@article{Zhu2020,
abstract = {Swine wastewater (SW) represents an important source of antibiotic resistance genes (ARGs) in the environment. However, few studies have assessed the occurrence and removal of ARGs in the whole wastewater treatment process followed by its farmland application. This study investigated the ARGs profiles in an integrated SW treatment system and its receiving soil, as well as their relationships with SW parameters and bacterial communities. Results revealed that sulfonamide, tetracycline and aminoglycoside resistance genes were dominant in SW. The relative abundance of total ARGs in SW was reduced by 84{\%} after the treatments. Among the SW treatment units, anaerobic digestion, primary sedimentation and constructed wetland contributed to ARGs removal while secondary sedimentation increased the total ARGs abundance. Farmland irrigation of the treated SW resulted in enrichment of persistent ARGs in the receiving soil, which might be attributed to the propagation of potential bacterial hosts and high horizontal gene transferability. Redundancy analysis indicated that the relative abundance of total ARGs was significantly correlated with total nitrogen, total phosphorus, antibiotics and bacterial communities. The shift in bacterial community was the major driving factor for ARGs alteration during SW treatment process. Our results highlight the effect of treated SW irrigation on the antibiotic resistome in agricultural environment, and can contribute in improving SW treatment system for better antibiotic resistance control.},
author = {Zhu, Ning and Jin, Hongmei and Ye, Xiaomei and Liu, Wei and Li, Danyang and Shah, Ghulam Mustafa and Zhu, Yanyun},
doi = {10.1016/j.scitotenv.2020.137654},
issn = {18791026},
journal = {Science of the Total Environment},
keywords = {Antibiotic resistance genes,Bacterial community,Mobile genetic element,Soil,Wastewater treatment},
month = {jun},
publisher = {Elsevier B.V.},
title = {{Fate and driving factors of antibiotic resistance genes in an integrated swine wastewater treatment system: From wastewater to soil}},
volume = {721},
year = {2020}
}
@misc{Zhang2019,
abstract = {Rhizoctonia solani is a plant pathogenic fungus, which can infect a wide range of economic crops including rice. In this case, biological control of this pathogen is one of the fundmental way to effectively control this pathogen. The Pseudomonas parafulva strain PRS09-11288 was isolated from rice rhizosphere and shows biocontrol ability against R. solani. Here, we analyzed the P. parafulva genome, which is {\~{}} 4.7 Mb, with 4310 coding sequences, 76 tRNAs, and 7 rRNAs. Genome analysis identified a phenazine biosynthetic pathway, which can produce antibiotic phenazine-1-carboxylic acid (PCA). This compound is responsible for biocontrol ability against R. solani K{\"{u}}hn, which is one of the most serious fungus disease on rice. Analysis of the phenazine biosynthesis gene mutant, ΔphzF, which is very important in this pathway, confirmed the relationship between the pathway and PCA production using LC-MS profiles. The annotated full genome sequence of this strain sheds light on the role of P. parafulva PRS09-11288 as a biocontrol bacterium.},

author = {Zhang, Yu and Chen, Ping and Ye, Guoyou and Lin, Haiyan and Ren, Deyong and Guo, Longbiao and Zhu, Bo and Wang, Zhongwei},
booktitle = {Current Microbiology},
doi = {10.1007/s00284-018-1441-0},
issn = {14320991},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {9},
pages = {1087--1091},
publisher = {Springer New York LLC},
title = {{Complete Genome Sequence of Pseudomonas Parafulva PRS09-11288, a Biocontrol Strain Produces the Antibiotic Phenazine-1-carboxylic Acid}},
volume = {76},
year = {2019}
}
@article{Zhang2020,
abstract = {Strains of the environmental bacterium Myroides odoratimimus can cause human infections. However, treating M. odoratimimus infections can be difficult because of multidrug resistance in this organism. In this study, we isolated strain M. odoratimimus G13 from pastureland in Tibet, China. The minimum inhibitory concentration analysis suggested that strain G13 has resistance to multiple antibiotics, with an MIC for tetracycline of 168 mg/L. Whole-genome sequencing and bioinformatic analysis revealed that the genome of G13 was rich in virulence factor-encoding genes and antibiotic resistance genes (ARGs). The mobilizable genomic island MGI1313 was also identified and characterized, and six resistance genes related to four types of antibiotics were annotated in MGI1313. Conjugation assays indicated that MGI1313 could be transferred from G13 to Escherichia coli 25DN by horizontal gene transfer, resulting in multidrug-resistant E. coli conjugants. In conclusion, multidrug-resistant M. odoratimimus G13 and the mobility of MGI1313 raise the risk of difficult-to-treat bacterial infections and should be under close surveillance.},
author = {Zhang, Peipei and Liu, Meng and Fu, Jiafang and Zhong, Chuanqing and Zong, Gongli and Cao, Guangxiang},
doi = {10.1016/j.scitotenv.2020.137970},
issn = {18791026},
journal = {Science of the Total Environment},
keywords = {Antibiotic resistance genes,Conjugation,Horizontal gene transfer,MGI1313,Mobilizable genomic island},
month = {jun},
publisher = {Elsevier B.V.},
title = {{Identification of a mobilizable, multidrug-resistant genomic island in Myroides odoratimimus isolated from Tibetan pasture}},
volume = {723},
year = {2020}
}
@misc{Zhang2017,
abstract = {Objectives In recent years, Klebsiella pneumoniae has emerged as a leading cause of nosocomial infection owing to the rising prevalence of multidrug-resistant strains, particularly carbapenem-resistant isolates. In this study, the complete genome sequence of carbapenem-

resistant K. pneumoniae SWU01 was determined. Methods Antimicrobial susceptibilities and hypermucoviscous phenotype were determined by the disk diffusion method and positive string test, respectively. Multilocus sequence typing (MLST) was performed using the K. pneumoniae MLST database, and capsular serotype was analysed using the BIGSdb-Kp database with the nucleotide sequence of the variable region (CD1-VR2-CD2) of wzc. The complete genome sequence was obtained via the PacBio RS II platform, and antimicrobial resistance genes were identified using ResFinder 2.1. Results SWU01 was resistant to all antibiotics tested except polymyxin B and minocycline. This strain showed a hypermucoviscous phenotype with serotype K47 belonging to the ST11 clone. The complete genome consists of a 5 536 506-bp circular chromosome and a 162 552-bp plasmid, with a G+C content of 57.4{\%}. A total of 5537 protein-coding sequences, 85 tRNAs, 25 rRNAs, 12 non-coding RNA genes and 157 pseudogenes were identified in the genome. Thirteen acquired antibiotic resistance genes were detected (eight in the chromosome and five in the plasmid). Conclusions Here we present the first whole-genome sequence of a carbapenem-resistant hypermucoviscous K. pneumoniae isolate SWU01 with capsular serotype K47 belonging to ST11 from a patient in China, which may serve as a reference sequence for further understanding of the pathogenesis and multidrug resistance mechanisms of this species.},
author = {Zhang, Luhua and Li, Ying and Shen, Wei and Wang, Shan Mei and Wang, Guangxi and Zhou, Yingshun},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2017.09.001},
issn = {22137173},
keywords = {China,Complete genome sequence,K47,Klebsiella pneumoniae,Lista{_}Filtrada,Multidrug resistance},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
pages = {87--89},
publisher = {Elsevier Ltd},
title = {{Whole-genome sequence of a carbapenem-resistant hypermucoviscous Klebsiella pneumoniae isolate SWU01 with capsular serotype K47 belonging to ST11 from a patient in China}},
volume = {11},
year = {2017}
}
@misc{Zhang2017a,
abstract = {Objectives In recent years, Klebsiella pneumoniae has emerged as a leading cause of nosocomial infection owing to the rising prevalence of multidrug-resistant strains, particularly carbapenem-resistant isolates. In this study, the complete genome sequence of carbapenem-resistant K. pneumoniae SWU01 was determined. Methods Antimicrobial susceptibilities and hypermucoviscous phenotype were determined by the disk diffusion method and positive string test, respectively. Multilocus sequence typing (MLST) was performed using the K. pneumoniae MLST database, and capsular serotype was analysed using the BIGSdb-Kp database with the nucleotide sequence of the variable region (CD1-VR2-CD2) of wzc. The complete genome sequence was obtained via the PacBio RS II platform, and antimicrobial resistance genes were identified using ResFinder 2.1. Results SWU01 was resistant to all antibiotics tested except polymyxin B and minocycline. This strain showed a hypermucoviscous phenotype with serotype K47 belonging to the ST11 clone. The complete genome consists of

a 5 536 506-bp circular chromosome and a 162 552-bp plasmid, with a G+C content of 57.4{\%}. A total of 5537 protein-coding sequences, 85 tRNAs, 25 rRNAs, 12 non-coding RNA genes and 157 pseudogenes were identified in the genome. Thirteen acquired antibiotic resistance genes were detected (eight in the chromosome and five in the plasmid). Conclusions Here we present the first whole-genome sequence of a carbapenem-resistant hypermucoviscous K. pneumoniae isolate SWU01 with capsular serotype K47 belonging to ST11 from a patient in China, which may serve as a reference sequence for further understanding of the pathogenesis and multidrug resistance mechanisms of this species.},
author = {Zhang, Luhua and Li, Ying and Shen, Wei and Wang, Shan Mei and Wang, Guangxi and Zhou, Yingshun},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2017.09.001},
issn = {22137173},
keywords = {China,Complete genome sequence,K47,Klebsiella pneumoniae,Lista{_}Filtrada,Multidrug resistance},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
pages = {87--89},
publisher = {Elsevier Ltd},
title = {{Whole-genome sequence of a carbapenem-resistant hypermucoviscous Klebsiella pneumoniae isolate SWU01 with capsular serotype K47 belonging to ST11 from a patient in China}},
volume = {11},
year = {2017}
}
@article{Zhang2017b,
abstract = {Bacterial endophytes with capacity to promote plant growth and improve plant tolerance against biotic and abiotic stresses have importance in agricultural practice and phytoremediation. A plant growth-promoting endophyte named Klebsiella sp. LTGPAF-6F, which was isolated from the roots of the desert plant Alhagi sparsifolia in north-west China, exhibits the ability to enhance the growth of wheat under drought stress. The complete genome sequence of this strain consists of one circular chromosome and two circular plasmids. From the genome, we identified genes related to the plant growth promotion and stress tolerance, such as nitrogen fixation, production of indole-3-acetic acid, acetoin, 2,3-butanediol, spermidine and trehalose. This genome sequence provides a basis for understanding the beneficial interactions between LTGPAF-6F and host plants, and will facilitate its applications as biotechnological agents in agriculture.},
author = {Zhang, Lei and Zhong, Jun and Liu, Hao and Xin, Kaiyun and Chen, Chaoqiong and Li, Qiqi and Wei, Yahong and Wang, Yao and Chen, Fei and Shen, Xihui},
doi = {10.1016/j.jbiotec.2017.02.008},
issn = {1873-4863},
journal = {Journal of biotechnology},
keywords = {2,3-Butanediol (PubChem CID: 262),Acetoin (PubChem CID: 179),Bacterial endophyte,Complete genome,Drought resistance-promoting,Indole-3-acetic acid (PubChem CID: 802),Lista{_}Filtrada,Nitrogen fixation,Spermidine,Spermidine (PubChem CID: 1102),Trehalose,Trehalose (PubChem CID: 7427)},
mendeley-tags = {Lista{_}Filtrada},

month = {mar},
pages = {36--39},
pmid = {28223006},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of the drought resistance-promoting endophyte Klebsiella sp. LTGPAF-6F.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28223006},
volume = {246},
year = {2017}
}
@article{Zhang2017c,
abstract = {The lytic cold-active bacteriophage VSW-3, belonging to the Podoviridae family and infecting the host Pseudomonas fluorescens SW-3, was isolated from the Napahai plateau wetland in China. With the development of sequencing technology, the study of Pseudomonas genomic diversity has increased; however, knowledge of cold-active phages infecting Pseudomonas is limited. The newly sequenced phage VSW-3 was classified based on virion morphology by transmission electron microscope. Sequence analysis revealed that the genome size was 40,556 bp with an overall GC content of 57.54 {\%} and 46 open reading frames. The genome was organized into several modules containing genes for packaging, structural proteins, replication/transcription, and phage lysis. The sequence contained 45 potential promoters, 3 transcription terminators, and yet no tRNAs. This is the first report of cold-active Pseudomonas fluorescens bacteriophage genome sequencing.},
author = {Zhang, Chunjing and Zhang, Zhongyao and Li, Jiankai and Qin, Kunhao and Wei, Yunlin and Zhang, Qi and Lin, Lianbing and Ji, Xiuling},
doi = {10.1007/s11262-016-1403-1},
issn = {1572994X},
journal = {Virus Genes},
keywords = {Cold-active phage,Genome sequence analysis,Lista{_}Filtrada,Plateau wetland,Podoviridae,Pseudomonas fluorescens},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
number = {1},
pages = {146--150},
publisher = {Springer New York LLC},
title = {{Complete genome sequence of the lytic cold-active Pseudomonas fluorescens bacteriophage VSW-3 from Napahai plateau wetland}},
volume = {53},
year = {2017}
}
@article{Yanzhen2016,
author = {Yanzhen, Mei and Yang, Liu and Xiangting, Xu and Wei, He},
doi = {10.1016/j.jbiotec.2016.03.019},
keywords = {Degradation,Genome,Pseudomonas fragi P121,Toxic compounds},
month = {apr},
pmid = {26988396},
publisher = {Elsevier B.V.},
title = {{No Title}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26988396},
volume = {224},
year = {2016}

}
@article{Xu2020,
abstract = {Emergence of antibiotic resistance is a global public health concern. The relationships between antibiotic use, the gut community composition, normal physiology and metabolism, and individual and public health are still being defined. Shifts in composition of bacteria, antibiotic resistance genes (ARGs) and mobile genetic elements (MGEs) after antibiotic treatment are not well-understood. This project used next-generation sequencing, custom-built metagenomics pipeline and differential abundance analysis to study the effect of antibiotic monotherapy on resistome and taxonomic composition in the gut of Balb/c mice infected with E. coli via transurethral catheterization to investigate the evolution and emergence of antibiotic resistance. There is a longitudinal decrease of gut microbiota diversity after antibiotic treatment. Various ARGs are enriched within the gut microbiota despite an overall reduction of the diversity and total amount of bacteria after antibiotic treatment. Sometimes treatment with a specific class of antibiotics selected for ARGs that resist antibiotics of a completely different class (e.g. treatment of ciprofloxacin or fosfomycin selected for cepA that resists ampicillin). Relative abundance of some MGEs increased substantially after antibiotic treatment (e.g. transposases in the ciprofloxacin group). Antibiotic treatment caused a remarkable reduction in diversity of gut bacterial microbiota but enrichment of certain types of ARGs and MGEs. These results demonstrate an emergence of cross-resistance as well as a profound change in the gut resistome following oral treatment of antibiotics.},
author = {Xu, Lei and Surathu, Anil and Raplee, Isaac and Chockalingam, Ashok and Stewart, Sharron and Walker, Lacey and Sacks, Leonard and Patel, Vikram and Li, Zhihua and Rouse, Rodney},
doi = {10.1186/s12864-020-6665-2},
issn = {1471-2164},
journal = {BMC Genomics},
keywords = {Animal Genetics and Genomics,Life Sciences,Lista{_}Filtrada,Microarrays,Microbial Genetics and Genomics,Plant Genetics and Genomics,Proteomics,general},
mendeley-tags = {Lista{_}Filtrada},
number = {1},
pages = {263},
publisher = {BioMed Central},
title = {{The effect of antibiotics on the gut microbiome: a metagenomics analysis of microbial shift and gut antibiotic resistance in antibiotic treated mice}},
url = {https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-020-6665-2},
volume = {21},
year = {2020}
}
@article{Wibberg2014,
abstract = {Pseudomonas pseudoalcaligenes CECT5344, a Gram-negative bacterium isolated from the Guadalquir River (C{\'{o}}rdoba, Spain), is able to utilize different cyano-derivatives. Here, the complete genome sequence of P. pseudoalcaligenes CECT5344 harboring a 4,686,340bp circular chromosome encoding 4513 genes and featuring a GC-content of 62.34{\%} is reported. Necessarily, remaining gaps in the genome had to

be closed by assembly of few long reads obtained from PacBio single molecule real-time sequencing. Here, the first complete genome sequence for the species P. pseudoalcaligenes is presented.},
author = {Wibberg, Daniel and Luque-Almagro, V{\'{i}}ctor M and Ige{\~{n}}o, Ma Isabel and Bremges, Andreas and Rold{\'{a}}n, Ma Dolores and Merch{\'{a}}n, Faustino and S{\'{a}}ez, Lara P and Guijo, Ma Isabel and Manso, Ma Isabel and Mac{\'{i}}as, Daniel and Cabello, Purificaci{\'{o}}n and Becerra, Gracia and Ib{\'{a}}{\~{n}}ez, Ma Isabel and Carmona, Ma Isabel and Escribano, Ma Mar{\'{i}}a Paz and Castillo, Francisco and Sczyrba, Alexander and Moreno-Vivi{\'{a}}n, Conrado and Blasco, Rafael and P{\"{u}}hler, Alfred and Schl{\"{u}}ter, Andreas},
doi = {10.1016/j.jbiotec.2014.02.004},
issn = {1873-4863},
journal = {Journal of biotechnology},
keywords = {Bioplastic,Cyanide,Cyanide assimilation,Cyanide resistance,Nitrilase},
month = {apr},
number = {1},
pages = {67--8},
pmid = {24553071},
title = {{Complete genome sequence of the cyanide-degrading bacterium Pseudomonas pseudoalcaligenes CECT5344.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/24553071},
volume = {175},
year = {2014}
}
@article{Wibberg2014a,
abstract = {Pseudomonas pseudoalcaligenes CECT5344, a Gram-negative bacterium isolated from the Guadalquir River (C{\'{o}}rdoba, Spain), is able to utilize different cyano-derivatives. Here, the complete genome sequence of P. pseudoalcaligenes CECT5344 harboring a 4,686,340. bp circular chromosome encoding 4513 genes and featuring a GC-content of 62.34{\%} is reported. Necessarily, remaining gaps in the genome had to be closed by assembly of few long reads obtained from PacBio single molecule real-time sequencing. Here, the first complete genome sequence for the species P. pseudoalcaligenes is presented. {\textcopyright} 2014 Elsevier B.V.},
author = {Wibberg, Daniel and Luque-Almagro, V{\'{i}}ctor M. and Ige{\~{n}}o, Ma; Isabel and Bremges, Andreas and Rold{\'{a}}n, Ma; Dolores and Merch{\'{a}}n, Faustino and S{\'{a}}ez, Lara P. and Guijo, Ma; Isabel and Manso, Ma; Isabel and Mac{\'{i}}as, Daniel and Cabello, Purificaci{\'{o}}n and Becerra, Gracia and Ib{\'{a}}{\~{n}}ez, Ma; Isabel and Carmona, Ma; Isabel and Escribano, Ma; Mar{\'{i}}a Paz and Castillo, Francisco and Sczyrba, Alexander and Moreno-Vivi{\'{a}}n, Conrado and Blasco, Rafael and P{\"{u}}hler, Alfred and Schl{\"{u}}ter, Andreas},
doi = {10.1016/j.jbiotec.2014.02.004},
issn = {01681656},
journal = {Journal of Biotechnology},
keywords = {Bioplastic,Cyanide,Cyanide assimilation,Cyanide resistance,Nitrilase},
month = {apr},
number = {1},
pages = {67--68},

title = {{Complete genome sequence of the cyanide-degrading bacterium Pseudomonas pseudoalcaligenes CECT5344}},
volume = {175},
year = {2014}
}
@article{Wibberg2014b,
abstract = {Pseudomonas pseudoalcaligenes CECT5344, a Gram-negative bacterium isolated from the Guadalquir River (C{\'{o}}rdoba, Spain), is able to utilize different cyano-derivatives. Here, the complete genome sequence of P. pseudoalcaligenes CECT5344 harboring a 4,686,340. bp circular chromosome encoding 4513 genes and featuring a GC-content of 62.34{\%} is reported. Necessarily, remaining gaps in the genome had to be closed by assembly of few long reads obtained from PacBio single molecule real-time sequencing. Here, the first complete genome sequence for the species P. pseudoalcaligenes is presented. {\textcopyright} 2014 Elsevier B.V.},
author = {Wibberg, Daniel and Luque-Almagro, V{\'{i}}ctor M. and Ige{\~{n}}o, Ma; Isabel and Bremges, Andreas and Rold{\'{a}}n, Ma; Dolores and Merch{\'{a}}n, Faustino and S{\'{a}}ez, Lara P. and Guijo, Ma; Isabel and Manso, Ma; Isabel and Mac{\'{i}}as, Daniel and Cabello, Purificaci{\'{o}}n and Becerra, Gracia and Ib{\'{a}}{\~{n}}ez, Ma; Isabel and Carmona, Ma; Isabel and Escribano, Ma; Mar{\'{i}}a Paz and Castillo, Francisco and Sczyrba, Alexander and Moreno-Vivi{\'{a}}n, Conrado and Blasco, Rafael and P{\"{u}}hler, Alfred and Schl{\"{u}}ter, Andreas},
doi = {10.1016/j.jbiotec.2014.02.004},
issn = {01681656},
journal = {Journal of Biotechnology},
keywords = {Bioplastic,Cyanide,Cyanide assimilation,Cyanide resistance,Nitrilase},
month = {apr},
number = {1},
pages = {67--68},
title = {{Complete genome sequence of the cyanide-degrading bacterium Pseudomonas pseudoalcaligenes CECT5344}},
volume = {175},
year = {2014}
}
@article{Wibberg2014c,
abstract = {Pseudomonas pseudoalcaligenes CECT5344, a Gram-negative bacterium isolated from the Guadalquir River (C{\'{o}}rdoba, Spain), is able to utilize different cyano-derivatives. Here, the complete genome sequence of P. pseudoalcaligenes CECT5344 harboring a 4,686,340. bp circular chromosome encoding 4513 genes and featuring a GC-content of 62.34{\%} is reported. Necessarily, remaining gaps in the genome had to be closed by assembly of few long reads obtained from PacBio single molecule real-time sequencing. Here, the first complete genome sequence for the species P. pseudoalcaligenes is presented. {\textcopyright} 2014 Elsevier B.V.},
author = {Wibberg, Daniel and Luque-Almagro, V{\'{i}}ctor M. and Ige{\~{n}}o, Ma; Isabel and Bremges, Andreas and Rold{\'{a}}n, Ma; Dolores and Merch{\'{a}}n, Faustino and S{\'{a}}ez, Lara P. and Guijo, Ma; Isabel and Manso, Ma; Isabel and Mac{\'{i}}as, Daniel and Cabello, Purificaci{\'{o}}n and Becerra, Gracia and Ib{\'{a}}{\~{n}}ez, Ma; Isabel and Carmona, Ma; Isabel and Escribano, Ma; Mar{\'{i}}a Paz and Castillo,

Francisco and Sczyrba, Alexander and Moreno-Vivi{\'{a}}n, Conrado and Blasco, Rafael and P{\"{u}}hler, Alfred and Schl{\"{u}}ter, Andreas},
doi = {10.1016/j.jbiotec.2014.02.004},
issn = {01681656},
journal = {Journal of Biotechnology},
keywords = {Bioplastic,Cyanide,Cyanide assimilation,Cyanide resistance,Nitrilase},
month = {apr},
number = {1},
pages = {67--68},
title = {{Complete genome sequence of the cyanide-degrading bacterium Pseudomonas pseudoalcaligenes CECT5344}},
volume = {175},
year = {2014}
}
@article{Wibberg2016,
abstract = {Pseudomonas pseudoalcaligenes CECT5344 tolerates cyanide and is also able to utilize cyanide and cyano-derivatives as a nitrogen source under alkaline conditions. The strain is considered as candidate for bioremediation of habitats contaminated with cyanide-containing liquid wastes. Information on the genome sequence of the strain CECT5344 became available previously. The P. pseudoalcaligenes CECT5344 genome was now resequenced by applying the single molecule, real-time (SMRT{\textregistered}) sequencing technique developed by Pacific Biosciences. The complete and finished genome sequence of the strain consists of a 4,696,984 bp chromosome featuring a GC-content of 62.34{\%}. Comparative analyses between the new and previous versions of the P. pseudoalcaligenes CECT5344 genome sequence revealed additional regions in the new sequence that were missed in the older version. These additional regions mostly represent mobile genetic elements. Moreover, five additional genes predicted to play a role in sulfoxide reduction are present in the newly established genome sequence. The P. pseudoalcaligenes CECT5344 genome sequence is highly related to the genome sequences of different Pseudomonas mendocina strains. Approximately, 70{\%} of all genes are shared between P. pseudoalcaligenes and P. mendocina. In contrast to P. mendocina, putative pathogenicity genes were not identified in the P. pseudoalcaligenes CECT5344 genome. P. pseudoalcaligenes CECT5344 possesses unique genes for nitrilases and mercury resistance proteins that are of importance for survival in habitats contaminated with cyano- and mercury compounds. As an additional feature of the SMRT sequencing technology, the methylome of P. pseudoalcaligenes was established. Six sequence motifs featuring methylated adenine residues (m6A) were identified in the genome. The genome encodes several methyltransferases, some of which may be considered for methylation of the m6A motifs identified. The complete genome sequence of the strain CECT5344 now provides the basis for exploitation of genetic features for biotechnological purposes.},
author = {Wibberg, Daniel and Bremges, Andreas and Dammann-Kalinowski, Tanja and Maus, Irena and Ige{\~{n}}o, M{\textordfeminine} Isabel and Vogelsang, Ralph and K{\"{o}}nig, Christoph and Luque-Almagro, V{\'{i}}ctor M. and Rold{\'{a}}n, M{\textordfeminine} Dolores and Sczyrba, Alexander and Moreno-Vivi{\'{a}}n, Conrado and Blasco, Rafael and P{\"{u}}hler, Alfred and Schl{\"{u}}ter, Andreas},
doi = {10.1016/j.jbiotec.2016.04.008},

issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {Bioremediation,Core genome,Mercury
resistance,Methylome,Nitrilase,Restriction/modification system},
month = {aug},
pages = {61--68},
publisher = {Elsevier B.V.},
title = {{Finished genome sequence and methylome of the cyanide-degrading
Pseudomonas pseudoalcaligenes strain CECT5344 as resolved by single-
molecule real-time sequencing}},
volume = {232},
year = {2016}
}
@article{Whitfield2020,
abstract = {Our understanding of the biofilm matrix components utilized
by Gram-positive bacteria, and the signalling pathways that regulate
their production are largely unknown. In a companion study, we developed
a computational pipeline for the unbiased identification of homologous
bacterial operons and applied this algorithm to the analysis of synthase-
dependent exopolysaccharide biosynthetic systems. Here, we explore the
finding that many species of Gram-positive bacteria have operons with
similarity to the Pseudomonas aeruginosa pel locus. Our characterization
of the pelDEADAFG operon from Bacillus cereus ATCC 10987, presented
herein, demonstrates that this locus is required for biofilm formation
and produces a polysaccharide structurally similar to Pel. We show that
the degenerate GGDEF domain of the B. cereus PelD ortholog binds cyclic-
3',5'-dimeric guanosine monophosphate (c-di-GMP), and that this binding
is required for biofilm formation. Finally, we identify a diguanylate
cyclase, CdgF, and a c-di-GMP phosphodiesterase, CdgE, that reciprocally
regulate the production of Pel. The discovery of this novel c-di-GMP
regulatory circuit significantly contributes to our limited understanding
of c-di-GMP signalling in Gram-positive organisms. Furthermore,
conservation of the core pelDEADAFG locus amongst many species of
bacilli, clostridia, streptococci, and actinobacteria suggests that Pel
may be a common biofilm matrix component in many Gram-positive
bacteria.},
author = {Whitfield, Gregory B. and Marmont, Lindsey S. and Bundalovic-
Torma, Cedoljub and Razvi, Erum and Roach, Elyse J. and Khursigara, Cezar
M. and Parkinson, John and Howell, P. Lynne},
doi = {10.1371/journal.ppat.1008281},
editor = {Lee, Vincent T.},
issn = {1553-7374},
journal = {PLOS Pathogens},
number = {4},
pages = {e1008281},
publisher = {Public Library of Science},
title = {{Discovery and characterization of a Gram-positive Pel
polysaccharide biosynthetic gene cluster}},
url = {https://dx.plos.org/10.1371/journal.ppat.1008281},
volume = {16},
year = {2020}
}
@article{Volozhantsev2016,

abstract = {A novel bacteriophage, vB{_}KpnP{_}KpV289, lytic for hypermucoviscous strains of Klebsiella pneumoniae, was attributed to the family Podoviridae, subfamily Autographivirinae, genus T7likevirus based on transmission electron microscopy and genome analysis. The complete genome of the bacteriophage vB{_}KpnP{_}KpV289 consists of a linear double-stranded DNA of 41,054 bp including 179-bp direct-repeat sequences at the ends and 51 open reading frames (ORFs). The G+C content is 52.56 {\%}. The phage was shown to lyse 15 out of 140 (10.7 {\%}) K. pneumoniae strains belonged to the capsular types K-1, K-2, and K-57 and strains without a determined capsular type, including a hypermucoviscous strain of the novel sequence type ST-1554.},
author = {Volozhantsev, Nikolay V and Myakinina, Vera P and Popova, Anastasia V and Kislichkina, Angelina A and Komisarova, Ekaterina V and Knyazeva, Anastasia I and Krasilnikova, Valentina M and Fursova, Nadezhda K and Svetoch, Eduard A},
doi = {10.1007/s00705-015-2680-z},
issn = {1432-8798},
journal = {Archives of virology},
month = {feb},
number = {2},
pages = {499--501},
pmid = {26577901},
publisher = {Springer-Verlag Wien},
title = {{Complete genome sequence of novel T7-like virus vB{_}KpnP{_}KpV289 with lytic activity against Klebsiella pneumoniae.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26577901},
volume = {161},
year = {2016}
}
@article{Volozhantsev2016a,
abstract = {A novel bacteriophage, vB{_}KpnP{_}KpV289, lytic for hypermucoviscous strains of Klebsiella pneumoniae, was attributed to the family Podoviridae, subfamily Autographivirinae, genus T7likevirus based on transmission electron microscopy and genome analysis. The complete genome of the bacteriophage vB{_}KpnP{_}KpV289 consists of a linear double-stranded DNA of 41,054 bp including 179-bp direct-repeat sequences at the ends and 51 open reading frames (ORFs). The G+C content is 52.56 {\%}. The phage was shown to lyse 15 out of 140 (10.7 {\%}) K. pneumoniae strains belonged to the capsular types K-1, K-2, and K-57 and strains without a determined capsular type, including a hypermucoviscous strain of the novel sequence type ST-1554.},
author = {Volozhantsev, Nikolay V. and Myakinina, Vera P. and Popova, Anastasia V. and Kislichkina, Angelina A. and Komisarova, Ekaterina V. and Knyazeva, Anastasia I. and Krasilnikova, Valentina M. and Fursova, Nadezhda K. and Svetoch, Eduard A.},
doi = {10.1007/s00705-015-2680-z},
issn = {03048608},
journal = {Archives of Virology},
month = {feb},
number = {2},
pages = {499--501},
publisher = {Springer-Verlag Wien},

title = {{Complete genome sequence of novel T7-like virus vB{_}KpnP{_}KpV289 with lytic activity against Klebsiella pneumoniae}},
volume = {161},
year = {2016}
}
@article{Turton2018,
abstract = {Purpose. Klebsiella pneumoniae is a concern because of its multidrug resistance and the ability of hypervirulent types, especially capsular type K1-clonal complex 23 (K1-CC23), to cause community-acquired, life-threatening infections. Hypervirulent types carry an array of virulence genes including rmpA/rmpA2, coding for capsule up-regulation. We sought to identify isolates carrying these elements among submissions to the UK national reference laboratory during 2016. Methodology. Virulence elements and carbapenemase genes were sought by PCR or from whole genome sequences. Isolates were typed by variable number tandem repeat analysis or by multi locus sequence typing from whole genome sequences. Long read nanopore sequencing was carried out on two isolates. Results/Key findings. Twelve of 1090 isolates (1.1 {\%}) belonged to hypervirulent K1-CC23, with one carrying blaOXA-48 (KpvST23L{_}OXA-48). A further 24 rmpA/rmpA2-positive isolates were detected: eight belonged to hypervirulent types of capsular types K2 and K54; and 14 belonged to 'non-hypervirulent' ST147, ST15 and ST383 and also carried carbapenemase gene(s). Virulence, heavy metal and antibiotic resistance gene contents were compared from whole genome sequences of KpvST23L{_}OXA-48 and one of the ST147 isolates carrying blaNDM-1. They carried 94/96 and 26/96 of the virulence genes sought, and 23/23 and 9/23 of the heavy metal resistance genes, respectively. In the ST147 isolate, rmpA/rmpA2 and the aerobactin siderophore cluster were on a large virulence plasmid together with resistance genes. The yersiniabactin cluster was widely present among carbapenemase gene-positive isolates, including among those that were rmpA/rmpA2-negative. Conclusion. Our results highlight a combination of virulence and resistance genes, which could lead to untreatable invasive infections.},
author = {Turton, Jane F. and Payne, Zo{\"{e}} and Coward, Amy and Hopkins, Katie L. and Turton, Jack A. and Doumith, Michel and Woodford, Neil},
doi = {10.1099/jmm.0.000653},
issn = {00222615},
journal = {Journal of Medical Microbiology},
keywords = {Aerobactin,Carbapenemase,Hypervirulence,Klebsiella pneumoniae,RmpA,Virulence plasmid,Yersiniabactin},
month = {jan},
number = {1},
pages = {118--128},
publisher = {Microbiology Society},
title = {{Virulence genes in isolates of Klebsiella pneumoniae from the UK during 2016, including among carbapenemase gene-positive hypervirulent K1-st23 and 'non-hypervirulent' types ST147, ST15 and ST383}},
volume = {67},
year = {2018}
}
@article{Turton2018a,
abstract = {Capsular type K54 of Klebsiella pneumoniae is associated with hypervirulence and we sought to discover the basis for this among

isolates submitted to the UK reference laboratory between 2012 and 2017. Isolates were typed by variable number tandem repeat analysis, and capsular type and virulence elements sought by PCR. The most prevalent type found (15/31 isolates) corresponded to clonal group (CG) 29 and included five representatives carrying rmpA, rmpA2 (regulators of mucoid phenotype), iutA and iroD (from the aerobactin and salmochelin siderophore clusters) associated with virulence plasmids. These included isolate KpvK54, recovered from pus. The remaining isolates did not carry a virulence plasmid. We also noted 11 further related isolates, including NCTC 9159, not of capsular type K54, but nevertheless sometimes associated with sepsis and abscesses. Whole-genome sequencing showed that KpvK54 carried a large virulence plasmid and an ICEKp3-like structure carrying the yersiniabactin cluster, absent in NCTC 9159. Comparative chromosomal analysis with an additional four genomes showed that KpvK54 shared further genes with K1-ST23 hypervirulent isolates, and with LS358, a K54-ST29 isolate from liver abscess puncture fluid. While CG29 isolates displayed varying degrees of virulence, some, especially those with the virulence plasmid (all K54), were clearly associated with hypervirulence.},
author = {Turton, J. F. and Payne, Z. and Micah, K. and Turton, J. A.},
doi = {10.1017/S0950268818001826},
issn = {14694409},
journal = {Epidemiology and Infection},
keywords = {Klebsiella,Lista{_}Filtrada,typing},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
number = {14},
pages = {1813--1823},
publisher = {Cambridge University Press},
title = {{Capsular type K54, clonal group 29 and virulence plasmids: An analysis of K54 and non-K54 closely related isolates of Klebsiella pneumoniae}},
volume = {146},
year = {2018}
}
@article{Sutterlin2017,
abstract = {Background Silver-based products have been marketed as an alternative to antibiotics, and their consumption has increased. Bacteria may, however, develop resistance to silver. Aim To study the presence of genes encoding silver resistance (silE, silP, silS) over time in three clinically important Enterobacteriaceae genera. Methods Using polymerase chain reaction (PCR), 752 bloodstream isolates from the years 1990–2010 were investigated. Age, gender, and ward of patients were registered, and the susceptibility to antibiotics and silver nitrate was tested. Clonality and single nucleotide polymorphism were assessed with repetitive element sequence-based PCR, multi-locus sequence typing, and whole-genome sequencing. Findings Genes encoding silver resistance were detected most frequently in Enterobacter spp. (48{\%}), followed by Klebsiella spp. (41{\%}) and Escherichia coli 4{\%}. Phenotypical resistance to silver nitrate was found in Enterobacter (13{\%}) and Klebsiella (3{\%}) isolates. The lowest carriage rate of sil genes was observed in blood isolates from the neonatology ward (24{\%}), and the highest in blood isolates from the oncology/haematology wards (66{\%}). Presence of sil genes was observed in international high-risk clones.

Sequences of the sil and pco clusters indicated that a single mutational event in the silS gene could have caused the phenotypic resistance. Conclusion Despite a restricted consumption of silver-based products in Swedish health care, silver resistance genes are widely represented in clinical isolates of Enterobacter and Klebsiella species. To avoid further selection and spread of silver-resistant bacteria with a high potential for healthcare-associated infections, the use of silver-based products needs to be controlled and the silver resistance monitored.},
author = {S{\"{u}}tterlin, S. and Dahl{\"{o}}, M. and Tellgren-Roth, C. and Schaal, W. and Melhus},
doi = {10.1016/j.jhin.2017.04.017},
issn = {15322939},
journal = {Journal of Hospital Infection},
keywords = {Enterobacter,Enterobacteriaceae,Heavy metal resistance,Klebsiella,Silver resistance,sil-operon},
month = {jul},
number = {3},
pages = {256--261},
publisher = {W.B. Saunders Ltd},
title = {{High frequency of silver resistance genes in invasive isolates of Enterobacter and Klebsiella species}},
volume = {96},
year = {2017}
}
@article{Sonda2018,
abstract = {This study aimed to use whole-genome sequencing to determine virulence and antimicrobial resistance genes in K. pneumoniae isolated from patients in a tertiary care hospital in Kilimanjaro. K. pneumoniae isolates from patients attending Kilimanjaro Christian Medical Centre between August 2013 and August 2015 were fully genome-sequenced and analysed locally. Sequence analysis was done for identification of virulence and AMR genes. Plasmid and multi-locus sequence typing and capsular or capsular (K) typing were performed and phylogeny was done to ascertain K. pneumoniae relatedness. Stata 13 (College Station, TX, 77845, USA) was used to determine Cohen's kappa coefficient of agreement between the phenotypically tested and sequence-predicted resistance. A total of 16 (47.1{\%}) sequence types (STs) and 10 (29.4{\%}) K types were identified in 30 (88.2{\%}) and 17 (50.0{\%}) of all analysed isolates, respectively. K. pneumoniae ST17 were 6 (17.6{\%}). The commonest determinants were blaCTX-M-15 in 16 (47.1{\%}) isolates, blaSHV in 30 (88.2{\%}), blaOXA-1 in 8 (23.5{\%}) and blaTEM-1 in 18 (52.9{\%}) isolates. Resistance genes for aminoglycosides were detected in 21 (61.8{\%}) isolates, fluoroquinolones in 13 (38.2{\%}) and quinolones 34 (100{\%}). Ceftazidime and ceftriaxone showed the strongest agreement between phenotype- and sequence-based resistance results: 93.8{\%}, kappa = 0.87 and p = 0.0002. Yersiniabactin determinant was detected in 12 (35.3{\%}) of K. pneumoniae. The proportion of AMR and virulence determinants detected in K. pneumoniae is alarming. WGS-based diagnostic approach has showed promising potentials in clinical microbiology, hospital outbreak source tracing virulence and AMR detection at KCMC.},
author = {Sonda, Tolbert and Kumburu, Happiness and van Zwetselaar, Marco and Alifrangis, Michael and Mmbaga, Blandina T and Lund, Ole and Kibiki, Gibson S and Aarestrup, Frank M},
doi = {10.1007/s10096-018-3324-5},

issn = {1435-4373},
journal = {European journal of clinical microbiology {\&} infectious diseases : official publication of the European Society of Clinical Microbiology},
keywords = {Antimicrobial resistance,K. pneumoniae,Lista{_}Filtrada,Tanzania,Virulence,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
number = {10},
pages = {1901--1914},
pmid = {30030694},
publisher = {Springer Verlag},
title = {{Molecular epidemiology of virulence and antimicrobial resistance determinants in Klebsiella pneumoniae from hospitalised patients in Kilimanjaro, Tanzania.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30030694},
volume = {37},
year = {2018}
}
@article{Smulski2020,
abstract = {Due to increasing bacterial antibiotic resistance and the consumers' tendency to choose organic products, cattle farmers are interested in alternative methods of calf diarrhoea treatment. This is a major challenge for veterinarians. Few methods of non-antibiotic treatment that bring satisfactory results have been reported in the related literature so far. In this article, the authors compare different non-antibiotic methods of diarrhoea prevention and treatment in calves. Among the alternatives discussed are herbs, probiotics, prebiotics and synbiotics, lactoferrin, and bacteriophages. It was found that the best results could be achieved through the use of pro-, pre- and synbiotics. However, the authors would like to point out that with the expansion of knowledge about the practical use of broad-scale bacteriophages, they could be the best alternative to antibiotics.},
author = {Smulski, Sebastian and Turlewicz-Podbielska, Hanna and Wylandowska, Agata and W{\l}odarek, Jan},
doi = {10.2478/jvetres-2020-0002},
issn = {2450-8608},
journal = {Journal of Veterinary Research},
month = {jan},
number = {0},
publisher = {Walter de Gruyter GmbH},
title = {{Non-antibiotic possibilities in prevention and treatment of calf diarrhoea}},
volume = {0},
year = {2020}
}
@article{Smith2020,
abstract = {{\textless}p{\textgreater} {\textless}italic{\textgreater}Ornithobacterium rhinotracheale{\textless}/italic{\textgreater} (ORT) is a causative agent of respiratory tract infections in avian hosts worldwide, but is a particular problem for commercial turkey production. Little is known about the ecologic and evolutionary dynamics of ORT, which makes prevention and control of this pathogen a challenge. The purpose of this

study was to gain insight into the genetic relationships between ORT populations through comparative genomics of clinical isolates from different US turkey producers. ORT clinical isolates were collected from four major US turkey producers and several independent turkey growers from the upper Midwest and Southeast, and whole-genome sequencing was performed. Genomes were compared phylogenetically using single nucleotide polymorphism (SNP)-based analysis, and then assemblies and annotations were performed to identify genes encoding putative virulence factors and antimicrobial resistance determinants. A pangenome approach was also used to establish a core set of genes consistently present in ORT, and to highlight differences in gene content between phylogenetic clades. A total of 1,457 non-recombinant SNPs were identified from 157 ORT genomes, and four distinct phylogenetic clades were identified. Isolates clustered by company on the phylogenetic tree, however, each company had isolates in multiple clades with similar collection dates, indicating that there are multiple ORT strains circulating within each of the companies examined. Additionally, several antimicrobial resistance proteins, putative virulence factors, and the pOR1 plasmid were associated with particular clades and multi-locus sequence types, which may explain why the same strains seem to have persisted in the same turkey operations for decades. {\textless}/p{\textgreater}},
author = {Smith, Emily A. and Miller, Elizabeth A. and Weber, Bonnie P. and {Munoz Aguayo}, Jeannette and {Flores Figueroa}, Cristian and Huisinga, Jared and Nezworski, Jill and Kromm, Michelle and Wileman, Ben and Johnson, Timothy J.},
doi = {10.1128/AEM.02874-19},
issn = {0099-2240},
journal = {Applied and Environmental Microbiology},
month = {apr},
title = {{Genomic landscape of {\textless}i{\textgreater}Ornithobacterium rhinotracheale{\textless}/i{\textgreater} in commercial turkey production in the United States}},
url = {http://aem.asm.org/lookup/doi/10.1128/AEM.02874-19},
year = {2020}
}
@article{Shin2015,
abstract = {Here we report the full genome sequence of Klesiella oxytoca M1, isolated from Manripo area of South Korea. The strain K. oxytoca M1 is able to produce either 2,3-butanediol or acetoin selectively by controlling the pH and temperature.},
author = {Shin, Sang Heum and Roh, Hanseong and Kim, Juhyeok and Cho, Sukhyeong and Um, Youngsoon and Lee, Jinwon and Ryu, Yeon Woo and Chong, Hyonyong and Yang, Kap Seok},
doi = {10.1016/j.jbiotec.2015.01.015},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {2,3-Butanediol,Acetoin,Klesiella oxytoca M1},
month = {mar},
pages = {1--2},
publisher = {Elsevier},
title = {{Complete genome sequence of Klebsiella oxytoca M1, isolated from Manripo area of South Korea}},
volume = {198},
year = {2015}

}
@article{Shimazaki2020,
abstract = {Autosomal recessive cerebellar ataxias comprise many types of diseases. The most frequent autosomal recessive cerebellar ataxias are Friedreich ataxia, but other types are relatively rare. We encountered a consanguineous family with two cases of late-onset cerebellar ataxia with neuropathy. We performed whole-exome sequencing in one patient and confirmed by Sanger sequencing in other family members. Neurological examination revealed cerebellar ataxia, hand tremor, and neck dystonia, distal muscle wasting, and diminished tendon reflexes. The patients had no conjunctival telangiectasia or immunodeficiency. Blood examination revealed slightly elevated α-fetoprotein. Brain MRI demonstrated marked cerebellar atrophy and mild brainstem atrophy. The electrophysiologic study and nerve biopsy showed axonal neuropathy. Whole-exome sequencing revealed a novel homozygous missense variant (NM{_}000051.3: c.496G {\textgreater} C) in the ataxia-telangiectasia mutated gene. This homozygous variant was found in another patient, co-segregated within the family members-this variant results in aberrant splicing (skipping exon 5) on RT-PCR analysis. We identified the ataxia-telangiectasia mutated variant in an adult, late-onset autosomal recessive cerebellar ataxias family. We should consider ataxia-telangiectasia even in late-onset autosomal recessive cerebellar ataxias without telangiectasia or immunodeficiency.},
author = {Shimazaki, Haruo and Kobayashi, Junya and Sugaya, Ryo and Nakano, Imaharu and Fujimoto, Shigeru},
doi = {10.31083/j.jin.2020.01.1239},
issn = {0219-6352},
journal = {Journal of integrative neuroscience},
keywords = {Autosomal recessive cerebellar ataxia,ataxia-telangiectasia mutated,muscle atrophy,neuropathy,splicing mutation,whole-exome sequencing},
month = {mar},
number = {1},
pages = {125--129},
pmid = {32259893},
title = {{Late-onset autosomal recessive cerebellar ataxia and neuropathy with a novel splicing mutation in the ATM gene.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32259893},
volume = {19},
year = {2020}
}
@article{Shen2017,
abstract = {Prokaryotic CRISPR-Cas system provides adaptive immunity against invasive genetic elements. Bacteria of the genus Klebsiella are important nosocomial opportunistic pathogens. However, information of CRISPR-Cas system in Klebsiella remains largely unknown. Here, we analyzed the CRISPR-Cas systems of 68 complete genomes of Klebsiella representing four species. All the elements for CRISPR-Cas system (cas genes, repeats, leader sequences, and PAMs) were characterized. Besides the typical Type I-E and I-F CRISPR-Cas systems, a new Subtype I system located in the ABC transport system-glyoxalase region was found. The conservation of the new subtype CRISPR system between different species showed new evidence for CRISPR horizontal transfer. CRISPR polymorphism was strongly correlated both with species and multilocus sequence types.

Some results indicated the function of adaptive immunity: most spacers (112 of 124) matched to prophages and plasmids and no matching housekeeping genes; new spacer acquisition was observed within the same sequence type (ST) and same clonal complex; the identical spacers were observed only in the ancient position (far from the leader) between different STs and clonal complexes. Interestingly, a high ratio of self-targeting spacers (7.5{\%}, 31 of 416) was found in CRISPR-bearing Klebsiella pneumoniae (61{\%}, 11 of 18). In some strains, there even were multiple full matching self-targeting spacers. Some self-targeting spacers were conserved even between different STs. These results indicated that some unknown mechanisms existed to compromise the function of self-targets of CRISPR-Cas systems in K. pneumoniae.},
author = {Shen, Juntao and Lv, Li and Wang, Xudong and Xiu, Zhilong and Chen, Guoqiang},
doi = {10.1002/jobm.201600589},
issn = {15214028},
journal = {Journal of Basic Microbiology},
keywords = {CRISPR-Cas,Klebsiella,MLST,mobile elements,self-target},
month = {apr},
number = {4},
pages = {325--336},
publisher = {Wiley-VCH Verlag},
title = {{Comparative analysis of CRISPR-Cas systems in Klebsiella genomes}},
volume = {57},
year = {2017}
}
@article{Shankar2018,
abstract = {This study characterizes KPC-2 producing Klebsiella pneumoniae belonging to ST101. Whole genome sequencing using the Ion Torrent PGM platform with 400 bp chemistry was performed. blaKPC-2 was found on an IncFIIK plasmid associated with ISKpn6 and ISKpn7 without Tn4401. This is the first report of KPC-2 K. pneumoniae from bacteremia in India. The isolate also coded for other resistance genes such as aadA1, aadA2, armA, aac(3)-Ild, aac(6′)-Ild for aminoglycoside; blaSHV-11, blaTEM-1B, blaOXA-9, for β-lactams and aac(6′)-Ild, oqxA, oqxB, qnrB1 for fluoroquinolones. It belonged to the K17 capsular type. India is endemic to New Delhi metallo-β-lactamase and OXA48-like carbapenemases and K. pneumoniae carbapenemase (KPC) is seldom reported. With high rates of carbapenem resistance, emergence of KPC in India will challenge patient management. The isolate was susceptible to colistin. The patient had a fatal outcome.},
author = {Shankar, Chaitra and Shankar, Baby Abirami and Manesh, Abi and Veeraraghavan, Balaji},
doi = {10.1099/jmm.0.000767},
issn = {00222615},
journal = {Journal of Medical Microbiology},
keywords = {Bacteraemia,IncFIIK,India,K.Pneumoniae,KPC-2,ST101},
month = {jul},
number = {7},
pages = {927--930},
publisher = {Microbiology Society},
title = {{KPC-2 producing ST101 Klebsiella pneumoniae from bloodstream infection in India}},

volume = {67},
year = {2018}
}
@article{Shang2015,
abstract = {The complete genome of Klebsiella phage P13 was sequenced and analyzed. Bacteriophage P13 has a double-stranded linear DNA with a length of 45,976 bp and a G+C content of 51.7 {\%}, which is slightly lower than that of Klebsiellapneumoniae KCTC 2242. The codon biases of phage P13 are very similar to those of SP6-like phages and K.pneumoniae KCTC 2242. Bioinformatics analysis shows that the phage P13 genome has 282 open reading frames (ORFs) that are greater than 100 bp in length, and 50 of these ORFs were identified as predicted genes with an average length of 833 bp. Among these genes, 41 show homology to known proteins in the GenBank database. The functions of the 24 putative proteins were investigated, and 13 of these were found to be highly conserved. According to the homology analysis of the 50 predicted genes and the whole genome, phage P13 is homologous to SP6-like phages. Furthermore, the morphological characteristics of phage P13 suggest that it belongs to the SP6-like viral genus of the Podoviridae subfamily Autographivirinae. Two hypothetical genes encoding an extracellular polysaccharide depolymerase were predicted using PSI-BLAST. This analysis serves as groundwork for further research and application of the enzyme.},
author = {Shang, Anqi and Liu, Yang and Wang, Jianlei and Mo, Zhaolan and Li, Guiyang and Mou, Haijin},
doi = {10.1007/s11262-014-1138-9},
issn = {1572994X},
journal = {Virus Genes},
keywords = {Complete genome sequencing,EPS depolymerase,Genomic comparison,Klebsiella phage P13,Predicted genes},
number = {1},
pages = {118--128},
publisher = {Kluwer Academic Publishers},
title = {{Complete nucleotide sequence of Klebsiella phage P13 and prediction of an EPS depolymerase gene}},
volume = {50},
year = {2015}
}
@article{See-Too2016,
abstract = {Pseudomonas sp. strain L10.10 (N DSM 101070) is a psychrotolerant bacterium which was isolated from Lagoon Island, Antarctica. Analysis of its complete genome sequence indicates its possible role as a plant-growth promoting bacterium, including nitrogen-fixing ability and indole acetic acid (IAA)-producing trait, with additional suggestion of plant disease prevention attributes via hydrogen cyanide production.},
author = {See-Too, Wah Seng and Lim, Yan Lue and Ee, Robson and Convey, Peter and Pearce, David A. and Yin, Wai Fong and Chan, Kok Gan},
doi = {10.1016/j.jbiotec.2016.02.017},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {Hydrogen cyanide,Indole acetic acid,Nitrogen fixing,Plant disease control,Plant growth-promoting rhizobacteria},
month = {mar},
pages = {84--85},

publisher = {Elsevier B.V.},
title = {{Complete genome of Pseudomonas sp. strain L10.10, a psychrotolerant biofertilizer that could promote plant growth}},
volume = {222},
year = {2016}
}
@article{Schneider2020,
abstract = {Background: Acute respiratory infection (ARI) accounts for over two-thirds of total antibiotic prescriptions although most are caused by viruses that do not benefit from antibiotics. Most antibiotics are prescribed in the outpatients setting. Antibiotic overuse leads to antibiotic-related adverse events (AEs), inclusive of secondary infections, resistance, and increased costs. Point-of-care tests (POCT) may reduce unnecessary antibiotics. A cost analysis was performed to assess diagnostic POCT options to identify patients with an ARI that may benefit from antibiotics in a United Kingdom (UK) outpatient setting.Methods: Healthcare savings were estimated using a budget impact analysis based on UK National Institute for Health and Care Excellence (NICE) data and direct costs (antibiotics, AEs, POCTs) derived from published literature. Otitis media, sinusitis, pharyngitis and bronchitis were considered the most common ARIs. Antibiotic-related AE costs were calculated using re-consultation costs for anaphylaxis, Stevens-Johnson syndrome, allergies/diarrhea/nausea, C. difficile infection (CDI). Potential cost-savings from POCTs was assessed by evaluating NICE guideline-referenced POCTs (CRP, FebriDx, Sarasota, FL) as well as a target product profile (TPP).Results: Fifty-percent (7,718,283) of ARI consultations resulted in antibiotics while guideline-based prescribing suggest appropriate antibiotic prescriptions are warranted 9{\%} (1,444,877) of ARI consultations. Direct antibiotic costs for actual ARI consultations associated with antibiotics was {\pounds}24,003,866 vs. {\pounds}4,493,568 for guideline-based, "appropriate" antibiotic prescriptions. Antibiotic-related AEs and re-consultations for actual vs. appropriate prescribing totaled {\pounds}302,496,486 vs. {\pounds}63,854,269. ARI prescribing plus AE costs totaled {\pounds}326,729,943 annually without the use of delayed prescribing practices or POCT while the addition of delayed prescribing plus POCT totaled {\pounds}60,114,564-{\pounds}78,148,933 depending on the POCT.Conclusions: Adding POCT to outpatient triage of ARI can reduce unnecessary antibiotics and antibiotic-related AEs, resulting in substantial cost savings. Further, near patient diagnostic testing can benefit health systems and patients by avoiding exposure to unnecessary drugs, side effects and antibiotic resistant pathogens.Key points for decision makersMany patients are unnecessarily treated with antibiotics for respiratory infections.Antibiotic misuse leads to unnecessary adverse events, secondary infections, re-consultations, antimicrobial resistance and increased costs.Point-of-care diagnostic tests used to guide antibiotic prescriptions will avoid unnecessary adverse health effects and expenses.},
author = {Schneider, John E and Boehme, Catharina and Borisch, Bettina and Dittrich, Sabine},
doi = {10.1080/13696998.2020.1736872},
issn = {1941-837X},
journal = {Journal of medical economics},

keywords = {Acute respiratory infection,C-reactive protein (CRP),C53,FebriDx,I15,I19,antibiotic-related adverse events,host response biomarkers,myxovirus resistance protein A (MxA),point-of-care tests (POCT)},
month = {apr},
pages = {1--10},
pmid = {32259465},
title = {{Application of a simple point-of-care test to reduce UK healthcare costs and adverse events in outpatient acute respiratory infections.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32259465},
year = {2020}
}
@article{Scheberl2020,
abstract = {Much recent effort has been directed toward the development of novel antimicrobial materials able to defeat new and antibiotic resistant pathogens. In this report, we study the efficacy of cationic poly(phenylene ethynylene), polythiophene, and oligo(phenylene ethynylene) electrolytes against laboratory strains of Pseudomonas aeruginosa, Staphylococcus aureus and Staphylococcus epidermidis. The focus of the study is to quantitatively evaluate the speed and extent of dark and light-activated antimicrobial activity. Using cell plating with serial dilutions, we determined that planktonic bacteria suspensions exposed to the antimicrobials (at 10 μg/mL) result in several log kills at 10 min both in the dark and under UV irradiation (360 nm) for all eight synthetic antimicrobials. However, there are significant differences in the ease of killing the different pathogens. In most trials, there is significantly greater killing under light-irradiation, indicating these materials may be used as versatile disinfectants.},
author = {Scheberl, Andrea and Khalil, Mohammed L and Maghsoodi, Fahimeh and Strach, Edward W and Yang, Jianzhong and Chi, Eva Y and Schanze, Kirk S and Reimhult, Erik and Whitten, David G},
doi = {10.1021/acsami.0c02939},
issn = {1944-8252},
journal = {ACS applied materials {\&} interfaces},
keywords = {Pseudomonas aeruginosa,Staphylococcus aureus,antimicrobial polyelectrolytes,conjugated polyelectrolytes,oligomeric electrolytes,poly(phenylene)-ethynylene polyelectrolytes,poly-3-hexyl-thiophene polyelectrolytes},
month = {apr},
pmid = {32259428},
title = {{Quantitative Determination of Dark and Light-Activated Antimicrobial Activity of Poly(Phenylene Ethynylene), Polythiophene, and Oligo(Phenylene Ethynylene) Electrolytes.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32259428},
year = {2020}
}
@article{Scheberl2020a,
abstract = {Much recent effort has been directed toward the development of novel antimicrobial materials able to defeat new and antibiotic resistant pathogens. In this report, we study the efficacy of cationic poly(phenylene ethynylene), polythiophene, and oligo(phenylene ethynylene) electrolytes against laboratory strains of Pseudomonas aeruginosa, Staphylococcus aureus and Staphylococcus epidermidis. The

focus of the study is to quantitatively evaluate the speed and extent of dark and light-activated antimicrobial activity. Using cell plating with serial dilutions, we determined that planktonic bacteria suspensions exposed to the antimicrobials (at 10 μg/mL) result in several log kills at 10 min both in the dark and under UV irradiation (360 nm) for all eight synthetic antimicrobials. However, there are significant differences in the ease of killing the different pathogens. In most trials, there is significantly greater killing under light-irradiation, indicating these materials may be used as versatile disinfectants.},
author = {Scheberl, Andrea and Khalil, Mohammed L and Maghsoodi, Fahimeh and Strach, Edward W and Yang, Jianzhong and Chi, Eva Y and Schanze, Kirk S and Reimhult, Erik and Whitten, David G},
doi = {10.1021/acsami.0c02939},
issn = {1944-8252},
journal = {ACS applied materials {\&} interfaces},
month = {apr},
pmid = {32259428},
title = {{Quantitative Determination of Dark and Light-Activated Antimicrobial Activity of Poly(Phenylene Ethynylene), Polythiophene, and Oligo(Phenylene Ethynylene) Electrolytes.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32259428},
year = {2020}
}
@article{Ruckert2015,
abstract = {Rhodococcus erythropolis BG43 was isolated from soil and characterized as a degrader of the quorum sensing signal molecules 2-heptyl-3-hydroxy-4(1. H)-quinolone (the Pseudomonas quinolone signal, PQS) and 2-heptyl-4(1. H)-quinolone, produced by Pseudomonas aeruginosa. The complete genome of R. erythropolis BG43 consists of a circular chromosome and three plasmids, one of them circular and two linear ones. In total, 6158 protein-coding regions were identified. With this genome sequence, the genetic basis of its quorum-quenching ability and possible biotechnological applications can be explored further.},
author = {R{\"{u}}ckert, Christian and Birmes, Franziska S. and M{\"{u}}ller, Christine and Niewerth, Heiko and Winkler, Anika and Fetzner, Susanne and Kalinowski, J{\"{o}}rn},
doi = {10.1016/j.jbiotec.2015.07.014},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {Pseudomonas aeruginosa,Quorum quenching},
month = {oct},
pages = {99--100},
publisher = {Elsevier},
title = {{Complete genome sequence of Rhodococcus erythropolis BG43 (DSM 46869), a degrader of Pseudomonas aeruginosa quorum sensing signal molecules}},
volume = {211},
year = {2015}
}
@article{Rhizobium2013,
abstract = {Although multiple sequence alignments (MSAs) are essential for a wide range of applications from structure modeling to prediction of functional sites, construction of accurate MSAs for distantly related proteins remains a largely unsolved problem. The rapidly increasing

database of spatial structures is a valuable source to improve alignment quality. We explore the use of 3D structural information to guide sequence alignments constructed by our MSA program PROMALS. The resulting tool, PROMALS3D, automatically identifies homologs with known 3D structures for the input sequences, derives structural constraints through structure-based alignments and combines them with sequence constraints to construct consistency-based multiple sequence alignments. The output is a consensus alignment that brings together sequence and structural information about input proteins and their homologs. PROMALS3D can also align sequences of multiple input structures, with the output representing a multiple structure-based alignment refined in combination with sequence constraints. The advantage of PROMALS3D is that it gives researchers an easy way to produce high-quality alignments consistent with both sequences and structures of proteins. PROMALS3D outperforms a number of existing methods for constructing multiple sequence or structural alignments using both reference-dependent and reference-independent evaluation methods.},
author = {Rhizobium, Growth-promoting Endophyte},
doi = {10.1093/nar},
isbn = {1471210510},
issn = {1362-4962; 0305-1048},
journal = {Nucleic acids research},
keywords = {Databases,Protein,Sequence Alignment/methods,Sequence Analysis,Software,Structural Homology},
number = {1256879},
pages = {13--14},
title = {{Complete Genome Sequence of the Sesbania Symbiont and Rice}},
volume = {1},
year = {2013}
}
@article{Pang2016,
abstract = {Klebsiella pneumoniae J1 is a Gram-negative strain, which belongs to a protein-based microbial flocculant-producing bacterium. However, little genetic information is known about this species. Here we carried out a whole-genome sequence analysis of this strain and report the complete genome sequence of this organism and its genetic basis for carbohydrate metabolism, capsule biosynthesis and transport system.},
author = {Pang, Changlong and Li, Ang and Cui, Di and Yang, Jixian and Ma, Fang and Guo, Haijuan},
doi = {10.1016/j.jbiotec.2016.01.020},
issn = {1873-4863},
journal = {Journal of biotechnology},
keywords = {CRISPRs clusters,Complete genome sequence,Klebsiella pneumoniae J1,Lista{_}Filtrada,Microbial flocculant-producing bacterium},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
pages = {90--1},
pmid = {26806487},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of Klebsiella pneumoniae J1, a protein-based microbial flocculant-producing bacterium.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26806487},
volume = {220},

year = {2016}
}
@article{Pang2016a,
abstract = {Klebsiella pneumoniae J1 is a Gram-negative strain, which belongs to a protein-based microbial flocculant-producing bacterium. However, little genetic information is known about this species. Here we carried out a whole-genome sequence analysis of this strain and report the complete genome sequence of this organism and its genetic basis for carbohydrate metabolism, capsule biosynthesis and transport system.},
author = {Pang, Changlong and Li, Ang and Cui, Di and Yang, Jixian and Ma, Fang and Guo, Haijuan},
doi = {10.1016/j.jbiotec.2016.01.020},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {CRISPRs clusters,Complete genome sequence,Klebsiella pneumoniae J1,Lista{_}Filtrada,Microbial flocculant-producing bacterium},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
pages = {90--91},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of Klebsiella pneumoniae J1, a protein-based microbial flocculant-producing bacterium}},
volume = {220},
year = {2016}
}
@article{Pang2016b,
abstract = {Klebsiella pneumoniae J1 is a Gram-negative strain, which belongs to a protein-based microbial flocculant-producing bacterium. However, little genetic information is known about this species. Here we carried out a whole-genome sequence analysis of this strain and report the complete genome sequence of this organism and its genetic basis for carbohydrate metabolism, capsule biosynthesis and transport system.},
author = {Pang, Changlong and Li, Ang and Cui, Di and Yang, Jixian and Ma, Fang and Guo, Haijuan},
doi = {10.1016/j.jbiotec.2016.01.020},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {CRISPRs clusters,Complete genome sequence,Klebsiella pneumoniae J1,Microbial flocculant-producing bacterium},
month = {feb},
pages = {90--91},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of Klebsiella pneumoniae J1, a protein-based microbial flocculant-producing bacterium}},
volume = {220},
year = {2016}
}
@article{Pan2020,
author = {Pan, Xiong and Lin, Li and Zhang, Weihong and Dong, Lei and Yang, Yuyi},
doi = {10.1016/j.envpol.2020.114470},
issn = {02697491},
journal = {Environmental Pollution},

month = {mar},
pages = {114470},
publisher = {Elsevier BV},
title = {{Metagenome sequencing to unveil the resistome in a deep subtropical lake on the Yunnan-Guizhou Plateau, China}},
year = {2020}
}
@article{Osakunor2020,
abstract = {Helminth parasites have been shown to have systemic effects in the host. Using shotgun metagenomic sequencing, we characterise the gut microbiome and resistome of 113 Zimbabwean preschool-aged children (1-5 years). We test the hypothesis that infection with the human helminth parasite, Schistosoma haematobium, is associated with changes in gut microbial and antimicrobial resistance gene abundance/diversity. Here, we show that bacteria phyla Bacteroidetes, Firmicutes, Proteobacteria, and fungi phyla Ascomycota, Microsporidia, Zoopagomycota dominate the microbiome. The abundance of Proteobacteria, Ascomycota, and Basidiomycota differ between schistosome-infected versus uninfected children. Specifically, infection is associated with increases in Pseudomonas, Stenotrophomonas, Derxia, Thalassospira, Aspergillus, Tricholoma, and Periglandula, with a decrease in Azospirillum. We find 262 AMR genes, from 12 functional drug classes, but no association with individual-specific data. To our knowledge, we describe a novel metagenomic dataset of Zimbabwean preschool-aged children, indicating an association between urogenital schistosome infection and changes in the gut microbiome.},
author = {Osakunor, Derick N M and Munk, Patrick and Mduluza, Takafira and Petersen, Thomas N and Brinch, Christian and Ivens, Alasdair and Chimponda, Theresa and Amanfo, Seth A and Murray, Janice and Woolhouse, Mark E J and Aarestrup, Frank M and Mutapi, Francisca},
doi = {10.1038/s42003-020-0859-7},
issn = {2399-3642},
journal = {Communications biology},
month = {apr},
number = {1},
pages = {155},
pmid = {32242065},
title = {{The gut microbiome but not the resistome is associated with urogenital schistosomiasis in preschool-aged children.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32242065 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC7118151},
volume = {3},
year = {2020}
}
@misc{Nuesch-Inderbinen2018,
abstract = {Objectives: Carbapenem-resistant Klebsiella pneumoniae have emerged worldwide and represent a major threat to human health. Here we report the genome sequence of K. pneumoniae 002SK2, an NDM-9- and CTX-M-15-producing strain isolated from wastewater in Switzerland and belonging to the international high-risk clone sequence type 147 (ST147). Methods: Whole-genome sequencing of K. pneumoniae 002SK2 was performed using Pacific Biosciences (PacBio) single-molecule, real-time (SMRT) technology RS2 reads (C4/P6 chemistry). De novo assembly was performed using Canu assembler, and sequences were annotated using the NCBI Prokaryotic Genome

Annotation Pipeline (PGAP). Results: The genome of K. pneumoniae 002SK2 consists of a 5.4-Mbp chromosome containing blaSHV-11 and fosA6, a 159-kb IncFIB(K) plasmid carrying the heavy metal resistance genes ars and sil, and a 77-kb IncR plasmid containing blaCTX-M-15, blaNDM-9, blaOXA-9 and blaTEM-1. Conclusions: Multidrug-resistant K. pneumoniae harbouring blaNDM-9 and blaCTX-M-15 are spreading into the environment, most probably via wastewater from clinical settings.},
author = {N{\"{u}}esch-Inderbinen, Magdalena and Zurfluh, Katrin and Stevens, Marc J.A. and Stephan, Roger},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2018.03.001},
issn = {22137173},
keywords = {Genome analysis,Klebsiella pneumoniae,Lista{_}Filtrada,ST147,blaCTX-M-15,blaNDM-9},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
pages = {53--54},
publisher = {Elsevier Ltd},
title = {{Complete and assembled genome sequence of an NDM-9- and CTX-M-15-producing Klebsiella pneumoniae ST147 wastewater isolate from Switzerland}},
volume = {13},
year = {2018}
}
@misc{Nuesch-Inderbinen2018a,
abstract = {Objectives: Carbapenem-resistant Klebsiella pneumoniae have emerged worldwide and represent a major threat to human health. Here we report the genome sequence of K. pneumoniae 002SK2, an NDM-9- and CTX-M-15-producing strain isolated from wastewater in Switzerland and belonging to the international high-risk clone sequence type 147 (ST147). Methods: Whole-genome sequencing of K. pneumoniae 002SK2 was performed using Pacific Biosciences (PacBio) single-molecule, real-time (SMRT) technology RS2 reads (C4/P6 chemistry). De novo assembly was performed using Canu assembler, and sequences were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). Results: The genome of K. pneumoniae 002SK2 consists of a 5.4-Mbp chromosome containing blaSHV-11 and fosA6, a 159-kb IncFIB(K) plasmid carrying the heavy metal resistance genes ars and sil, and a 77-kb IncR plasmid containing blaCTX-M-15, blaNDM-9, blaOXA-9 and blaTEM-1. Conclusions: Multidrug-resistant K. pneumoniae harbouring blaNDM-9 and blaCTX-M-15 are spreading into the environment, most probably via wastewater from clinical settings.},
author = {N{\"{u}}esch-Inderbinen, Magdalena and Zurfluh, Katrin and Stevens, Marc J.A. and Stephan, Roger},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2018.03.001},
issn = {22137173},
keywords = {Genome analysis,Klebsiella pneumoniae,Lista{_}Filtrada,ST147,blaCTX-M-15,blaNDM-9},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
pages = {53--54},
publisher = {Elsevier Ltd},

title = {{Complete and assembled genome sequence of an NDM-9- and CTX-M-15-producing Klebsiella pneumoniae ST147 wastewater isolate from Switzerland}},
volume = {13},
year = {2018}
}
@misc{Nuesch-Inderbinen2018b,
abstract = {Objectives: Carbapenem-resistant Klebsiella pneumoniae have emerged worldwide and represent a major threat to human health. Here we report the genome sequence of K. pneumoniae 002SK2, an NDM-9- and CTX-M-15-producing strain isolated from wastewater in Switzerland and belonging to the international high-risk clone sequence type 147 (ST147). Methods: Whole-genome sequencing of K. pneumoniae 002SK2 was performed using Pacific Biosciences (PacBio) single-molecule, real-time (SMRT) technology RS2 reads (C4/P6 chemistry). De novo assembly was performed using Canu assembler, and sequences were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). Results: The genome of K. pneumoniae 002SK2 consists of a 5.4-Mbp chromosome containing blaSHV-11 and fosA6, a 159-kb IncFIB(K) plasmid carrying the heavy metal resistance genes ars and sil, and a 77-kb IncR plasmid containing blaCTX-M-15, blaNDM-9, blaOXA-9 and blaTEM-1. Conclusions: Multidrug-resistant K. pneumoniae harbouring blaNDM-9 and blaCTX-M-15 are spreading into the environment, most probably via wastewater from clinical settings.},
author = {N{\"{u}}esch-Inderbinen, Magdalena and Zurfluh, Katrin and Stevens, Marc J.A. and Stephan, Roger},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2018.03.001},
issn = {22137173},
keywords = {Genome analysis,Klebsiella pneumoniae,Lista{_}Filtrada,ST147,blaCTX-M-15,blaNDM-9},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
pages = {53--54},
publisher = {Elsevier Ltd},
title = {{Complete and assembled genome sequence of an NDM-9- and CTX-M-15-producing Klebsiella pneumoniae ST147 wastewater isolate from Switzerland}},
volume = {13},
year = {2018}
}
@article{Nuesch-Inderbinen2018c,
abstract = {OBJECTIVES Carbapenem-resistant Klebsiella pneumoniae have emerged worldwide and represent a major threat to human health. Here we report the genome sequence of K. pneumoniae 002SK2, an NDM-9- and CTX-M-15-producing strain isolated from wastewater in Switzerland and belonging to the international high-risk clone sequence type 147 (ST147). METHODS Whole-genome sequencing of K. pneumoniae 002SK2 was performed using Pacific Biosciences (PacBio) single-molecule, real-time (SMRT) technology RS2 reads (C4/P6 chemistry). De novo assembly was performed using Canu assembler, and sequences were annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). RESULTS The genome of K. pneumoniae 002SK2 consists of a 5.4-Mbp chromosome containing blaSHV-11 and fosA6, a 159-kb IncFIB(K) plasmid carrying the heavy metal resistance genes ars and sil, and a 77-kb IncR plasmid containing blaCTX-M-15, blaNDM-9, blaOXA-9 and

blaTEM-1. CONCLUSIONS Multidrug-resistant K. pneumoniae harbouring blaNDM-9 and blaCTX-M-15 are spreading into the environment, most probably via wastewater from clinical settings.},
author = {N{\"{u}}esch-Inderbinen, Magdalena and Zurfluh, Katrin and Stevens, Marc J A and Stephan, Roger},
doi = {10.1016/j.jgar.2018.03.001},
issn = {2213-7173},
journal = {Journal of global antimicrobial resistance},
keywords = {Genome analysis,Klebsiella pneumoniae,Lista{_}Filtrada,ST147,bla(CTX-M-15),bla(NDM-9)},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
pages = {53--54},
pmid = {29551728},
publisher = {Elsevier Ltd},
title = {{Complete and assembled genome sequence of an NDM-9- and CTX-M-15-producing Klebsiella pneumoniae ST147 wastewater isolate from Switzerland.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/29551728},
volume = {13},
year = {2018}
}
@article{Nelson2002,
abstract = {Pseudomonas putida is a metabolically versatile saprophytic soil bacterium that has been certified as a biosafety host for the cloning of foreign genes. The bacterium also has considerable potential for biotechnological applications. Sequence analysis of the 6.18 Mb genome of strain KT2440 reveals diverse transport and metabolic systems. Although there is a high level of genome conservation with the pathogenic Pseudomonad Pseudomonas aeruginosa (85{\%} of the predicted coding regions are shared), key virulence factors including exotoxin A and type III secretion systems are absent. Analysis of the genome gives insight into the non-pathogenic nature of P. putida and points to potential new applications in agriculture, biocatalysis, bioremediation and bioplastic production.},
author = {Nelson, K. E. and Weinel, C. and Paulsen, I. T. and Dodson, R. J. and Hilbert, H. and {Martins dos Santos}, V. A.P. and Fouts, D. E. and Gill, S. R. and Pop, M. and Holmes, M. and Brinkac, L. and Beanan, M. and DeBoy, R. T. and Daugherty, S. and Kolonay, J. and Madupu, R. and Nelson, W. and White, O. and Peterson, J. and Khouri, H. and Hance, I. and {Chris Lee}, P. and Holtzapple, E. and Scanlan, D. and Tran, K. and Moazzez, A. and Utterback, T. and Rizzo, M. and Lee, K. and Kosack, D. and Moestl, D. and Wedler, H. and Lauber, J. and Stjepandic, D. and Hoheisel, J. and Straetz, M. and Heim, S. and Kiewitz, C. and Eisen, J. and Timmis, K. N. and D{\"{u}}sterh{\"{o}}ft, A. and T{\"{u}}mmler, B. and Fraser, C. M.},
doi = {10.1046/j.1462-2920.2002.00366.x},
issn = {14622912},
journal = {Environmental Microbiology},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
number = {12},
pages = {799--808},
pmid = {12534463},

title = {{Complete genome sequence and comparative analysis of the
metabolically versatile Pseudomonas putida KT2440}},
volume = {4},
year = {2002}
}
@article{NeetuKumraTaneja2007,
abstract = {Objectives: To develop simple, rapid, low-cost and robust
assays for screening drugs against dormant
and actively growing mycobacteria.
Methods: Actively growing aerobic and hypoxia-adapted dormant cultures of
Mycobacterium tuberculosis, Mycobacterium bovis BCG and Mycobacterium
smegmatis were tested for susceptibility to standard antimicrobial drugs
by resazurin reduction assay. The visual and fluorimetric MICs were
compared with those obtained by the standard cfu assay.
Results: Drug MICs for M. tuberculosis and M. bovis BCG were determined
by the aerobic resazurin
microplate assay (REMA) and correlated well with those obtained by the
cfu assay. Metronidazole and
nitrofurans showed comparable bactericidal activity in the hypoxic
resazurin reduction assay (HyRRA).
The HyRRA assay was noted to be superior to the cfu assay in that it
distinguished between metabolically active dormant bacteria and non-
viable organisms, unlike the cfu assay that could not differentiate
between these two populations. The HyRRA assay performed with good
concordance in both
fluorimetric and visual formats to distinguish between bactericidal and
bacteriostatic effects of a drug.
Conclusions: The REMA and HyRRA assays will be useful for anti-tubercular
anti-dormancy compound
screening and drug susceptibility testing in a safe, reliable, easy and
cost-effective manner particularly
in low resource countries. The application of the assays in M. smegmatis
or M. bovis BCG offers the
distinct advantage of rapidly and safely screening anti-tubercular
compounds in a high-thro},
author = {{Neetu Kumra Taneja} and {Jaya Sivaswami Tya}},
doi = {10.1093/JAC},
journal = {Journal of Antimicrobial Chemotherapy},
number = {1},
pages = {1--4},
publisher = {Oxford Academic},
title = {{Resazurin reduction assays for screening of anti-tubercular
compounds against dormant and actively growing Mycobacterium
tuberculosis, Mycobacterium bovis BCG and Mycobacterium smegmatis}},
volume = {43},
year = {2007}
}
@article{NeetuKumraTaneja2007a,
abstract = {Objectives: To develop simple, rapid, low-cost and robust
assays for screening drugs against dormant
and actively growing mycobacteria.
Methods: Actively growing aerobic and hypoxia-adapted dormant cultures of
Mycobacterium tuberculosis, Mycobacterium bovis BCG and Mycobacterium

smegmatis were tested for susceptibility to standard antimicrobial drugs by resazurin reduction assay. The visual and fluorimetric MICs were compared with those obtained by the standard cfu assay.
Results: Drug MICs for M. tuberculosis and M. bovis BCG were determined by the aerobic resazurin
microplate assay (REMA) and correlated well with those obtained by the cfu assay. Metronidazole and
nitrofurans showed comparable bactericidal activity in the hypoxic resazurin reduction assay (HyRRA).
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fluorimetric and visual formats to distinguish between bactericidal and bacteriostatic effects of a drug.
Conclusions: The REMA and HyRRA assays will be useful for anti-tubercular anti-dormancy compound
screening and drug susceptibility testing in a safe, reliable, easy and cost-effective manner particularly
in low resource countries. The application of the assays in M. smegmatis or M. bovis BCG offers the
distinct advantage of rapidly and safely screening anti-tubercular compounds in a high-thro},
author = {{Neetu Kumra Taneja} and {Jaya Sivaswami Tya}},
doi = {10.1093/JAC},
journal = {Journal of Antimicrobial Chemotherapy},
number = {1},
pages = {1--4},
publisher = {Oxford Academic},
title = {{Resazurin reduction assays for screening of anti-tubercular compounds against dormant and actively growing Mycobacterium tuberculosis, Mycobacterium bovis BCG and Mycobacterium smegmatis}},
volume = {43},
year = {2007}
}
@article{Meletis2019,
abstract = {The emergence and spread of NDM-1-encoding Klebsiella pneumoniae is causing worldwide concern, whereas a second epicenter of their dissemination after the Indian subcontinent is thought to be located in the Balkans. In this study, the complete genome sequencing of an NDM-1-producing ST11 K. pneumoniae isolated in a private laboratory in Greece is presented. The genome sequencing was performed on Illumina MiniSeq. Multilocus Sequence Typing was determined using a BLAST-based approach whereas antimicrobial resistance genes and plasmid replicons were identified by ResFinder and PlasmidFinder respectively. The capsular serotype was determined by the nucleotide sequence of the wzc gene. The Rapid Annotation System Technology server v2.0 was used for genome annotation. The isolate was classified to Sequence Type 11 and to the K24 capsular serotype. Its genome consisted of 5,549,974 bp with a G + C content of 57.26{\%}. The resistome included 16 antibiotic resistance genes, 12 located in plasmids and 4 in the chromosome. The whole genome sequence of the isolate has been deposited at GenBank to serve as future

reference in the study of the epidemiology and antibiotic resistance mechanisms of carbapenemase-producing Enterobacteriaceae.},
author = {Meletis, Georgios and Chatzopoulou, Fani and Chatzidimitriou, Dimitrios and Tsingerlioti, Fani and Botziori, Christina and Tzimagiorgis, Georgios and Skoura, Lemonia},
doi = {10.1089/mdr.2017.0411},
issn = {19318448},
journal = {Microbial Drug Resistance},
keywords = {Balkans,Greece,Klebsiella pneumoniae,Lista{_}Filtrada,NDM-1,ST11,whole genome sequence},
mendeley-tags = {Lista{_}Filtrada},
month = {jan},
number = {1},
pages = {80--86},
publisher = {Mary Ann Liebert Inc.},
title = {{Whole Genome Sequencing of NDM-1-Producing ST11 Klebsiella pneumoniae Isolated in a Private Laboratory in Greece}},
volume = {25},
year = {2019}
}
@article{Martin2017,
abstract = {Background Carbapenemase-producing Enterobacteriaceae (CPE), including KPC-producing Klebsiella pneumoniae (KPC-Kpn), are an increasing threat to patient safety. Objectives To use WGS to investigate the extent and complexity of carbapenemase gene dissemination in a controlled KPC outbreak. Materials and methods Enterobacteriaceae with reduced ertapenem susceptibility recovered from rectal screening swabs/clinical samples, during a 3 month KPC outbreak (2013-14), were investigated for carbapenemase production, antimicrobial susceptibility, variable-number-tandem-repeat profile and WGS [short-read (Illumina), long-read (MinION)]. Short-read sequences were used for MLST and plasmid/Tn4401 fingerprinting, and long-read sequence assemblies for plasmid identification. Phylogenetic analysis used IQTree followed by ClonalFrameML, and outbreak transmission dynamics were inferred using SCOTTI. Results Twenty patients harboured KPC-positive isolates (6 infected, 14 colonized), and 23 distinct KPC-producing Enterobacteriaceae were identified. Four distinct KPC plasmids were characterized but of 20 KPC-Kpn (from six STs), 17 isolates shared a single pKpQIL-D2 KPC plasmid. All isolates had an identical transposon (Tn4401a), except one KPC-Kpn (ST661) with a single nucleotide variant. A sporadic case of KPC-Kpn (ST491) with Tn4401a-carrying pKpQIL-D2 plasmid was identified 10 months before the outbreak. This plasmid was later seen in two other species and other KPC-Kpn (ST14,ST661) including clonal spread of KPC-Kpn (ST661) from a symptomatic case to nine ward contacts. Conclusions WGS of outbreak KPC isolates demonstrated blaKPC dissemination via horizontal transposition (Tn4401a), plasmid spread (pKpQIL-D2) and clonal spread (K. pneumoniae ST661). Despite rapid outbreak control, considerable dissemination of blaKPC still occurred among K. pneumoniae and other Enterobacteriaceae, emphasizing its high transmission potential and the need for enhanced control efforts.},
author = {Martin, Jessica and Phan, Hang T T and Findlay, Jacqueline and Stoesser, Nicole and Pankhurst, Louise and Navickaite, Indre and {De Maio}, Nicola and Eyre, David W and Toogood, Giles and Orsi, Nicolas M and Kirby, Andrew and Young, Nicola and Turton, Jane F and Hill, Robert L

R and Hopkins, Katie L and Woodford, Neil and Peto, Tim E A and Walker, A Sarah and Crook, Derrick W and Wilcox, Mark H},
doi = {10.1093/jac/dkx264},
issn = {1460-2091},
journal = {The Journal of antimicrobial chemotherapy},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {nov},
number = {11},
pages = {3025--3034},
pmid = {28961793},
title = {{Covert dissemination of carbapenemase-producing Klebsiella pneumoniae (KPC) in a successfully controlled outbreak: long- and short-read whole-genome sequencing demonstrate multiple genetic modes of transmission.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28961793 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5890743},
volume = {72},
year = {2017}
}
@article{Magill2015,
abstract = {A complete nucleotide sequence of the new Pseudomonas aeruginosa Luz24likevirus phiCHU was obtained. This virus was shown to have a unique host range whereby it grew poorly on the standard laboratory strain PAO1, but infected 26 of 46 clinical isolates screened, and strains harbouring IncP2 plasmid pMG53. It was demonstrated that phiCHU has single-strand interruptions in its genome. Analysis of the phiCHU genome also suggested that recombination event(s) participated in the evolution of the leftmost portion of the genome, presumably encoding early genes.},
author = {Magill, Damian J and Shaburova, Olga V and Chesnokova, Elena N and Pleteneva, Elena A and Krylov, Victor N and Kulakov, Leonid A},
doi = {10.1093/femsle/fnv045},
issn = {1574-6968},
journal = {FEMS microbiology letters},
keywords = {antibiotic resistance,bacteriophage,phage therapy},
month = {may},
number = {9},
pmid = {25825475},
title = {{Complete nucleotide sequence of phiCHU: a Luz24likevirus infecting Pseudomonas aeruginosa and displaying a unique host range.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/25825475},
volume = {362},
year = {2015}
}
@article{Liu2018,
abstract = {Objectives: We previously described the novel qnrVC6 and blaIMP-45 carrying megaplasmid pBM413. This study aimed to investigate the complete genome of multidrug-resistance P. aeruginosa Guangzhou-Pae617, a clinical isolate from the sputum of a patient who was suffering from respiratory disease in Guangzhou, China. Methods: The genome was sequenced using Illumina Hiseq 2500 and PacBio RS II sequencers and assembled de novo using HGAP. The genome was automatically and manually annotated. Results: The genome of P. aeruginosa Guangzhou-Pae617 is

6,430,493 bp containing 5881 predicted genes with an average G + C content of 66.43{\%}. The genome showed high similarity to two new sequenced P. aeruginosa strains isolated from New York, USA. From the whole genome sequence, we identified a type IV pilin, two large prophages, 15 antibiotic resistant genes, 5 genes involved in the “Infectious diseases” pathways, and 335 virulence factors. Conclusions: The antibiotic resistance and virulence factors in the genome of P. aeruginosa strain Guangzhou-Pae617 were identified by complete genomic analysis. It contributes to further study on antibiotic resistance mechanism and clinical control of P. aeruginosa.},
author = {Liu, Junyan and Li, Lin and Peters, Brian M. and Li, Bing and Chen, Dingqiang and Xu, Zhenbo and Shirtliff, Mark E.},
doi = {10.1016/j.micpath.2018.02.049},
issn = {10961208},
journal = {Microbial Pathogenesis},
keywords = {Complete genomic analysis,Lista{_}Filtrada,Multidrug-resistance,Pseudomonas aeruginosa,Virulence},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
pages = {265--269},
publisher = {Academic Press},
title = {{Complete genomic analysis of multidrug-resistance Pseudomonas aeruginosa Guangzhou-Pae617, the host of megaplasmid pBM413}},
volume = {117},
year = {2018}
}
@article{Liu2019,
abstract = {Purpose. The emergence and spread of carbapenem-resistant hypervirulent Klebsiella pneumoniae (CR-hvKP) is causing worldwide concern, whereas NDM-producing hvKP is still rare. Here we report the complete genome sequence characteristics of an NDM-1-producing ST23 type clinical hvKP in PR China. Methodology. Capsular polysaccharide serotyping was performed by PCR. The complete genome sequence of isolate 3214 was obtained using both the Illumina Hiseq platform and Pacbio RS platform. Multilocus sequence type was identified by submitting the genome sequence to mlst 2.0 and the antimicrobial resistance genes and plasmid replicons were identified using Res- Finder and PlasmidFinder, respectively. Transferability of the blaNDM-1-bearing plasmid was determined by conjugation experiment, S1 pulsed-field gel electrophoresis and Southern hybridization. Results. Isolate 3214 was classified to ST23 and belonged to the K1 capsular serotype. The isolate's total genome size was 6 171 644 bp with a G+C content of 56.39{\%}, consisting of a 5 448 209 bp chromosome and seven plasmids. The resistome included 18 types of antibiotic resistance genes. Fourteen resistance genes including blaNDM-1and blaCTX-M-14were located on plasmids and five also including blaCTX-M-14were in the chromosome. Plasmid pNDM{_}3214 carrying blaNDM-1harboured six types of resistance genes surrounded by insertion sequences and was conjugative. The worldwide pLVPK-like virulence plasmid harbouring rmpA2 and rmpA was also found in this isolate. Conclusion. This study provides basic information of phenotypic and genomic features of ST23 CR-hvKP isolate 3214. Our data highlights the potential risk of spread of NDM-1-producing ST23 hvKP.},
author = {Liu, Bao Tao and Su, Wei Qi},
doi = {10.1099/jmm.0.000996},

issn = {14735644},
journal = {Journal of Medical Microbiology},
keywords = {Hypervirulent Klebsiella
pneumoniae,Lista{_}Filtrada,NDM,ST23,Whole genome sequence},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
number = {6},
pages = {866--873},
publisher = {Microbiology Society},
title = {{Whole genome sequencing of NDM-1-producing serotype k1 st23
hypervirulent klebsiella pneumoniae in china}},
volume = {68},
year = {2019}
}
@article{Li2015,
abstract = {Pseudomonas plecoglossicida NyZ12 (CCTCC AB 2015057), a Gram-
negative bacterium isolated from soil, has the ability to degrade
cyclohexylamine. The complete genome sequence of this strain (6,233,254bp
of chromosome length) is presented, with information about the genes of
characteristic enzymes responsible for cyclohexylamine oxidation to
cyclohexanone and the integrated gene cluster for the metabolic pathway
of cyclohexanone oxidation to adipate.},
author = {Li, Xin and Li, Cun-Zhi and Mao, Ling-Qi and Yan, Da-Zhong and
Zhou, Ning-Yi},
doi = {10.1016/j.jbiotec.2015.02.011},
issn = {1873-4863},
journal = {Journal of biotechnology},
keywords = {Cyclohexylamine oxidation,Gene cluster,Genome
sequence,Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
pages = {29--30},
pmid = {25701176},
publisher = {Elsevier},
title = {{Complete genome sequence of the cyclohexylamine-degrading
Pseudomonas plecoglossicida NyZ12.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/25701176},
volume = {199},
year = {2015}
}
@article{Li2015a,
abstract = {Pseudomonas plecoglossicida NyZ12 (CCTCC AB 2015057), a Gram-
negative bacterium isolated from soil, has the ability to degrade
cyclohexylamine. The complete genome sequence of this strain (6,233,254.
bp of chromosome length) is presented, with information about the genes
of characteristic enzymes responsible for cyclohexylamine oxidation to
cyclohexanone and the integrated gene cluster for the metabolic pathway
of cyclohexanone oxidation to adipate.},
author = {Li, Xin and Li, Cun Zhi and Mao, Ling Qi and Yan, Da Zhong and
Zhou, Ning Yi},
doi = {10.1016/j.jbiotec.2015.02.011},
issn = {18734863},
journal = {Journal of Biotechnology},

keywords = {Cyclohexylamine oxidation,Gene cluster,Genome
sequence,Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
pages = {29--30},
publisher = {Elsevier},
title = {{Complete genome sequence of the cyclohexylamine-degrading
Pseudomonas plecoglossicida NyZ12}},
volume = {199},
year = {2015}
}
@article{Li2015b,
abstract = {Pseudomonas plecoglossicida NyZ12 (CCTCC AB 2015057), a Gram-
negative bacterium isolated from soil, has the ability to degrade
cyclohexylamine. The complete genome sequence of this strain (6,233,254.
bp of chromosome length) is presented, with information about the genes
of characteristic enzymes responsible for cyclohexylamine oxidation to
cyclohexanone and the integrated gene cluster for the metabolic pathway
of cyclohexanone oxidation to adipate.},
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journal = {Journal of Biotechnology},
keywords = {Cyclohexylamine oxidation,Gene cluster,Genome
sequence,Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
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title = {{Complete genome sequence of the cyclohexylamine-degrading
Pseudomonas plecoglossicida NyZ12}},
volume = {199},
year = {2015}
}
@article{Li2018,
abstract = {The complete genomic sequence of Pseudomonas fluorescens
bacteriophage PFP1, isolated from sewage samples collected in Liaoning
Province, China, were sequenced in this study and found to be 40,914 bp
long. The PFP1 genome is composed of linear double-stranded DNA with
55.81{\%} G+C content and 45 putative protein-coding genes, and no rRNA
and tRNA genes. Comparative genomics and phylogenetic analysis revealed
that the Pseudomonas fluorescens phage PFP1 is a new member of the genus
T7virus. This information can be used to develop novel phage-based
control strategies against Pseudomonas fluorescens.},
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doi = {10.1007/s00705-018-3979-3},
issn = {1432-8798},
journal = {Archives of virology},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
number = {12},

pages = {3423--3426},
pmid = {30120569},
publisher = {Springer-Verlag Wien},
title = {{Complete genome sequence of PFP1, a novel T7-like Pseudomonas fluorescens bacteriophage.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30120569},
volume = {163},
year = {2018}
}
@article{Lee2017,
abstract = {Antimicrobial-producing, cold-adapted microorganisms have great potential for biotechnological applications in food, pharmaceutical, and cosmetic industries. Pseudomonas antarctica PAMC 27494, a psychrophile exhibiting antimicrobial activity, was isolated from an Antarctic freshwater sample. Here we report the complete genome of P. antarctica PAMC 27494. The strain contains a gene cluster encoding microcin B which inhibits DNA regulations by targeting the DNA gyrase. PAMC 27494 may produce R-type pyocins and also contains a complete set of proteins for the biosynthesis of adenosylcobalamin and possibly induces plant growth by supplying pyrroloquinoline quionone molecules.},
author = {Lee, Jaejin and Cho, Yong Joon and Yang, Jae Young and Jung, You Jung and Hong, Soon Gyu and Kim, Ok Sun},
doi = {10.1016/j.jbiotec.2017.08.013},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {Complete genome,Lista{_}Filtrada,Microcin B,Pseudomonas antarctica,Psychrophile},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
pages = {15--18},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of Pseudomonas antarctica PAMC 27494, a bacteriocin-producing psychrophile isolated from Antarctica}},
volume = {259},
year = {2017}
}
@misc{Le2013,
abstract = {PURPOSE OF REVIEW: The advent of high-throughput whole-genome sequencing has the potential to revolutionize the conduct of outbreak investigation. Because of its ultimate resolution power for differentiating between closely related pathogen strains, whole-genome sequencing could augment the traditional epidemiologic investigations of infectious disease outbreaks. RECENT FINDINGS: The combination of whole-genome sequencing and intensive epidemiologic analysis provided new insights on the sources and transmission dynamics of large-scale epidemics caused by Escherichia coli and Vibrio cholerae, nosocomial outbreaks caused by methicillin-resistant Staphylococcus aureus, Klebsiella pneumoniae, Mycobacterium abscessus, community-centered outbreaks caused by Mycobacterium tuberculosis, and natural disaster-Associated outbreaks caused by environmentally acquired molds. SUMMARY: When combined with traditional epidemiologic investigation, whole-genome sequencing has proven useful for elucidating the sources and transmission dynamics of disease outbreaks. Development of a fully automated bioinformatics pipeline for the analysis of whole-genome sequence data is

much needed to make this powerful tool more widely accessible. {\textcopyright} 2013 Wolters Kluwer Health Lippincott Williams {\&} Wilkins.},
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booktitle = {Current Opinion in Critical Care},
doi = {10.1097/MCC.0b013e3283636b8c},
issn = {10705295},
keywords = {Foodborne outbreaks,Infection control,Nosocomial infection,Outbreak investigation,Whole-genome sequencing},
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number = {5},
pages = {432--439},
title = {{Selected insights from application of whole-genome sequencing for outbreak investigations}},
volume = {19},
year = {2013}
}
@article{Kwak2015,
abstract = {Pseudomonas rhizosphaerae IH5T (=DSM 16299T), isolated from the rhizospheric soil of grass growing in Spain, has been reported as a novel species of the genus Pseudomonas harboring insoluble phosphorus solubilizing activity. To understanding the multifunctional biofertilizer better, we report the complete genome sequence of P. rhizosphaerae IH5T.},
author = {Kwak, Yunyoung and Jung, Byung Kwon and Shin, Jae Ho},
doi = {10.1016/j.jbiotec.2014.11.031},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {Phosphate-solubilizer,Pseudomonas rhizosphaerae,Single molecule real-time sequencing,Whole genome sequence},
month = {jan},
pages = {137--138},
publisher = {Elsevier},
title = {{Complete genome sequence of Pseudomonas rhizosphaerae IH5T (=DSM 16299T), a phosphate-solubilizing rhizobacterium for bacterial biofertilizer}},
volume = {193},
year = {2015}
}
@article{Kumar2019,
abstract = {Pseudomonas frederiksbergensis ERDD5:01 is a psychrotrophic bacteria isolated from the glacial stream flowing from East Rathong glacier in Sikkim Himalaya. The strain showed survivability at high altitude stress conditions like freezing, frequent freeze-thaw cycles, and UV-C radiations. The complete genome of 5,746,824 bp circular chromosome and a plasmid of 371,027 bp was sequenced to understand the genetic basis of its survival strategy. Multiple copies of cold-associated genes encoding cold active chaperons, general stress response, osmotic stress, oxidative stress, membrane/cell wall alteration, carbon storage/starvation and, DNA repair mechanisms supported its survivability at extreme cold and radiations corroborating with the bacterial physiological findings. The molecular cold adaptation analysis in comparison with the genome of 15 mesophilic Pseudomonas species revealed

functional insight into the strategies of cold adaptation. The genomic data also revealed the presence of industrially important enzymes.},
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issn = {10898646},
journal = {Genomics},
keywords = {Cold and radiation resistance,Complete genome sequence,Industrial enzymes,Lista{_}Filtrada,Molecular cold adaptation,Pseudomonas frederiksbergensis ERDD5:01,SMRT sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {may},
number = {3},
pages = {492--499},
publisher = {Academic Press Inc.},
title = {{Complete genome sequence of Pseudomonas frederiksbergensis ERDD5:01 revealed genetic bases for survivability at high altitude ecosystem and bioprospection potential}},
volume = {111},
year = {2019}
}
@article{Kuepper2015,
abstract = {Pseudomonas putida S12 is a solvent-tolerant gamma-proteobacterium with an extensive track record for production of industrially relevant chemicals. Here we report the annotated complete genome sequence of this organism, including the megaplasmid pTTS12 which encodes many of the unique features of the S12 strain.},
author = {Kuepper, J. and Ruijssenaars, H. J. and Blank, L. M. and de Winde, J. H. and Wierckx, N.},
doi = {10.1016/j.jbiotec.2015.02.027},
issn = {18734863},
journal = {Journal of Biotechnology},
keywords = {Biocatalysis,Complete genome sequence,Lista{_}Filtrada,Pseudomonas putida S12,Solvent tolerance,Styrene},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
pages = {17--18},
publisher = {Elsevier},
title = {{Complete genome sequence of solvent-tolerant pseudomonas putida S12 including megaplasmid pTTS12}},
volume = {200},
year = {2015}
}
@article{Kohler2013,
abstract = {Pseudomonas sp. VLB120 was isolated in Stuttgart, Germany, as a styrene degrading organism. The complete genome sequence includes genomic information of solvent tolerance mechanisms, metabolic pathways for various organic compounds, and the megaplasmid pSTY. {\textcopyright} 2013 Elsevier B.V.},
author = {K{\"{o}}hler, Kirsten A.K. and R{\"{u}}ckert, Christian and Schatschneider, Sarah and Vorh{\"{o}}lter, Frank J{\"{o}}rg and Szczepanowski, Rafael and Blank, Lars M. and Niehaus, Karsten and

Goesmann, Alexander and P{\"{u}}hler, Alfred and Kalinowski, J{\"{o}}rn and Schmid, Andreas},
doi = {10.1016/j.jbiotec.2013.10.016},
issn = {01681656},
journal = {Journal of Biotechnology},
keywords = {Biofilm,Genome sequence,Lista{_}Filtrada,Pseudomonas VLB120,Solvent tolerance,Styrene},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
number = {4},
pages = {729--730},
title = {{Complete genome sequence of Pseudomonas sp. strain VLB120 a solvent tolerant, styrene degrading bacterium, isolated from forest soil}},
volume = {168},
year = {2013}
}
@article{Klochko2016,
abstract = {Meticillin-resistant Staphylococcus aureus (MRSA) is a serious public health threat causing outbreaks of clinical infection around the world. Mupirocin is a promising anti-MRSA drug, however mupirocin-resistant strains of S. aureus are emerging at an increasing rate. The newly discovered antibiotic batumin may contribute to anti-MRSA therapy. The objective of this work was to identify possible molecular targets for batumin as well as mechanisms of its antistaphylococcal activity using computational molecular docking and by analysing the complete genome sequence of the batumin-producer Pseudomonas batumici UCM B-321. It was found that batumin acted very similarly to mupirocin by inhibiting aminoacyl tRNA synthetases. A previous hypothesis considering the trans-enoyl-CoA reductase FabI as a prime molecular target of batumin was rejected. However, indirect inhibition of fatty acid biosynthesis in sensitive bacteria does take place as a part of stringent response repression triggered by accumulation of uncharged tRNA molecules. Paralogues of diverse leucine-tRNA synthetases in the genome of P. batumici indicated that this protein might be the prime target of batumin. A batumin biosynthesis operon comprising 28 genes was found to be acquired through horizontal gene transfer. It was hypothesised that, in contrast to mupirocin, batumin could inhibit a broader range of aminoacyl tRNA synthetases and that acquired resistance to mupirocin might not endow S. aureus strains with resistance against batumin.},
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doi = {10.1016/j.ijantimicag.2015.10.006},
issn = {18727913},
journal = {International Journal of Antimicrobial Agents},
keywords = {Antistaphylococcal antibiotic,Batumin,Genome,Molecular docking,Mupirocin,Pseudomonas batumici},
month = {jan},
number = {1},
pages = {56--61},
publisher = {Elsevier B.V.},
title = {{Prospects of a new antistaphylococcal drug batumin revealed by molecular docking and analysis of the complete genome sequence of the batumin-producer Pseudomonas batumici UCM B-321}},

volume = {47},
year = {2016}
}
@article{Kholodilov,
abstract = {In recent decades, many new flavi-like viruses have been discovered predominantly in different invertebrates and, as was recently shown, some of them may cause disease in humans. The Jingmenvirus (JMV) group holds a special place among flaviviruses and flavi-like viruses because they have a segmented ssRNA(+) genome. We detected Alongshan virus (ALSV), which is a representative of the JMV group, in ten pools of adult Ixodes persulcatus ticks collected in two geographically-separated Russian regions. Three of the ten strains were isolated in the tick cell line IRE/CTVM19. One of the strains persisted in the IRE/CTVM19 cells without cytopathic effect for three years. Most ALSV virions purified from tick cells were spherical with a diameter of approximately 40.5 nm. In addition, we found smaller particles of approximately 13.1 nm in diameter. We obtained full genome sequences of all four segments of two of the isolated ALSV strains, and partial sequences of one segment from the third strain. Phylogenetic analysis on genome segment 2 of the JMV group clustered our novel strains with other ALSV strains. We found evidence for the existence of a novel upstream open reading frame in the glycoprotein-coding segment of ALSV and other members of the JMV group.},
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doi = {10.3390/v12040362},
journal = {Viruses},
title = {{Isolation and Characterisation of Alongshan Virus in Russia}},
url = {https://www.mdpi.com/1999-4915/12/4/362?utm{_}source=researcher{_}app{\&}utm{_}medium=referral{\&}utm{_}campaign=RESR{_}MRKT{_}Researcher{_}inbound}
}
@article{Kaminski2018,
abstract = {Microorganisms classified in to the Pseudomonas genus are a ubiquitous bacteria inhabiting variety of environmental niches and have been isolated from soil, sediment, water and different parts of higher organisms (plants and animals). Members of this genus are known for their metabolic versatility and are able to utilize different chemical compounds as a source of carbon, nitrogen or phosphorus, which makes them an interesting microorganism for bioremediation or bio-transformation. Moreover, Pseudomonas sp. has been described as a microorganism that can easily adapt to new environmental conditions due to its resistance to the presence of high concentrations of heavy metals or chemical pollution. Here we present the isolation and analysis of Pseudomonas silesiensis sp. nov. strain A3T isolated from peaty soil used in a biological wastewater treatment plant exploited by a pesticide packaging company. Phylogenetic MLSA analysis of 4 housekeeping genes (16S rRNA, gyrB, rpoD and rpoB), complete genome sequence comparison (ANIb, Tetranucleotide identity, digital DDH), FAME analysis, and other biochemical tests indicate the A3T strain (type strain PCM 2856T = DSM 103370T) differs significantly from the closest relative species and therefore represents a new species

within the Pseudomonas genus. Moreover, bioinformatic analysis of the complete sequenced genome showed that it consists of 6,823,539 bp with a 59.58 mol{\%} G + C content and does not contain any additional plasmids. Genome annotation predicted the presence of 6066 genes, of which 5875 are coding proteins and 96 are RNA genes.},
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doi = {10.1016/j.syapm.2017.09.002},
issn = {16180984},
journal = {Systematic and Applied Microbiology},
keywords = {Complete genome assembly,Complete genome sequence,Pesticide,Pseudomonas,Soil,Wastewater treatment plant},
month = {jan},
number = {1},
pages = {13--22},
publisher = {Elsevier GmbH},
title = {{Pseudomonas silesiensis sp. nov. strain A3T isolated from a biological pesticide sewage treatment plant and analysis of the complete genome sequence}},
volume = {41},
year = {2018}
}
@article{Jiang2014,
abstract = {Pseudomonas aurantiaca Strain JD37, a Gram-negative bacterium isolated from potato rhizosphere soil (Shanghai, China), is a plant growth-promoting rhizobacterium. The JD37 genome consists of only one chromosome with no plasmids. Its genome contains genes involved plant growth promoting, biological control, and other function. Here, we present the complete genome sequence of P. aurantiaca JD37. As far as we know, this is the first whole-genome of this species.},
author = {Jiang, Qiuyue and Xiao, Jing and Zhou, Chenhao and Mu, Yonglin and Xu, Bin and He, Qingling and Xiao, Ming},
doi = {10.1016/j.jbiotec.2014.10.021},
issn = {1873-4863},
journal = {Journal of biotechnology},
month = {dec},
pages = {85--6},
pmid = {25456057},
title = {{Complete genome sequence of the plant growth-promoting rhizobacterium Pseudomonas aurantiaca strain JD37.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/25456057},
volume = {192 Pt A},
year = {2014}
}
@article{Jia2020,
abstract = {For comprehensive insights into the effects of multiple disinfection regimes on antibiotic resistome in drinking water, this study utilized metagenomic approaches to reveal the changing patterns of antibiotic resistance genes (ARGs) and bacterial community as well as their associations. A total of 297 ARGs within 17 types were detected in the drinking water, and their total relative abundance ranged from 195.49 ± 24.85 to 626.31 ± 38.61 copies of ARGs per cell. The total ARG abundance was significantly increased after the antimicrobial resin and ultraviolet (AR/UV) disinfection while significantly decreased after the

ozone and chlorine (O3/Cl2) disinfection and remained stable after AR/Cl2 disinfection. Overall, 18 ARGs including bacA, mexT, and blaOXA-12, mainly affiliated to bacitracin, multidrug, and beta-lactam, were persistent and discriminative during all the disinfection strategies in drinking water, and they were considered as key ARGs that represent the antibiotic resistome during drinking water disinfection. Additionally, possible hosts of 50{\%} key ARGs were revealed based on co-occurrence network. During multiple disinfection processes, the change of Fusobacteriales and Aeromonadaceae in abundance mainly contributed to the abundance shift of bacA, and Pseudomonas mainly increased the abundance of mexT. These findings indicated that bacterial community shift may be the key factor driving the change of antibiotic resistome during disinfection. The strong association between antibiotic resistome alteration and bacterial community shift proposed in this study may enhance our understanding of the underlying mechanism of the disinfection effects on antibiotic resistance and benefit effective measures to improve safety of drinking water.},
author = {Jia, Shuyu and Bian, Kaiqin and Shi, Peng and Ye, Lin and Liu, Chang Hong},
doi = {10.1016/j.watres.2020.115721},
issn = {18792448},
journal = {Water Research},
keywords = {Antibiotic resistance genes,Bacterial community shift,Disinfection strategy,Drinking water,High-throughput sequencing},
month = {jun},
publisher = {Elsevier Ltd},
title = {{Metagenomic profiling of antibiotic resistance genes and their associations with bacterial community during multiple disinfection regimes in a full-scale drinking water treatment plant}},
volume = {176},
year = {2020}
}
@article{Jia2019,
abstract = {OBJECTIVES Klebsiella pneumoniae has emerged worldwide as a major cause of severe infections owing to the rising prevalence of multidrug-resistant strains in clinical settings. This study aimed to investigate the genomic features of pandrug-resistant K. pneumoniae strain KP2 with high colistin and tigecycline resistance isolated from a patient in China. METHODS The antimicrobial susceptibility of K. pneumoniae KP2 was determined by microdilution broth assay. Whole genomic DNA was extracted and was sequenced using an Illumina HiSeq X10 platform. De novo genome assembly was performed using Unicycler, and the draft genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The sequence type (ST), capsular type, antimicrobial resistance and virulence-related genes were identified from the genome sequence. Core genome multilocus sequence typing (cgMLST) analysis was performed by BacWGSTdb server. RESULTS Klebsiella pneumoniae KP2 was resistant to all antimicrobial agents tested, including colistin and tigecycline. The genome size was calculated as 5 729 339bp, with 5772 protein-coding sequences and a G+C content of 57.0{\%}. The isolate was assigned to ST11 with capsular serotype KL64. Several antimicrobial resistance genes and virulence genes as well as genomic islands and multiple insertion sequences were identified in the genome sequence. The closest relative of K. pneumoniae KP2 was another isolate from Hangzhou

that differed by only 45 cgMLST loci. CONCLUSION The genome sequence data presented in this study can serve as an important reference sequence for further understanding of the antimicrobial resistance mechanisms and virulence potential of this bacterial species.},
author = {Jia, Huiqiong and Chen, Hangfei and Ruan, Zhi},
doi = {10.1016/j.jgar.2019.08.013},
issn = {2213-7173},
journal = {Journal of global antimicrobial resistance},
keywords = {KL64,Klebsiella pneumoniae,Lista{_}Filtrada,Pandrug resistance,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
pages = {40--42},
pmid = {31449964},
publisher = {Elsevier Ltd},
title = {{Unravelling the genome sequence of a pandrug-resistant Klebsiella pneumoniae isolate with sequence type 11 and capsular serotype KL64 from China.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/31449964},
volume = {19},
year = {2019}
}
@misc{Jia2019a,
abstract = {Objectives: Klebsiella pneumoniae has emerged worldwide as a major cause of severe infections owing to the rising prevalence of multidrug-resistant strains in clinical settings. This study aimed to investigate the genomic features of pandrug-resistant K. pneumoniae strain KP2 with high colistin and tigecycline resistance isolated from a patient in China. Methods: The antimicrobial susceptibility of K. pneumoniae KP2 was determined by microdilution broth assay. Whole genomic DNA was extracted and was sequenced using an Illumina HiSeq X10 platform. De novo genome assembly was performed using Unicycler, and the draft genome was annotated using the NCBI Prokaryotic Genome Annotation Pipeline (PGAP). The sequence type (ST), capsular type, antimicrobial resistance and virulence-related genes were identified from the genome sequence. Core genome multilocus sequence typing (cgMLST) analysis was performed by BacWGSTdb server. Results: Klebsiella pneumoniae KP2 was resistant to all antimicrobial agents tested, including colistin and tigecycline. The genome size was calculated as 5 729 339 bp, with 5772 protein-coding sequences and a G + C content of 57.0{\%}. The isolate was assigned to ST11 with capsular serotype KL64. Several antimicrobial resistance genes and virulence genes as well as genomic islands and multiple insertion sequences were identified in the genome sequence. The closest relative of K. pneumoniae KP2 was another isolate from Hangzhou that differed by only 45 cgMLST loci. Conclusion: The genome sequence data presented in this study can serve as an important reference sequence for further understanding of the antimicrobial resistance mechanisms and virulence potential of this bacterial species.},
author = {Jia, Huiqiong and Chen, Hangfei and Ruan, Zhi},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2019.08.013},
issn = {22137173},
keywords = {KL64,Klebsiella pneumoniae,Lista{_}Filtrada,Pandrug resistance,Whole-genome sequencing},

mendeley-tags = {Lista{_}Filtrada},
month = {dec},
pages = {40--42},
publisher = {Elsevier Ltd},
title = {{Unravelling the genome sequence of a pandrug-resistant Klebsiella pneumoniae isolate with sequence type 11 and capsular serotype KL64 from China}},
volume = {19},
year = {2019}
}
@article{Ji2020,
author = {Ji, Beihong and Liu, Shuhan and He, Xibing and Man, Viet Hoang and Xie, Xiang-Qun and Wang, Junmei},
doi = {10.1021/acschemneuro.9b00696},
issn = {1948-7193},
journal = {ACS Chemical Neuroscience},
month = {mar},
publisher = {American Chemical Society (ACS)},
title = {{Prediction of the binding affinities and selectivity for CB1 and CB2 ligands using homology modeling, molecular docking, molecular dynamics simulations, and MM-PBSA binding free energy calculations}},
year = {2020}
}
@article{JasperJ.KoehorstJesseC.J.vanDamEdoardoSaccentiVitorA.P.MartinsdosSantos2017,
abstract = {Summary: To unlock the full potential of genome data and to enhance data interoperability and reusability of genome annotations we have developed SAPP, a Semantic Annotation Platform with Provenance. SAPP is designed as an infrastructure supporting FAIR de novo computational gen- omics but can also be used to process and analyze existing genome annotations. SAPP automatic- ally predicts, tracks and stores structural and functional annotations and associated dataset- and element-wise provenance in a Linked Data format, thereby enabling information mining and re- trieval with Semantic Web technologies. This greatly reduces the administrative burden of han- dling multiple analysis tools and versions thereof and facilitates multi-level large scale comparative analysis. Availability and implementation: SAPP is written in JAVA and freely available at https://gitlab.com/ sapp and runs on Unix-like operating systems. The documentation, examples and a tutorial are available at https://sapp.gitlab.io.},
author = {{Jasper J. Koehorst, Jesse C. J. van Dam, Edoardo Saccenti, Vitor A. P. Martins dos Santos}, Maria Suarez-Diez and Peter J. Schaap},
doi = {10.1093/BIOINFORMATICS},
journal = {Oxford},
number = {8},
pages = {1401--1403},
publisher = {Oxford Academic},
title = {{Imported from https://www.researchgate.net/publication/321428915{_}SAPP{_}functional{_}genome{_}annotation{_}and{_}analysis{_}through{_}a{_}semantic{_}framework{_}using{_}FAIR{_}principles}},
url = {https://www.researchgate.net/publication/321428915{_}SAPP{_}functional

{_}genome{_}annotation{_}and{_}analysis{_}through{_}a{_}semantic{\
}framework{}using{_}FAIR{_}principles},
volume = {34},
year = {2017}
}
@article{Hwang2020,
author = {Hwang, Junsang and Bang, Ina and Kim, Donghyuk and Shin, Seung
Chul and Chin, Young-Wook and Kim, Tae-Wan and Kim, Hyo Jin},
doi = {10.1007/s13205-020-02174-9},
issn = {2190-572X},
journal = {3 Biotech},
month = {apr},
number = {4},
pages = {185},
title = {{Genome sequence of the potential probiotic eukaryote
Saccharomyces cerevisiae KCCM 51299}},
url = {http://link.springer.com/10.1007/s13205-020-02174-9},
volume = {10},
year = {2020}
}
@article{Hunter2020,
abstract = {The ability to serially monitor tumor-derived cell-free DNA
(cfDNA) brings with it the potential to measure response to anticancer
therapies and detect minimal residual disease (MRD). This report
describes a patient with HER2-positive metastatic breast cancer with an
exceptional response to trastuzumab and nab-paclitaxel who remains in
complete remission several years after cessation of therapy. Next-
generation sequencing of the patient's primary tumor tissue showed
several mutations, including an oncogenic hotspot PIK3CA mutation. A
sample of cfDNA was collected 6 years after her last therapy and then
analyzed for mutant PIK3CA using digital PCR. No detectable mutations
associated with the primary tumor were found despite assaying
{\textgreater}10,000 genome equivalents, suggesting that the patient had
achieved a molecular remission. Results of this case study suggest that
serial monitoring of MRD using liquid biopsies could provide a useful
method for individualizing treatment plans for patients with metastatic
disease with extreme responses to therapy. However, large-scale clinical
studies are needed to validate and implement these techniques for patient
care.},
author = {Hunter, Natasha and Croessmann, Sarah and Cravero, Karen and
Shinn, Daniel and Hurley, Paula J and Park, Ben Ho},
doi = {10.6004/jnccn.2019.7381},
issn = {1540-1413},
journal = {Journal of the National Comprehensive Cancer Network : JNCCN},
month = {apr},
number = {4},
pages = {375--379},
pmid = {32259780},
title = {{Undetectable Tumor Cell-Free DNA in a Patient With Metastatic
Breast Cancer With Complete Response and Long-Term Remission.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32259780},
volume = {18},
year = {2020}
}

@article{Huang2020,
author = {Huang, Wei and Hu, Hui and Zhang, Qiong and Wang, Ning and Yang, Xiangliang and Guo, An-Yuan},
doi = {10.3389/fbioe.2020.00088},
journal = {Frontiers in Bioengineering and Biotechnology},
month = {mar},
publisher = {Frontiers Media SA},
title = {{Genome-Wide DNA Methylation Enhances Stemness in the Mechanical Selection of Tumor-Repopulating Cells}},
volume = {8},
year = {2020}
}
@article{Hu2015,
abstract = {Pseudomonas stutzeri SLG510A3-8, isolated from oil-contaminated soil in Shengli Oilfield, China, has the potential to be applied for microbial enhanced oil recovery. Here, we reported the complete genome sequence of this bacterium. It has a 4,650,155bp circular chromosome encoding 4450 genes, and the genome consists of genes that are involved in denitrification, chemotaxis, benzoate degradation, molecule transportation, and other functions. The genome contains a complete set of genes for type I secretion system in comparison with sequences of other P. stutzeri strains.},
author = {Hu, Bing and Nie, Yong and Geng, Shuang and Wu, Xiao-Lei},
doi = {10.1016/j.jbiotec.2015.06.421},
issn = {1873-4863},
journal = {Journal of biotechnology},
keywords = {Complete genome sequencing,Lista{_}Filtrada,Microbial enhanced oil recovery,Pseudomonas stutzeri SLG510A3-8},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
pages = {1--2},
pmid = {26144046},
publisher = {Elsevier},
title = {{Complete genome sequence of the petroleum-emulsifying bacterium Pseudomonas stutzeri SLG510A3-8.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26144046},
volume = {211},
year = {2015}
}
@article{Hu2015a,
abstract = {Pseudomonas stutzeri SLG510A3-8, isolated from oil-contaminated soil in Shengli Oilfield, China, has the potential to be applied for microbial enhanced oil recovery. Here, we reported the complete genome sequence of this bacterium. It has a 4,650,155. bp circular chromosome encoding 4450 genes, and the genome consists of genes that are involved in denitrification, chemotaxis, benzoate degradation, molecule transportation, and other functions. The genome contains a complete set of genes for type I secretion system in comparison with sequences of other P. stutzeri strains.},
author = {Hu, Bing and Nie, Yong and Geng, Shuang and Wu, Xiao Lei},
doi = {10.1016/j.jbiotec.2015.06.421},
issn = {18734863},
journal = {Journal of Biotechnology},

keywords = {Complete genome sequencing,Lista{_}Filtrada,Microbial enhanced oil recovery,Pseudomonas stutzeri SLG510A3-8},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
pages = {1--2},
publisher = {Elsevier},
title = {{Complete genome sequence of the petroleum-emulsifying bacterium Pseudomonas stutzeri SLG510A3-8}},
volume = {211},
year = {2015}
}
@article{Holden2018,
abstract = {Klebsiella pneumoniae is rapidly acquiring resistance to all known antibiotics, including carbapenems. Multilocus sequence type ST258 (sequence type 258), carrying a gene encoding the K. pneumoniae carbapenemase (blaKPC) on a transmissible plasmid, is the most prevalent carbapenem-resistant Enterobacteriaceae (CRE) in the United States and has disseminated worldwide. Previously, whole-genome sequencing identified core genome single nucleotide variants that divide ST258 into two distinct clades, ST258a and ST258b. Furthermore, a subset of ST258b strains have a 347-base deletion within the enterobactin (Ent) exporter gene entS Despite the predicted inability of these strains to secrete the siderophore Ent, this clade is prevalent among clinical isolates, indicating that a full-length entS gene is not necessary for infection. To compare the transcriptional responses of ST258 subtypes to iron limitation, we performed transcriptome sequencing (RNA-Seq) in minimal medium alone or supplemented with iron or human serum and measured gene expression patterns. Iron limitation induced differential expression of distinct iron acquisition pathways when comparing ST258a and ST258b strains, including the upregulation of the hemin transport operon in entS partial deletion isolates. To measure how K. pneumoniae strains vary in iron chelation and siderophore production, we performed in vitro chrome azurol S (CAS) and Arnow assays as well as mass spectrometry. We determined that both ST258a and ST258b strains grow under iron-depleted conditions, can utilize hemin for growth, and secrete Ent, despite the partial entS deletion in a subset of ST258b strains. All carbapenem-resistant (CR) K. pneumoniae strains tested were susceptible to growth inhibition by the Ent-sequestering innate immune protein lipocalin 2.IMPORTANCE Carbapenem-resistant Enterobacteriaceae, including K. pneumoniae, are a major health care concern worldwide because they cause a wide range of infection and are resistant to all or nearly all antibiotics. To cause infection, these bacteria must acquire iron, and a major mechanism of acquiring iron is by secreting a molecule called enterobactin that strips iron from host proteins. However, a subset of carbapenem-resistant K. pneumoniae strains that lack a portion of the entS gene that is required for enterobactin secretion was recently discovered. To understand how these mutant strains obtain iron, we studied their transcriptional responses, bacterial growth, and enterobactin secretion under iron-limited conditions. We found that strains both with mutated and intact entS genes grow under iron-limiting conditions, secrete enterobactin, and utilize an alternate iron source, hemin, for growth. Our data indicate that carbapenem-resistant K. pneumoniae can use varied methods for iron uptake during infection.},

author = {Holden, Victoria I and Wright, Meredith S and Houle, S{\'{e}}bastien and Collingwood, Abigail and Dozois, Charles M and Adams, Mark D and Bachman, Michael A},
doi = {10.1128/mSphere.00125-18},
issn = {2379-5042},
journal = {mSphere},
keywords = {CRE,Klebsiella pneumoniae,Lista{_}Filtrada,ST258,carbapenems,entS,enterobactin,hemin},
mendeley-tags = {Lista{_}Filtrada},
number = {2},
pmid = {29669884},
title = {{Iron Acquisition and Siderophore Release by Carbapenem-Resistant Sequence Type 258 Klebsiella pneumoniae.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/29669884 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5907654},
volume = {3},
year = {2018}
}
@misc{HenriquesNormark2002,
abstract = {Antibiotic resistance is a clinical and socioeconomical problem that is here to stay. Resistance can be natural or acquired. Some bacterial species, such as Pseudomonas aeruginosa, show a high intrinsic resistance to a number of antibiotics whereas others are normally highly antibiotic susceptible such as group A streptococci. Acquired resistance evolve via genetic alterations in the microbes own genome or by horizontal transfer of resistance genes located on various types of mobile DNA elements. Mutation frequencies to resistance can vary dramatically depending on the mechanism of resistance and whether or not the organism exhibits a mutator phenotype. Resistance usually has a biological cost for the microorganism, but compensatory mutations accumulate rapidly that abolish this fitness cost, explaining why many types of resistances may never disappear in a bacterial population. Resistance frequently occurs stepwise making it important to identify organisms with low level resistance that otherwise may constitute the genetic platform for development of higher resistance levels. Self-replicating plasmids, prophages, transposons, integrons and resistance islands all represent DNA elements that frequently carry resistance genes into sensitive organisms. These elements add DNA to the microbe and utilize site-specific recombinases/integrases for their integration into the genome. However, resistance may also be created by homologous recombination events creating mosaic genes where each piece of the gene may come from a different microbe. The selection with antibiotics have informed us much about the various genetic mechanisms that are responsible for microbial evolution.},
author = {{Henriques Normark}, B. and Normark, S.},
booktitle = {Journal of Internal Medicine},
doi = {10.1046/j.1365-2796.2002.01026.x},
issn = {09546820},
keywords = {Antibiotic resistance,Compensation,Cost,Evolution,Mechanisms,Reversion},
number = {2},
pages = {91--106},
pmid = {12190884},
title = {{Evolution and spread of antibiotic resistance}},

volume = {252},
year = {2002}
}
@article{Haley2020,
abstract = {Preweaned dairy calves and lactating dairy cows are known reservoirs of antibiotic-resistant bacteria. To further understand the differences in the resistomes and microbial communities between the two, we sequenced the metagenomes of fecal composite samples from preweaned dairy calves and lactating dairy cows on 17 commercial dairy farms (n = 34 samples). Results indicated significant differences in the structures of the microbial communities (analysis of similarities [ANOSIM] R = 0.81, p = 0.001) and resistomes (ANOSIM R = 0.93 to 0.96, p = 0.001) between the two age groups. Firmicutes, Bacteroidetes, Proteobacteria, and Actinobacteria were the predominant members of the communities, but when the groups were compared, Bacteroidetes and Verrumicrobia were significantly more abundant in calf fecal composite samples, whereas Firmicutes, Spirochaetes, Deinococcus-Thermus, Lentisphaerae, Planctomycetes, Chlorofexi, and Saccharibacteria-(TM7) were more abundant in lactating cow samples. Diverse suites of antibiotic resistance genes (ARGs) were identified in all samples, with the most frequently detected being assigned to tetracycline and aminoglycoside resistance. When the two groups were compared, ARGs were significantly more abundant in composite fecal samples from calves than those from lactating cows (calf median ARG abundance = 1.8 × 100 ARG/16S ribosomal RNA [rRNA], cow median ARG abundance = 1.7 × 10-1 ARG/16S rRNA) and at the antibiotic resistance class level, the relative abundance of tetracycline, trimethoprim, aminoglycoside, macrolide-lincosamide-streptogramin B, β-lactam, and phenicol resistance genes was significantly higher in calf samples than in cow samples. Results of this study indicate that composite feces from preweaned calves harbor different bacterial communities and resistomes than composite feces from lactating cows, with a greater abundance of resistance genes detected in preweaned calf feces.},
author = {Haley, Bradd J and Kim, Seon-Woo and Salaheen, Serajus and Hovingh, Ernest and {Van Kessel}, Jo Ann S},
doi = {10.1089/fpd.2019.2768},
issn = {1556-7125},
journal = {Foodborne pathogens and disease},
keywords = {antibiotic resistance,dairy microbiology,metagenomics,microbial communities},
month = {mar},
pmid = {32176535},
publisher = {Mary Ann Liebert Inc},
title = {{Differences in the Microbial Community and Resistome Structures of Feces from Preweaned Calves and Lactating Dairy Cows in Commercial Dairy Herds.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32176535},
year = {2020}
}
@article{Guerrero-Araya2020,
abstract = {Clostridium difficile B1/NAP1/RT027/ST01 has been responsible for outbreaks of antibiotic-associated diarrhoea in clinical settings worldwide and is associated with severe disease presentations and increased mortality rates. Two fluoroquinolone-resistant (FQR) lineages of the epidemic B1/NAP1/RT027/ST01 strain emerged in the USA in the early

1990s and disseminated trans continentally (FQR1 and FQR2). However, it is unclear when and from where they entered Latin America (LA) and whether isolates from LA exhibit unique genomic features when compared to B1/NAP1/RT027/ST01 isolates from other regions of the world. To answer the first issue we compared whole-genome sequences (WGS) of 25 clinical isolates typed as NAP1, RT027 or ST01 in Costa Rica (n=16), Chile (n=5), Honduras (n=3) and Mexico (n=1) to WGS of 129 global isolates from the same genotype using Bayesian phylogenomics. The second question was addressed through a detailed analysis of the number and type of mutations of the LA isolates and their mobile resistome. All but two B1/NAP1/RT027/ST01 isolates from LA belong to the FQR2 lineage (n=23, 92 {\%}), confirming its widespread distribution. As indicated by analysis of a dataset composed of 154 WGS, the B1/NAP1/RT027/ST01 strain was introduced into the four LA countries analysed between 1998 and 2005 from North America (twice) and Europe (at least four times). These events occurred soon after the emergence of the FQR lineages and more than one decade before the first report of the detection of the B1/NAP1/RT027/ST01 in LA. A total of 552 SNPs were identified across all genomes examined (3.8-4.3 Mb) in pairwise comparisons to the R20291 reference genome. Moreover, pairwise SNP distances were among the smallest distances determined in this species so far (0 to 55). Despite this high level of genomic conservation, 39 unique SNPs (7 {\%}) in genes that play roles in the infection process (i.e. slpA) or antibiotic resistance (i.e. rpoB, fusA) distinguished the LA isolates. In addition, isolates from Chile, Honduras and Mexico had twice as many antibiotic resistance genes (ARGs, n=4) than related isolates from other regions. Their unique set of ARGs includes a cfr-like gene and tetM, which were found as part of putative mobile genetic elements whose sequences resemble undescribed integrative and conjugative elements. These results show multiple, independent introductions of B1/NAP1/RT027/ST01 isolates from the FQR1 and FQR2 lineages from different geographical sources into LA and a rather rapid accumulation of distinct mutations and acquired ARG by the LA isolates.},
author = {Guerrero-Araya, Enzo and Meneses, Claudio and Castro-Nallar, Eduardo and {Guzm{\'{a}}n D}, Ana M and {\'{A}}lvarez-Lobos, Manuel and Quesada-G{\'{o}}mez, Carlos and Paredes-Sabja, Daniel and Rodr{\'{i}}guez, C{\'{e}}sar},
doi = {10.1099/mgen.0.000355},
issn = {2057-5858},
journal = {Microbial genomics},
keywords = {B1/NAP1/RT027/ST01 strain,Clostridium difficile,Latin America,Lista{_}Filtrada,MGEs,phylogenomics},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
pmid = {32176604},
publisher = {Microbiology Society},
title = {{Origin, genomic diversity and microevolution of the Clostridium difficile B1/NAP1/RT027/ST01 strain in Costa Rica, Chile, Honduras and Mexico.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32176604},
year = {2020}
}
@article{Gu2018,
abstract = {Background Hypervirulent Klebsiella pneumoniae strains often cause life-threatening community-acquired infections in young and healthy

hosts, but are usually sensitive to antibiotics. In this study, we investigated a fatal outbreak of ventilator-associated pneumonia caused by a new emerging hypervirulent K pneumoniae strain. Methods The outbreak occurred in the integrated intensive care unit of a new branch of the Second Affiliated Hospital of Zhejiang University (Hangzhou, China). We collected 21 carbapenem-resistant K pneumoniae strains from five patients and characterised these strains for their antimicrobial susceptibility, multilocus sequence types, and genetic relatedness using VITEK-2 compact system, multilocus sequence typing, and whole genome sequencing. We selected one representative isolate from each patient to establish the virulence potential using a human neutrophil assay and Galleria mellonella model and to establish the genetic basis of their hypervirulence phenotype. Findings All five patients had undergone surgery for multiple trauma and subsequently received mechanical ventilation. The patients were aged 53–73 years and were admitted to the intensive care unit between late February and April, 2016. They all had severe pneumonia, carbapenem-resistant K pneumoniae infections, and poor responses to antibiotic treatment and died due to severe lung infection, multiorgan failure, or septic shock. All five representative carbapenem-resistant K pneumoniae strains belonged to the ST11 type, which is the most prevalent carbapenem-resistant K pneumoniae type in China, and originated from the same clone. The strains were positive on the string test, had survival of about 80{\%} after 1 h incubation in human neutrophils, and killed 100{\%} of wax moth larvae (G mellonella) inoculated with 1 × 10 6 colony-forming units of the specimens within 24 h, suggesting that they were hypervirulent K pneumoniae. Genomic analyses showed that the emergence of these ST11 carbapenem-resistant hypervirulent K pneumoniae strains was due to the acquisition of a roughly 170 kbp pLVPK-like virulence plasmid by classic ST11 carbapenem-resistant K pneumoniae strains. We also detected these strains in specimens collected in other regions of China. Interpretation The ST11 carbapenem-resistant hypervirulent K pneumoniae strains pose a substantial threat to human health because they are simultaneously hypervirulent, multidrug resistant, and highly transmissible. Control measures should be implemented to prevent further dissemination of such organisms in the hospital setting and the community. Funding Chinese National Key Basic Research and Development Program and Collaborative Research Fund of Hong Kong Research Grant Council.},
author = {Gu, Danxia and Dong, Ning and Zheng, Zhiwei and Lin, Di and Huang, Man and Wang, Lihua and Chan, Edward Wai Chi and Shu, Lingbin and Yu, Jiang and Zhang, Rong and Chen, Sheng},
doi = {10.1016/S1473-3099(17)30489-9},
issn = {14744457},
journal = {The Lancet Infectious Diseases},
month = {jan},
number = {1},
pages = {37--46},
publisher = {Lancet Publishing Group},
title = {{A fatal outbreak of ST11 carbapenem-resistant hypervirulent Klebsiella pneumoniae in a Chinese hospital: a molecular epidemiological study}},
volume = {18},
year = {2018}
}

@article{Gona2019,
abstract = {The aim of this study was to analyze the alarming spread of NDM-1- and OXA-48-co-producing Klebsiella pneumoniae clinical isolates, collected between October 2016 and January 2018 in a neonatal intensive care unit of the University Hospital, Catania, Italy, through whole genome sequencing. All confirmed carbapenem-resistant K. pneumoniae (CRKp) isolates were characterized pheno- and geno-typically, as well as by whole genome sequencing (WGS). A total of 13 CRKp isolates were identified from 13 patients. Pulsed-field gel electrophoresis (PFGE) was performed, and the multilocus sequence typing (MLST) scheme used was based on the gene sequence as published on the MLST Pasteur website. Core genome MLST (cgMLST) was also performed. All isolates co-carried blaoxa-48 and blaNDM-1 genes located on different plasmids belonging to the IncM/L and IncA/C2 groups, respectively. The 13 strains had identical PFGE profiles. MLST and cgMLST showed that K. pneumoniae was dominated by CRKp ST101 and two novel STs (ST3666 and ST3367), identified after submission to the MLST database for ST assignment. All isolates shared the same virulence factors such as type 3 fimbriae, genes for yersiniabactin biosynthesis, yersiniabactin receptor, and iron ABC transporter. They carried the wzi137 variant associated with the K17 serotype. To the best of our knowledge, this is the first report of two novel STs, 3366 and 3367, NDM-OXA-48-co-producing K. pneumoniae clinical isolates, in Italy.},
author = {Gona, Floriana and Bongiorno, Dafne and Aprile, Ausilia and Corazza, Erika and Pasqua, Betta and Scuderi, Maria Grazia and Chiacchiaretta, Matteo and Cirillo, Daniela Maria and Stefani, Stefania and Mezzatesta, Maria Lina},
doi = {10.1007/s10096-019-03597-w},
issn = {14354373},
journal = {European Journal of Clinical Microbiology and Infectious Diseases},
keywords = {Carbapenemase,K. pneumoniae,NDM,OXA-48,ST101,ST3366,ST3367},
month = {sep},
number = {9},
pages = {1687--1691},
publisher = {Springer Verlag},
title = {{Emergence of two novel sequence types (3366 and 3367) NDM-1- and OXA-48-co-producing K. pneumoniae in Italy}},
volume = {38},
year = {2019}
}
@misc{Francisco2019,
abstract = {Objectives: KPC-producing Klebsiella pneumoniae is considered one of the most worrisome multidrug-resistant micro-organisms in nosocomial infections. It has also been reported in wastewater and urban rivers in the city of Sao Paulo, Brazil. Here we report the draft genome sequences of three KPC-2- and CTX-M-15-producing K. pneumoniae sequence type 437 (ST437) isolates obtained from two urban rivers and from a clinical sample of a patient in Sao Paulo. Methods: A genomic library was constructed using a Nextera XT Kit. An Illumina platform was used to perform whole-genome sequencing (WGS). Results: WGS of environmental isolates Kp148/PINH-4900 and Kp196/TIET-4200 and clinical isolate Kp314/11 resulted in estimated genome sizes of 5 464 058, 5 437 723 and 5 319 218 bp, respectively. Resistome analysis of the environmental and

clinical strains revealed the presence of resistance genes to the following antimicrobials in all strains: aminoglycosides [aac(6')-Ib-cr]; β-lactams (bla OXA-1 , bla SHV-11 , bla CTX-M-15 and bla KPC-2); fluoroquinolones [aac(6′)-Ib-cr, oqxA and oqxB]; fosfomycin (fosA KP); macrolides [mph(A)]; phenicols (catB4); sulfonamides (sul1); and trimethoprim (dfrA30). The tetracycline resistance gene tetA was identified in Kp148/PINH-4900 and Kp314/11 only; the aminoglycoside resistance gene aph(3′)-Ia was found only in environmental isolates, and aadA2 only in Kp314/11; and the phenicol resistance gene catA1 was identified only in Kp148/PINH-4900. Conclusions: The draft genome sequences of these strains help us to elucidate the dissemination of resistance genes in micro-organisms inside and outside the hospital and are useful for further comparisons between clinical and environmental strains.},
author = {Francisco, Gabriela Rodrigues and Bueno, Maria Fernanda C. and Cerdeira, Louise and Lincopan, Nilton and Ienne, Susan and Souza, Tiago A. and {de Oliveira Garcia}, Doroti},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2018.12.003},
issn = {22137173},
keywords = {CTX-M-15,Clinical sample,KPC,Klebsiella pneumoniae,Lista{_}Filtrada,ST437,Urban river},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
pages = {74--75},
publisher = {Elsevier Ltd},
title = {{Draft genome sequences of KPC-2- and CTX-M-15-producing Klebsiella pneumoniae ST437 isolated from a clinical sample and urban rivers in Sao Paulo, Brazil}},
volume = {16},
year = {2019}
}
@article{Fontana2020,
abstract = {Aim: Carbapenemase-resistant Enterobacteriaceae represents a major concern in hospital setting. Materials {\&} methods: The evolutionary history of carbapenem-resistant Klebsiella pneumonia strains was analyzed by core genome multilocus sequence typing and Bayesian phylogenesis by whole genomes sequencing. Results: A great increase carbapenem-resistant K. pneumoniae causing blood stream infection was observed in the years 2015-2016. At multilocus sequence typing (MLST), they were prevalently ST512 and ST101. ST512 were core genome (cg)MLST 53, while ST101 mainly cgMLST453. The minimum-spanning tree, based on cgMLST, showed strains clustering based on the different STs. By Bayesian phylogenetic analysis, maximum clade credibility tree showed that strains were introduced in the year 2005 with the most probable location in the ICU ward. Two outbreaks by ST101 and ST512 strains with Tower T8 as the probable location were evidenced. Conclusion: Molecular epidemiology is a powerful tool to track the way of transmission of resistant bacteria within the hospital setting.},
author = {Fontana, Carla and Angeletti, Silvia and Mirandola, Walter and Cella, Eleonora and Alessia, Lai and Zehender, Gianguglielmo and Favaro, Marco and Leoni, Davide and Rose, Diego Delle and Gherardi, Giovanni and Florio, Lucia De and Salemi, Marco and Andreoni, Massimo and Sarmati, Loredana and Ciccozzi, Massimo},

doi = {10.2217/fmb-2019-0074},
issn = {17460921},
journal = {Future Microbiology},
keywords = {Klebsiella pneumoniae,Lista{_}Filtrada,carabapenemase resistance,nosocomial infection,phylogenetic analysis,whole genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
number = {3},
pages = {203--212},
publisher = {Future Medicine Ltd.},
title = {{Whole genome sequencing of carbapenem-resistant Klebsiella pneumoniae: Evolutionary analysis for outbreak investigation}},
volume = {15},
year = {2020}
}
@article{Fang2016,
abstract = {Pseudomonas azotoformans is a Gram-negative bacterium and infects cereal grains, especially rice. P. azotoformans S4 from soil sample derived from Lijiang, Yunnan Province, China, appeared to be strong inhibitory activity against Fusarium fujikurio, a serious rice fungal pathogen. Here, we present the complete genome of P. azotoformans S4, which consists of 6,859,618bp with a circle chromosome, 5991 coding DNA sequences, 70 tRNA and 19 rRNA. The genomic analysis revealed that 9 candidate gene clusters are involved in the biosynthesis of secondary metabolites.},
author = {Fang, Yang and Wu, Lijuan and Chen, Guoqing and Feng, Guozhong},
doi = {10.1016/j.jbiotec.2016.04.020},
issn = {1873-4863},
journal = {Journal of biotechnology},
keywords = {Gene cluster,Genome sequence,Pseudomonas azotoformans,Secondary metabolism},
month = {jun},
pages = {25--26},
pmid = {27080451},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of Pseudomonas azotoformans S4, a potential biocontrol bacterium.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/27080451 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4869038},
volume = {227},
year = {2016}
}
@article{Ding2020,
author = {Ding, Long-Jun and Zhou, Xin-Yuan and Zhu, Yong-Guan},
doi = {10.1016/j.envint.2020.105702},
issn = {01604120},
journal = {Environment International},
month = {jun},
pages = {105702},
title = {{Microbiome and antibiotic resistome in household dust from Beijing, China}},
url = {https://linkinghub.elsevier.com/retrieve/pii/S0160412020306760},

volume = {139},
year = {2020}
}
@article{DeCarvalho2020,
abstract = {CTX-M-type extended-spectrum β-lactamase (ESBL)-producing Escherichia coli clones have been increasingly reported worldwide. In this regard, although discussions of transmission routes of these bacteria are in evidence, molecular data are lacking to elucidate the epidemiological impacts of ESBL producers in wild animals. In this study, we have screened 90 wild animals living in a surrounding area of S{\~{a}}o Paulo, the largest metropolitan city in South America, to monitor the presence of multidrug-resistant (MDR) Gram-negative bacteria. Using a genomic approach, we have analyzed eight ceftriaxone-resistant E. coli. Resistome analyses revealed that all E. coli strains carried blaCTX-M- type genes, prevalent in human infections, besides other clinically relevant resistance genes to aminoglycosides, β-lactams, phenicols, tetracyclines, sulfonamides, trimethoprim, fosfomycin, and quinolones. Additionally, E. coli strains belonged to international sequence types (STs) ST38, ST58, ST212, ST744, ST1158 and ST1251, and carried several virulence-associated genes. Our findings suggest spread and adaptation of international clones of CTX-M-producing E. coli beyond urban settings, including wildlife from shared environments.},
author = {de Carvalho, Marcelo P N and Fernandes, Miriam R and Sellera, F{\'{a}}bio P and Lopes, Ralf and Monte, Daniel F and Hipp{\'{o}}lito, Al{\'{i}}cia G and Milanelo, Liliane and Raso, T{\^{a}}nia F and Lincopan, Nilton},
doi = {10.1111/tbed.13558},
issn = {1865-1682},
journal = {Transboundary and emerging diseases},
keywords = {ESBL,Enterobacterales,MDR bacteria,resistome,wildlife},
month = {apr},
pmid = {32239649},
title = {{International clones of extended-spectrum-β-lactamase (CTX-M)-producing Escherichia coli in peri-urban wild animals, Brazil.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32239649},
year = {2020}
}
@article{Danda2020,
abstract = {INTRODUCTION: Alkaptonuria (AKU) is a rare metabolic disease. The global incidence is 1:100,000 to 1:250,000. However, identification of a founder mutation in a gypsy population from India prompted us to study the prevalence of AKU in this population and to do molecular typing in referred cases of AKU from the rest of India., OBJECTIVE: To determine the prevalence of AKU in the gypsy population predominantly residing in the seven districts of Tamil Nadu. To determine the molecular characteristic of AKU cases referred to our clinic from various parts of India., METHOD: Urine spot test to detect homogentisic acid followed by quantitative estimation using high-performance liquid chromatography in 499 participants from the gypsy population and confirming the founder mutation in those with high levels by sequencing. Sequence the homogentisate 1,2-dioxygenase (HGD) gene to identify mutations and variants in 29 AKU non-gypsy cases., RESULTS: The founder mutation was detected in homozygous state in 41/499 AKU-affected individuals of the gypsy community giving a high prevalence of 8.4{\%}. Low back pain, knee

pain, and eye and ear pigmentation were the most common symptoms and signs respectively. The commonest mutation identified in the non-gypsy AKU cases was p.Ala122Val., CONCLUSION: High prevalence of AKU in the inbred gypsy population at 8.4{\%} was detected confirming the founder effect. Urine screening provided a cost-effective method to detect the disease early. Mutation spectrum is varied in the rest of the Indian population. This study identified maximum number of mutations in exon 6 of the HGD gene.Key Points* High prevalence (8.4{\%}) of alkaptonuria (AKU) in the gypsy population due to founder mutation in the HGD gene.* Inbreeding exemplifies the founder effects of this rare genetic disorder.* Urinary screening is a cost-effective method in this community for early detection of AKU and intervention.* The mutation spectrum causing AKU is diverse in the rest of the Indian population.},
author = {Danda, Sumita and Mohan, Sony and Devaraj, Prabavathi and Dutta, Atanu K. and Nampoothiri, Sheela and Yesodharan, Dhanya and Phadke, Shubha R. and Jalan, Anil B. and Thangaraj, K. and Verma, Ishwar Chandra and Danda, Debashish and Jebaraj, Isaac},
doi = {10.1007/s10067-020-05020-8},
issn = {0770-3198},
journal = {Clinical Rheumatology},
month = {mar},
publisher = {Springer Science and Business Media LLC},
title = {{Founder effects of the homogentisate 1,2-dioxygenase (HGD) gene in a gypsy population and mutation spectrum in the gene among alkaptonuria patients from India}},
year = {2020}
}
@article{DaSilvaDuarte2020,
author = {{da Silva Duarte}, Vin{\'{i}}cius and Treu, Laura and Sartori, Cristina and Dias, Roberto Sousa and {da Silva Paes}, Isabela and Vieira, Marcella Silva and Santana, Gabriele Rocha and Marcondes, Marcos In{\'{a}}cio and Giacomini, Alessio and Corich, Viviana and Campanaro, Stefano and da Silva, Cynthia Canedo and de Paula, S{\'{e}}rgio Oliveira},
doi = {10.1038/s41598-020-62499-6},
issn = {20452322},
journal = {Scientific Reports},
month = {dec},
number = {1},
publisher = {Springer Science and Business Media LLC},
title = {{Milk microbial composition of Brazilian dairy cows entering the dry period and genomic comparison between Staphylococcus aureus strains susceptible to the bacteriophage vB{_}SauM-UFV{_}DC4}},
volume = {10},
year = {2020}
}
@misc{Chatzopoulou2018,
abstract = {Objectives: The emergence and spread of transferable β-lactamases among Enterobacteriaceae is a major problem both to human and veterinary medicine and is an important contributing factor to the development of multidrug-resistant bacterial isolates. In the present study, whole-genome sequencing of a Klebsiella pneumoniae isolate (LKP817909) resistant to first- and second-generation cephalosporins and non-susceptible to fluoroquinolones, isolated from a urine sample of a

hospitalised dog, was performed. Methods: Genome sequencing was performed on an Illumina MiniSeq Sequencing System. Multilocus sequence typing (MLST) was performed using a BLAST-based approach, whereas antimicrobial resistance genes and plasmid replicons were identified by ResFinder and PlasmidFinder, respectively. The Rapid Annotation using Subsystem Technology (RAST) server v.2.0 was used for genome annotation. Results: Data analyses revealed the complete resistome of isolate LKP817909, which included the cefotaximase-M{\"{u}}nchen-11 (CTX-M-11) extended-spectrum β-lactamase together with 11 other resistance genes. Ten resistance genes were located on plasmids and two on the chromosome. Conclusions: To the best of our knowledge, this is the first detection of a CTX-M-11-producing K. pneumoniae isolated from a canine. The whole genome sequence of the isolate has been deposited at GenBank to serve as a future reference.},
author = {Chatzopoulou, Fani and Meletis, Georgios and Polidoro, Giulia and Oikonomidis, Ioannis L. and Dimopoulou, Irene and Mavrovouniotis, Ilias and Anagnostou, Tilemahos L.},
booktitle = {Journal of Global Antimicrobial Resistance},
doi = {10.1016/j.jgar.2018.06.019},
issn = {22137173},
keywords = {CTX-M-11,Canine,Greece,Klebsiella pneumoniae,Lista{_}Filtrada,ST194,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
pages = {126--128},
publisher = {Elsevier Ltd},
title = {{Whole-genome sequencing of a CTX-M-11-encoding and quinolone-non-susceptible Klebsiella pneumoniae ST194 isolate from a hospitalised dog in Greece}},
volume = {14},
year = {2018}
}
@article{Charifson2019,
author = {Charifson, Mia A and Trumble, Benjamin C},
doi = {10.1093/EMPH},
journal = {Evolution, Medicine, and Public Health},
keywords = {mismatch,polycystic ovary syndrome},
number = {1},
pages = {50--63},
publisher = {Oxford Academic},
title = {{Imported from http://paulturke.com/research.html}},
volume = {2019},
year = {2019}
}
@article{Campbell2020,
abstract = {The gut microbiome can vary across differences in host lifestyle, geography, and host species. By comparing closely related host species across varying lifestyles and geography, we can evaluate the relative contributions of these factors in structuring the composition and functions of the microbiome. Here we show that the gut microbial taxa, microbial gene family composition, and resistomes of great apes and humans are more related by host lifestyle than geography. We show that captive chimpanzees and gorillas are enriched for microbial genera commonly found in non-Westernized humans. Captive ape microbiomes also

had up to {\~{}}34-fold higher abundance and up to {\~{}}5-fold higher richness of all antibiotic resistance genes compared with wild apes. Through functional metagenomics, we identified a number of novel antibiotic resistance genes, including a gene conferring resistance to colistin, an antibiotic of last resort. Finally, by comparing our study cohorts to human and ape gut microbiomes from a diverse range of environments and lifestyles, we find that the influence of host lifestyle is robust to various geographic locations.},
author = {Campbell, Tayte P. and Sun, Xiaoqing and Patel, Vishal H. and Sanz, Crickette and Morgan, David and Dantas, Gautam},
doi = {10.1038/s41396-020-0634-2},
issn = {1751-7362},
journal = {The ISME Journal},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
publisher = {Springer Science and Business Media LLC},
title = {{The microbiome and resistome of chimpanzees, gorillas, and humans across host lifestyle and geography}},
year = {2020}
}
@article{Buedts2020,
author = {Buedts, Lieselot and Smits, Sanne and Ameye, Genevi{\`{e}}ve and Lehnert, Stefan and Ding, Jia and Delforge, Michel and Vermeesch, Joris and Boeckx, Nancy and Tousseyn, Thomas and Michaux, Lucienne and Vandenberghe, Peter and Dewaele, Barbara},
doi = {10.1002/gcc.22848},
issn = {10452257},
journal = {Genes, Chromosomes and Cancer},
month = {apr},
title = {{Ultra-low depth sequencing of plasma cell DNA for the detection of copy number aberrations in multiple myeloma}},
url = {http://doi.wiley.com/10.1002/gcc.22848},
year = {2020}
}
@article{Belda2016,
abstract = {By the time the complete genome sequence of the soil bacterium Pseudomonas putida KT2440 was published in 2002 (Nelson et al.,) this bacterium was considered a potential agent for environmental bioremediation of industrial waste and a good colonizer of the rhizosphere. However, neither the annotation tools available at that time nor the scarcely available omics data—let alone metabolic modeling and other nowadays common systems biology approaches—allowed them to anticipate the astonishing capacities that are encoded in the genetic complement of this unique microorganism. In this work we have adopted a suite of state-of-the-art genomic analysis tools to revisit the functional and metabolic information encoded in the chromosomal sequence of strain KT2440. We identified 242 new protein-coding genes and re-annotated the functions of 1548 genes, which are linked to almost 4900 PubMed references. Catabolic pathways for 92 compounds (carbon, nitrogen and phosphorus sources) that could not be accommodated by the previously constructed metabolic models were also predicted. The resulting examination not only accounts for some of the known stress tolerance traits known in P. putida but also recognizes the capacity of this

bacterium to perform difficult redox reactions, thereby multiplying its value as a platform microorganism for industrial biotechnology.},
author = {Belda, Eugeni and van Heck, Ruben G.A. and {Jos{\'{e}} Lopez-Sanchez}, Maria and Cruveiller, St{\'{e}}phane and Barbe, Val{\'{e}}rie and Fraser, Claire and Klenk, Hans Peter and Petersen, J{\"{o}}rn and Morgat, Anne and Nikel, Pablo I. and Vallenet, David and Rouy, Zo{\'{e}} and Sekowska, Agnieszka and {Martins dos Santos}, Vitor A.P. and de Lorenzo, V{\'{i}}ctor and Danchin, Antoine and M{\'{e}}digue, Claudine},
doi = {10.1111/1462-2920.13230},
issn = {14622920},
journal = {Environmental Microbiology},
month = {oct},
number = {10},
pages = {3403--3424},
publisher = {Blackwell Publishing Ltd},
title = {{The revisited genome of Pseudomonas putida KT2440 enlightens its value as a robust metabolic chassis}},
volume = {18},
year = {2016}
}
@article{Bardet2018,
abstract = {Culturomics is a new postgenomics field that explores the microbial diversity of the human gut coupled with taxono-genomic strategy. Culturomics, and the microbiome science more generally, are anticipated to transform global health diagnostics and inform the ways in which gut microbial diversity contributes to human health and disease, and by extension, to personalized medicine. Using culturomics, we report in this study the description of strain CB1T (=CSUR P1334=DSM 29075), a new species isolated from a stool specimen from a 37-year-old Brazilian woman. This description includes phenotypic characteristics and complete genome sequence and annotation. Strain CB1T is a gram-negative aerobic and motile bacillus, exhibits neither catalase nor oxidase activities, and presents a 98.3{\%} 16S rRNA sequence similarity with Pseudomonas putida. The 4,723,534 bp long genome contains 4239 protein-coding genes and 74 RNA genes, including 15 rRNA genes (5 16S rRNA, 4 23S rRNA, and 6 5S rRNA) and 59 tRNA genes. Strain CB1T was named Pseudomonas massiliensis sp. nov. and classified into the family Pseudomonadaceae. This study demonstrates the usefulness of microbial culturomics in exploration of human microbiota in diverse geographies and offers new promise for incorporating new omics technologies for innovation in diagnostic medicine and global health.},
author = {Bardet, Lucie and Cimmino, Teresa and Buffet, Cl{\'{e}}mence and Michelle, Caroline and Rathored, Jaishriram and Tandina, Fatalmoudou and Lagier, Jean-Christophe and Khelaifia, Saber and Abrah{\~{a}}o, J{\^{o}}natas and Raoult, Didier and Rolain, Jean-Marc},
doi = {10.1089/omi.2017.0027},
issn = {1557-8100},
journal = {Omics : a journal of integrative biology},
keywords = {Pseudomonas massiliensis,global health,microbial culturomics,system diagnostics,taxono-genomics},
month = {feb},
number = {2},
pages = {164--175},
pmid = {28650741},

publisher = {Mary Ann Liebert Inc.},
title = {{Microbial Culturomics Application for Global Health: Noncontiguous Finished Genome Sequence and Description of Pseudomonas massiliensis Strain CB-1T sp. nov. in Brazil.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28650741},
volume = {22},
year = {2018}
}
@article{Araya-Flores2020,
abstract = {Lipoic acid (LA) and its reduced form (dihydrolipoic acid, DHLA) have unique antioxidant properties among such molecules. Moreover, after a process termed lipoylation, LA is an essential prosthetic group covalently-attached to several key multi-subunit enzymatic complexes involved in primary metabolism, including E2 subunits of pyruvate dehydrogenase (PDH). The metabolic pathway of lipoylation has been extensively studied in Escherichia coli and Arabidopsis thaliana in which protein modification occurs via two routes: de novo synthesis and salvage. Common to both pathways, lipoyl synthase (LIP1 in plants, LipA in bacteria, EC 2.8.1.8) inserts sulphur atoms into the molecule in a final, activating step. However, despite the detection of LA and DHLA in other plant species, including tomato (Solanum lycopersicum), no plant LIP1s have been characterised to date from species other than Arabidopsis. In this work, we present the identification and characterisation of two LIPs from tomato, SlLIP1 and SlLIP1p. Consistent with in silico data, both are widely-expressed, particularly in reproductive organs. In line with bioinformatic predictions, we determine that yellow fluorescent protein tagged versions of SlLIP1 and SlLIP1p are mitochondrially- and plastidially-localised, respectively. Both possess the molecular hallmarks and domains of well-characterised bacterial LipAs. When heterologously-expressed in an E. coli lipA mutant, both are capable of complementing specific growth phenotypes and increasing lipoylation levels of E2 subunits of PDH in vivo, demonstrating that they do indeed function as lipoyl synthases.},
author = {Araya-Flores, Jorge and Miranda, Sim{\'{o}}n and Covarrubias, Mar{\'{i}}a Paz and Stange, Claudia and Handford, Michael},
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issn = {1873-2690},
journal = {Plant physiology and biochemistry : PPB},
keywords = {Heterologous complementation,LIP1,Lipoic acid,Lipoyl synthase,Lipoylation,Pyruvate dehydrogenase,Solanum lycopersicum},
month = {mar},
pages = {264--270},
pmid = {32244096},
publisher = {Elsevier BV},
title = {{Solanum lycopersicum (tomato) possesses mitochondrial and plastidial lipoyl synthases capable of increasing lipoylation levels when expressed in bacteria.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32244096},
volume = {151},
year = {2020}
}
@article{,
doi = {10.1093/FEMSLE/FNV045},
title = {{(No Title)}}

}
@article{,
pmid = {24695768},
title = {{(No Title)}}
}
@article{,
pmid = {25449545},
title = {{(No Title)}}
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@article{,
pmid = {24161918},
title = {{(No Title)}}
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@article{,
pmid = {28551853},
title = {{(No Title)}}
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@article{,
pmid = {22354942},
title = {{(No Title)}}
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@article{,
pmid = {26913973},
title = {{(No Title)}}
}
@misc{,
title = {{Complete genome sequence caterium pseudomonas - PubMed - NCBI}},
url = {https://www.ncbi.nlm.nih.gov/pubmed/?term=Complete+genome+sequence+caterium+pseudomonas https://www.ncbi.nlm.nih.gov/pubmed},
urldate = {2020-04-09}
}
@article{Castillo2019,
abstract = {Klebsiella pneumoniae is a commonly antibiotic-resistant human pathogen. This report describes the complete genome sequence and important features of Sin4, a siphophage infecting carbapenemase-producing K. pneumoniae . By its genome size, predicted packaging mechanism, protein similarity, and classification given to its closest relatives, Sin4 was determined to be a T1-like phage.},
author = {Castillo, Micah and Tran, Rainie and Newkirk, Heather and Liu, Mei and Gill, Jason J. and Ramsey, Jolene},
doi = {10.1128/mra.01048-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Castillo et al. - 2019 - Complete Genome Sequence of Sin4, a Siphophage Infecting Carbapenemase-Producing Klebsiella pneumoniae.pdf:pdf;::},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {,Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {39},
pmid = {31558644},

publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Sin4, a Siphophage Infecting Carbapenemase-Producing Klebsiella pneumoniae}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/31558644 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6763659},
volume = {8},
year = {2019}
}
@article{Zhou2017,
abstract = {At present, the most used methods for Klebsiella pneumoniae subtyping are multilocus sequence typing (MLST) and pulsed-field gel electrophoresis (PFGE). However, the discriminatory power of MLST could not meet the need for distinguishing outbreak and non-outbreak isolates and the PFGE is time-consuming and labor-intensive. A core genome multilocus sequence typing (cgMLST) scheme for whole-genome sequence-based typing of K. pneumoniae was developed for solving the disadvantages of these traditional molecular subtyping methods. Firstly, we used the complete genome of K. pneumoniae strain HKUOPLC as the reference genome and 907 genomes of K. pneumoniae download from NCBI database as original genome dataset to determine cgMLST target genes. A total of 1,143 genes were retained as cgMLST target genes. Secondly, we used 26 K. pneumoniae strains from a nosocomial infection outbreak to evaluate the cgMLST scheme. cgMLST enabled clustering of outbreak strains with {\textless}10 alleles difference and unambiguous separation from unrelated outgroup strains. Moreover, cgMLST revealed that there may be several sub-clones of epidemic ST11 clone. In conclusion, the novel cgMLST scheme not only showed higher discriminatory power compared with PFGE and MLST in outbreak investigations but also showed ability to reveal more population structure characteristics than MLST.},
author = {Zhou, Haijian and Liu, Wenbing and Qin, Tian and Liu, Chen and Ren, Hongyu},
doi = {10.3389/fmicb.2017.00371},
file = {::},
issn = {1664302X},
journal = {Frontiers in Microbiology},
keywords = {Core genome multilocus sequence typing,Klebsiella pneumoniae,Outbreak investigation,Population structure analysis,Whole-genome sequence},
month = {mar},
number = {MAR},
publisher = {Frontiers Research Foundation},
title = {{Defining and evaluating a core genome multilocus sequence typing scheme for whole-genome sequence-based typing of Klebsiella pneumoniae}},
volume = {8},
year = {2017}
}
@article{Xing2017,
abstract = {Klebsiella pneumoniae is the most common clinically important opportunistic bacterial pathogen and its infection is often iatrogenic. Its drug resistance poses a grave threat to public health. The genomic data reported here comprise an important resource for research on phage therapy in the control of drug-resistant bacteria.},

author = {Xing, Shaozhen and Pan, Xiangchun and Sun, Qiang and Pei, Guangqian and An, Xiaoping and Mi, Zhiqiang and Huang, Yong and Zhao, Baohua and Tong, Yigang},
doi = {10.1128/genomeA.00055-17},
file = {::},
issn = {2169-8287},
journal = {Genome announcements},
month = {may},
number = {19},
pmid = {28495757},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of a Novel Multidrug-Resistant Klebsiella pneumoniae Phage, vB{_}Kpn{_}IME260.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28495757 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5427192},
volume = {5},
year = {2017}
}
@article{Wu2017,
abstract = {Pseudomonas stutzeri 273 is a marine bacterium producing exopolysaccharide 273 (EPS273) with high anti-biofilm activity against P. aeruginosa PAO1. Here, the complete genome of P.stutzeri 273 was sequenced and the genome contained a circular 5.03 Mb chromosome. With extensive analysis of the genome, a genetic locus containing 18 genes was predicted to be involved in the biosynthesis of EPS273. In order to confirm this prediction, two adjacent genes (eps273-H and eps273-I) encoding glycosyltransferases and one gene (eps273-O) encoding tyrosine protein kinase within the genetic locus were deleted and biosynthesis of EPS273 was checked in parallel. The molecular weight profile of EPS purified from the mutant Δeps273-HI was obviously different from that purified from wild-type P.stutzeri 273, while the corresponding EPS was hardly detected from the mutant Δeps273-O, which indicated the involvement of the proposed 18-gene cluster in the biosynthesis of EPS273. Moreover, the mutant Δeps273-HI had the biofilm formed earlier compared with the wild type, and the mutant Δeps273-O almost completely lost the ability of biofilm formation. Therefore, EPS273 might facilitate the biofilm formation for its producing strain P.stutzeri 273 while inhibiting the biofilm formation of P. aeruginosa PAO1. This study can contribute to better understanding of the biosynthesis of EPS273 and disclose the biological function of EPS273 for its producing strain P.stutzeri 273.},
author = {Wu, Shimei and Zheng, Rikuan and Sha, Zhenxia and Sun, Chaomin},
doi = {10.3390/md15070218},
file = {::},
issn = {1660-3397},
journal = {Marine drugs},
keywords = {Lista{_}Filtrada,Pseudomonas stutzeri,biofilm,biosynthesis,exopolysaccharide,genome},
mendeley-tags = {Lista{_}Filtrada},
month = {jul},
number = {7},
pmid = {28698510},
publisher = {MDPI AG},

title = {{Genome Sequence of Pseudomonas stutzeri 273 and Identification of the Exopolysaccharide EPS273 Biosynthesis Locus.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28698510 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5532660},
volume = {15},
year = {2017}
}
@article{Wick2017,
abstract = {Illumina sequencing platforms have enabled widespread bacterial whole genome sequencing. While Illumina data is appropriate for many analyses, its short read length limits its ability to resolve genomic structure. This has major implications for tracking the spread of mobile genetic elements, including those which carry antimicrobial resistance determinants. Fully resolving a bacterial genome requires long-read sequencing such as those generated by Oxford Nanopore Technologies (ONT) platforms. Here we describe our use of the ONT MinION to sequence 12 isolates of Klebsiella pneumoniae on a single flow cell. We assembled each genome using a combination of ONT reads and previously available Illumina reads, and little to no manual intervention was needed to achieve fully resolved assemblies using the Unicycler hybrid assembler. Assembling only ONT reads with Canu was less effective, resulting in fewer resolved genomes and higher error rates even following error correction with Nanopolish. We demonstrate that multiplexed ONT sequencing is a valuable tool for high-throughput bacterial genome finishing. Specifically, we advocate the use of Illumina sequencing as a first analysis step, followed by ONT reads as needed to resolve genomic structure.},
author = {Wick, Ryan R. and Judd, Louise M. and Gorrie, Claire L. and Holt, Kathryn E.},
doi = {10.1099/mgen.0.000132},
file = {::},
issn = {20575858},
journal = {Microbial Genomics},
keywords = {Genome assembly,Hybrid assembly,Klebsiella pneumoniae,Long-read sequencing,Multiplex sequencing,Oxford nanopore},
month = {oct},
number = {10},
pmid = {29177090},
publisher = {Microbiology Society},
title = {{Completing bacterial genome assemblies with multiplex MinION sequencing}},
volume = {3},
year = {2017}
}
@article{Wang2018,
abstract = {Hypervirulent K. pneumoniae variants (hvKP) have been increasingly reported worldwide, causing metastasis of severe infections such as liver abscesses and bacteremia. The capsular serotype K2 hvKP strains show diverse multi-locus sequence types (MLSTs), but with limited genetics and virulence information. In this study, we report a hypermucoviscous K. pneumoniae strain, RJF293, isolated from a human bloodstream sample in a Chinese hospital. It caused a metastatic infection and fatal septic shock in a critical patient. The microbiological features and genetic background were investigated with

multiple approaches. The Strain RJF293 was determined to be multilocis sequence type (ST) 374 and serotype K2, displayed a median lethal dose (LD50) of 1.5 × 102 CFU in BALB/c mice and was as virulent as the ST23 K1 serotype hvKP strain NTUH-K2044 in a mouse lethality assay. Whole genome sequencing revealed that the RJF293 genome codes for 32 putative virulence factors and exhibits a unique presence/absence pattern in comparison to the other 105 completely sequenced K. pneumoniae genomes. Whole genome SNP-based phylogenetic analysis revealed that strain RJF293 formed a single clade, distant from those containing either ST66 or ST86 hvKP. Compared to the other sequenced hvKP chromosomes, RJF293 contains several strain variable regions, including one prophage, one ICEKp1 family integrative and conjugative element and six large genomic islands. The sequencing of the first complete genome of an ST374 K2 hvKP clinical strain should reinforce our understanding of the epidemiology and virulence mechanisms of this bloodstream infection-causing hvKP with clinical significance.},
author = {Wang, Xiaoli and Xie, Yingzhou and Li, Gang and Liu, Jialin and Li, Xiaobin and Tian, Lijun and Sun, Jingyong and Ou, Hong Yu and Qu, Hongping},
doi = {10.1080/21505594.2017.1421894},
file = {::},
issn = {21505608},
journal = {Virulence},
keywords = {Bloodstream infection,Capsular serotype K2,Comparative genomic analysis,Hypervirulent,Klebsiella pneumoniae,ST374},
month = {jan},
number = {1},
pages = {510--521},
publisher = {Taylor and Francis Inc.},
title = {{Whole-Genome-Sequencing characterization of bloodstream infection-causing hypervirulent Klebsiella pneumoniae of capsular serotype K2 and ST374}},
volume = {9},
year = {2018}
}
@article{Tran2019,
abstract = { Klebsiella pneumoniae infection is a serious concern in hospital settings due to the continuing emergence of multidrug-resistant strains. The study of K. pneumoniae phages may help the development of new treatment strategies. Here, the complete genome sequence of K. pneumoniae phage Patroon, a T3/T7-like phage, is presented. },
author = {Tran, Rainie and Kongari, Rohit and Lessor, Lauren and Gill, Jason J. and Liu, Mei},
doi = {10.1128/mra.00461-19},
file = {::},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
month = {may},
number = {21},
publisher = {American Society for Microbiology},
title = {{ Complete Genome Sequence of Klebsiella pneumoniae Podophage Patroon }},
volume = {8},
year = {2019}

}
@article{Sheppard2016,
abstract = {Carbapenem resistance in Klebsiella pneumoniae, frequently conferred by the blaKPC gene, is a major public health threat. We sequenced a blaKPC-containing strain of K. pneumoniae belonging to the emergent lineage ST941, in order to better understand the evolution of blaKPC within this species.},
author = {Sheppard, Anna E and Stoesser, Nicole and Sebra, Robert and Kasarskis, Andrew and Deikus, Gintaras and Anson, Luke and Walker, A Sarah and Peto, Tim E and Crook, Derrick W and Mathers, Amy J},
doi = {10.1128/genomeA.01649-15},
file = {::},
issn = {2169-8287},
journal = {Genome announcements},
month = {jan},
number = {1},
pmid = {26823590},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of KPC-Producing Klebsiella pneumoniae Strain CAV1193.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26823590 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4732343},
volume = {4},
year = {2016}
}
@article{Sekizuka2018,
abstract = { Antimicrobial resistance genes (ARGs) and the bacteria that harbor them are widely distributed in the environment, especially in surface water, sewage treatment plant effluent, soil, and animal waste. In this study, we isolated a KPC-2-producing Klebsiella pneumoniae strain (GSU10-3) from a sampling site in Tokyo Bay, Japan, near a wastewater treatment plant (WWTP) and determined its complete genome sequence. Strain GSU10-3 is resistant to most β-lactam antibiotics and other antimicrobial agents (quinolones and aminoglycosides). This strain is classified as sequence type 11 (ST11), and a core genome phylogenetic analysis indicated that strain GSU10-3 is closely related to KPC-2-positive Chinese clinical isolates from 2011 to 2017 and is clearly distinct from strains isolated from the European Union (EU), United States, and other Asian countries. Strain GSU10-3 harbors four plasmids, including a bla KPC-2 -positive plasmid, pGSU10-3-3 (66.2 kb), which is smaller than other bla KPC-2 -positive plasmids and notably carries dual replicons (IncFII [pHN7A8] and IncN). Such downsizing and the presence of dual replicons may promote its maintenance and stable replication, contributing to its broad host range with low fitness costs. A second plasmid, pGSU10-3-1 (159.0 kb), an IncA/C2 replicon, carries a class 1 integron (containing intI1 , dfrA12 , aadA2 , qacEΔ1 , and sul1) with a high degree of similarity to a broad-host-range plasmid present in the family Enterobacteriaceae . The plasmid pGSU10-3-2 (134.8 kb), an IncFII(K) replicon, carries the IS 26 -mediated ARGs [aac (6') Ib-cr , bla OXA-1 , catB4 (truncated), and aac (3) -IId], tet (A), and a copper/arsenate resistance locus. GSU10-3 is the first nonclinical KPC-2-producing environmental Enterobacteriaceae isolate from Japan for which the whole genome has been sequenced. IMPORTANCE We isolated and determined the complete genome sequence of a KPC-2-producing K.

pneumoniae strain from a sampling site in Tokyo Bay, Japan, near a wastewater treatment plant (WWTP). In Japan, the KPC type has been very rarely detected, while IMP is the most predominant type of carbapenemase in clinical carbapenemase-producing Enterobacteriaceae (CPE) isolates. Although laboratory testing thus far suggested that Japan may be virtually free of KPC-producing Enterobacteriaceae , we have detected it from effluent from a WWTP. Antimicrobial resistance (AMR) monitoring of WWTP effluent may contribute to the early detection of future AMR bacterial dissemination in clinical settings and communities; indeed, it will help illuminate the whole picture in which environmental contamination through WWTP effluent plays a part. },
author = {Sekizuka, Tsuyoshi and Yatsu, Koji and Inamine, Yuba and Segawa, Takaya and Nishio, Miho and Kishi, Norimi and Kuroda, Makoto},
doi = {10.1128/msphere.00314-18},
file = {::},
issn = {2379-5042},
journal = {mSphere},
month = {sep},
number = {5},
publisher = {American Society for Microbiology},
title = {{ Complete Genome Sequence of a bla KPC-2 -Positive Klebsiella pneumoniae Strain Isolated from the Effluent of an Urban Sewage Treatment Plant in Japan }},
volume = {3},
year = {2018}
}
@article{Provasek2015,
abstract = {Klebsiella pneumoniae is a leading cause of nosocomial infections in the United States. Due to the emergence of multidrugresistant strains, phages targeting K. pneumoniae may be a useful alternative against this pathogen. Here, we announce the complete genome of K. pneumoniae pseudo-T-even myophage Matisse and describe its features.},
author = {Provasek, Vincent E. and Lessor, Lauren E. and Cahill, Jesse L. and Rasche, Eric S. and {Kuty Everett}, Gabriel F.},
doi = {10.1128/genomeA.01136-15},
file = {::},
issn = {21698287},
journal = {Genome Announcements},
number = {5},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of carbapenemase-producing Klebsiella pneumoniae myophage Matisse}},
volume = {3},
year = {2015}
}
@article{Nowicki2017,
abstract = {In this paper, we describe two independent isolates of a new member of the subfamily Autographivirinae, Pseudomonas phage KNP. The type strain (KNP) has a linear, 40,491-bp-long genome with GC content of 57.3{\%}, and 50 coding DNA sequences (CDSs). The genome of the second strain (WRT) contains one CDS less, encodes a significantly different tail fiber protein and is shorter (40,214 bp; GC content, 57.4{\%}). Phylogenetic analysis indicates that both KNP and WRT belong to the genus

T7virus. Together with genetically similar Pseudomonas phages (gh-1, phiPSA2, phiPsa17, PPPL-1, shl2, phi15, PPpW-4, UNO-SLW4, phiIBB-PF7A, Pf-10, and Phi-S1), they form a divergent yet coherent group that stands apart from the T7-like viruses (sensu lato). Analysis of the diversity of this group and its relatedness to other members of the subfamily Autographivirinae led us to the conclusion that this group might be considered as a candidate for a new genus.},
author = {Nowicki, Grzegorz and Walkowiak-Nowicka, Karolina and Zemleduch-Barylska, Agata and Mleczko, Anna and Fr{\c{a}}ckowiak, Patryk and Nowaczyk, Natalia and Kozdrowska, Emilia and Barylski, Jakub},
doi = {10.1007/s00705-017-3419-9},
file = {::},
issn = {03048608},
journal = {Archives of Virology},
month = {sep},
number = {9},
pages = {2907--2911},
publisher = {Springer-Verlag Wien},
title = {{Complete genome sequences of two novel autographiviruses infecting a bacterium from the Pseudomonas fluorescens group}},
volume = {162},
year = {2017}
}
@article{Nguyen2019,
abstract = {May is a newly isolated myophage that infects multidrug-resistant strains of Klebsiella pneumoniae, a pathogen that is associated with antibiotic-resistant infections in humans. The genome of May has been shown to be similar to that of phage Vi01.},
author = {Nguyen, Katherine T and Bonasera, Rachele and Benson, Garret and Hernandez-Morales, Adriana C and Gill, Jason J and Liu, Mei},
doi = {10.1128/MRA.00252-19},
file = {::},
issn = {2576-098X},
journal = {Microbiology resource announcements},
month = {may},
number = {19},
pmid = {31072899},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Myophage May.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/31072899 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6509524},
volume = {8},
year = {2019}
}
@article{Min2019,
abstract = { Klebsiella pneumoniae is an opportunistic pathogen associated with hospital-acquired infections. This report describes the complete genome of the K. pneumoniae myophage Mulock, which appears to be a temperate myophage distantly related to other Klebsiella myophages in morphogenesis genes and is partially syntenic with the canonical Escherichia phage lambda in genes encoding lambda-like functions. },
author = {Min, Lorna and Lessor, Lauren and O'Leary, Chandler and Bonasera, Rachele and Gill, Jason and Liu, Mei},
doi = {10.1128/mra.01338-19},

file = {::},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
month = {nov},
number = {46},
publisher = {American Society for Microbiology},
title = {{ Complete Genome Sequence of Klebsiella pneumoniae Myophage Mulock }},
volume = {8},
year = {2019}
}
@article{Martinez2019,
abstract = { Klebsiella pneumoniae is a multidrug-resistant bacterium causing many severe hospital-acquired infections. Here, we describe siphophage Sweeny that infects K. pneumoniae . Of its 78 predicted protein-encoding genes, a functional assignment was given to 36 of them. Sweeny is most closely related to T1-like phages at the protein level. },
author = {Martinez, Nicholas and Williams, Eric and Newkirk, Heather and Liu, Mei and Gill, Jason J. and Ramsey, Jolene},
doi = {10.1128/mra.01047-19},
file = {::},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
month = {sep},
number = {39},
publisher = {American Society for Microbiology},
title = {{ Complete Genome Sequence of Klebsiella pneumoniae Phage Sweeny }},
volume = {8},
year = {2019}
}
@article{Lu2015,
abstract = {We report here the complete genome sequence of Klebsiella pneumoniae strain HKUOPLC, isolated from a giant panda fecal sample collected from Ocean Park, Hong Kong. The complete genome of this bacterium may contribute to the discovery of efficient cellulose-degrading pathways.},
author = {Lu, Matthew Guan-Xi and Jiang, Jingwei and Liu, Lirui and Ma, Angel Po-Yee and Leung, Frederick Chi-Ching},
doi = {10.1128/genomeA.01318-15},
file = {::},
issn = {2169-8287},
journal = {Genome announcements},
month = {nov},
number = {6},
pmid = {26564041},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Strain HKUOPLC, a Cellulose-Degrading Bacterium Isolated from Giant Panda Feces.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26564041 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4972777},
volume = {3},
year = {2015}

}
@article{Lu2015a,
abstract = {We report here the complete genome sequence of Klebsiella variicola strain HKUOPLA, isolated from a giant panda feces sample collected from Ocean Park, Hong Kong. The complete genome of this bacterium may contribute toward the discovery of efficient cellulose-degrading pathways.},
author = {Lu, Matthew Guan-Xi and Jiang, Jingwei and Liu, Lirui and Ma, Angel Po-Yee and Leung, Frederick Chi-Ching},
doi = {10.1128/genomeA.01200-15},
file = {::},
issn = {2169-8287},
journal = {Genome announcements},
month = {oct},
number = {5},
pmid = {26472841},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella variicola Strain HKUOPLA, a Cellulose-Degrading Bacterium Isolated from Giant Panda Feces.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26472841 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4611693},
volume = {3},
year = {2015}
}
@article{Lin2015,
abstract = {Klebsiella variicola strain DX120E (=CGMCC 1.14935) is an endophytic nitrogen-fixing bacterium isolated from sugarcane crops grown in Guangxi, China and promotes sugarcane growth. Here we summarize the features of the strain DX120E and describe its complete genome sequence. The genome contains one circular chromosome and two plasmids, and contains 5,718,434 nucleotides with 57.1{\%} GC content, 5,172 protein-coding genes, 25 rRNA genes, 87 tRNA genes, 7 ncRNA genes, 25 pseudo genes, and 2 CRISPR repeats.},
author = {Lin, Li and Wei, Chunyan and Chen, Mingyue and Wang, Hongcheng and Li, Yuanyuan and Yang, Litao and Yang, Litao and An, Qianli},
doi = {10.1186/s40793-015-0004-2},
file = {::},
issn = {19443277},
journal = {Standards in Genomic Sciences},
keywords = {Endophyte,Klebsiella pneumoniae,Klebsiella variicola,Nitrogen fixation,Pathogenicity,Plant growth-promoting bacteria,Sugarcane},
month = {may},
number = {MAY2015},
publisher = {BioMed Central Ltd.},
title = {{Complete genome sequence of endophytic nitrogen-fixing Klebsiella variicola strain DX120E}},
volume = {10},
year = {2015}
}
@article{Kawato2015,
abstract = {Pseudomonas plecoglossicida is a lethal pathogen of ayu (Plecoglossus altivelis) in Japan and is responsible for substantial economic costs to ayu culture. Previously, we demonstrated the efficacy

of phage therapy against P. plecoglossicida infection using two lytic phages (PPpW-3 and PPpW-4) (S. C. Park, I. Shimamura, M. Fukunaga, K. Mori, and T. Nakai, Appl Environ Microbiol 66:1416-1422, 2000, http://dx.doi.org/10.1128/AEM.66.4.1416-1422.2000; S. C. Park and T. Nakai, Dis Aquat Org 53:33-39, 2003, http://dx.doi.org/10.3354/dao053033). In the present study, the complete genome sequences of these therapeutic P. plecoglossicida phages were determined and analyzed for deleterious factors as therapeutic agents. The genome of PPpW-3 (myovirus) consisted of 43,564 bp with a GC content of 61.1{\%} and 66 predicted open reading frames (ORFs). Approximately half of the genes were similar to the genes of the Escherichia coli phage vB{_}EcoM{_}ECO1230-10 (myovirus). The genome of PPpW-4 (podovirus) consisted of 41,386 bp with a GC content of 56.8{\%} and 50 predicted ORFs. More than 70{\%} of the genes were similar to the genes of Pseudomonas fluorescens phage ϕIBB-PF7A and Pseudomonas putida phage ϕ15 (podoviruses). The whole-genome analysis revealed that no known virulence genes were present in PPpW-3 and PPpW-4. An integrase gene was found in PPpW-3, but other factors used for lysogeny were not confirmed. The PCR detection of phage genes in phage-resistant variants provided no evidence of lysogenic activity in PPpW-3 and PPpW-4. We conclude that these two lytic phages qualify as therapeutic agents.},
author = {Kawato, Yasuhiko and Yasuike, Motoshige and Nakamura, Yoji and Shigenobu, Yuya and Fujiwara, Atushi and Sano, Motohiko and Nakai, Toshihiro},
doi = {10.1128/AEM.03038-14},
file = {::},
issn = {10985336},
journal = {Applied and Environmental Microbiology},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {3},
pages = {874--881},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence analysis of two Pseudomonas plecoglossicida phages, potential therapeutic agents}},
volume = {81},
year = {2015}
}
@article{Kalischuk2015,
abstract = {Pectobacterium atrosepticum is a common phytopathogen causing significant economic losses worldwide. To develop a biocontrol strategy for this blackleg pathogen of solanaceous plants, P. atrosepticum bacteriophage Peat1 was isolated and its genome completely sequenced. Interestingly, morphological and sequence analyses of the 45,633-bp genome revealed that phage Peat1 is a member of the family Podoviridae and most closely resembles the Klebsiella pneumoniae bacteriophage KP34. This is the first published complete genome sequence of a phytopathogenic P. atrosepticum bacteriophage, and details provide important information for the development of biocontrol by advancing our understanding of phage-phytopathogen interactions.},
author = {Kalischuk, Melanie and Hachey, John and Kawchuk, Lawrence},
doi = {10.1128/genomeA.00760-15},
file = {::},
issn = {2169-8287},

journal = {Genome announcements},
month = {aug},
number = {4},
pmid = {26272557},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Phytopathogenic Pectobacterium atrosepticum Bacteriophage Peat1.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26272557 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4536668},
volume = {3},
year = {2015}
}
@article{Jiang2014a,
abstract = {Background: The giant panda (Ailuropoda melanoleuca) is an endangered species well-known for ingesting bamboo as a major part of their diet despite the fact that it belongs to order Carnivora. However, the giant panda's draft genome shows no direct evidence of enzymatic genes responsible for cellulose digestion. To explore this phenomenon, we study the giant panda's gut microbiota using genomic approaches in order to better understand their physiological processes as well as any potential microbial cellulose digestion processes. Results: A complete genome of isolated Klebsiella oxytoca HKOPL1 of 5.9 Mb has been successfully sequenced, closed and comprehensively annotated against various databases. Genome comparisons within the Klebsiella genus and K. oxytoca species have also been performed. A total of 5,772 genes were predicted, and among them, 211 potential virulence genes, 35 pathogenicity island-like regions, 1,615 potential horizontal transferring genes, 23 potential antibiotics resistant genes, a potential prophage integrated region, 8 genes in 2,3-Butanediol production pathway and 3 genes in the cellulose degradation pathway could be identified and discussed based on the comparative genomic studies between the complete genome sequence of K. oxytoca HKOPL1 and other Klebsiella strains. A functional study shows that K. oxytoca HKOPL1 can degrade cellulose within 72 hours. Phylogenomic studies indicate that K. oxytoca HKOPL1 is clustered with K. oxytoca strains 1686 and E718. Conclusions: K. oxytoca HKOPL1 is a gram-negative bacterium able to degrade cellulose. We report here the first complete genome sequence of K. oxytoca isolated from giant panda feces. These studies have provided further insight into the role of gut microbiota in giant panda digestive physiology. In addition, K. oxytoca HKOPL1 has the potential for biofuel application in terms of cellulose degradation and potential for the production of 2,3-Butanediol (an important industrial raw material).},
author = {Jiang, Jingwei and Tun, Hein Min and Mauroo, Nathalie France and Ma, Angel Po Yee and Chan, San Yuen and Leung, Frederick C.},
doi = {10.1186/1756-0500-7-827},
file = {::},
issn = {17560500},
journal = {BMC Research Notes},
keywords = {Biofuel,Cellulose degradation,Complete genome sequence,Giant panda,Gut microbiota,Klebsiella oxytoca},
month = {nov},
number = {1},
publisher = {BioMed Central Ltd.},

title = {{Complete genome sequence and comparative genome analysis of Klebsiella oxytoca HKOPL1 isolated from giant panda feces}},
volume = {7},
year = {2014}
}
@article{Gutierrez-Barranquero2017,
abstract = {Background: The pPT23A family of plasmids appears to be indigenous to the plant pathogen Pseudomonas syringae and these plasmids are widely distributed and widely transferred among pathovars of P. syringae and related species. pPT23A-family plasmids (PFPs) are sources of accessory genes for their hosts that can include genes important for virulence and epiphytic colonization of plant leaf surfaces. The occurrence of repeated sequences including duplicated insertion sequences on PFPs has made obtaining closed plasmid genome sequences difficult. Therefore, our objective was to obtain complete genome sequences from PFPs from divergent P. syringae pathovars and also from strains of P. syringae pv. syringae isolated from different hosts. Results: The eight plasmids sequenced ranged in length from 61.6 to 73.8kb and encoded from 65 to 83 annotated orfs. Virulence genes including type III secretion system effectors were encoded on two plasmids, and one of these, pPt0893-29 from P. syringae pv. tabaci, encoded a wide variety of putative virulence determinants. The PFPs from P. syringae pv. syringae mostly encoded genes of importance to ecological fitness including the rulAB determinant conferring tolerance to ultraviolet radiation. Heavy metal resistance genes encoding resistance to copper and arsenic were also present in a few plasmids. The discovery of part of the chromosomal genomic island GI6 from P. syringae pv. syringae B728a in two PFPs from two P. syringae pv. syringae hosts is further evidence of past intergenetic transfers between plasmid and chromosomal DNA. Phylogenetic analyses also revealed new subgroups of the pPT23A plasmid family and confirmed that plasmid phylogeny is incongruent with P. syringae pathovar or host of isolation. In addition, conserved genes among seven sequenced plasmids within the same phylogenetic group were limited to plasmid-specific functions including maintenance and transfer functions. Conclusions: Our sequence analysis further revealed that PFPs from P. syringae encode suites of accessory genes that are selected at species (universal distribution), pathovar (interpathovar distribution), and population levels (intrapathovar distribution). The conservation of type IV secretion systems encoding conjugation functions also presumably contributes to the distribution of these plasmids within P. syringae populations.},
author = {Guti{\'{e}}rrez-Barranquero, Jos{\'{e}} A. and Cazorla, Francisco M. and de Vicente, Antonio and Sundin, George W.},
doi = {10.1186/s12864-017-3763-x},
file = {::},
issn = {14712164},
journal = {BMC Genomics},
keywords = {Copper resistance,Genomic island,P. syringae,Plasmid phylogeny,hopBD1,rulAB},
month = {may},
number = {1},
publisher = {BioMed Central Ltd.},
title = {{Complete sequence and comparative genomic analysis of eight native Pseudomonas syringae plasmids belonging to the pPT23A family}},

volume = {18},
year = {2017}
}
@article{Erickson2018,
abstract = {Klebsiella pneumoniae is a Gram-negative bacterium associated with the gastrointestinal tract and is a significant nosocomial pathogen due to its antibiotic resistance. Phage therapy against K. pneumoniae may prove useful in treating infections caused by this bacterium. This announcement describes the genome of the T5-like K. pneumoniae siphophage Sugarland.},
author = {Erickson, Samuel G and Lessor, Lauren and O'Leary, Chandler J and Gill, Jason J and Liu, Mei},
doi = {10.1128/MRA.01014-18},
file = {::},
issn = {2576-098X},
journal = {Microbiology resource announcements},
month = {nov},
number = {19},
pmid = {30533796},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Siphophage Sugarland.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30533796 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6256483},
volume = {7},
year = {2018}
}
@article{Erickson2018a,
abstract = { Klebsiella pneumoniae is a Gram-negative bacterium associated with the gastrointestinal tract and is a significant nosocomial pathogen due to its antibiotic resistance. Phage therapy against K. pneumoniae may prove useful in treating infections caused by this bacterium. This announcement describes the genome of the T5-like K. pneumoniae siphophage Sugarland. },
author = {Erickson, Samuel G. and Lessor, Lauren and O'Leary, Chandler J. and Gill, Jason J. and Liu, Mei},
doi = {10.1128/mra.01014-18},
file = {::},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
month = {nov},
number = {19},
publisher = {American Society for Microbiology},
title = {{ Complete Genome Sequence of Klebsiella pneumoniae Siphophage Sugarland }},
volume = {7},
year = {2018}
}
@article{Elliott2016,
abstract = {Klebsiella quasipneumoniae subsp. similipneumoniae strain ATCC 700603, formerly known as K. pneumoniae K6, is known for producing extended-spectrum β-lactamase (ESBL) enzymes that can hydrolyze oxyimino-β-lactams, resulting in resistance to these drugs. We herein report the complete genome of strain ATCC 700603 and show that the ESBL genes are plasmid-encoded.},

author = {Elliott, Alysha G. and Ganesamoorthy, Devika and Coin, Lachlan and Cooper, Matthew A. and Cao, Minh Duc},
doi = {10.1128/genomeA.00438-16},
file = {::},
issn = {21698287},
journal = {Genome Announcements},
number = {3},
pmid = {27231369},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of Klebsiella quasipneumoniae subsp. similipneumoniae strain ATCC 700603}},
volume = {4},
year = {2016}
}
@article{Detheridge2018,
abstract = {Two strains of Pseudomonas putida, Psp-LUP and Psp-SPAR, capable of growth on the quinolizidine alkaloids, lupanine and sparteine respectively, were studied here. We report the isolation of Psp-SPAR and the complete genome sequencing of both bacteria. Both were confirmed to belong to P. putida, Psp-LUP close to the type isolate of the species (NBRC14164T) and Psp-SPAR close to strains KT2440 and F1. Psp-SPAR did not grow on lupanine but did contain a gene encoding a putative quinolizidine-17-hydroxylase peptide which exhibited high similarity (76{\%}identity) to the lupanine-17-hydroxylase characterised from Psp-LUP.},
author = {Detheridge, Andrew P and Griffith, Gareth W and Hopper, David J},
doi = {10.1007/s00284-018-1573-2},
file = {::},
issn = {1432-0991},
journal = {Current microbiology},
month = {dec},
number = {12},
pages = {1649--1654},
pmid = {30267141},
publisher = {Springer New York LLC},
title = {{Genome Sequence Analysis of Two Pseudomonas putida Strains to Identify a 17-Hydroxylase Putatively Involved in Sparteine Degradation.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30267141 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6208669},
volume = {75},
year = {2018}
}
@article{Carl2017,
abstract = {We describe here the genome sequence of the novel temperate Klebsiella pneumoniae phage KPP5665-2 isolated from a Klebsiella pneumoniae strain recovered from milk in Germany in 2016. The phage exhibited a narrow host range and a siphoviridal morphology. KPP5665-2-related prophage sequences were detected in whole-genome sequencing (WGS) data of various Klebsiella species isolates.},
author = {Carl, Gaby and J{\"{a}}ckel, Claudia and Gr{\"{u}}tzke, Josephine and Hertwig, Stefan and Grobbel, Mirjam and Malorny, Burkhard and Rau, J{\"{o}}rg and K{\"{a}}sbohrer, Annemarie and Hammerl, Jens A},

doi = {10.1128/genomeA.01118-17},
file = {::},
issn = {2169-8287},
journal = {Genome announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
number = {43},
pmid = {29074652},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of the Temperate Klebsiella pneumoniae Phage KPP5665-2.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/29074652 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5658490},
volume = {5},
year = {2017}
}
@article{Zhou2016,
abstract = {The study describes the transmission of a CTX-M-15-producing ST15 Klebsiella pneumoniae between patients treated in a single center and the subsequent inter-institutional spread by patient referral occurring between May 2012 and September 2013. A suspected epidemiological link between clinical K. pneumoniae isolates was supported by patient contact tracing and genomic phylogenetic analysis from May to November 2012. By May 2013, a patient treated in three institutions in two cities was involved in an expanding cluster caused by this high-risk clone (HiRiC) (local expansion, CTX-M-15 producing, and containing hypervirulence factors). A clone-specific multiplex PCR was developed for patient screening by which another patient was identified in September 2013. Genomic phylogenetic analysis including published ST15 genomes revealed a close homology with isolates previously found in the USA. Environmental contamination and lack of consistent patient screening were identified as being responsible for the clone dissemination. The investigation addresses the advantages of whole-genome sequencing in the early detection of HiRiC with a high propensity of nosocomial transmission and prolonged circulation in the regional patient population. Our study suggests the necessity for inter-institutional/regional collaboration for infection/outbreak management of K. pneumoniae HiRiCs.},
author = {Zhou, Kai and Lokate, Mariette and Deurenberg, Ruud H and Tepper, Marga and Arends, Jan P and Raangs, Erwin G C and Lo-Ten-Foe, Jerome and Grundmann, Hajo and Rossen, John W A and Friedrich, Alexander W},
doi = {10.1038/srep20840},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Zhou et al. - 2016 - Use of whole-genome sequencing to trace, control and characterize the regional expansion of extended-spectrum β-lac.pdf:pdf},
issn = {2045-2322},
journal = {Scientific reports},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
pages = {20840},

pmid = {26864946},
publisher = {Nature Publishing Group},
title = {{Use of whole-genome sequencing to trace, control and characterize the regional expansion of extended-spectrum β-lactamase producing ST15 Klebsiella pneumoniae.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26864946 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4749987},
volume = {6},
year = {2016}
}
@article{Zheng2020,
abstract = {The massive use of antibiotics in healthcare and agriculture has led to their artificial accumulation in natural habitats, which risks the structure and function of the microbial communities in ecosystems, threatens food and water security, and accelerates the development of resistome. Ideally, antibiotics should remain fully active in clinical services while becoming deactivated rapidly once released into the environment, but none of the current antibiotics meet this criterion. Here, we show a nanoantibiotic design that epitomizes the concept of carrying a built-in "OFF" switch responsive to natural stimuli. The environmentally benign nanoantibiotics consist of cellulose backbones covalently grafted with hydrophilic polymer brushes that by themselves are antimicrobially inactive. In their nanostructured forms in services, these cellulose-based polymer molecular brushes are potent killers for both Gram-positive and Gram-negative bacteria, including clinical multidrug-resistant strains; after services and being discharged into the environment, they are shredded into antimicrobially inactive pieces by cellulases that do not exist in the human body but are abundant in natural habitats. This study illuminates a new concept of mitigating the environmental footprints of antibiotics with rationally designed nanoantibiotics that can be dismantled and disabled by bioorthogonal chemistry occurring exclusively in natural habitats.},
author = {Zheng, Wan and Anzaldua, Miguel and Arora, Ankita and Jiang, Yunjiang and McIntyre, Kelly and Doerfert, Michael and Winter, Theodora and Mishra, Abhijit and Ma, Hairong and Liang, Hongjun},
doi = {10.1021/acs.biomac.0c00163},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Zheng et al. - 2020 - Environmentally Benign Nanoantibiotics with a Built-in Deactivation Switch Responsive to Natural Habitats.pdf:pdf},
issn = {1526-4602},
journal = {Biomacromolecules},
month = {apr},
pmid = {32202760},
publisher = {American Chemical Society (ACS)},
title = {{Environmentally Benign Nanoantibiotics with a Built-in Deactivation Switch Responsive to Natural Habitats.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32202760},
year = {2020}
}
@article{Yu2018,
abstract = {The bacterial strain M5a1 is a model strain for studying the molecular genetics of N2-fixation and molecular engineering of microbial production of platform chemicals 1,3-propanediol and 2,3-butanediol.

Here, we present the complete genome sequence of the strain M5al, which belongs to a novel species closely related to Klebsiella michiganensis. M5al secretes plant cell wall-degrading enzymes and colonizes rice roots but does not cause soft rot disease. M5al also produces siderophores and contains the gene clusters for synthesis and transport of yersiniabactin which is a critical virulence factor for Klebsiella pathogens in causing human disease. We propose that the model strain M5al can be genetically modified to study bacterial N2-fixation in association with non-legume plants and production of 1,3-propanediol and 2,3-butanediol through degradation of plant cell wall biomass.},
author = {Yu, Zhili and Li, Shuying and Li, Yuanyuan and Jiang, Zhuang and Zhou, Jinru and An, Qianli},
doi = {10.1016/j.btre.2017.11.006},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Yu et al. - 2018 - Complete genome sequence of N2-fixing model strain Klebsiella sp. nov. M5al, which produces plant cell wall-degrading.pdf:pdf},
issn = {2215017X},
journal = {Biotechnology Reports},
keywords = {Carbohydrate-active enzyme,Klebsiella michiganensis,Klebsiella oxytoca,Lista{_}Filtrada,Nitrogen fixation,Type II secretion system},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
pages = {6--9},
publisher = {Elsevier B.V.},
title = {{Complete genome sequence of N2-fixing model strain Klebsiella sp. nov. M5al, which produces plant cell wall-degrading enzymes and siderophores}},
volume = {17},
year = {2018}
}
@article{Yang2019,
abstract = {Background: As a result of the growing prevalence of the plasmid-mediated mobile colistin resistance gene mcr-1 among Gram-negative bacteria, the surveillance of mcr-1 has been globally applied. In our study, we aimed to shed light on the possibility of transmission of mcr-1-resistant isolates through market retail fruits. Methods and results: Herein, 133 different fruit surface samples were collected and screened for the different MCR variants (mcr-1 to mcr-8) using PCR and confirmed with sequencing. We identify for the first time mcr-1-carrying Escherichia coli and Klebsiella pneumoniae from market retail fruits in Guangzhou, China. Minimum inhibitory concentrations were detected by the broth microdilution method. Liquid mating was performed to check the transferability of the mcr-1 gene. Pulsed field gel electrophoresis analysis of S1 nuclease-digested DNA and Southern blotting were performed to check the location of the mcr-1 gene. Then, whole-genome sequencing and in silico multilocus sequence typing analysis were performed. Conclusion: We showed that E. coli GB110 can mediate the spreading of antibiotic resistance genes through the food chain, while K. pneumoniae GB015 was considered to be the progenitor of the most successful multidrug-resistant clone. Since fruits are usually consumed fresh, this may serve as a direct source of mcr-1-producing bacteria in humans that

requires prompt surveillance and intervention to limit the spread of resistance.},
author = {Yang, Fan and Shen, Cong and Zheng, Xiaobin and Liu, Yan and Ahmed, Mohamed Abd El Gawad El Sayed and Zhao, Zihan and Liao, Kang and Shi, Yaling and Guo, Xin and Zhong, Ruoxuan and Xu, Zhimin and Tian, Guo Bao},
doi = {10.2147/IDR.S194635},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Yang et al. - 2019 - Plasmid-mediated colistin resistance gene mcr-1 in Escherichia coli and Klebsiella pneumoniae isolated from market.pdf:pdf},
issn = {11786973},
journal = {Infection and Drug Resistance},
keywords = {Colistin,Escherichia coli,Fruit,Klebsiella pneumoniae,Mcr-1},
pages = {385--389},
publisher = {Dove Medical Press Ltd.},
title = {{Plasmid-mediated colistin resistance gene mcr-1 in Escherichia coli and Klebsiella pneumoniae isolated from market retail fruits in Guangzhou, China}},
volume = {12},
year = {2019}
}
@article{Xu2020a,
abstract = {Purpose Imipenemase (IMP), an Ambler class B metallo-β-lactamase, is an important carbapenemase that confers resistance to almost all β-lactams. In this study, we characterized the genomic feature of an IMP-4-producing Klebsiella pneumoniae ST1873 strain, a rare sequence type (ST) isolated from an infant with a bloodstream infection in China. Patients and Methods K. pneumoniae strain, BKP19, was collected from a bloodstream infection in an infant who was hospitalized at the department of paediatrics. The whole genome sequence of the strain was sequenced using the Illumina NovaSeq 6000 platform and long-read MinION sequencer. Multilocus sequence typing, antimicrobial resistance gene identification, plasmid and phylogenetic relationship analysis of the strain were analysed by various bioinformatics approaches. Results K. pneumoniae BKP19 was resistant to multiple antimicrobials, including carbapenems. Eleven antimicrobial resistance genes corresponding to beta-lactam resistance, quinolone resistance, phenicol resistance and fosfomycin resistance could be identified in the genome. The carbapenem resistance gene blaIMP-4 was located in an IS26-associated class 1 integron of an IncN-type plasmid with 39,033 bp (pIMP-4-BKP19). Sequence alignment revealed that pIMP-4-BKP19 is closely related to the common plasmid carrying IMP-4 in K. pneumoniae (pIMP-HZ1-like plasmid) but is smaller, lacking the quinolone resistance gene qnrS1 and multiple tra gene orthologs. Conjugation experiment revealed that pIMP-4-BKP19 is a non-conjugative plasmid. According to in silico MLST analysis, K. pneumoniae strain BKP19 belongs to a sporadic clone ST1873. Conclusion In summary, our study reports the first genome sequence of a K. pneumoniae ST1873 strain harbouring the class B β-lactamase blaIMP-4 in an IncN-type plasmid recovered from an infant with a bloodstream infection in China. Considering the global emergence of IMP-4 carbapenemase, more attention must be paid to prevent its future prevalence.},
author = {Xu, Juan and Lin, Wenping and Chen, Yanmin and He, Fang},
doi = {10.2147/IDR.S247341},

file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Xu et al. - 2020 - Characterization of an IMP-4-Producing Klebsiella pneumoniae ST1873 Strain Recovered from an Infant with a Bloodstrea.pdf:pdf},
issn = {1178-6973},
journal = {Infection and drug resistance},
keywords = {IncN plasmid,Klebsiella pneumoniae,Lista{_}Filtrada,ST1873,blaIMP-4,bloodstream infection},
mendeley-tags = {Lista{_}Filtrada},
pages = {773--779},
pmid = {32210591},
publisher = {Dove Medical Press Ltd.},
title = {{Characterization of an IMP-4-Producing Klebsiella pneumoniae ST1873 Strain Recovered from an Infant with a Bloodstream Infection in China.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32210591 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC7069566},
volume = {13},
year = {2020}
}
@article{Wu2020,
abstract = {While advances in genomic sequencing have highlighted significant strain variability between and within Salmonella serovars, only a few protein variants have been directly related to evolutionary adaptation for survival, such as host specificity or differential virulence. The current study investigated whether allelic variation of the Salmonella adhesin/invasin PagN influences bacterial interaction with their receptors. The Salmonella enterica, subspecies enterica serovar Typhi (S. Typhi) allelic variant of PagN was found to bind significantly better to different enterocytes as well as to the extracellular matrix protein laminin than did the major Salmonella enterica, subspecies enterica serovar Typhimurium (S. Typhimurium) allele. The two alleles differed at amino acid residues 49 and 109 in two of the four predicted PagN surface loops, and residue substitution analysis revealed that a glutamic acid at residue 49 increased the adhesive and invasive properties of S. Typhi PagN. PagN sequence comparisons from 542 Salmonella strains for six representative S. enterica serovars and S. diarizonae further supported the role of glutamic acid at residues 49 and 109 in optimizing adhesion to cells and laminin, as well as for cell invasion. In summary, this study characterized unique residues in allelic variants of a virulence factor that participates in the colonization and invasive properties of different Salmonella stains, subspecies and serovars.},
author = {Wu, Yanping and Hu, Qiaoyun and Dehinwal, Ruchika and Rakov, Alexey V. and Grams, Nicholas and Clemens, Erin C. and Hofmann, Jennifer and Okeke, Iruka N. and Schifferli, Dieter M.},
doi = {10.3390/microorganisms8040489},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Wu et al. - 2020 - The Not so Good, the Bad and the Ugly Differential Bacterial Adhesion and Invasion Mediated by Salmonella PagN Alleli.pdf:pdf},
issn = {2076-2607},
journal = {Microorganisms},
keywords = {Lista{_}Filtrada},

mendeley-tags = {Lista{_}Filtrada},
number = {4},
pages = {489},
title = {{The Not so Good, the Bad and the Ugly: Differential Bacterial Adhesion and Invasion Mediated by Salmonella PagN Allelic Variants}},
url = {https://www.mdpi.com/2076-2607/8/4/489},
volume = {8},
year = {2020}
}
@article{Winsor2016,
abstract = {The Pseudomonas Genome Database (http://www.pseudomonas.com) is well known for the application of community-based annotation approaches for producing a high-quality Pseudomonas aeruginosa PAO1 genome annotation, and facilitating whole-genome comparative analyses with other Pseudomonasstrains. To aid analysis of potentially thousands of complete and draft genome assemblies, this database and analysis platform was upgraded to integrate curated genome annotations and isolate metadata with enhanced tools for larger scale comparative analysis and visualization. Manually curated gene annotations are supplemented with improved computational analyses that help identify putative drug targets and vaccine candidates or assist with evolutionary studies by identifying orthologs, pathogen-associated genes and genomic islands. The database schema has been updated to integrate isolate metadata that will facilitate more powerful analysis of genomes across datasets in the future. We continue to place an emphasis on providing high-quality updates to gene annotations through regular review of the scientific literature and using community-based approaches including a major new Pseudomonas community initiative for the assignment of high-quality gene ontology terms to genes. As we further expand from thousands of genomes, we plan to provide enhancements that will aid data visualization and analysis arising from whole-genome comparative studies including more pan-genome and population-based approaches.},
author = {Winsor, Geoffrey L. and Griffiths, Emma J. and Lo, Raymond and Dhillon, Bhavjinder K. and Shay, Julie A. and Brinkman, Fiona S.L.},
doi = {10.1093/nar/gkv1227},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Winsor et al. - 2016 - Enhanced annotations and features for comparing thousands of Pseudomonasgenomes in the Pseudomonas genome databas.pdf:pdf},
issn = {13624962},
journal = {Nucleic Acids Research},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {D1},
pages = {D646--D653},
pmid = {26578582},
publisher = {Oxford University Press},
title = {{Enhanced annotations and features for comparing thousands of Pseudomonasgenomes in the Pseudomonas genome database}},
volume = {44},
year = {2016}
}
@article{Wick2018,

abstract = {As whole-genome sequencing becomes an established component of the microbiologist's toolbox, it is imperative that researchers, clinical microbiologists, and public health professionals have access to genomic analysis tools for the rapid extraction of epidemiologically and clinically relevant information. For the Gram-negative hospital pathogens such as Klebsiella pneumoniae, initial efforts have focused on the detection and surveillance of antimicrobial resistance genes and clones. However, with the resurgence of interest in alternative infection control strategies targeting Klebsiella surface polysaccharides, the ability to extract information about these antigens is increasingly important. Here we present Kaptive Web, an online tool for the rapid typing of Klebsiella K and O loci, which encode the polysaccharide capsule and lipopolysaccharide O antigen, respectively. Kaptive Web enables users to upload and analyze genome assemblies in a web browser. The results can be downloaded in tabular format or explored in detail via the graphical interface, making it accessible for users at all levels of computational expertise. We demonstrate Kaptive Web's utility by analyzing 500 K. pneumoniae genomes. We identify extensive K and O locus diversity among 201 genomes belonging to the carba-penemase-associated clonal group 258 (25 K and 6 O loci). The characterization of a further 309 genomes indicated that such diversity is common among the multidrug-resistant clones and that these loci represent useful epidemiological markers for strain subtyping. These findings reinforce the need for rapid, reliable, and accessible typing methods such as Kaptive Web. Kaptive Web is available for use at http://kaptive.holtlab.net/, and the source code is available at https://github.com/kelwyres/Kaptive-Web.},
author = {Wick, Ryan R. and Heinz, Eva and Holt, Kathryn E. and Wyres, Kelly L.},
doi = {10.1128/JCM.00197-18},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Wick et al. - 2018 - Kaptive web User-Friendly capsule and lipopolysaccharide serotype prediction for Klebsiella genomes.pdf:pdf},
issn = {1098660X},
journal = {Journal of Clinical Microbiology},
keywords = {Capsular polysaccharide,Capsule,Genome analysis,Genomics,Klebsiella,Lipopolysaccharide,Lista{_}Filtrada,Molecular epidemiology},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
number = {6},
publisher = {American Society for Microbiology},
title = {{Kaptive web: User-Friendly capsule and lipopolysaccharide serotype prediction for Klebsiella genomes}},
volume = {56},
year = {2018}
}
@article{Wen2020,
abstract = {Despite the commercial importance of the Concord grape, its origin has remained unresolved for over 150 years without a comprehensive phylogenetic analysis. In this study we aimed to reconstruct the evolutionary history of the Concord grape using sequence data from four nuclear markers (AT103, GAI1, PHYA, and SQD1), six plastid markers (matK, psbA-trnH, petN-trnC, ycf1, trnL-F, and trnS-G), and the plastid genome.

We sampled extensively the Vitis species native to northeastern North America as well as representative species from Europe and Asia, including the commercially important Vitis vinifera (wine grape), a native European species with hermaphroditic flowers, and its wild progenitor, V. vinifera subsp. sylvestris. We also sequenced the plastid genome of one accession of the Concord grape and compared the plastid genome data to the recently published data set of Vitis plastomes. Phylogenetic analyses of the plastid and nuclear data using maximum likelihood and Bayesian inference support the hybrid origin of the Concord grape. The results clearly pinpoint the wine grape, V. vinifera, as the maternal donor and the fox grape, Vitis labrusca, which is common in northeastern North America, as the paternal donor. Moreover, we infer that the breeding history of the Concord grape must have involved the backcrossing of the F1 hybrid with the paternal parent V. labrusca. This backcrossing also explains the higher morphological similarity of the Concord grape to V. labrusca than to V. vinifera. This study provides concrete genetic evidence for the hybrid origin of a widespread Vitis cultivar and is, therefore, promising for similar future studies focused on resolving ambiguous origins of major crops or to create successful hybrid fruit crops.},
author = {Wen, Jun and Herron, Sterling A and Yang, Xue and Liu, Bin-Bin and Zuo, Yun-Juan and Harris, A J and Kalburgi, Yash and Johnson, Gabriel and Zimmer, Elizabeth A},
doi = {10.3389/fpls.2020.00263},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Wen et al. - 2020 - Nuclear and Chloroplast Sequences Resolve the Enigmatic Origin of the Concord Grape.pdf:pdf},
issn = {1664-462X},
journal = {Frontiers in plant science},
keywords = {Concord grape,Lista{_}Filtrada,Vitaceae,Vitis,grape,origin},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
pages = {263},
pmid = {32256506},
publisher = {Frontiers Media SA},
title = {{Nuclear and Chloroplast Sequences Resolve the Enigmatic Origin of the Concord Grape.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32256506 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC7092692},
volume = {11},
year = {2020}
}
@article{Wang2020,
abstract = {Gut microbiota is a reservoir of antibiotic resistance genes (ARGs). Yet, limited information is available regarding the presence (metagenomic DNA level) and expression profiles (metatranscriptomic RNA level) of ARGs in gut microbiota. Here, we used both metagenomic and metatranscriptomic approaches to comprehensively reveal the abundance, diversity, and expression of ARGs in human, chicken, and pig gut microbiomes in China. Based on deep sequencing data and ARG databases, a total of 330 ARGs associated with 21 antibiotic classes were identified in 18 human, chicken, and pig fecal samples. Metatranscriptomic analysis revealed that 49.4, 66.5, and 56.6{\%} of ARGs identified in human, chicken, and pig gut microbiota, respectively, were expressed, indicating that a large proportion of ARGs were not transcriptionally active.

Further analysis demonstrated that transcript abundance of tetracycline, aminoglycoside, and beta-lactam resistance genes was mainly contributed by acquired ARGs. We also found that various biocide, chemical, and metal resistance genes were actively transcribed in human and animal guts. The combination of metagenomic and metatranscriptomic analysis in this study allowed us to specifically link ARGs to their transcripts, providing a comprehensive view of the prevalence and expression of ARGs in gut microbiota. Taken together, these data deepen our understanding of the distribution, evolution, and dissemination of ARGs and metal resistance genes in human, chicken, and pig gut microbiota.},
author = {Wang, Yanan and Hu, Yongfei and Liu, Fei and Cao, Jian and Lv, Na and Zhu, Baoli and Zhang, Gaiping and Gao, George Fu},
doi = {10.1016/j.envint.2020.105649},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Wang et al. - 2020 - Integrated metagenomic and metatranscriptomic profiling reveals differentially expressed resistomes in human, chick.pdf:pdf},
issn = {18736750},
journal = {Environment International},
keywords = {Acquired ARGs,Gut resistome,Mcr-1,Metagenomics,Metatranscriptomics},
month = {may},
publisher = {Elsevier Ltd},
title = {{Integrated metagenomic and metatranscriptomic profiling reveals differentially expressed resistomes in human, chicken, and pig gut microbiomes}},
volume = {138},
year = {2020}
}
@article{Villa2016,
abstract = {Klebsiella pneumoniae sequence type (ST) 307, carrying blaKPC-3, blaCTX-M-15, blaOXA-1, aac(6')-Ib-cr, and qnrB1 genes, is replacing the predominant hyperepidemic ST258 clone in Italy. Whole-genome and complete plasmid sequencing of one ST307 strain was performed and new features were identified.},
author = {Villa, Laura and Feudi, Claudia and Fortini, Daniela and Iacono, Michele and Bonura, Celestino and Endimiani, Andrea and Mammina, Caterina and Carattoli, Alessandra},
doi = {10.1128/genomeA.00213-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Villa et al. - 2016 - Complete genome sequence of KPC-3- and CTX-M-15-producing Klebsiella pneumoniae sequence type 307.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {2},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of KPC-3- and CTX-M-15-producing Klebsiella pneumoniae sequence type 307}},
volume = {4},
year = {2016}
}

@article{Villa2017,
abstract = {The global spread of Klebsiella pneumoniae producing Klebsiella pneumoniae carbapenemase (KPC) has been mainly associated with the dissemination of high-risk clones. In the last decade, hospital outbreaks involving KPC-producing K. pneumoniae have been predominantly attributed to isolates belonging to clonal group (CG) 258. However, results of recent epidemiological analysis indicate that KPC-producing sequence type (ST) 307, is emerging in different parts of the world and is a candidate to become a prevalent high-risk clone in the near future. Here we show that the ST307 genome encodes genetic features that may provide an advantage in adaptation to the hospital environment and the human host. Sequence analysis revealed novel plasmid-located virulence factors, including a cluster for glycogen synthesis. Glycogen production is considered to be one of the possible adaptive responses to long-term survival and growth in environments outside the host. Chromosomally-encoded virulence traits in the clone comprised fimbriae, an integrative conjugative element carrying the yersiniabactin siderophore, and two different capsular loci. Compared with the ST258 clone, capsulated ST307 isolates showed higher resistance to complement-mediated killing. The acquired genetic features identified in the genome of this new emerging clone may contribute to increased persistence of ST307 in the hospital environment and shed light on its potential epidemiological success.},
author = {Villa, Laura and Feudi, Claudia and Fortini, Daniela and Brisse, Sylvain and Passet, Virginie and Bonura, Celestino and Endimiani, Andrea and Mammina, Caterina and Ocampo, Ana Maria and Jimenez, Judy Natalia and Doumith, Michel and Woodford, Neil and Hopkins, Katie and Carattoli, Alessandra},
doi = {10.1099/mgen.0.000110},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Villa et al. - 2017 - Diversity, virulence, and antimicrobial resistance of the KPCproducing klebsiella pneumoniae ST307 clone.pdf:pdf},
issn = {20575858},
journal = {Microbial Genomics},
keywords = {Capsule,KPC,Lista{_}Filtrada,Plasmid,ST259,ST307,WGS},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
number = {4},
publisher = {Microbiology Society},
title = {{Diversity, virulence, and antimicrobial resistance of the KPCproducing klebsiella pneumoniae ST307 clone}},
volume = {3},
year = {2017}
}
@article{Vestergaard2016,
abstract = {Combination therapy with several antibiotics is one strategy that has been applied in order to limit the spread of antimicrobial resistance. We compared the de novo evolution of resistance during combination therapy with the-lactam ceftazidime and the fluoroquinolone ciprofloxacin with the resistance evolved after single-drug exposure. Combination therapy selected for mutants that displayed broad-spectrum resistance, and a major resistance mechanism was mutational inactivation of the repressor gene mexR that regulates the multidrug efflux operon mexAB-oprM. Deregulation of this operon led to a broad-spectrum

resistance phenotype that decreased susceptibility to the combination of drugs applied during selection as well as to unrelated antibiotic classes. Mutants isolated after single-drug exposure displayed narrow-spectrum resistance and carried mutations in the MexCD-OprJ efflux pump regulator gene nfxB conferring ciprofloxacin resistance, or in the gene encoding the non-essential penicillin-binding protein DacB conferring ceftazidime resistance. Reconstruction of resistance mutations by allelic replacement and in vitro fitness assays revealed that in contrast to single antibiotic use, combination therapy consistently selected for mutants with enhanced fitness expressing broad-spectrum resistance mechanisms.},
author = {Vestergaard, M ; and Paulander, W ; and Marvig, R L and Clasen, J ; and Jochumsen, N ; and Molin, S ; and Folkesson, . .},
doi = {10.1016/j.ijantimicag.2015.09.014},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Vestergaard et al. - 2016 - Pseudomonas aeruginosa.pdf:pdf},
journal = {International Journal of Antimicrobial Agents},
keywords = {Antibiotics,Combination therapy,Drug efflux,Fluoroquinolones,Lactams,Lista{_}Filtrada,Multidrug resistance-},
mendeley-tags = {Lista{_}Filtrada},
pages = {48--55},
publisher = {APA},
title = {{Pseudomonas aeruginosa}},
url = {https://www.sciencedirect.com/science/article/pii/S0924857915003350},
volume = {47},
year = {2016}
}
@article{VanDorp2019,
abstract = {Carbapenem-resistant Klebsiella pneumoniae (CRKP) increasingly cause high-mortality outbreaks in hospital settings globally. Following a patient fatality at a hospital in Beijing due to a blaKPC-2-positive CRKP infection, close monitoring was put in place over the course of 14 months to characterize all blaKPC-2-positive CRKP in circulation in the hospital. Whole genome sequences were generated for 100 isolates from blaKPC-2-positive isolates from infected patients, carriers and the hospital environment. Phylogenetic analyses identified a closely related cluster of 82 sequence type 11 (ST11) isolates circulating in the hospital for at least a year prior to admission of the index patient. The majority of inferred transmissions for these isolates involved patients in intensive care units. Whilst the 82 ST11 isolates collected during the surveillance effort all had closely related chromosomes, we observed extensive diversity in their antimicrobial resistance (AMR) phenotypes. We were able to reconstruct the major genomic changes underpinning this variation in AMR profiles, including multiple gains and losses of entire plasmids and recombination events between plasmids, including transposition of blaKPC-2. We also identified specific cases where variation in plasmid copy number correlated with the level of phenotypic resistance to drugs, suggesting that the number of resistance elements carried by a strain may play a role in determining the level of AMR. Our findings highlight the epidemiological value of whole genome sequencing for investigating multi-drug-resistant hospital

infections and illustrate that standard typing schemes cannot capture the extraordinarily fast genome evolution of CRKP isolates.},
author = {van Dorp, Lucy and Wang, Qi and Shaw, Liam P and Acman, Mislav and Brynildsrud, Ola B and Eldholm, Vegard and Wang, Ruobing and Gao, Hua and Yin, Yuyao and Chen, Hongbin and Ding, Chuling and Farrer, Rhys A and Didelot, Xavier and Balloux, Francois and Wang, Hui},
doi = {10.1099/mgen.0.000263},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/van Dorp et al. - 2019 - Rapid phenotypic evolution in multidrug-resistant Klebsiella pneumoniae hospital outbreak strains.pdf:pdf},
issn = {2057-5858},
journal = {Microbial genomics},
keywords = {Lista{_}Filtrada,antimicrobial resistance,carbapenem-resistant Klebsiella pneumoniae (CRKP),horizontal gene transfer,nosocomial pathogens,plasmids,transmission chains},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
number = {4},
pages = {1--11},
pmid = {30939107},
publisher = {Microbiology Society},
title = {{Rapid phenotypic evolution in multidrug-resistant Klebsiella pneumoniae hospital outbreak strains.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30939107 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6521586},
volume = {5},
year = {2019}
}
@article{VanBeek2019,
abstract = {Background: Two epidemiologically-unrelated clusters of Klebsiella pneumoniae carbapenemase (KPC)producing K. pneumoniae were detected among several healthcare facilities (HCF) in Finland by routine surveillance using whole genome sequencing (WGS). Aim: The objective was to investigate transmission chains to stop further spread of the responsible strain. Methods: In this observational retrospective study, cases were defined as patients with K. pneumoniae KPC-3sequence type (ST)512 strain detected in Finland from August 2013 to May 2018. Environmental specimens were obtained from surfaces, sinks and toilets in affected wards. WGS was performed on K. pneumoniae cultures using Illumina MiSeq platform and data were analysed using Ridom SeqShere software K. pneumoniae core genome multilocus sequence typing (cgMLST) scheme. Epidemiological information of the cases was provided by HCFs. Results: We identified 20 cases in six HCFs: cluster1 included 18 cases in five HCFs and cluster2 two cases in one HCF. In cluster1, a link with a foreign country was unclear, 6/18 cases without overlapping stay had occupied the same room in one of the five HCFs within{\textgreater}3years. In cluster2, the index case was transferred from abroad, both cases occupied the same room 8months apart. A strain identical to that of the two cases in cgMLST was isolated from the toilet of the room, suggesting a clonal origin. Conclusions: The clusters were mostly related to case transfer between facilities and likely involved environmental transmission. We show that CPE surveillance using WGS and

collaboration between hospitals are crucial to identify clusters and trace transmission chains.},
author = {van Beek, Janko and R{\"{a}}is{\"{a}}nen, Kati and Broas, Markku and Kauranen, Jari and K{\"{a}}hk{\"{o}}l{\"{a}}, Arja and Laine, Janne and Mustonen, Eeva and Nurkkala, Tuija and Puhto, Teija and Sinkkonen, Jaana and Torvinen, Senja and Vornanen, Tarja and Vuento, Risto and Jalava, Jari and Lyytik{\"{a}}inen, Outi},
doi = {10.2807/1560-7917.ES.2019.24.38.1800522},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/van Beek et al. - 2019 - Tracing local and regional clusters of carbapenemase-producing Klebsiella pneumoniae ST512 with whole genome se.pdf:pdf},
issn = {15607917},
journal = {Eurosurveillance},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {38},
publisher = {European Centre for Disease Prevention and Control (ECDC)},
title = {{Tracing local and regional clusters of carbapenemase-producing Klebsiella pneumoniae ST512 with whole genome sequencing, Finland, 2013 to 2018}},
volume = {24},
year = {2019}
}
@article{Takeuchi2014,
abstract = {The biocontrol strain Pseudomonas sp. Cab57 was isolated from the rhizosphere of shepherd's purse growing in a field in Hokkaido by screening the antibiotic producers. The whole genome sequence of this strain was obtained by paired-end and whole-genome shotgun sequencing, and the gaps between the contigs were closed using gap-spanning PCR products. The P. sp. Cab57 genome is organized into a single circular chromosome with 6,827,892 bp, 63.3{\%} G+C content, and 6,186 predicted protein-coding sequences. Based on 16S rRNA gene analysis and whole genome analysis, strain Cab57 was identified as P. protegens. As reported in P. protegens CHA0 and Pf-5, four gene clusters (phl, prn, plt, and hcn) encoding the typical antibiotic metabolites and the reported genes associated with Gac/Rsm signal transduction pathway of these strains are fully conserved in the Cab57 genome. Actually strain Cab57 exhibited typical Gac/Rsm activities and antibiotic production, and these activities were enhanced by knocking out the retS gene (for a sensor kinase acting as an antagonist of GacS). Two large segments (79 and 115 kb) lacking in the Cab57 genome, as compared with the Pf-5 genome, accounted for the majority of the difference (247 kb) between these genomes. One of these segments was the complete rhizoxin analog biosynthesis gene cluster (ca. 79 kb) and another one was the 115-kb mobile genomic island. A whole genome comparison of those relative strains revealed that each strain has unique gene clusters involved in metabolism such as nitrite/nitrate assimilation, which was identified in the Cab57 genome. These findings suggest that P. protegens is a ubiquitous bacterium that controls its biocontrol traits while building up strain-specific genomic repertoires for the biosynthesis of secondary metabolites and niche adaptation. {\textcopyright} 2014 Takeuchi et al.},
author = {Takeuchi, Kasumi and Noda, Naomi and Someya, Nobutaka},

doi = {10.1371/journal.pone.0093683},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Takeuchi, Noda, Someya - 2014 - Complete genome sequence of the biocontrol strain Pseudomonas protegens Cab57 discovered in Japan reveal.pdf:pdf},
issn = {19326203},
journal = {PLoS ONE},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
number = {4},
publisher = {Public Library of Science},
title = {{Complete genome sequence of the biocontrol strain Pseudomonas protegens Cab57 discovered in Japan reveals strain-specific diversity of this species}},
volume = {9},
year = {2014}
}
@article{Tada2017,
abstract = {Methods: Twenty-seven clinical isolates of carbapenem-resistant Klebsiella pneumoniae with MICs ≥4 mg/L for imipenem or meropenem were obtained from inpatients in a hospital in Vietnam. Antimicrobial susceptibility tests and whole genome sequencing were performed. Multilocus sequence typing and the presence of drug resistant genes were determined and a maximum-likelihood phylogenetic tree was constructed by SNP alignment of whole genome sequencing data. Results: All the isolates harbored one of genes encoding carbapenemases, including KPC-2, NDM-1, NDM-4 and OXA-48. Of the isolates, 13 were resistant to arbekacin with MICs ≥256 mg/L and to amikacin with MICs ≥512 mg/L. These isolates harbored a gene encoding a 16S rRNA methylase, either RmtB or RmtC. Eighteen and 4 isolates belonged to international clones, ST15 and ST16, respectively. None of the isolates had colistin-resistant factors. Conclusion: Carbapenem-resistant K. pneumoniae isolates belonged to international clones spread in a medical setting in Vietnam, and that these isolates harbored genes encoding various combinations of carbapenemases and 16S rRNA methylases. This is the first report of KPC-2, NDM-4 and OXA-48 producers in a medical setting in Vietnam.},
author = {Tada, Tatsuya and Tsuchiya, Mitsuhiro and Shimada, Kayo and Nga, Tran Thi Thanh and Thu, Le Thi Anh and Phu, Truong Thien and Ohmagari, Norio and Kirikae, Teruo},
doi = {10.1186/s12879-017-2570-y},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Tada et al. - 2017 - Dissemination of Carbapenem-resistant Klebsiella pneumoniae clinical isolates with various combinations of Carbapen.pdf:pdf},
issn = {14712334},
journal = {BMC Infectious Diseases},
keywords = {Carbapenem-resistant Klebsiella pneumoniae,Carbapenemase,MLST,Molecular epidemiology},
month = {jul},
number = {1},
publisher = {BioMed Central Ltd.},
title = {{Dissemination of Carbapenem-resistant Klebsiella pneumoniae clinical isolates with various combinations of Carbapenemases (KPC-2,

NDM-1, NDM-4, and OXA-48) and 16S rRNA Methylases (RmtB and RmtC) in Vietnam}},
volume = {17},
year = {2017}
}
@article{Sun2020,
abstract = {Anthropogenic environments have been implicated in enrichment and exchange of antibiotic resistance genes and bacteria. Here we study the impact of confined and controlled swine farm environments on temporal changes in the gut microbiome and resistome of veterinary students with occupational exposure for 3 months. By analyzing 16S rRNA and whole metagenome shotgun sequencing data in tandem with culture-based methods, we show that farm exposure shapes the gut microbiome of students, resulting in enrichment of potentially pathogenic taxa and antimicrobial resistance genes. Comparison of students' gut microbiomes and resistomes to farm workers' and environmental samples revealed extensive sharing of resistance genes and bacteria following exposure and after three months of their visit. Notably, antibiotic resistance genes were found in similar genetic contexts in student samples and farm environmental samples. Dynamic Bayesian network modeling predicted that the observed changes partially reverse over a 4-6 month period. Our results indicate that acute changes in a human's living environment can persistently shape their gut microbiota and antibiotic resistome.},
author = {Sun, Jian and Liao, Xiao Ping and D'Souza, Alaric W. and Boolchandani, Manish and Li, Sheng Hui and Cheng, Ke and {Luis Mart{\'{i}}nez}, Jos{\'{e}} and Li, Liang and Feng, You Jun and Fang, Liang Xing and Huang, Ting and Xia, Jing and Yu, Yang and Zhou, Yu Feng and Sun, Yong Xue and Deng, Xian Bo and Zeng, Zhen Ling and Jiang, Hong Xia and Fang, Bing Hu and Tang, You Zhi and Lian, Xin Lei and Zhang, Rong Min and Fang, Zhi Wei and Yan, Qiu Long and Dantas, Gautam and Liu, Ya Hong},
doi = {10.1038/s41467-020-15222-y},
file = {:C$\backslash$Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Sun et al. - 2020 - Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms.pdf:pdf},
issn = {20411723},
journal = {Nature Communications},
month = {dec},
number = {1},
pmid = {32188862},
publisher = {Nature Research},
title = {{Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms}},
volume = {11},
year = {2020}
}
@article{Sui2018,
abstract = {Background: Carbapenem-resistant Klebsiella pneumoniae (CRKP) is a major cause of nosocomial infections worldwide. The transmission route of CRKP isolates within an outbreak is rarely described. This study aimed to reveal the molecular characteristics and transmission route of CRKP isolates within an outbreak of nosocomial infection. Methods: Collecting case information, active screening and targeted environmental monitoring were carried out. The antibiotic susceptibility, drug-

resistant genes, molecular subtype and whole genome sequence of CRKP strains were analyzed. Results: Between October and December 2011, 26 CRKP isolates were collected from eight patients in a surgical intensive care unit and subsequent transfer wards of Beijing Tongren hospital, China. All 26 isolates harbored bla KPC-2 , bla SHV-1 , and bla CTX-M-15 genes, had the same or similar pulsed-field gel electrophoresis patterns, and belonged to the sequence type 11 (ST11) clone. By comprehensive consideration of genomic and epidemiological information, a putative transmission map was constructed, including identifying one case as an independent event distinct from the other seven cases, and revealing two transmissions starting from the same case. Conclusions: This study provided the first report confirming an outbreak caused by K. pneumoniae ST11 clone co-harboring the bla KPC-2 , bla CTX-M-15 , and bla SHV-1 genes, and suggested that comprehensive consideration of genomic and epidemiological data can yield a fine transmission map of an outbreak and facilitate the control of nosocomial transmission.},
author = {Sui, Wenjun and Zhou, Haijian and Du, Pengcheng and Wang, Lijun and Qin, Tian and Wang, Mei and Ren, Hongyu and Huang, Yanfei and Hou, Jing and Chen, Chen and Lu, Xinxin},
doi = {10.1186/s13756-018-0363-8},
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issn = {20472994},
journal = {Antimicrobial Resistance and Infection Control},
keywords = {Carbapenemases,K. pneumoniae,KPC-2,Lista{_}Filtrada,Outbreak,Whole genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
number = {1},
publisher = {BioMed Central Ltd.},
title = {{Whole genome sequence revealed the fine transmission map of carbapenem-resistant Klebsiella pneumonia isolates within a nosocomial outbreak}},
volume = {7},
year = {2018}
}
@article{Stover2000,
abstract = {Pseudomonas aeruginosa is a ubiquitous environmental bacterium that is one of the top three causes of opportunistic human infections. A major factor in its prominence as a pathogen is its intrinsic resistance to antibiotics and disinfectants. Here we report the complete sequence of P. aeruginosa strain PAO1. At 6.3 million base pairs, this is the largest bacterial genome sequenced, and the sequence provides insights into the basis of the versatility and intrinsic drug resistance of P. aeruginosa. Consistent with its larger genome size and environmental adaptability, P. aeruginosa contains the highest proportion of regulatory genes observed for a bacterial genome and a large number of genes involved in the catabolism, transport and efflux of organic compounds as well as four potential chemotaxis systems. We propose that the size and complexity of the P. aeruginosa genome reflect an evolutionary adaptation permitting it to thrive in diverse environments and resist the effects of a variety of antimicrobial substances.},

author = {Stover, C. K. and Pham, X. Q. and Erwin, A. L. and Mizoguchi, S. D. and Warrener, P. and Hickey, M. J. and Brinkman, F. S.L. and Hufnagle, W. O. and Kowallk, D. J. and Lagrou, M. and Garber, R. L. and Goltry, L. and Tolentino, E. and Westbrock-Wadman, S. and Yuan, Y. and Brody, L. L. and Coulter, S. N. and Folger, K. R. and Kas, A. and Larbig, K. and Lim, R. and Smith, K. and Spencer, D. and Wong, G. K.S. and Wu, Z. and Paulsen, I. T. and Relzer, J. and Saler, M. H. and Hancock, R. E.W. and Lory, S. and Olson, M. V.},
doi = {10.1038/35023079},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Stover et al. - 2000 - Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.pdf:pdf},
issn = {00280836},
journal = {Nature},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {aug},
number = {6799},
pages = {959--964},
pmid = {10984043},
title = {{Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen}},
volume = {406},
year = {2000}
}
@article{Stoesser2014,
abstract = {NDM-producing Klebsiella pneumoniae strains represent major clinical and infection control challenges, particularly in re-source-limited settings with high rates of antimicrobial resistance. Determining whether transmission occurs at a gene, plasmid, or bacterial strain level and within hospital and/or the community has implications for monitoring and controlling spread. Whole-genome sequencing (WGS) is the highest-resolution typing method available for transmission epidemiology. We sequenced carbapenem-resistant K. pneumoniae isolates from 26 individuals involved in several infection case clusters in a Nepali neonatal unit and 68 other clinical Gram-negative isolates from a similar time frame, using Illumina and PacBio technologies. Within-outbreak chromosomal and closed-plasmid structures were generated and used as data set-specific references. Three temporally separated case clusters were caused by a single NDM K. pneumoniae strain with a conserved set of four plasmids, one being a 304,526-bp plasmid carrying blaNDM-1. The plasmids contained a large number of antimicrobial/heavy metal resistance and plasmid maintenance genes, which may have explained their persistence. No obvious environmental/human reservoir was found. There was no evidence of transmission of outbreak plasmids to other Gram-negative clinical isolates, although blaNDM variants were present in other isolates in different genetic contexts. WGS can effectively define complex antimicrobial resistance epidemiology. Wider sampling frames are required to contextualize outbreaks. Infection control may be effective in terminating outbreaks caused by particular strains, even in areas with widespread resistance, although this study could not demonstrate evidence supporting specific interventions. Larger, detailed studies are needed to characterize resistance genes, vectors, and host strains involved in disease, to enable effective intervention.},

author = {Stoesser, N. and Giess, A. and Batty, E. M. and Sheppard, A. E. and Walker, A. S. and Wilson, D. J. and Didelot, X. and Bashir, A. and Sebra, R. and Kasarskis, A. and Sthapit, B. and Shakya, M. and Kelly, D. and Pollard, A. J. and Peto, T. E.A. and Crook, D. W. and Donnelly, P. and Thorson, S. and Amatya, P. and Joshi, S.},
doi = {10.1128/AAC.03900-14},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Stoesser et al. - 2014 - Genome sequencing of an extended series of NDM-producing Klebsiella pneumoniae isolates from neonatal infection.pdf:pdf},
issn = {10986596},
journal = {Antimicrobial Agents and Chemotherapy},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
number = {12},
pages = {7347--7357},
publisher = {American Society for Microbiology},
title = {{Genome sequencing of an extended series of NDM-producing Klebsiella pneumoniae isolates from neonatal infections in a Nepali hospital characterizes the extent of community- Versus hospital-associated transmission in an endemic setting}},
volume = {58},
year = {2014}
}
@article{Shen2018,
abstract = {Objectives mcr-1-mediated colistin resistance in bacteria is concerning, as colistin is used in treating multidrug-resistant bacterial infections. And mcr-1-producing bacteria have been identified in multiple sources. Up to 248 million people use public transportation daily in China, however; public transportation hasn't been studied as a potential source of community-based transmission of mcr-1. Herein we investigated mcr-1-producing isolates from public transportation and explored the genomic characteristics of them. Methods Surface samples were collected from public transportation in Guangzhou, China, from October 2016 to April 2017. Polymerase chain reaction was performed to detect mcr-1 gene, plasmid replicon type and phylogenetic group. Minimum inhibitory concentrations (MICs) were determined by microdilution method. S1-nuclease digestion and pulsed-field gel electrophoresis (S1-PFGE) and Southern blotting were performed with mcr-1-harboring plasmids. Whole-genome sequencing was performed with mcr-1-producing isolates. Results Of the 737 samples with bacterial growth, 26 isolates were positive for mcr-1, including 23 Escherichia coli and 3 Klebsiella pneumoniae isolates. The E. coli isolates belonged to phylogroups A and B1. Most mcr-1-producing isolates were resistant to ampicillin (25), cefotaxime (21), fosfomycin (16), and gentamicin (15). S1-PFGE, Southern blotting and replicon typing showed that mcr-1 was mainly located on {\~{}}33.3 kb to {\~{}}220 kb IncX4, IncI2 and IncHI2 plasmids in E. coli, while located on {\~{}}33.3 kb untyped plasmid in K. pneumoniae. Several sequence types (ST), including ST2253, ST101, ST10 complex and ST37, were revealed. Between 53 and 66 (mean = 61.8) resistance genes were identified among mcr-1-producing isolates. Conclusions Public transportation may serve as a source of mcr-1-producing bacteria.},

author = {Shen, Cong and Feng, Siyuan and Chen, Hongtao and Dai, Min and Paterson, David L and Zheng, Xiaobin and Wu, Xingui and Zhong, Lan-Lan and Liu, Yan and Xia, Yong and Ma, Rui and Huang, Xi and Tian, Guo-Bao},
doi = {10.1093/cid/ciy661},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Shen et al. - 2018 - Transmission of mcr-1-Producing Multidrug-resistant Enterobacteriaceae in Public Transportation in Guangzhou, China.pdf:pdf},
issn = {1537-6591},
journal = {Clinical infectious diseases : an official publication of the Infectious Diseases Society of America},
number = {suppl{_}2},
pages = {S217--S224},
pmid = {30423047},
title = {{Transmission of mcr-1-Producing Multidrug-resistant Enterobacteriaceae in Public Transportation in Guangzhou, China.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30423047},
volume = {67},
year = {2018}
}
@article{Seth-Smith2019,
abstract = {Whole genome sequencing (WGS) has become the new gold standard for bacterial outbreak investigation, due to the high resolution available for typing. While sequencing is currently predominantly performed on Illumina devices, the preceding library preparation can be performed using various protocols. Enzymatic fragmentation library preparation protocols are fast, have minimal hands-on time, and work with small quantities of DNA. The aim of our study was to compare three library preparation protocols for molecular typing: Nextera XT (Illumina); Nextera Flex (Illumina); and QIAseq FX (Qiagen). We selected 12 ATCC strains from human Gram-positive and Gram-negative pathogens with {\%}G+C-content ranging from 27{\%} (Fusobacterium nucleatum) to 73{\%} (Micrococcus luteus), each having a high quality complete genome assembly available, to allow in-depth analysis of the resulting Illumina sequence data quality. Additionally, we selected isolates from previously analyzed cases of vancomycin-resistant Enterococcus faecium (VRE) (n = 7) and a local outbreak of Klebsiella aerogenes (n = 5). The number of protocol steps and time required were compared, in order to test the suitability for routine laboratory work. Data analyses were performed with standard tools commonly used in outbreak situations: Ridom SeqSphere+ for cgMLST; CLC genomics workbench for SNP analysis; and open source programs. Nextera Flex and QIAseq FX were found to be less sensitive than Nextera XT to variable {\%}G+C-content, resulting in an almost uniform distribution of read-depth. Therefore, low coverage regions are reduced to a minimum resulting in a more complete representation of the genome. Thus, with these two protocols, more alleles were detected in the cgMLST analysis, producing a higher resolution of closely related isolates. Furthermore, they result in a more complete representation of accessory genes. In particular, the high data quality and relative simplicity of the workflow of Nextera Flex stood out in this comparison. This thorough comparison within an ISO/IEC 17025 accredited environment will be of interest to those aiming to optimize their clinical microbiological genome sequencing.},

author = {Seth-Smith, Helena M B and Bonfiglio, Ferdinando and Cu{\'{e}}nod, Aline and Reist, Josiane and Egli, Adrian and W{\"{u}}thrich, Daniel},
doi = {10.3389/fpubh.2019.00241},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Seth-Smith et al. - 2019 - Evaluation of Rapid Library Preparation Protocols for Whole Genome Sequencing Based Outbreak Investigation.pdf:pdf},
issn = {2296-2565},
journal = {Frontiers in public health},
keywords = {Illumina,Lista{_}Filtrada,NGS,bacteria,comparison,library,next generation sequencing,prokaryotes,whole genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
number = {AUG},
pages = {241},
pmid = {31508405},
publisher = {Frontiers Media S.A.},
title = {{Evaluation of Rapid Library Preparation Protocols for Whole Genome Sequencing Based Outbreak Investigation.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/31508405 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6719548},
volume = {7},
year = {2019}
}
@article{Sekizuka2018a,
abstract = {A novel species of carbapenemase-producing Enterobacteriaceae (CPE) was isolated from a patient diagnosed with sigmoid colon diverticulitis. At first, laboratory testing suggested it was Klebsiella oxytoca or Pantoea sp.; however, a complete genome sequence of the isolate, MRY16-398, revealed that it could be novel species, most similar to [Kluyvera] intestini, of which taxonomic nomenclature is still under discussion. Orthologous conserved gene analysis among 42 related bacterial strains indicated that MRY16-398 was classified as the newly proposed genus Metakosakonia. Further, MRY16-398 was found to harbor the blaIMP-6 gene-positive class 1 integron (In722) in plasmid pMRY16-398{_}2 (IncN replicon, 47.4 kb in size). This finding implies that rare and opportunistic bacteria could be potential infectious agents. In conclusion, our results highlight the need for continuous monitoring for CPE even in nonpathogenic bacteria in the nosocomial environment.},
author = {Sekizuka, Tsuyoshi and Matsui, Mari and Takahashi, Tomiyo and Hayashi, Michiko and Suzuki, Satowa and Tokaji, Akihiko and Kuroda, Makoto},
doi = {10.3389/fmicb.2018.02853},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Sekizuka et al. - 2018 - Complete Genome Sequence of blaIMP-6-Positive Metakosakonia sp. MRY16-398 Isolate From the Ascites of a Diverti.pdf:pdf},
issn = {1664-302X},
journal = {Frontiers in microbiology},
keywords = {IncN,Kluyvera,Metakosakonia,blaIMP-6,carbapenemase},
month = {nov},
number = {NOV},
pages = {2853},

pmid = {30524415},
publisher = {Frontiers Media S.A.},
title = {{Complete Genome Sequence of blaIMP-6-Positive Metakosakonia sp. MRY16-398 Isolate From the Ascites of a Diverticulitis Patient.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30524415 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6262049},
volume = {9},
year = {2018}
}
@article{Saldana2019,
abstract = {Carbapenem-resistant Klebsiella pneumoniae , a bacterium of the family Enterobacteriaceae , is a high-priority antibiotic-resistant pathogen that causes nosocomial infections. Here, we describe the isolation and annotation of the K. pneumoniae siphophage Shelby, a T1-like siphophage encoding 78 proteins, of which 34 have a predicted function.},
author = {Saldana, Robert and Newkirk, Heather and Liu, Mei and Gill, Jason J. and Ramsey, Jolene},
doi = {10.1128/mra.01037-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Saldana et al. - 2019 - Complete Genome Sequence of Shelby, a Siphophage Infecting Carbapenemase-Producing Klebsiella pneumoniae.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {38},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Shelby, a Siphophage Infecting Carbapenemase-Producing Klebsiella pneumoniae}},
volume = {8},
year = {2019}
}
@article{Salazar2019,
abstract = {Carbapenemase-producing Klebsiella pneumoniae poses a significant public health threat due to its resistance to antibiotics. Siphophage Seifer was isolated and characterized as part of an effort to develop phage therapeutics to control this pathogen. This report describes the complete genome sequence of phage Seifer, which is a distant member of the χ-like siphovirus phage cluster.},
author = {Salazar, Adam J. and Lessor, Lauren and O'Leary, Chandler and Gill, Jason and Liu, Mei},
doi = {10.1128/mra.01289-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Salazar et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Siphophage Seifer.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {nov},
number = {46},

publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Siphophage Seifer}},
volume = {8},
year = {2019}
}
@article{Ruppe2017,
abstract = {Objectives Whole-genome sequencing (WGS) is a promising tool for identifying transmission pathways in outbreaks caused by multidrug-resistant bacteria. However, it is uncertain how the data produced by WGS can be best integrated into epidemiologic investigations. Methods We tested various genomic analyses to identify clonal groups in two distinct outbreaks of Klebsiella pneumoniae carbapenemase-producing K. pneumoniae that occurred in Switzerland in 2013 and 2015. In blinded fashion, we sequenced 12 strains involved in the two outbreaks, respectively, and six that were epidemiologically unrelated. We analysed genomic commonalities from conserved genes to plasmid-borne antibiotic resistance genes (ARGs) and contrasted these results with available epidemiologic evidence. Results Using WGS, blinded analysts correctly identified the two clusters of strains from the two outbreaks. Nonetheless, the 2015 index strain was found to be slightly different (1–3 single nucleotide variants) from the strains recovered from secondary cases, likely because prior long-term carriage (3 years) by the index patient allowed for genetic mutations over time. Also, we observed occasional loss of ARG-bearing plasmidic fragments in outbreak-causing strains. Conclusions Retrospective WGS analysis was successful in identifying clonal groups in both outbreaks. Still, data should be analysed with caution in cases of previous long-term carriage of the studied bacteria.},
author = {Rupp{\'{e}}, E. and Olearo, F. and Pires, D. and Baud, D. and Renzi, G. and Cherkaoui, A. and Goldenberger, D. and Huttner, A. and Fran{\c{c}}ois, P. and Harbarth, S. and Schrenzel, J.},
doi = {10.1016/j.cmi.2017.01.015},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Rupp{\'{e}} et al. - 2017 - Clonal or not clonal Investigating hospital outbreaks of KPC-producing Klebsiella pneumoniae with whole-genome seq.pdf:pdf},
issn = {14690691},
journal = {Clinical Microbiology and Infection},
keywords = {Carbapenemase,Clone,Evolution,Genomics,Klebsiella pneumoniae,Lista{_}Filtrada,Molecular typing,Outbreak,Whole-genome sequencing (WGS)},
mendeley-tags = {Lista{_}Filtrada},
month = {jul},
number = {7},
pages = {470--475},
publisher = {Elsevier B.V.},
title = {{Clonal or not clonal? Investigating hospital outbreaks of KPC-producing Klebsiella pneumoniae with whole-genome sequencing}},
volume = {23},
year = {2017}
}
@article{Ruan2020,
abstract = {Background: The prevalence of multidrug-resistant Klebsiella pneumoniae is increasingly being implicated worldwide in a variety of

infections with high mortalities. Here, we report the complete genome sequence of K. pneumoniae strain KP58, a pandrug-resistant K. pneumoniae strain that exhibits high levels of resistance to colistin and tigecycline in China. Methods: The K. pneumoniae strain KP58 was recovered from a urine sample of a female patient hospitalized in a tertiary hospital in Hangzhou, China. Antimicrobial susceptibility testing was performed and the minimum inhibitory concentrations (MICs) were determined. Whole-genome sequencing was performed using Illumina and Oxford nanopore sequencing technologies. Genomic features, antimicrobial resistance genes and virulence genes were comprehensively analysed by various bioinformatics approaches. In addition, genomic epidemiological and phylogenetic analyses of K. pneumoniae KP58 and closely related isolates were performed using the core genome multilocus sequence typing (cgMLST) analysis in BacWGSTdb, an online bacterial whole-genome sequence typing and source tracking database. Results: K. pneumoniae KP58 was resistant to all antimicrobial agents tested, including tigecycline and colistin. Combining the two sequencing technologies allowed a high-quality complete genome sequence of K. pneumoniae KP58 comprising one circular chromosome and five circular plasmids to be obtained. This strain harbours a variety of acquired antimicrobial resistance and virulence determinants. It also carried an ISKpn26-like insertion in the disrupted mgrB gene, which confers colistin resistance. The tigecycline resistance was associated with overexpression of the AcrAB efflux system. The closest relative of K. pneumoniae KP58 was another clinical isolate recovered from Hangzhou that differed by only 10 cgMLST loci. Conclusion: The dataset presented in this study provides essential insights into the evolution of antimicrobial-resistant K. pneumoniae in hospital settings and assists in the development of effective control strategies. Appropriate surveillance and control measures are essential to prevent its further dissemination.},
author = {Ruan, Zhi and Wu, Jianyong and Chen, Hangfei and Draz, Mohamed S. and Xu, Juan and He, Fang},
doi = {10.2147/IDR.S240404},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Ruan et al. - 2020 - Hybrid genome assembly and annotation of a pandrug-resistant klebsiella pneumoniae strain using nanopore and illumi.pdf:pdf},
issn = {11786973},
journal = {Infection and Drug Resistance},
keywords = {Hybrid assembly,Klebsiella pneumoniae,Lista{_}Filtrada,Nanopore,Pandrug resistance,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
pages = {199--206},
publisher = {Dove Medical Press Ltd.},
title = {{Hybrid genome assembly and annotation of a pandrug-resistant klebsiella pneumoniae strain using nanopore and illumina sequencing}},
volume = {13},
year = {2020}
}
@article{Roguet2020,
abstract = {Sewage overflows, agricultural runoff, and stormwater discharges introduce fecal pollution into surface waters. Distinguishing these sources is critical for evaluating water quality and formulating

remediation strategies. With the falling costs of sequencing, microbial community-based water quality assessment tools are under development. However, their application is limited by the need to build reference libraries, which requires extensive sampling of sources and bioinformatic expertise. Here, we introduce FORest Enteric Source IdentifiCation (FORENSIC; https://forensic.sfs.uwm.edu/), an online, library-independent source tracking platform based on random forest classification and 16S rRNA gene amplicon sequences to identify in environmental samples common fecal contamination sources, including humans, domestic pets, and agricultural animals. FORENSIC relies on a broad reference signature database of Bacteroidales and Clostridiales , two predominant bacterial groups that have coevolved with their hosts. As a result, these groups demonstrate cohesive and reliable assemblage patterns within mammalian species or among species sharing the same diet/physiology. We created a scalable and extensible platform that we tested for global applicability using samples collected in distant geographic locations. This Web application offers a fast and intuitive approach for fecal source identification, particularly in sewage-contaminated waters. IMPORTANCE FORENSIC is an online platform to identify sources of fecal pollution without the need to create reference libraries. FORENSIC is based on the ability of random forest classification to extract cohesive source microbial signatures to create classifiers despite individual variability and to detect the signatures in environmental samples. We primarily focused on defining sewage signals, which are associated with a high human health risk in polluted waters. To test for fecal contamination sources, the platform only requires paired-end reads targeting the V4 or V6 regions of the 16S rRNA gene. We demonstrated that we could use V4V5 reads trimmed to the V4 positions to generate the reference signature. The systematic workflow we describe to create and validate the signatures could be applied to many disciplines. With the increasing gap between advancing technology and practical applications, this platform makes sequence-based water quality assessments accessible to the public health and water resource communities.},
author = {Roguet, Ad{\'{e}}la{\"{i}}de and Esen, {\"{O}}zcan C. and Eren, A. Murat and Newton, Ryan J. and McLellan, Sandra L.},
doi = {10.1128/msystems.00869-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Roguet et al. - 2020 - FORENSIC an Online Platform for Fecal Source Identification.pdf:pdf},
issn = {2379-5077},
journal = {mSystems},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
number = {2},
pmid = {32184364},
publisher = {American Society for Microbiology},
title = {{FORENSIC: an Online Platform for Fecal Source Identification}},
volume = {5},
year = {2020}
}
@article{Rimoldi2017,

abstract = {Background: The emergence of carbapenem-resistant Klebsiella pneumoniae strains is threatening antimicrobial treatment. Methods: Sixty-eight carbapenemase-producing K. pneumoniae strains isolated at Luigi Sacco University Hospital-ASST Fatebenefratelli Sacco (Milan, Italy) between 2012 and 2014 were characterised microbiologically and molecularly. They were tested for drug susceptibility and carbapenemase phenotypes, investigated by means of repetitive extra-genic palindromic polymerase chain reaction (REP-PCR), and fully sequenced by means of next-generation sequencing for the in silico analysis of multi-locus sequence typing (MLST), their resistome, virulome and plasmid content, and their core single nucleotide polymorphism (SNP) genotypes. Results: All of the samples were resistant to carbapenems, other β-lactams and ciprofloxacin; many were resistant to aminoglycosides and tigecycline and seven were resistant to colistin. Resistome analysis revealed the presence of blaKPC genes and, less frequently blaSHV, blaTEM, blaCTX-M and blaOXA, which are related to resistance to carbapenem and other β-lactams. Other genes conferring resistance to aminoglycoside, fluoroquinolone, phenicol, sulphonamide, tetracycline, trimethoprim and macrolide-lincosamide-streptogramin were also detected. Genes related to AcrAB-TolC efflux pump-dependent and pump-independent tigecycline resistance mechanisms were investigated, but it was not possible to clearly correlate the genomic features with tigecycline resistance because of the presence of a common mutation in susceptible, intermediate and resistant strains. Concerning colistin resistance, the mgrB gene was disrupted by an IS5-like element, and the mobile mcr-1 and mcr-2 genes were not detected in two cases. The virulome profile revealed type-3 fimbriae and iron uptake system genes, which are important during the colonisation stage in the mammalian host environment. The in silico detected plasmid replicons were classified as IncFIB(pQil), IncFIB(K), ColRNAI, IncX1, IncX3, IncFII(K), IncN, IncL/M(pMU407) and IncFIA(HI1). REP-PCR showed five major clusters, and MLST revealed six different sequence types: 512, 258, 307, 1519, 745 and 101. Core SNP genotyping, which led to four clusters, correlated with the MLST data. Isolates of the same sequencing type often had common genetic traits, but the SNP analysis allowed greater strain tracking and discrimination than either the REP-PCR or MLST analysis. Conclusion: Our findings support the importance of implementing bacterial genomics in clinical medicine in order to complement traditional methods and overcome their limited resolution.},
author = {Rimoldi, Sara Giordana and Gentile, Bernardina and Pagani, Cristina and {Di Gregorio}, Annamaria and Anselmo, Anna and Palozzi, Anna Maria and Fortunato, Antonella and Pittiglio, Valentina and Ridolfo, Anna Lisa and Gismondo, Maria Rita and Rizzardini, Giuliano and Lista, Florigio},
doi = {10.1186/s12879-017-2760-7},
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issn = {14712334},
journal = {BMC Infectious Diseases},
keywords = {Bacteria epidemiology,Carbapenem-resistant Klebsiella pneumoniae,Lista{_}Filtrada,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},

month = {oct},
number = {1},
publisher = {BioMed Central Ltd.},
title = {{Whole genome sequencing for the molecular characterization of carbapenem-resistant Klebsiella pneumoniae strains isolated at the Italian ASST Fatebenefratelli Sacco Hospital, 2012-2014}},
volume = {17},
year = {2017}
}
@article{Richardson2019,
abstract = {Klebsiella pneumoniae is an opportunistic pathogen that is the cause of several hospital-acquired infections. Bacteriophages that target this bacterium could be used therapeutically as novel antimicrobial agents. Here, we present the complete genome sequence of the T1-like K. pneumoniae phage Sanco.},
author = {Richardson, Ryan W. and Lessor, Lauren and O'Leary, Chandler and Gill, Jason and Liu, Mei},
doi = {10.1128/mra.01252-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Richardson et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Siphophage Sanco.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {oct},
number = {44},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Siphophage Sanco}},
volume = {8},
year = {2019}
}
@article{Reuter2013,
abstract = {IMPORTANCE The latest generation of benchtop DNA sequencing platforms can provide an accurate whole-genome sequence (WGS) for a broad range of bacteria in less than a day. These could be used to more effectively contain the spread of multidrug-resistant pathogens. OBJECTIVE To compareWGS with standard clinical microbiology practice for the investigation of nosocomial outbreaks caused by multidrug-resistant bacteria, the identification of genetic determinants of antimicrobial resistance, and typing of other clinically important pathogens. DESIGN, SETTING, AND PARTICIPANTS A laboratory-based study of hospital inpatients with a range of bacterial infections at Cambridge University Hospitals NHS Foundation Trust, a secondary and tertiary referral center in England, comparingWGS with standard diagnostic microbiology using stored bacterial isolates and clinical information. MAIN OUTCOMES AND MEASURES Specimens were taken and processed as part of routine clinical care, and cultured isolates stored and referred for additional reference laboratory testing as necessary. Isolates underwent DNA extraction and library preparation prior to sequencing on the Illumina MiSeq platform. Bioinformatic analyses were performed by persons blinded to the clinical, epidemiologic, and antimicrobial susceptibility data. RESULTS We investigated 2 putative nosocomial outbreaks, one caused by

vancomycinresistant Enterococcus faecium and the other by carbapenem-resistant Enterobacter cloacae; WGS accurately discriminated between outbreak and nonoutbreak isolates and was superior to conventional typingmethods.We comparedWGS with standard methods for the identification of the mechanism of carbapenem resistance in a range of gram-negative bacteria (Acinetobacter baumannii, E cloacae, Escherichia coli, and Klebsiella pneumoniae). This demonstrated concordance between phenotypic and genotypic results, and the ability to determine whether resistance was attributable to the presence of carbapenemases or other resistance mechanisms. Whole-genome sequencing was used to recapitulate reference laboratory typing of clinical isolates of Neisseria meningitidis and to provide extended phylogenetic analyses of these. CONCLUSIONS AND RELEVANCE The speed, accuracy, and depth of information provided by WGS platforms to confirm or refute outbreaks in hospitals and the community, and to accurately define transmission of multidrug-resistant and other organisms, represents an important advance.},
author = {Reuter, Sandra and Ellington, Matthew J. and Cartwright, Edward J.P. and K{\"{o}}ser, Claudio U. and T{\"{o}}r{\"{o}}k, M. Est{\'{e}}e and Gouliouris, Theodore and Harris, Simon R. and Brown, Nicholas M. and Holden, Matthew T.G. and Quail, Mike and Parkhill, Julian and Smith, Geoffrey P. and Bentley, Stephen D. and Peacock, Sharon J.},
doi = {10.1001/jamainternmed.2013.7734},
file = {:C$\backslash$Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Reuter et al. - 2013 - Rapid bacterial whole-genome sequencing to enhance diagnostic and public health microbiology.pdf:pdf},
issn = {21686106},
journal = {JAMA Internal Medicine},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {15},
pages = {1397--1404},
pmid = {23857503},
title = {{Rapid bacterial whole-genome sequencing to enhance diagnostic and public health microbiology}},
volume = {173},
year = {2013}
}
@article{Rafiq2016,
abstract = {Klebsiella pneumoniae U25 is a multidrug resistant strain isolated from a tertiary care hospital in Chennai, India. Here, we report the complete annotated genome sequence of strain U25 obtained using PacBio RSII. This is the first report of the whole genome of K. pneumoniae species from Chennai. It consists of a single circular chromosome of size 5,491,870-bp and two plasmids of size 211,813 and 172,619-bp. The genes associated with multidrug resistance were identified. The chromosome of U25 was found to have eight antibiotic resistant genes [blaOXA-1, blaSHV-28, aac(6')1b-cr, catB3, oqxAB, dfrA1]. The plasmid pMGRU25-001 was found to have only one resistant gene (catA1) while plasmid pMGRU25-002 had 20 resistant genes [strAB, aadA1, aac(6')-Ib, aac(3)-IId, sul1,2, blaTEM-1A,1B, blaOXA-9, blaCTX-M-15, blaSHV-11, cmlA1, erm(B), mph(A)]. A mutation in the porin OmpK36 was identified which is likely to be associated with the intermediate resistance to carbapenems in the absence of carbapenemase genes. U25 is one of the few K. pneumoniae strains to harbour clustered regularly interspaced short

palindromic repeats (CRISPR) systems. Two CRISPR arrays corresponding to Cas3 family helicase were identified in the genome. When compared to K. pneumoniae NTUHK2044, a transposase gene InsH of IS5-13 was found inserted.},
author = {Rafiq, Zumaana and Sam, Nithin and Vaidyanathan, Rama},
doi = {10.1590/0074-02760150423},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Rafiq, Sam, Vaidyanathan - 2016 - Whole genome sequence of Klebsiella pneumoniae U25, a hypermucoviscous, multidrug resistant, biofilm p.pdf:pdf},
issn = {16788060},
journal = {Memorias do Instituto Oswaldo Cruz},
keywords = {CRISPR,Carbapenem resistant OMPK36 porin mutant,India,Klebsiella pneumoniae genome sequence,Lista{_}Filtrada,Multidrug resistant},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
number = {2},
pages = {144--146},
publisher = {Fundacao Oswaldo Cruz},
title = {{Whole genome sequence of Klebsiella pneumoniae U25, a hypermucoviscous, multidrug resistant, biofilm producing isolate from India}},
volume = {111},
year = {2016}
}
@article{Powell2019,
abstract = {Carbapenemase-producing Klebsiella pneumoniae is an important opportunistic pathogen due to its drug resistance. This study reports on the isolation and characterization of a podophage, named Pylas, infecting this bacterium. The complete genome of phage Pylas is described, and it is distantly related to the well-studied phage N4.},
author = {Powell, Jeffery E. and Lessor, Lauren and O'Leary, Chandler and Gill, Jason and Liu, Mei},
doi = {10.1128/mra.01287-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Powell et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Podophage Pylas.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {nov},
number = {46},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Podophage Pylas}},
volume = {8},
year = {2019}
}
@article{Palmieri2018,
abstract = {The prevalence of multidrug-resistant gram-negative bacteria has continuously increased over the past few years; bacterial strains producing AmpC β-lactamases and/or extended-spectrum β-

lactamases (ESBLs) are of particular concern. We combined high-resolution whole genome sequencing and phenotypic data to elucidate the mechanisms of resistance to cephamycin and β-lactamase in Korean Klebsiella pneumoniae strains, in which no AmpC-encoding genes were detected by PCR. We identified several genes that alone or in combination can potentially explain the resistance phenotype. We showed that different mechanisms could explain the resistance phenotype, emphasizing the limitations of the PCR and the importance of distinguishing closely-related gene variants.},
author = {Palmieri, Mattia and Schicklin, Stephane and Pelegrin, Andreu Coello and Chatellier, Sonia and Franceschi, Christine and Mirande, Caroline and Park, Yeon Joon and {Van Belkum}, Alex},
doi = {10.3343/alm.2018.38.4.367},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Palmieri et al. - 2018 - Phenotypic and genomic characterization of AmpC-producing Klebsiella pneumoniae from Korea.pdf:pdf},
issn = {22343814},
journal = {Annals of Laboratory Medicine},
keywords = {AmpC,Antibiotic resistance,Klebsiella pneumoniae,Korea,Lista{_}Filtrada,Whole Genome Sequencing},
mendeley-tags = {Lista{_}Filtrada},
number = {4},
pages = {367--370},
publisher = {Seoul National University, Institute for Cognitive Science},
title = {{Phenotypic and genomic characterization of AmpC-producing Klebsiella pneumoniae from Korea}},
volume = {38},
year = {2018}
}
@article{Olalekan2020,
abstract = {Objectives: Carbapenem-resistant Enterobacterales are a global problem, however little is known about the burden and origin of carbapenem resistance in Africa. The objectives of this study were to determine the proportion of carbapenem-resistant isolates among extended-spectrum β-lactamase-producing Enterobacterales (ESBL-E), to identify the underlying mechanisms of resistance and to assess the population structure of carbapenem-resistant isolates from Nigeria. Methods: ESBL-E isolates (n = 175) from infections were collected at four hospitals in Lagos, Nigeria, from July 2016 to January 2018 and were screened for carbapenem resistance using a VITEK{\textregistered}2 automated system. All carbapenem-resistant ESBL-E (CRE) were screened for blaKPC, blaCTX-M, blaCMY-2, blaNDM, blaVIM, blaIMP, blaOXA-181 and blaOXA-48 genes. Genotyping of randomly selected isolates was performed by whole-genome sequencing. Results: The isolates included Escherichia coli (n = 113; 64.6{\%}) and Klebsiella pneumoniae (n = 62; 35.4{\%}). Of the 175 ESBL-E isolates, 48 (27.4{\%}) were resistant to carbapenems (15 E. coli and 33 K. pneumoniae). CRE isolates carried blaNDM (n = 30; 62.5{\%}), blaNDM + blaOXA-181 (n = 10; 20.8{\%}), blaOXA-181 (n = 2; 4.2{\%}) and blaNDM + blaOXA-48 (n = 1; 2.1{\%}); no carbapenemase gene was detected in 5 isolates (10.4{\%}). The isolates showed low diversity and were mainly associated with multilocus sequence typing (MLST) sequence types ST410 for E. coli and ST395 and ST147 for K. pneumoniae. Conclusion: Carbapenem resistance is frequent among ESBL-E in Nigeria and

is mainly associated with blaNDM. Genotyping suggested that the observed clones possibly originated from Southeast Asia.},
author = {Olalekan, Adesola and Onwugamba, Francis and Iwalokun, Bamidele and Mellmann, Alexander and Becker, Karsten and Schaumburg, Frieder},
doi = {10.1016/j.jgar.2019.09.007},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Olalekan et al. - 2020 - High proportion of carbapenemase-producing Escherichia coli and Klebsiella pneumoniae among extended-spectrum β.pdf:pdf},
issn = {22137173},
journal = {Journal of Global Antimicrobial Resistance},
keywords = {Carbapenem-resistant Enterobacterales,Ceftazidime/avibactam,Extended-spectrum β-lactamase,Nigeria,blaNDM,blaOXA-181},
month = {jun},
pages = {8--12},
publisher = {Elsevier Ltd},
title = {{High proportion of carbapenemase-producing Escherichia coli and Klebsiella pneumoniae among extended-spectrum β-lactamase-producers in Nigerian hospitals}},
volume = {21},
year = {2020}
}
@article{Nordberg2018,
abstract = {Objectives: To analyse Klebsiella pneumoniae (KP) isolates from an outbreak of extended-spectrum β-lactamase (ESBL)-producing KP and Escherichia coli (EC) among infants admitted to neonatal intensive care units and to determine the duration of the intestinal colonization. Methods: We performed a prospective cohort study of intestinal ESBL-KP/ESBL-EC colonized neonates after a 5-month outbreak in two neonatal intensive care units. Whole genome sequencing, multilocus sequence typing, core genome multilocus sequence typing, pulsed-field electrophoresis and PCR for blaCTX-M were performed on the first isolates. Stool cultures were performed every second month after discharge until 2 years after discharge and at 5 years of age. The last positive samples were analysed with pulsed-field gel electrophoresis and PCR for blaCTX-M. The intestinal relative dominance of ESBL-producing Enterobacteriaceae was determined. Results: Thirteen of 17 patients colonized with ESBL-KP/ESBL-EC survived. Isolates from 16 of 17 patients were available for analysis and featured the same strain type of ESBL-KP: sequence type 101. The strain had capsule type K29 and harboured blaCTX-M-15. The virulence genes irp1, irp2, iutA, kfu and mrk were detected in all isolates. The median length of colonization was 12.5 months (range, 5–68 months). After 2 years, two of 13 patients were carriers of ESBL-KP and one of 13 of ESBL-EC. At 5 years of age, one neonate was colonized with ESBL-EC. No infant experienced an ESBL-KP/EC-infection during follow-up. Conclusions: Two years after discharge, almost one fourth of the study participants were ESBL/KP-EC carriers. ESBL-KP sequence type 101 persisted in two of 13 children for 23 to 26 months. One patient was colonized with ESBL-EC at age 5 years.},
author = {Nordberg, V. and Jonsson, K. and Giske, C. G. and Iversen, A. and Aspevall, O. and Jonsson, B. and Camporeale, A. and Norman, M. and Nav{\'{e}}r, L.},
doi = {10.1016/j.cmi.2017.12.028},

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issn = {14690691},
journal = {Clinical Microbiology and Infection},
keywords = {ESBL,Intestinal colonization,Klebsiella pneumoniae,Neonatal,Sequence type},
month = {sep},
number = {9},
pages = {1004--1009},
publisher = {Elsevier B.V.},
title = {{Neonatal intestinal colonization with extended-spectrum β-lactamase–producing Enterobacteriaceae—a 5-year follow-up study}},
volume = {24},
year = {2018}
}
@article{Nguyen2019a,
abstract = { May is a newly isolated myophage that infects multidrug-resistant strains of Klebsiella pneumoniae , a pathogen that is associated with antibiotic-resistant infections in humans. The genome of May has been shown to be similar to that of phage Vi01. },
author = {Nguyen, Katherine T. and Bonasera, Rachele and Benson, Garret and Hernandez-Morales, Adriana C. and Gill, Jason J. and Liu, Mei},
doi = {10.1128/mra.00252-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Nguyen et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Myophage May.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
month = {may},
number = {19},
publisher = {American Society for Microbiology},
title = {{ Complete Genome Sequence of Klebsiella pneumoniae Myophage May }},
volume = {8},
year = {2019}
}
@article{Nguyen2015,
abstract = {Klebsiella pneumoniae is a Gram-negative bacterium in the family Enterobacteriaceae. It is associated with numerous nosocomial infections, including respiratory and urinary tract infections in humans. The following reports the complete genome sequence of K. pneumoniae carbapenemase-producing K. pneumoniae T1-like siphophage Sushi and describes its major features.},
author = {Nguyen, Dat T and Lessor, Lauren E and Cahill, Jesse L and Rasche, Eric S and {Kuty Everett}, Gabriel F},
doi = {10.1128/genomeA.00994-15},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Nguyen et al. - 2015 - Complete Genome Sequence of Klebsiella pneumoniae Carbapenemase-Producing K. pneumoniae Siphophage Sushi.pdf:pdf},
issn = {2169-8287},

journal = {Genome announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {5},
pmid = {26337889},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Carbapenemase-Producing K. pneumoniae Siphophage Sushi.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26337889 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4559738},
volume = {3},
year = {2015}
}
@article{Newkirk2019,
abstract = {Klebsiella pneumoniae is an opportunistic pathogen that has become an increasing problem in nosocomial infections. Studying phages that infect K. pneumoniae may lead to improvements in phage therapeutics for treating these infections. Here, the full genome sequence of Menlow, a Vi01-like phage, is introduced and described.},
author = {Newkirk, Heather N. and Lessor, Lauren and Gill, Jason J. and Liu, Mei},
doi = {10.1128/mra.00192-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Newkirk et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Myophage Menlow.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
number = {17},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Myophage Menlow}},
volume = {8},
year = {2019}
}
@article{Movert2013,
abstract = {Group B streptococcus (GBS) is a leading neonatal pathogen and a growing cause of invasive disease in the elderly, with clinical manifestations such as pneumonia and sepsis. Despite its clinical importance, little is known about innate immunity against GBS in humans. Here, we analyze the role of human group IIA secreted phospholipase A2 (sPLA2-IIA), a bactericidal enzyme induced during acute inflammation, in innate immunity against GBS. We show that clinical GBS isolates are highly sensitive to killing by sPLA2-IIA but not by human antimicrobial peptides. Using transgenic mice that express human sPLA2-IIA, we demonstrate that this enzyme is crucial for host protection against systemic infection and lung challenge by GBS. We found that acute sera from humans diagnosed with invasive GBS disease contain increased levels of sPLA2-IIA compared with normal sera from healthy individuals, indicating that GBS induces an sPLA2-IIA response in blood during human infection. We demonstrate that clinically relevant GBS strains are

rapidly killed in these acute sera. We also demonstrate that the bactericidal effect is entirely due to sPLA2-IIA, showing that sPLA2-IIA might represent an important component of humoral innate immunity against GBS. Our data provide experimental and clinical evidence that sPLA2-IIA protects humans against GBS infections.},
author = {Movert, Elin and Wu, Yongzheng and Lambeau, G{\'{e}}rard and Kahn, Fredrik and Touqui, Lhousseine and Areschoug, Thomas},
doi = {10.1093/INFDIS},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Movert et al. - 2013 - Using Patient Pathways to Accelerate the Drive to Ending Tuberculosis.pdf:pdf},
isbn = {1537-6613 (Electronic)$\backslash$r0022-1899 (Linking)},
journal = {Journal of Infectious Diseases},
keywords = {Antimicrobial molecules,Bactericidal,Group B streptococcus,Innate immunity},
number = {12},
pages = {2025--2035},
publisher = {Oxford Academic},
title = {{Using Patient Pathways to Accelerate the Drive to Ending Tuberculosis}},
url = {https://academic.oup.com/jid/issue/216/suppl{_}7},
volume = {208},
year = {2013}
}
@article{Morohoshi2017,
abstract = {Pseudomonas chlororaphis subsp. aurantiaca StFRB508 regulates phenazine production through N-acyl-l-homoserine lactone (AHL)-mediated quorum sensing. Two sets of AHL-synthase and AHL-receptor genes, phzI/phzR and aurI/aurR, have been identified from the incomplete draft genome of StFRB508. In the present study, the complete genome of StFRB508, comprising a single chromosome of 6,997,933 bp, was sequenced. The complete genome sequence revealed the presence of a third quorum-sensing gene set, designated as csaI/csaR. An LC-MS/MS analysis revealed that StFRB508 produced six types of AHLs, with the most important AHL being N-(3-hydroxyhexanoyl)-l-homoserine lactone (3-OH-C6-HSL). PhzI mainly catalyzed the biosynthesis of 3-OH-C6-HSL, while AurI and CsaI catalyzed that of N-hexanoyl-l-homoserine lactone and N-(3-oxohexanoyl)-l-homoserine lactone, respectively. A mutation in phzI decreased phenazine production, whereas that in aurI or csaI did not. A phzI aurI csaI triple mutant (508ΔPACI) did not produce phenazine. Phenazine production by 508ΔPACI was stimulated by exogenous AHLs and 3-OH-C6-HSL exerted the strongest effects on phenazine production at the lowest concentration tested (0.1 μM). The plant protection efficacy of 508ΔPACI against an oomycete pathogen was lower than that of wild-type StFRB508. These results demonstrate that the triplicate quorum-sensing system plays an important role in phenazine production by and the biocontrol activity of StFRB508.},
author = {Morohoshi, Tomohiro and Yamaguchi, Takahito and Xie, Xiaonan and Wang, Wen-Zhao and Takeuchi, Kasumi and Someya, Nobutaka},
doi = {10.1264/jsme2.ME16162},
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issn = {1347-4405},
journal = {Microbes and environments},
keywords = {Acylhomoserine
lactone,Biocontrol,Lista{_}Filtrada,Phenazine,Pseudomonas
chlororaphis,Quorum sensing},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
number = {1},
pages = {47--53},
pmid = {28239068},
publisher = {Japanese Society of Microbial Ecology},
title = {{Complete Genome Sequence of Pseudomonas chlororaphis subsp.
aurantiaca Reveals a Triplicate Quorum-Sensing Mechanism for Regulation
of Phenazine Production.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28239068
http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5371074},
volume = {32},
year = {2017}
}
@article{Mohsin2020,
abstract = {OBJECTIVES To report the draft genome sequences of two
multidrug-resistant bacteria,Bacteroides thetaiotaomicron F9-2 and
Escherichia coli 09-02E, isolated from stool samples of a healthy
resident in Vietnam. METHODS Genome sequences were determined using the
MiSeq and MinION platforms. Genomic assembly was performed using Platanus
and Canu. The DDBJ Fast Annotation and Submission Tool were used for
genome annotation. RESULTS The genome ofB. thetaiotaomicron F9-2
comprised 6,283,774 bp with a 42.7{\%} GC content and 4,802 protein-
coding sequences, whereas the E. coli 09-02E genome comprised 5,246,320
bp with a 50.6{\%} GC content and 4,991 protein-coding sequences. Both
strains harbored common antibiotic resistance genes, such as those for
sulfonamide (sul2) and aminoglycoside (strA and strB). However, the sul2-
strA-strB cassette was located on the chromosome and plasmid of strains
F9-2 and 09-02E, respectively. These genes were flanked by different
insertion sequences. CONCLUSIONS Considering their diversities in the
human gut resistome, these strains would be of considerable interest for
detailed comparative genomic analysis. Notably, the samesul2 cassette was
found in facultative and obligate anaerobic bacterial isolates (resident
in humans). However, the differential location of the cassette indicates
a possible mechanism of gene transfer among gut microbes.},
author = {Mohsin, Mashkoor and Tanaka, Kaori and Kawahara, Ryuji and
Kondo, Shinji and Noguchi, Hideki and Motooka, Daisuke and Nakamura,
Shota and Khong, Diep Thi and Nguyen, Thang Nam and Hoang, Trong Nang and
Yamamoto, Yoshimasa},
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comparative analysis of the genomes of Bacteroides thetaiotaomicron and
Escherichi(2).pdf:pdf},
issn = {2213-7173},
journal = {Journal of global antimicrobial resistance},
keywords = {Anaerobe,Antibiotic resistance gene,Bacteroides
thetaiotaomicron,Escherichia coli,Gut microbes,Whole-genome
sequencing,sul2},

month = {mar},
pmid = {32200128},
publisher = {Elsevier BV},
title = {{Whole-genome sequencing and comparative analysis of the genomes of Bacteroides thetaiotaomicron and Escherichia coli isolated from a healthy resident in Vietnam.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32200128},
year = {2020}
}
@article{Miro2020,
abstract = {Whole-genome sequencing (WGS)-based typing methods have emerged as promising and highly discriminative epidemiological tools. In this study, we combined gene-by-gene allele calling and core genome single nucleotide polymorphism (cgSNP) approaches to investigate the genetic relatedness of a well-characterized collection of OXA-48-producing Klebsiella pneumoniae isolates. We included isolates from the predominant sequence type ST405 (n = 31) OXA-48-producing K. pneumoniae clone and isolates from ST101 (n = 3), ST14 (n = 1), ST17 (n = 1), and ST1233 (n = 1), obtained from eight Catalan hospitals. Core-genome multilocus sequence typing (cgMLST) schemes from Institut Pasteur's BIGSdb-Kp (634 genes) and SeqSphere+ (2,365 genes), and a SeqSphere+ whole-genome MLST (wgMLST) scheme (4,891 genes) were used. Allele differences or allelic mismatches and the genetic distance, as the proportion of allele differences, were used to interpret the results from a gene-by-gene approach, whereas the number of SNPs was used for the cgSNP analysis. We observed between 0–10 and 0–14 allele differences among the predominant ST405 using cgMLST and wgMLST from SeqSphere+, respectively, and {\textless}2 allelic mismatches when using Institut Pasteur's BIGSdb-Kp cgMLST scheme. For ST101, we observed 14 and 54 allele differences when using cgMLST and wgMLST SeqSphere+, respectively, and 2–5 allelic mismatches for BIGSdb-Kp cgMLST. A low genetic distance ({\textless}0.0035, a previously established threshold for epidemiological link) was generally in concordance with a low number of allele differences ({\textless}8) when using the SeqSphere+ cgMLST scheme. The cgSNP analysis showed 6–29 SNPs in isolates with identical allelic SeqSphere+ cgMLST profiles and 16–61 cgSNPs among ST405 isolates. Furthermore, comparison of WGS-based typing results with previously obtained MLST and pulsed-field gel electrophoresis (PFGE) data showed some differences, demonstrating the different molecular principles underlying these techniques. In conclusion, the use of the different WGS-based typing methods that were used to elucidate the genetic relatedness of clonal OXA-48-producing K. pneumoniae all led to the same conclusions. Furthermore, threshold parameters in WGS-based typing methods should be applied with caution and should be used in combination with clinical epidemiological data and population and species characteristics.},
author = {Miro, Elisenda and Rossen, John W.A. and Chlebowicz, Monika A. and Harmsen, Dag and Brisse, Sylvain and Passet, Virginie and Navarro, Ferran and Friedrich, Alex W. and Garc{\'{i}}a-Cobos, S.},
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issn = {1664302X},

journal = {Frontiers in Microbiology},
keywords = {K. pneumoniae,Lista{_}Filtrada,OXA-48,WGS,cgMLST,molecular epidemiology,wgMLST},
mendeley-tags = {Lista{_}Filtrada},
month = {jan},
publisher = {Frontiers Media S.A.},
title = {{Core/Whole Genome Multilocus Sequence Typing and Core Genome SNP-Based Typing of OXA-48-Producing Klebsiella pneumoniae Clinical Isolates From Spain}},
volume = {10},
year = {2020}
}
@article{Mijalis2015,
abstract = {Klebsiella pneumoniae is a Gram-negative pathogen frequently associated with antibiotic-resistant nosocomial infections. Bacteriophage therapy against K. pneumoniae may be possible to combat these infections. The following describes the complete genome sequence and key features of the pseudo-T-even K. pneumoniae carbapenemase (KPC)-producing K. pneumoniae myophage Miro.},
author = {Mijalis, Eleni M and Lessor, Lauren E and Cahill, Jesse L and Rasche, Eric S and {Kuty Everett}, Gabriel F},
doi = {10.1128/genomeA.01137-15},
file = {:C$\backslash$$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Mijalis et al. - 2015 - Complete Genome Sequence of Klebsiella pneumoniae Carbapenemase-Producing K. pneumoniae Myophage Miro.pdf:pdf},
issn = {2169-8287},
journal = {Genome announcements},
keywords = {Lista{_}Filtrada},
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pmid = {26430050},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Carbapenemase-Producing K. pneumoniae Myophage Miro.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26430050 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4591322},
volume = {3},
year = {2015}
}
@article{Meletis2020,
abstract = {Objectives: Greece is endemic for KPC-encoding Klebsiella pneumoniae; however, until now, reports have referred only to hospital isolates. In this study, seven KPC-encoding K. pneumoniae isolated in private laboratories from non-hospitalised patients were characterised. Methods: Whole-genome sequencing was performed on an Illumina MiniSeq Sequencing System. Multilocus sequence typing (MLST) was performed using a BLAST-based approach, and antimicrobial resistance genes and plasmid replicons were identified using ResFinder and PlasmidFinder, respectively. The Rapid Annotation using Subsystem Technology (RAST) v.2.0 server was used for genome annotation of virulence, pathogenesis and defence genes. Results: Six isolates belonged to the major MLST sequence type 258 (ST258) and one to ST39. The resistome included genes

encoding resistance mechanisms to β-lactams, aminoglycosides, quinolones, sulfonamides, trimethoprim, fosfomycin and phenicols, conferring multidrug-resistant phenotypes. Moreover, various genes involved in virulence, pathogenesis and defence have been identified. Conclusions: It is highly probable that these isolates were acquired during previous hospitalisation in Greek hospitals. The presence of KPC-encoding K. pneumoniae in non-hospitalised patients is alarming, although it is not yet possible to assess its actual impact.},
author = {Meletis, Georgios and Chatzopoulou, Fani and Fragkouli, Aikaterini and Alexandridou, Magdalini and Mavrovouniotis, Ilias and Chatzinikolaou, Anastasia and Chatzidimitriou, Dimitrios},
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issn = {22137173},
journal = {Journal of Global Antimicrobial Resistance},
keywords = {Greece,KPC,Klebsiella pneumoniae,Lista{_}Filtrada,ST258,ST39,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
pages = {78--81},
publisher = {Elsevier Ltd},
title = {{Whole-genome sequencing study of KPC-encoding Klebsiella pneumoniae isolated in Greek private laboratories from non-hospitalised patients}},
volume = {20},
year = {2020}
}
@article{Mcclelland2001,
author = {Mcclelland, Michael and Sanderson, Kenneth E and Spieth, John and Clifton, Sandra W and Latreille, Phil and Courtney, Laura and Porwollik, Steffen and Ali, Johar and Dante, Mike and Du, Feiyu and Hou, Shunfang and Layman, Dan and Grewal, Neenu and Mulvaney, Elizabeth and Ryan, Ellen and Sun, Hui},
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isbn = {0028-0836 (Print)$\backslash$n0028-0836 (Linking)},
issn = {0028-0836},
number = {October},
pmid = {11677609},
title = {{Complete-genome-sequence-of-Sa-8d48a7a1-5360-41bf-9afa-cb52873a57cc}},
volume = {413},
year = {2001}
}
@article{Martinez-Garcia2015,
abstract = {The genome sequence of more than 100 Pseudomonas syringae strains has been sequenced to date; however only few of them have been fully assembled, including P. syringae pv. syringae B728a. Different strains of pv. syringae cause different diseases and have different host

specificities; so, UMAF0158 is a P. syringae pv. syringae strain related to B728a but instead of being a bean pathogen it causes apical necrosis of mango trees, and the two strains belong to different phylotypes of pv.syringae and clades of P. syringae. In this study we report the complete sequence and annotation of P. syringae pv. syringae UMAF0158 chromosome and plasmid pPSS158. A comparative analysis with the available sequenced genomes of other 25 P. syringae strains, both closed (the reference genomes DC3000, 1448A and B728a) and draft genomes was performed. The 5.8 Mb UMAF0158 chromosome has 59.3{\%} GC content and comprises 5017 predicted protein-coding genes. Bioinformatics analysis revealed the presence of genes potentially implicated in the virulence and epiphytic fitness of this strain. We identified several genetic features, which are absent in B728a, that may explain the ability of UMAF0158 to colonize and infect mango trees: the mangotoxin biosynthetic operon mbo, a gene cluster for cellulose production, two different type III and two type VI secretion systems, and a particular T3SS effector repertoire. A mutant strain defective in the rhizobial-like T3SS Rhc showed no differences compared to wild-type during its interaction with host and non-host plants and worms. Here we report the first complete sequence of the chromosome of a pv. syringae strain pathogenic to a woody plant host. Our data also shed light on the genetic factors that possibly determine the pathogenic and epiphytic lifestyle of UMAF0158. This work provides the basis for further analysis on specific mechanisms that enable this strain to infect woody plants and for the functional analysis of host specificity in the P. syringae complex.},
author = {Mart{\'{i}}nez-Garc{\'{i}}a, Pedro Manuel and Rodr{\'{i}}guez-Palenzuela, Pablo and Arrebola, Eva and Carri{\'{o}}n, V{\'{i}}ctor J and Guti{\'{e}}rrez-Barranquero, Jos{\'{e}} Antonio and P{\'{e}}rez-Garc{\'{i}}a, Alejandro and Ramos, Cayo and Cazorla, Francisco M and de Vicente, Antonio},
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issn = {1932-6203},
journal = {PloS one},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {aug},
number = {8},
pages = {e0136101},
pmid = {26313942},
publisher = {Public Library of Science},
title = {{Bioinformatics Analysis of the Complete Genome Sequence of the Mango Tree Pathogen Pseudomonas syringae pv. syringae UMAF0158 Reveals Traits Relevant to Virulence and Epiphytic Lifestyle.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/26313942 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4551802},
volume = {10},
year = {2015}
}
@article{Mannion2020,

abstract = { Cotton-top tamarins (CTTs) are an ideal model of human inflammatory bowel disease (IBD) because these animals develop multigenerational, lower bowel cancer. We previously isolated and characterized a novel enterohepatic Helicobacter species, Helicobacter saguini , from CTTs with IBD and documented that H. saguini infection in germfree C57BL IL-10 -/- mice recapitulates IBD, suggesting that H. saguini influences IBD etiopathogenesis. In this study, we utilized a germfree IL-10 -/- model to illustrate that H. saguini infection can naturally transmit and infect four generations and cause significant intestinal inflammatory pathology. Additionally, whole-genome sequencing of representative H. saguini isolates from each generation of IL-10 -/- mice revealed gene mutations suggestive of multigenerational evolution. Overall, these results support that specific bacterial species with pathogenic potential, like H. saguini , are transmissible microorganisms in the etiopathogenesis of IBD in CTTs and reinforces the importance of specific microbiota in the pathogenesis of IBD in humans. IMPORTANCE While family history is a significant risk factor for developing inflammatory bowel disease (IBD), it is unclear whether the microbiome from parents is a transmissible influence on disease in their offspring. Furthermore, it is unknown whether IBD-associated microbes undergo genomic adaptations during multigenerational transmission and chronic colonization in their hosts. Herein, we show that a single bacterial species, Helicobacter saguini , isolated from a nonhuman primate species with familial IBD, is transmissible from parent to offspring in germfree IL-10 -/- mice and causes multigenerational IBD. Additionally, whole-genome sequence analysis of H. saguini isolated from different mouse generations identified microevolutions in environmental interaction, nutrient metabolism, and virulence factor genes that suggest that multigenerational transmission may promote adaptations related to colonization and survival in new hosts and chronic inflammatory environments. The findings from our study highlight the importance of specific bacterial species with pathogenic potential, like H. saguini , as transmissible microorganisms in the etiopathogenesis of IBD. },
author = {Mannion, Anthony and Shen, Zeli and Feng, Yan and Puglisi, Dylan and Muthupalani, Sureshkumar and Whary, Mark T. and Fox, James G.},
doi = {10.1128/msphere.00011-20},
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issn = {23795042},
journal = {mSphere},
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number = {2},
publisher = {American Society for Microbiology},
title = {{ Natural Transmission of Helicobacter saguini Causes Multigenerational Inflammatory Bowel Disease in C57/129 IL-10 -/- Mice }},
volume = {5},
year = {2020}
}
@article{Magalhaes2020,
abstract = {Pseudomonas aeruginosa is one of the main pathogens responsible for nosocomial infections, particularly in Intensive Care

Units (ICUs). Due to the complexity of P. aeruginosa ecology, only powerful typing methods can efficiently allow its surveillance and the detection during expanding outbreaks. An increase in P. aeruginosa incidence was observed in the ICUs of the Lausanne University Hospital between 2010 and 2014. All clinical and environmental isolates retrieved during this period were typed with Double locus sequence typing (DLST), which detected the presence of three major genotypes: DLST 1–18, DLST 1–21, and DLST 6–7. DLST 1–18 (ST1076) isolates were previously associated with an epidemiologically well-described outbreak in the burn unit. Nevertheless, DLST 1–21 (ST253) and DLST 6–7 (ST17) showed sporadic occurrence with only few cases of possible transmission between patients. Whole genome sequencing (WGS) was used to further investigate the epidemiology of these three major P. aeruginosa genotypes in the ICUs. WGS was able to differentiate between outbreak and non-outbreak isolates and confirm suspected epidemiological links. Additionally, whole-genome single nucleotide polymorphisms (SNPs) results considered isolates as closely related for which no epidemiological links were suspected, expanding the epidemiological investigation to unsuspected links. The combination of a first-line molecular typing tool (DLST) with a more discriminatory method (WGS) proved to be an accurate and cost-efficient typing strategy for the investigation of P. aeruginosa epidemiology in the ICUs.},
author = {Magalh{\~{a}}es, B{\'{a}}rbara and Valot, Benoit and Abdelbary, Mohamed M.H. and Prod'hom, Guy and Greub, Gilbert and Senn, Laurence and Blanc, Dominique S.},
doi = {10.3389/fpubh.2020.00003},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Magalh{\~{a}}es et al. - 2020 - Combining Standard Molecular Typing and Whole Genome Sequencing to Investigate Pseudomonas aeruginosa Epidemio.pdf:pdf},
issn = {22962565},
journal = {Frontiers in Public Health},
keywords = {Lista{_}Filtrada,Pseudomonas aeruginosa,double locus sequence typing,genomic epidemiology,molecular epidemiology,molecular typing,whole genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {jan},
publisher = {Frontiers Media S.A.},
title = {{Combining Standard Molecular Typing and Whole Genome Sequencing to Investigate Pseudomonas aeruginosa Epidemiology in Intensive Care Units}},
volume = {8},
year = {2020}
}
@article{Magalhaes2020a,
abstract = {Pseudomonas aeruginosa is one of the main pathogens responsible for nosocomial infections, particularly in Intensive Care Units (ICUs). Due to the complexity of P. aeruginosa ecology, only powerful typing methods can efficiently allow its surveillance and the detection during expanding outbreaks. An increase in P. aeruginosa incidence was observed in the ICUs of the Lausanne University Hospital between 2010 and 2014. All clinical and environmental isolates retrieved during this period were typed with Double locus sequence typing (DLST), which detected the presence of three major genotypes: DLST 1–18, DLST 1–

21, and DLST 6-7. DLST 1-18 (ST1076) isolates were previously associated with an epidemiologically well-described outbreak in the burn unit. Nevertheless, DLST 1-21 (ST253) and DLST 6-7 (ST17) showed sporadic occurrence with only few cases of possible transmission between patients. Whole genome sequencing (WGS) was used to further investigate the epidemiology of these three major P. aeruginosa genotypes in the ICUs. WGS was able to differentiate between outbreak and non-outbreak isolates and confirm suspected epidemiological links. Additionally, whole-genome single nucleotide polymorphisms (SNPs) results considered isolates as closely related for which no epidemiological links were suspected, expanding the epidemiological investigation to unsuspected links. The combination of a first-line molecular typing tool (DLST) with a more discriminatory method (WGS) proved to be an accurate and cost-efficient typing strategy for the investigation of P. aeruginosa epidemiology in the ICUs.},
author = {Magalh{\~{a}}es, B{\'{a}}rbara and Valot, Benoit and Abdelbary, Mohamed M.H. and Prod'hom, Guy and Greub, Gilbert and Senn, Laurence and Blanc, Dominique S.},
doi = {10.3389/fpubh.2020.00003},
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issn = {22962565},
journal = {Frontiers in Public Health},
keywords = {Lista{_}Filtrada,Pseudomonas aeruginosa,double locus sequence typing,genomic epidemiology,molecular epidemiology,molecular typing,whole genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {jan},
publisher = {Frontiers Media S.A.},
title = {{Combining Standard Molecular Typing and Whole Genome Sequencing to Investigate Pseudomonas aeruginosa Epidemiology in Intensive Care Units}},
volume = {8},
year = {2020}
}
@article{Machuca2019,
abstract = {The aim of this study was to characterize the population structure of 56 OXA-48-like-producing Klebsiella pneumoniae isolates, as well as extended-spectrum -lactamase (ESBL) and carbapenemase genes, recovered in 2014 and 2015 from 16 hospitals in southern Spain. XbaI pulsed-field gel electrophoresis and multilocus sequence typing were performed to assess clonal relatedness. Representative isolates belonging to OXA-48-like-producing and CTX-M-15-coproducing pulsotypes were selected for characterization of bla OXA-48-like - and bla CTX-M-15 - carrying plasmids by PCR-based replicon typing, IncF subtyping, whole-genome sequencing analysis, and typing of Tn1999 structures. Forty-three OXA-48-producing isolates (77{\%}) were recovered from clinical samples and 13 from rectal swabs. All isolates showed ertapenem MIC values of 1 mg/liter, although 70{\%} remained susceptible to imipenem and meropenem. Forty-nine isolates (88{\%}) produced OXA-48, 5 produced OXA-245, and 2 produced OXA-181. Twenty-eight different pulsotypes (5 detected in more than 1 hospital) and 16 sequence types (STs) were found. The most

prevalent clones were ST15 (29 isolates [52{\%}]) and ST11 (7 isolates [13{\%}]). Forty-five (80{\%}) isolates were also bla CTX-M-15 carriers. The bla CTX-M-15 gene was mostly (82{\%}) located on IncR plasmids, although ST15 and ST11 isolates also carried this gene on IncF plasmids. The composite transposon variant Tn1999.2-like was the most frequent. Among ST15 and ST11 isolates, different transposon variants were observed. The bla OXA-48 gene was mainly located on IncL plasmids, although IncM plasmids were also observed. The spread of OXA-48-like-producing K. pneumoniae in southern Spain is mainly due to ST15 and ST11 clones. Variation within clonal lineages could indicate different acquisition events for both ESBL and carbapenemase traits.},
author = {Machuca, Jes{\'{u}}s and L{\'{o}}pez-Cerero, Lorena and Fern{\'{a}}ndez-Cuenca, Felipe and Mora-Navas, Laura and Mediavilla-Gradolph, Concepci{\'{o}}n and L{\'{o}}pez-Rodr{\'{i}}guez, Inmaculada and Pascual, {\'{A}}lvaro},
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issn = {10986596},
journal = {Antimicrobial Agents and Chemotherapy},
keywords = {Klebsiella pneumoniae,OXA-48,Southern Spain},
month = {jan},
number = {1},
publisher = {American Society for Microbiology},
title = {{OXA-48-Like-Producing Klebsiella pneumoniae in Southern Spain in 2014–2015}},
volume = {63},
year = {2019}
}
@article{Ma2020,
abstract = {Background: Dysbiosis of human gut microbiota is associated with a wide range of metabolic disorders, including gestational diabetes mellitus (GDM). Yet whether gut microbiota dysbiosis participates in the etiology of GDM remains largely unknown. Objectives: Our study was initiated to determine whether the alternations in gut microbial composition during early pregnancy linked to the later development of GDM, and explore the feasibility of microbial biomarkers for the early prediction of GDM. Study design: This nested case-control study was based upon an early pregnancy follow-up cohort (ChiCTR1900020652). Gut microbiota profiles of 98 subjects with GDM and 98 matched healthy controls during the early pregnancy (10-15 weeks) were assessed via 16S rRNA gene amplicon sequencing of V4 region. The data set was randomly split into a discovery set and a validation set, the former was used to analyze the differences between GDM cases and controls in gut microbial composition and functional annotation, and to establish an early identification model of GDM, then the performance of the model was verified by the external validation set. Results: Bioinformatic analyses revealed changes to gut microbial composition with significant differences in relative abundance between the groups. Specifically, Eisenbergiella, Tyzzerella 4, and Lachnospiraceae NK4A136 were enriched in the GDM group, whereas Parabacteroides, Megasphaera, Eubacterium eligens group, etc. remained dominant in the controls. Correlation analysis revealed that GDM-enriched genera Eisenbergiella and Tyzzerella

4 were positively correlated with fasting blood glucose levels, while three control-enriched genera (Parabacteroides, Parasutterella, and Ruminococcaceae UCG 002) were the opposite. Further, GDM functional annotation modules revealed enrichment of modules for sphingolipid metabolism, starch and sucrose metabolism, etc., while lysine biosynthesis and nitrogen metabolism were reduced. Finally, five genera and two clinical indices were included in the linear discriminant analysis model for the prediction of GDM; the areas under receiver operating characteristic curves of the training and validation sets were 0.736 (95{\%} confidence interval: 0.663-0.808) and 0.696 (0.575-0.818), respectively. Conclusions: Gut bacterial dysbiosis in early pregnancy was found to be associated with the later development of GDM, and gut microbiota-targeted biomarkers might be utilized as potential predictors of GDM.},
author = {Ma, Shujuan and You, Yiping and Huang, Lingting and Long, Sisi and Zhang, Jiayue and Guo, Chuhao and Zhang, Na and Wu, Xinrui and Xiao, Yanni and Tan, Hongzhuan},
doi = {10.3389/fcimb.2020.00058},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Ma et al. - 2020 - Alterations in Gut Microbiota of Gestational Diabetes Patients During the First Trimester of Pregnancy.pdf:pdf},
issn = {22352988},
journal = {Frontiers in cellular and infection microbiology},
keywords = {biomarker,early prediction,gestational diabetes mellitus,gut microbiota,nested case-control study},
month = {feb},
pages = {58},
publisher = {NLM (Medline)},
title = {{Alterations in Gut Microbiota of Gestational Diabetes Patients During the First Trimester of Pregnancy}},
volume = {10},
year = {2020}
}
@article{Lomonaco2018,
abstract = {The emergence and dissemination of carbapenemases, bacterial enzymes able to inactivate most β-lactam antibiotics, in Enterobacteriaceae is of increasing concern. The concurrent spread of resistance against colistin, an antibiotic of last resort, further compounds this challenge further. Whole-genome sequencing (WGS) can play a significant role in the rapid and accurate detection/characterization of existing and emergent resistance determinants, an essential aspect of public health surveillance and response activities to combat the spread of antimicrobial resistant bacteria. In the current study, WGS data was used to characterize the genomic content of antimicrobial resistance genes, including those encoding carbapenemases, in 10 multidrug-resistant Klebsiella pneumoniae isolates from Pakistan. These clinical isolates represented five sequence types: ST11 (n = 3 isolates), ST14 (n = 3), ST15 (n = 1), ST101 (n = 2), and ST307 (n = 1). Resistance profiles against 25 clinically-relevant antimicrobials were determined by broth microdilution; resistant phenotypes were observed for at least 15 of the 25 antibiotics tested in all isolates except one. Specifically, 8/10 isolates were carbapenem-resistant and 7/10 isolates were colistin-resistant. The blaNDM-1 and blaOXA-48 carbapenemase genes were present in

7/10 and 5/10 isolates, respectively; including 2 isolates carrying both genes. No plasmid-mediated determinants for colistin resistance (e.g. mcr) were detected, but disruptions and mutations in chromosomal loci (i.e. mgrB and pmrB) previously reported to confer colistin resistance were observed. A blaOXA-48-carrying IncL/M-type plasmid was found in all blaOXA-48-positive isolates. The application of WGS to molecular epidemiology and surveillance studies, as exemplified here, will provide both a more complete understanding of the global distribution of MDR isolates and a robust surveillance tool useful for detecting emerging threats to public health.},
author = {Lomonaco, Sara and Crawford, Matthew A and Lascols, Christine and Timme, Ruth E and Anderson, Kevin and Hodge, David R and Fisher, Debra J and Pillai, Segaran P and Morse, Stephen A and Khan, Erum and Hughes, Molly A and Allard, Marc W and Sharma, Shashi K},
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issn = {1932-6203},
journal = {PloS one},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
number = {6},
pages = {e0198526},
pmid = {29883490},
publisher = {Public Library of Science},
title = {{Resistome of carbapenem- and colistin-resistant Klebsiella pneumoniae clinical isolates.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/29883490 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5993281},
volume = {13},
year = {2018}
}
@article{Liu2020,
abstract = {Rising concern about the use of antibiotics in food production has resulted in many studies on the occurrence of antibiotic resistance genes (ARGs) in animal-associated bacterial communities. There are few baseline data on the abundance of ARGs on farms where chickens are intensively raised with little or no use of antibiotics. This study used a high-throughput quantitative PCR array to survey two antibiotic-free chicken farms for the occurrence of ARGs and mobile genetic elements known to enhance the spread of ARGs. No antibiotics had been used on the study farms for five years prior to this study. The results provide a baseline for the occurrence of resistance genes in the chicken production system without direct selective pressure.},
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volume = {9},
year = {2020}
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@article{Liu2016,
abstract = {A novel lytic Salmonella bacteriophage was isolated by using Klebsiella pneumoniae as host cells. The phage's genome was determined to be 47,564 bp and has the highest similarity to Salmonella phage E1 and Salmonella phage 64795{_}sal3, with coverages of 61{\%} and 56{\%}, respectively. Here, we announce the phage's complete genome.},
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year = {2016}
}
@article{Liu2012,
author = {Liu, Pinglei and Li, Peng and Jiang, Xiaofei and Bi, Dexi and Xie, Yingzhou and Tai, Cui and Deng, Zixin and Rajakumar, Kumar and Ou, Hong-Yu},
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url = {http://jb.asm.org/},
year = {2012}
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@misc{Liu2012a,
abstract = {Klebsiella pneumoniae is an important pathogen commonly associated with opportunistic infections. Here we report the genome sequence of a strain, HS11286, isolated from human sputum in 2011 in Shanghai, China. It contains one chromosome (5.3 Mb), three multidrug

resistance plasmids ({\~{}}110 kb), including a carbapenemase producer, and three small plasmids ({\~{}}3 kb). {\textcopyright} 2012, American Society for Microbiology.},
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volume = {194},
year = {2012}
}
@article{Liu2018a,
abstract = {The aim of this study was to investigate the characteristics of carbapenem-resistant Klebsiella pneumoniae (CRKP) collected during an outbreak in a Chinese teaching hospital and to provide insights into the prevention and control of nosocomial infection. We collected unique CRKP clinical isolates from 2009 to 2013. Antibiotic-resistant genes were identified by polymerase chain reaction (PCR) and sequencing. The isolates were typed using pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST). Plasmids were classified using a PCR-based incompatibility/replicon typing method and a replicon sequence typing method. Conjugation experiments were performed to evaluate the transferability of carbapenem-resistant genes. Whole genome sequencing (WGS) was conducted to further investigate the genetic background of the isolates. Infection control practices were reviewed throughout the study period. Klebsiella pneumoniae sequence type (ST) 11 emerged in 2010 and acquired the blaKPC-2 gene by 2011. From 2011 to 2013, ST11 KPC-2-producing CRKP (G type) prevailed as the most common CRKP in our hospital, causing a prolonged outbreak. The majority of these CRKP strains possess an IncFII plasmid, with Tn1721-blaKPC-2-ΔTn3-IS26 bearing the genetic structure for blaKPC-2. Infection prevention control measures available at the time contained the initial outbreak, but had no effect on the spread of CRKP later. This study demonstrated the seriousness concerning the spread of KPC-2-producing ST11 CRKP in a Chinese hospital, indicating that current prevention and control strategies for carbapenem-resistant Enterobacteriaceae (CRE) nosocomial infection need to be investigated and adjusted.},
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number = {2},
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publisher = {Springer Verlag},
title = {{Emergence and establishment of KPC-2-producing ST11 Klebsiella pneumoniae in a general hospital in Shanghai, China}},
volume = {37},
year = {2018}
}
@article{Lin2016,
abstract = {Here, we announce the complete genome sequence of Klebsiella pneumoniae KP36, a strain isolated from a patient with a severe community-acquired urinary tract infection. This genome provides insights into the pathogenesis of a pandemic K. pneumoniae strain from a community-acquired urinary tract infection.},
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mendeley-tags = {Lista{_}Filtrada},
number = {6},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of community-acquired Klebsiella pneumoniae KP36, a strain isolated from a patient with an upper urinary tract infection}},
volume = {4},
year = {2016}
}
@article{Lepuschitz2019,
abstract = {In 2016, the Austrian Agency for Health and Food Safety started a pilot project to investigate antimicrobial resistance in surface water. Here we report on the characterisation of carbapenem resistant and ESBL-producing K. pneumoniae isolates from Austrian river water samples compared to 95 clinical isolates recently obtained in Austrian hospitals. Ten water samples were taken from four main rivers, collected upstream and downstream of major cities in 2016. For subtyping and comparison, public core genome multi locus sequence typing (cgMLST) schemes were used. The presence of AMR genes, virulence genes and plasmids was extracted from whole genome sequence (WGS) data. In total

three ESBL-producing strains and two carbapenem resistant strains were isolated. WGS based comparison of these five water isolates to 95 clinical isolates identified three clusters. Cluster 1 (ST11) and cluster 2 (ST985) consisted of doublets of carbapenem resistant strains (one water and one clinical isolate each). Cluster 3 (ST405) consisted of three ESBL-producing strains isolated from one water sample and two clinical specimens. The cities, in which patient isolates of cluster 2 and 3 were collected, were in concordance with the water sampling locations downstream from these cities. The genetic concordance between isolates from river water samples and patient isolates raises concerns regarding the release of wastewater treatment plant effluents into surface water. From a public health perspective these findings demand attention and strategies are required to minimize the spread of multiresistant strains to the environment.},
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issn = {1879-1026},
journal = {The Science of the total environment},
keywords = {Anthropogenic pollution,Lista{_}Filtrada,Multiresistance,Surface-water,Surveillance,Whole-genome sequencing},
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title = {{Whole genome sequencing reveals resemblance between ESBL-producing and carbapenem resistant Klebsiella pneumoniae isolates from Austrian rivers and clinical isolates from hospitals.}},
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volume = {662},
year = {2019}
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@article{LalGupta2020,
abstract = {Antibiotic or antimicrobial resistance (AR) facilitated by the vertical and/or horizontal transfer of antibiotic resistance genes (ARGs), is a serious global health challenge. While traditionally associated with pathogens in clinical environments, it is becoming increasingly clear that non-clinical environments may also be reservoirs of ARGs. The recent improvements in rapid and affordable next generation sequencing technologies along with sophisticated bioinformatics platforms has the potential to revolutionize diagnostic microbiology and microbial surveillance. Through the study and characterization of ARGs in bacterial genomes and complex metagenomes, we are now able to reveal the genetic scope of AR in single bacteria and complex communities, and obtain important insights into AR dynamics at species, population and community

levels, providing novel epidemiological and ecological perspectives. A suite of bioinformatics pipelines and ARG databases are currently available for genomic and metagenomic data analyses. However, different platforms may significantly vary and therefore, it is crucial to choose the tools that are most suitable for the specific analysis being conducted. This review provides a detailed account of available bioinformatics platforms for identification and characterization of ARGs and associated genetic elements within single bacterial isolates and complex environmental samples. It focuses primarily on currently available ARG databases, employing a comprehensive benchmarking pipeline to identify ARGs in four bacterial genomes (Aeromonas salmonicida, Bacillus cereus, Burkholderia sp. and Escherichia coli) and three shotgun metagenomes (human gut, poultry litter and soil) providing insight into which databases should be used for different analytical scenarios.},
author = {{Lal Gupta}, Chhedi and {Kumar Tiwari}, Rohit and Cytryn, Eddie},
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issn = {1873-6750},
journal = {Environment international},
keywords = {Antibiotic resistance genes,Bioinformatics,Environment,Lista{_}Filtrada,Metagenome,Mobile genetic elements,Pathogen,Resistome},
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pmid = {32234679},
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url = {http://www.ncbi.nlm.nih.gov/pubmed/32234679},
volume = {138},
year = {2020}
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@article{Kwon2016,
abstract = {The prevalence of Klebsiella pneumoniae coproducing carbapenemase metallo-β-lactamase 1 (NDM-1) and OXA-48 has been increasing globally since 2013. The complete genome of KP617 was sequenced and assembled into a circular chromosome and two plasmids. This sequence provides the genetic background for understanding the evolution of carbapenemase genes in K. pneumoniae KP617.},
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pmid = {26769936},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae subsp. pneumoniae KP617, Coproducing OXA-232 and NDM-1 Carbapenemases, Isolated in South Korea.}},
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volume = {4},
year = {2016}
}
@article{Koser2014,
abstract = {OBJECTIVES As a result of the introduction of rapid benchtop sequencers, the time required to subculture a bacterial pathogen to extract sufficient DNA for library preparation can now exceed the time to sequence said DNA. We have eliminated this rate-limiting step by developing a protocol to generate DNA libraries for whole-genome sequencing directly from single bacterial colonies grown on primary culture plates. METHODS We developed our protocol using single colonies of 17 bacterial pathogens responsible for severe human infection that were grown using standard diagnostic media and incubation conditions. We then applied this method to four clinical scenarios that currently require time-consuming reference laboratory tests: full identification and genotyping of salmonellae; identification of blaNDM-1, a highly transmissible carbapenemase resistance gene, in Klebsiella pneumoniae; detection of genes encoding staphylococcal toxins associated with specific disease syndromes; and monitoring of vaccine targets to detect vaccine escape in Neisseria meningitidis. RESULTS We validated our single-colony whole-genome sequencing protocol for all 40 combinations of pathogen and selective, non-selective or indicator media tested in this study. Moreover, we demonstrated the clinical value of this method compared with current reference laboratory tests. CONCLUSIONS This advance will facilitate the implementation of whole-genome sequencing into diagnostic and public health microbiology.},
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issn = {1460-2091},
journal = {The Journal of antimicrobial chemotherapy},
keywords = {Lista{_}Filtrada,antibiotic resistance,infectious diseases,typing},
mendeley-tags = {Lista{_}Filtrada},
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pmid = {24370932},

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url = {http://www.ncbi.nlm.nih.gov/pubmed/24370932 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC3977605},
volume = {69},
year = {2014}
}
@article{Korry2020,
abstract = {Antibiotic resistance is a current and expanding threat to the practice of modern medicine. Antibiotic therapy has been shown to perturb the composition of the host microbiome with significant health consequences. In addition, the gut microbiome is known to be a reservoir of antibiotic resistance genes. Work has demonstrated that antibiotics can alter the collection of antibiotic resistance genes within the microbiome through selection and horizontal gene transfer. While antibiotics also have the potential to impact the expression of resistance genes, metagenomic-based pipelines currently lack the ability to detect these shifts. Here, we utilized a dual sequencing approach combining shotgun metagenomics and metatranscriptomics to profile how three antibiotics, amoxicillin, doxycycline, and ciprofloxacin, impact the murine gut resistome at the DNA and RNA level. We found that each antibiotic induced broad, but untargeted impacts on the gene content of the resistome. In contrast, changes in ARG transcript abundance were more targeted to the antibiotic treatment. Doxycycline and amoxicillin induced the expression of tetracycline and beta-lactamase resistance genes, respectively. Furthermore, the increased beta-lactamase resistance gene transcripts could contribute to an observed bloom of Bacteroides thetaiotaomicron during amoxicillin treatment. Based on these findings, we propose that the utilization of a dual sequencing methodology provides a unique capacity to fully understand the response of the resistome to antibiotic perturbation. In particular, the analysis of transcripts reveals that the expression and utilization of resistance genes is far narrower than their abundance at the genomic level would suggest.},
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issn = {1664-302X},
journal = {Frontiers in microbiology},
keywords = {Lista{_}Filtrada,antibiotic resistance genes,antibiotics,metagenomics,metatranscriptomics,microbiome,resistome},
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month = {mar},
pages = {322},
pmid = {32210932},
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volume = {11},
year = {2020}

}
@article{Komisarova2017,
abstract = {The double-stranded DNA (dsDNA) bacteriophage vB{_}KpnM{_}KpV477, with a broad spectrum of lytic activity against Klebsiella pneumoniae, including strains of capsular serotypes K1, K2, and K57, was isolated from a clinical sample. The phage genome comprises 168,272 bp, with a G±C content of 39.3{\%}, and it contains 275 putative coding sequences (CDSs) and 17 tRNAs.},
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issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
number = {37},
publisher = {American Society for Microbiology},
title = {{Complete nucleotide sequence of Klebsiella pneumoniae bacteriophage vB{_}KpnM{_}KpV477}},
volume = {5},
year = {2017}
}
@article{Kluytmans-VanDenBergh2016,
abstract = {Molecular typing has become indispensable in the detection of nosocomial transmission of bacterial pathogens and the identification of sources and routes of transmission in outbreak settings, but current methods are labor-intensive, are difficult to standardize, or have limited resolution. Whole-genome multilocus sequence typing (wgMLST) has emerged as a whole-genome sequencing (WGS)-based gene-by-gene typing method that may overcome these limitations and has been applied successfully for several species in outbreak settings. In this study, genus-, genetic-complex-, and species-specific wgMLST schemes were developed for Citrobacter spp., the Enterobacter cloacae complex, Escherichia coli, Klebsiella oxytoca, and Klebsiella pneumoniae and used to type a national collection of 1,798 extended-spectrum-beta-lactamase-producing Enterobacteriaceae (ESBL-E) isolates obtained from patients in Dutch hospitals. Genus-, genetic-complex-, and species-specific thresholds for genetic distance that accurately distinguish between epidemiologically related and unrelated isolates were defined for Citrobacter spp., the E. cloacae complex, E. Coli, and K. pneumoniae. wgMLST was shown to have higher discriminatory power and typeability than in silico MLST. In conclusion, the wgMLST schemes developed in this study facilitate high-resolution WGS-based typing of the most prevalent ESBL-producing species in clinical practice and may contribute to further elucidation of the complex epidemiology of antimicrobial-resistant Enterobacteriaceae. wgMLST opens up possibilities for the creation of a Web-accessible database for the global surveillance of ESBL-producing bacterial clones.},
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number = {12},
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pmid = {27629900},
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}
@article{Klebsiella2017,
abstract = {Klebsiella pneumoniae is a human commensal and opportunistic patho-gen that has become a leading causative agent of hospital-based infections over the past few decades. The emergence and global expansion of hypervirulent and multidrug-resistant (MDR) clones of K. pneumoniae have been increasingly reported in community-acquired and nosocomial infections. Despite this, the population genomics and epi-demiology of MDR K. pneumoniae at the national level are still poorly understood. To obtain insights into these, we analyzed a systematic large-scale collection of inva-sive MDR K. pneumoniae isolates from hospitals across the United Kingdom and Ire-land. Using whole-genome phylogenetic analysis, we placed these in the context of previously sequenced K. pneumoniae populations from geographically diverse coun-tries and identified their virulence and drug resistance determinants. Our results demonstrate that United Kingdom and Ireland MDR isolates are a highly diverse population drawn from across the global phylogenetic tree of K. pneumoniae and represent multiple recent international introductions that are mainly from Europe but in some cases from more distant countries. In addition, we identified novel genetic deter-minants underlying resistance to beta-lactams, gentamicin, ciprofloxacin, and tetracy-clines, indicating that both increased virulence and resistance have emerged inde-pendently multiple times throughout the population. Our data show that MDR K. pneumoniae isolates in the United Kingdom and Ireland have multiple distinct origins and appear to be part of a globally circulating K. pneumoniae population. IMPORTANCE Klebsiella pneumoniae is a major human pathogen that has been impli-cated in infections in healthcare settings over the past few decades. Antimicrobial treat-ment of K. pneumoniae infections has become increasingly difficult as a consequence of the emergence and spread of strains that are resistant to multiple antimicrobials. To bet-ter understand the spread of resistant K. pneumoniae, we studied the genomes of a large-scale population of extensively antimicrobial-resistant K. pneumoniae in the United Kingdom and Ireland by utilizing the fine resolution that whole-genome sequencing

of pathogen genomes provides. Our results indicate that the K. pneumoniae population is highly diverse and that, in some cases, resistant strains appear to have spread across the country over a few years. In addition, we found evidence that some strains have ac-quired antimicrobial resistance genes independently, presumably in response to antimi-crobial treatment.},
author = {Klebsiella, Multidrug-resistant},
doi = {10.1128/mBio.01976-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Klebsiella - 2017 - crossm Evolution and Epidemiology of.pdf:pdf},
issn = {21507511},
journal = {mBio},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {jan},
number = {1},
pages = {1--13},
pmid = {28223459},
publisher = {American Society for Microbiology},
title = {{crossm Evolution and Epidemiology of}},
volume = {8},
year = {2017}
}
@article{Kitajima2018,
abstract = {We report here the complete genome sequence of Klebsiella quasipneumoniae strain S05, a bacterium capable of producing membrane fouling-causing soluble substances and capable of respiring on oxygen, nitrate, and an anodic electrode. The genomic information of strain S05 should help predict metabolic pathways associated with these unique biological properties of this bacterium.},
author = {Kitajima, Masaaki and Ishizaki, So and Jang, Jeonghwan and Ishii, Satoshi and Okabe, Satoshi},
doi = {10.1128/genomeA.00471-18},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Kitajima et al. - 2018 - Complete genome sequence of Klebsiella quasipneumoniae strain S05, a fouling-causing bacterium isolated from a.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {jun},
number = {23},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of Klebsiella quasipneumoniae strain S05, a fouling-causing bacterium isolated from a membrane bioreactor}},
volume = {6},
year = {2018}
}
@article{Kim2012,
abstract = {A novel Pseudomonas aeruginosa lytic bacteriophage (phage), PA1{\O}, was isolated, and its genome was sequenced completely. This phage is able to lyse not only P. aeruginosa but also Staphylococcus

aureus. Genome analysis of PA1{\O} showed that it is similar to a P. aeruginosa temperate phage, D3112, with the exception of the absence of a c repressor-encoding gene, which is known to play a critical role in the maintenance of the lysogenic state of D3112 in P. aeruginosa.},
author = {Kim, S. and Rahman, M. and Kim, J.},
doi = {10.1128/jvi.07191-11},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Kim, Rahman, Kim - 2012 - Complete Genome Sequence of Pseudomonas aeruginosa Lytic Bacteriophage PA1O Which Resembles Temperate Bacterio.pdf:pdf},
issn = {0022-538X},
journal = {Journal of Virology},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
number = {6},
pages = {3400--3401},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Pseudomonas aeruginosa Lytic Bacteriophage PA1O Which Resembles Temperate Bacteriophage D3112}},
volume = {86},
year = {2012}
}
@article{Kao2017,
abstract = {Carbapenem-resistant Klebsiella pneumoniae strain 1756 was isolated from a pus specimen from a Taiwanese patient. Here, the complete genome sequence of strain 1756 is presented.},
author = {Kao, Cheng-Yen and Yan, Jing-Jou and Lin, Yu-Chun and Zheng, Po-Xing and Wu, Jiunn-Jong},
doi = {10.1128/genomeA.00066-17},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Kao et al. - 2017 - Complete Genome Sequence of Carbapenem-Resistant Klebsiella pneumoniae Strain 1756, Isolated from a Pus Specimen.pdf:pdf},
issn = {2169-8287},
journal = {Genome announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
number = {13},
pmid = {28360152},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Carbapenem-Resistant Klebsiella pneumoniae Strain 1756, Isolated from a Pus Specimen.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28360152 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5374226},
volume = {5},
year = {2017}
}
@article{Joensen2015,
abstract = {Accurate and rapid typing of pathogens is essential for effective surveillance and outbreak detection. Conventional serotyping of Escherichia coli is a delicate, laborious, time-consuming, and expensive procedure. With whole-genome sequencing (WGS) becoming cheaper, it has

vast potential in routine typing and surveillance. The aim of this study was to establish a valid and publicly available tool for WGS-based in silico serotyping of E. coli applicable for routine typing and surveillance. A FASTA database of specific O-antigen processing system genes for O typing and flagellin genes for H typing was created as a component of the publicly available Web tools hosted by the Center for Genomic Epidemiology (CGE) (www.genomicepidemiology.org). All E. coli isolates available with WGS data and conventional serotype information were subjected to WGS-based serotyping employing this specific SerotypeFinder CGE tool. SerotypeFinder was evaluated on 682 E. coli genomes, 108 of which were sequenced for this study, where both the whole genome and the serotype were available. In total, 601 and 509 isolates were included for O and H typing, respectively. The O-antigen genes wzx, wzy, wzm, and wzt and the flagellin genes fliC, flkA, fllA, flmA, and flnA were detected in 569 and 508 genome sequences, respectively. SerotypeFinder for WGS-based O and H typing predicted 560 of 569 O types and 504 of 508 H types, consistent with conventional serotyping. In combination with other available WGS typing tools, E. coli serotyping can be performed solely from WGS data, providing faster and cheaper typing than current routine procedures and making WGS typing a superior alternative to conventional typing strategies.},
author = {Joensen, Katrine G and Tetzschner, Anna M M and Iguchi, Atsushi and Aarestrup, Frank M and Scheutz, Flemming},
doi = {10.1128/JCM.00008-15},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Joensen et al. - 2015 - Rapid and Easy In Silico Serotyping of Escherichia coli Isolates by Use of Whole-Genome Sequencing Data.pdf:pdf},
issn = {1098-660X},
journal = {Journal of clinical microbiology},
month = {aug},
number = {8},
pages = {2410--26},
pmid = {25972421},
publisher = {American Society for Microbiology},
title = {{Rapid and Easy In Silico Serotyping of Escherichia coli Isolates by Use of Whole-Genome Sequencing Data.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/25972421 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4508402},
volume = {53},
year = {2015}
}
@article{Jiang2015,
abstract = {An outbreak of carbapenem-resistant Klebsiella pneumoniae strains emerged at a hospital, and was tracked in order to understand the spread of these infectious pathogens. A total of 66 K. pneumoniae strains were collected from sterile samples in 2012. The MICs of 20 antimicrobial agents were determined for all strains. Molecular typing was performed with pulsed-field gel electrophoresis (PFGE). Twelve blaKPC-producing K. pneumoniae strains isolated from ten patients were selected for whole genome sequencing. Phylogenetic reconstruction of these 12 strains was performed by the use of single-nucleotide polymorphism (SNP) row sequences of each draft genome sequence. Plasmids from the 12 strains were separated by S1 digestion and PFGE. The 12 K. pneumoniae strains

isolated from the ten patients were deemed to be representative of the hospital outbreak, owing to their similar PFGE patterns. These 12 blaKPC-producing strains conferred multidrug resistance, which contrasted with the remaining 54, more susceptible, strains in the hospital. Differences in SNPs between each draft genome of the blaKPC-producing strains partitioned the 12 outbreak strains into three separate clades. The patients with each clade shared close hospital units. All 12 strains harboured at least one multidrug resistance plasmid. Strains showing high-level resistance may facilitate nosocomial dissemination and result in an infectious pathogen outbreak. Although the 12 blaKPC-producing K. pneumoniae strains possessed similar PFGE patterns, SNP variations throughout the genome allowed the strains to be divided into three clades. These results suggest that three independent transmission events led to hospital-wide dissemination of the outbreak strains.},
author = {Jiang, Y. and Wei, Z. and Wang, Y. and Hua, X. and Feng, Y. and Yu, Y.},
doi = {10.1016/j.cmi.2015.07.001},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Jiang et al. - 2015 - Tracking a hospital outbreak of KPC-producing ST11 Klebsiella pneumoniae with whole genome sequencing.pdf:pdf},
issn = {14690691},
journal = {Clinical Microbiology and Infection},
keywords = {Carbapenem resistance,Lista{_}Filtrada,Outbreak,Plasmid,SNP,Whole genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
month = {nov},
number = {11},
pages = {1001--1007},
publisher = {Elsevier},
title = {{Tracking a hospital outbreak of KPC-producing ST11 Klebsiella pneumoniae with whole genome sequencing}},
volume = {21},
year = {2015}
}
@article{Iwase2016,
abstract = {We report here the complete genome sequence ofKlebsiella pneumoniaestrain YH43, isolated from sweet potato. The genome consists of a single circular chromosome of 5,520,319 bp in length. It carries 8 copies of rRNA operons, 86 tRNA genes, 5,154 protein-coding genes, and thenifgene cluster for nitrogen fixation.},
author = {Iwase, Tadayuki and Ogura, Yoshitoshi and Hayashi, Tetsuya and Mizunoe, Yoshimitsu},
doi = {10.1128/genomeA.00242-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Iwase et al. - 2016 - Complete Genome Sequence of Klebsiella pneumoniae YH43.pdf:pdf},
issn = {2169-8287},
journal = {Genome announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
number = {2},

pmid = {27081127},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae YH43.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/27081127
http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC4832155},
volume = {4},
year = {2016}
}
@article{Iwase2016a,
abstract = {Klebsiella oxytoca can be either pathogenic or beneficial, depending on conditions. These opposing characteristics have not been fully elucidated. Here, we report the complete sequence of the K. oxytoca JKo3 genome, consisting of a single circular chromosome of 5,943,791 bp and four plasmids.},
author = {Iwase, Tadayuki and Ogura, Yoshitoshi and Hayashi, Tetsuya and Mizunoe, Yoshimitsu},
doi = {10.1128/genomeA.01221-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Iwase et al. - 2016 - Complete genome sequence of Klebsiella oxytoca strain JKo3.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {6},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of Klebsiella oxytoca strain JKo3}},
volume = {4},
year = {2016}
}
@article{Huff2020,
abstract = {Background Studies evaluating bacteria in insects can provide information about host-microorganism-environment interactions. The gut microbial community has a profound effect on different physiological functions of insects. Enterococcus spp. are part of the gut community in humans and other animals, as well as in insects. The presence and antimicrobial resistance profile of enterococci are well studied in different animals; however, data for Heliconius erato phyllis (Lepidoptera: Nymphalidae) do not yet exist. Therefore, the aims of this study were to evaluate the distribution of enterococcal species, their antimicrobial resistance profile and virulence genes, and the genetic relationships between enterococci isolated from fecal samples from sibling and non-sibling H. erato phyllis caterpillars collected from different sites in South Brazil. Methods Three H. erato phyllis females were captured (two from a forest fragment and one from an urban area), and kept individually in open-air insectaries. Eggs were collected and caterpillars (siblings and non-siblings) were fed daily with Passiflora suberosa leaves. Fecal samples (n = 12) were collected from fifth-instar caterpillars, inoculated in selective medium, and 15 bacterial colonies were randomly selected from each sample. Enterococci were identified by PCR and MALDI-TOF, analyzed by disk diffusion antimicrobial susceptibility tests, and screened for resistance and virulence genes by PCR. The genetic relationships between the strains were determined using pulsed-field gel electrophoresis (PFGE). Results A total of 178

enterococci strains were identified: E. casseliflavus (74.15{\%}; n = 132), E. mundtii (21.34{\%}; n = 38), E. faecalis (1.12{\%}; n = 2) and Enterococcus sp. (3.37{\%}; n = 6). High rates of resistance to rifampicin (56{\%}) and erythromycin (31{\%}) were observed; 120 (67.41{\%}) of the isolates showed resistance to at least one antibiotic and six (3.37{\%}) were multidrug-resistant.None of the erythromycin-resistant strains was positive for the erm(B) and msrC genes. The virulence genes esp, ace, and gelE were observed in 35{\%}, 7{\%}, and 1{\%} of the strains, respectively. PFGE separated the enterococci into 22 patterns, four being composed of strains from sibling caterpillars. Conclusion Enterococcus casseliflavus was the dominant species in fecal samples of fifth-instar caterpillars. Resistant enterococci strains may be related to environmental pollution or the resistome. The PFGE analysis showed genetic relationships between some strains, suggesting that the enterococci isolated from fecal samples of the sibling caterpillars might have come from common sources, e.g., via diet (herbivory) and/or vertical transmission (through the egg surface). Further studies will be conducted to better understand the role of Enterococcus in the microbial community of the gastrointestinal tract of these insects, and the mechanisms involved in acquisition and maintenance of enterococci.},
author = {Huff, Rosana and {Inhoque Pereira}, Rebeca and Pissetti, Caroline and {Mellender de Ara{\'{u}}jo}, Aldo and Alves d'Azevedo, Pedro and Frazzon, Jeverson and GuedesFrazzon, Ana Paula},
doi = {10.7717/peerj.8647},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Huff et al. - 2020 - Antimicrobial resistance and genetic relationships of enterococci from siblings and non-siblings Heliconius erato p.pdf:pdf},
issn = {2167-8359},
journal = {PeerJ},
keywords = {Antimicrobial profile,Enterococcal species,Enterococcus casseliflavus,Lepidoptera,Molecular typing},
month = {feb},
pages = {e8647},
pmid = {32149028},
publisher = {PeerJ},
title = {{Antimicrobial resistance and genetic relationships of enterococci from siblings and non-siblings Heliconius erato phyllis caterpillars.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32149028 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC7049460},
volume = {8},
year = {2020}
}
@article{Hudson2014,
abstract = {Multidrug-resistant Enterobacteriaceae are emerging as a serious infectious disease challenge. These strains can accumulate many antibiotic resistance genes though horizontal transfer of genetic elements, those for β-lactamases being of particular concern. Some β-lactamases are active on a broad spectrum of β-lactams including the last-resort carbapenems. The gene for the broad-spectrum and carbapenem-active metallo-β-lactamase NDM-1 is rapidly spreading. We present the complete genome of Klebsiella pneumoniae ATCC BAA-2146, the first U.S. isolate found to encode NDM-1, and describe its

repertoire of antibiotic-resistance genes and mutations, including genes for eight β-lactamases and 15 additional antibiotic-resistance enzymes. To elucidate the evolution of this rich repertoire, the mobile elements of the genome were characterized, including four plasmids with varying degrees of conservation and mosaicism and eleven chromosomal genomic islands. One island was identified by a novel phylogenomic approach, that further indicated the cps-lps polysaccharide synthesis locus, where operon translocation and fusion was noted. Unique plasmid segments and mosaic junctions were identified. Plasmid-borne blaCTX-M-15 was transposed recently to the chromosome by IS Ecp1. None of the eleven full copies of IS26, the most frequent IS element in the genome, had the expected 8-bp direct repeat of the integration target sequence, suggesting that each copy underwent homologous recombination subsequent to its last transposition event. Comparative analysis likewise indicates IS26 as a frequent recombinational junction between plasmid ancestors, and also indicates a resolvase site. In one novel use of high-throughput sequencing, homologously recombinant subpopulations of the bacterial culture were detected. In a second novel use, circular transposition intermediates were detected for the novel insertion sequence ISKpn21 of the ISNCY family, suggesting that it uses the two-step transposition mechanism of IS3. Robust genome-based phylogeny showed that a unified Klebsiella cluster contains Enterobacter aerogenes and Raoultella, suggesting the latter genus should be abandoned. {\textcopyright} 2014 Hudson et al.},
author = {Hudson, Corey M. and Bent, Zachary W. and Meagher, Robert J. and Williams, Kelly P.},
doi = {10.1371/journal.pone.0099209},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Hudson et al. - 2014 - Resistance determinants and mobile genetic elements of an NDM-1-encoding Klebsiella pneumoniae strain.pdf:pdf},
issn = {19326203},
journal = {PLoS ONE},
month = {jun},
number = {6},
publisher = {Public Library of Science},
title = {{Resistance determinants and mobile genetic elements of an NDM-1-encoding Klebsiella pneumoniae strain}},
volume = {9},
year = {2014}
}
@article{Hudson2014a,
author = {Hudson, CM and Bent, ZW and Meagher, RJ and Williams, KP},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Hudson et al. - 2014 - Determinantes de resistencia y elementos gen{\'{e}}ticos m{\'{o}}viles de una cepa de Klebsiella pneumoniae que codifica NDM-.pdf:pdf},
journal = {PloS one},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
title = {{Determinantes de resistencia y elementos gen{\'{e}}ticos m{\'{o}}viles de una cepa de Klebsiella pneumoniae que codifica NDM-1}},

url =
{https://journals.plos.org/plosone/article{\%}3Fid{\%}3D10.1371/journal.p
one.0099209},
year = {2014}
}
@article{Hua2014,
abstract = {Klbesiella pneumoniae is one of the most important human
pathogens and frequently causes many diseases. To facilitate the
comparative genome analysis in tigecycline resistance mechanism, we
report the complete chromosomal sequence of a multidrug-resistance K.
pneumoniae strain before tigecycline treatment for reference genome.},
author = {Hua, Xiaoting and Chen, Qiong and Li, Xi and Feng, Ye and Ruan,
Zhi and Yu, Yunsong},
doi = {10.1128/genomeA.01337-14},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley
Desktop/Downloaded/Hua et al. - 2014 - Complete genome sequence of
Klebsiella pneumoniae sequence type 17, a multidrug-resistant strain
isolated during tig.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {6},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of Klebsiella pneumoniae sequence type
17, a multidrug-resistant strain isolated during tigecycline treatment}},
volume = {2},
year = {2014}
}
@article{Heikal2017,
abstract = {Multidrug-resistant Klebsiella pneumoniae is a major cause of
hospital-acquired infections. Here, we report the complete genome
sequence of the multidrug-resistant, blaNDM-1-positive strain K.
pneumoniae K66-45, isolated from a hospitalized Norwegian patient.},
author = {Heikal, Adam and Samuelsen, {\O}rjan and Kristensen, Tom and
{\O}kstad, Ole Andreas},
doi = {10.1128/genomeA.00601-17},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley
Desktop/Downloaded/Heikal et al. - 2017 - Complete Genome Sequence of a
Multidrug-Resistant, blaNDM-1-Expressing Klebsiella pneumoniae K66-45
Clinical Isol.pdf:pdf},
issn = {2169-8287},
journal = {Genome announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {jul},
number = {27},
pmid = {28684580},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of a Multidrug-Resistant, blaNDM-1-
Expressing Klebsiella pneumoniae K66-45 Clinical Isolate from Norway.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28684580
http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5502861},
volume = {5},

year = {2017}
}
@article{Harb2019,
abstract = {Here, we describe the complete genome sequence of the T4-like Klebsiella pneumoniae myophage Marfa. In its 168,532-bp genome, Marfa has 289 genes, for which 122 gene functions were predicted. Many similar proteins are shared between Marfa and phage T4, as well as its closest phage relatives.},
author = {Harb, Laith and Boeckman, Justin and Newkirk, Heather and Liu, Mei and Gill, Jason J. and Ramsey, Jolene},
doi = {10.1128/mra.00748-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Harb et al. - 2019 - Complete Genome Sequence of the Novel Klebsiella pneumoniae Phage Marfa.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {jul},
number = {29},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of the Novel Klebsiella pneumoniae Phage Marfa}},
volume = {8},
year = {2019}
}
@article{Gramer2019,
abstract = {Klebsiella pneumoniae is a Gram-negative opportunistic pathogen and a leading cause of antibiotic-resistant nosocomial infections. The genome sequence of siphophage Skenny, which infects K. pneumoniae , is described here. Skenny encodes 78 genes and is closely related to Klebsiella phages KPN N141 and MezzoGao, which are T1-like phages.},
author = {Gramer, Jacob and Kenny, Sarah and Newkirk, Heather and Liu, Mei and Gill, Jason J. and Ramsey, Jolene},
doi = {10.1128/mra.01036-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Gramer et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Siphophage Skenny.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {39},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Siphophage Skenny}},
volume = {8},
year = {2019}
}
@article{Gonzalez2020,
abstract = {Helicobacter pylori is considered the most prevalent bacterial pathogen in humans. The increasing antibiotic resistance

evolved by this microorganism has raised alarm bells worldwide due to the significant reduction in the eradication rates of traditional standard therapies. A major challenge in this antibiotic resistance crisis is the identification of novel microbial targets whose inhibitors can overcome the currently circulating resistome. In the present study, we have validated the use of the essential response regulator ArsR as a novel and promising therapeutic target against H. pylori infections. A high-throughput screening of a repurposing chemical library using a fluorescence-based thermal shift assay identified several ArsR binders. At least four of these low-molecular weight compounds noticeably inhibited the DNA binding activity of ArsR and showed bactericidal effects against antibiotic-resistant strains of H. pylori. Among the ArsR inhibitors, a human secondary bile acid, lithocholic acid, quickly destroyed H. pylori cells and exhibited partial synergistic action in combination with clarithromycin or levofloxacin, while the antimicrobial effect of this compound against representative members of the normal human microbiota such as Escherichia coli and Staphylococcus epidermidis appeared irrelevant. Our results enhance the battery of novel therapeutic tools against refractory infections caused by multidrug-resistant H. pylori strains.},
author = {Gonz{\'{a}}lez, Andr{\'{e}}s and Casado, Javier and Chueca, Eduardo and Salillas, Sandra and Vel{\'{a}}zquez-Campoy, Adri{\'{a}}n and Sancho, Javier and Lanas, {\'{A}}ngel},
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file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Gonz{\'{a}}lez et al. - 2020 - Small Molecule Inhibitors of the Response Regulator ArsR Exhibit Bactericidal Activity against Helicobacter pyl.pdf:pdf},
issn = {2076-2607},
journal = {Microorganisms},
keywords = {ArsR,Helicobacter pylori,U-binders,antimicrobial therapy,response regulator},
month = {apr},
number = {4},
pages = {503},
pmid = {32244717},
title = {{Small Molecule Inhibitors of the Response Regulator ArsR Exhibit Bactericidal Activity against Helicobacter pylori.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/32244717},
volume = {8},
year = {2020}
}
@article{Gao2017,
abstract = {The Klebsiella pneumoniae phages SopranoGao, MezzoGao, and AltoGao were isolated from the Seneca Wastewater Treatment Plant in Germantown, MD. The following reports the complete genome sequence of these bacteriophages and describes their major features.},
author = {Gao, Sarah and Linden, Sara B. and Nelson, Daniel C.},
doi = {10.1128/genomeA.01009-17},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Gao, Linden, Nelson - 2017 - Complete genome sequence of Klebsiella pneumoniae phages SopranoGao, MezzoGao, and AltoGao.pdf:pdf},
issn = {21698287},

journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {nov},
number = {45},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of Klebsiella pneumoniae phages SopranoGao, MezzoGao, and AltoGao}},
volume = {5},
year = {2017}
}
@article{Errico2019,
abstract = {OBJECTIVES A prospective cohort study was conducted in Italy in order to describe the microbiologic aspects of colonization/infection by carbapenemase-producing Enterobacteriaceae (CPE) in donors and recipients of lung and liver transplants and the possible CPE transmission from donors to recipients. METHODS Between 15 January 2014 and 14 January 2015, all recipients of solid organ transplants (SOT) at ten lung and eight liver transplantation centres and the corresponding donors were enrolled. Screening cultures to detect CPE were performed in donors, and screening and clinical cultures in recipients with a 28-day microbiologic follow-up after receipt of SOT. Detection of carbapenemase genes by PCR, genotyping by multilocus sequence typing, and pulsed-field gel electrophoresis and whole-genome sequencing were performed. RESULTS Of 588 screened donors, 3.4{\%} were colonized with CPE. Of the liver first transplant recipients (n = 521), 2.5{\%} were colonized before receipt of SOT and 5{\%} acquired CPE during follow-up. CPE colonization was higher in lung first transplant recipients (n = 111, 2.7{\%} before SOT and 14.4{\%} after SOT). CPE infections occurred in 1.9{\%} and 5.3{\%} of liver or lung recipients, respectively. CPE isolates were mostly Klebsiella pneumoniae carbapenemase (KPC)-producing K. pneumoniae belonging to CG258. Three events of donor-recipient CPE transmission, confirmed by whole-genome sequencing and/or pulsed-field gel electrophoresis, occurred in lung recipients: two involving K. pneumoniae sequence type 512 and one Verona integron-encoded metallo-β-lactamase (VIM)-producing Enterobacter aerogenes. CONCLUSIONS This study showed a low risk of donor-recipient CPE transmission, indicating that donor CPE colonization does not necessarily represent a contraindication for donation unless colonization regards the organ to be transplanted. Donor and recipient screening remains essential to prevent CPE transmission and cross-infection in transplantation centres.},
author = {Errico, G and Gagliotti, C and Monaco, M and Masiero, L and Gaibani, P and Ambretti, S and Landini, M P and D'Arezzo, S and {Di Caro}, A and Parisi, S G and Pal{\`{u}}, G and Vespasiano, F and Morsillo, F and Moro, M L and Procaccio, F and Ricci, A and Grossi, P A and Pantosti, A and {Nanni Costa}, A and {SInT Collaborative Study Group}},
doi = {10.1016/j.cmi.2018.05.003},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Errico et al. - 2019 - Colonization and infection due to carbapenemase-producing Enterobacteriaceae in liver and lung transplant recipie.pdf:pdf},
issn = {1469-0691},

journal = {Clinical microbiology and infection : the official publication of the European Society of Clinical Microbiology and Infectious Diseases},
keywords = {CPE,Colonization,Donor-recipient transmission,Infection,Solid organ transplant},
month = {feb},
number = {2},
pages = {203--209},
pmid = {29800674},
publisher = {Elsevier B.V.},
title = {{Colonization and infection due to carbapenemase-producing Enterobacteriaceae in liver and lung transplant recipients and donor-derived transmission: a prospective cohort study conducted in Italy.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/29800674},
volume = {25},
year = {2019}
}
@article{Duan2013,
abstract = {The plant growth-promoting bacterium (PGPB) Pseudomonas sp. UW4, previously isolated from the rhizosphere of common reeds growing on the campus of the University of Waterloo, promotes plant growth in the presence of different environmental stresses, such as flooding, high concentrations of salt, cold, heavy metals, drought and phytopathogens. In this work, the genome sequence of UW4 was obtained by pyrosequencing and the gaps between the contigs were closed by directed PCR. The P. sp. UW4 genome contains a single circular chromosome that is 6,183,388 bp with a 60.05{\%} G+C content. The bacterial genome contains 5,423 predicted protein-coding sequences that occupy 87.2{\%} of the genome. Nineteen genomic islands (GIs) were predicted and thirty one complete putative insertion sequences were identified. Genes potentially involved in plant growth promotion such as indole-3-acetic acid (IAA) biosynthesis, trehalose production, siderophore production, acetoin synthesis, and phosphate solubilization were determined. Moreover, genes that contribute to the environmental fitness of UW4 were also observed including genes responsible for heavy metal resistance such as nickel, copper, cadmium, zinc, molybdate, cobalt, arsenate, and chromate. Whole-genome comparison with other completely sequenced Pseudomonas strains and phylogeny of four concatenated "housekeeping" genes (16S rRNA, gyrB, rpoB and rpoD) of 128 Pseudomonas strains revealed that UW4 belongs to the fluorescens group, jessenii subgroup. {\textcopyright} 2013 Duan et al.},
author = {Duan, Jin and Jiang, Wei and Cheng, Zhenyu and Heikkila, John J. and Glick, Bernard R.},
doi = {10.1371/journal.pone.0058640},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Duan et al. - 2013 - The Complete Genome Sequence of the Plant Growth-Promoting Bacterium Pseudomonas sp. UW4.pdf:pdf},
issn = {19326203},
journal = {PLoS ONE},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
number = {3},
title = {{The Complete Genome Sequence of the Plant Growth-Promoting Bacterium Pseudomonas sp. UW4}},

volume = {8},
year = {2013}
}
@article{Dinkelacker2018,
abstract = {Klebsiella pneumoniae and related species are frequent causes of nosocomial infections and outbreaks. Therefore, quick and reliable strain typing is crucial for the detection of transmission routes in the hospital. The aim of this study was to evaluate Fourier transform infrared spectroscopy (FTIR) and matrix-assisted laser desorption ionization-time of flight mass spectrometry (MALDI-TOF MS) as rapid methods for typing clinical Klebsiella isolates in comparison to whole-genome sequencing (WGS), which was considered the gold standard for typing and identification. Here, 68 clinical Klebsiella strains were analyzed by WGS, FTIR, and MALDI-TOF MS. FTIR showed high discriminatory power in comparison to the WGS reference, whereas MALDI-TOF MS exhibited a low ability to type the isolates. MALDI-TOF mass spectra were further analyzed for peaks that showed high specificity for different Klebsiella species. Phylogenetic analysis revealed that the Klebsiella isolates comprised three different species: K. pneumoniae, K. variicola, and K. quasipneumoniae Genome analysis showed that MALDI-TOF MS can be used to distinguish K. pneumoniae from K. variicola due to shifts of certain mass peaks. The peaks were tentatively identified as three ribosomal proteins (S15p, L28p, L31p) and one stress response protein (YjbJ), which exhibit amino acid differences between the two species. Overall, FTIR has high discriminatory power to recognize the clonal relationship of isolates, thus representing a valuable tool for rapid outbreak analysis and for the detection of transmission events due to fast turnaround times and low costs per sample. Furthermore, specific amino acid substitutions allow the discrimination of K. pneumoniae and K. variicola by MALDI-TOF MS.},
author = {Dinkelacker, Ariane G and Vogt, Sophia and Oberhettinger, Philipp and Mauder, Norman and Rau, J{\"{o}}rg and Kostrzewa, Markus and Rossen, John W A and Autenrieth, Ingo B and Peter, Silke and Liese, Jan},
doi = {10.1128/JCM.00843-18},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Dinkelacker et al. - 2018 - Typing and Species Identification of Clinical Klebsiella Isolates by Fourier Transform Infrared Spectroscopy.pdf:pdf},
issn = {1098-660X},
journal = {Journal of clinical microbiology},
keywords = {Fourier transform infrared spectroscopy,Klebsiella pneumoniae,Klebsiella variicola,Lista{_}Filtrada,MALDI-TOF mass spectrometry,bacterial typing},
mendeley-tags = {Lista{_}Filtrada},
month = {nov},
number = {11},
pmid = {30135233},
publisher = {American Society for Microbiology},
title = {{Typing and Species Identification of Clinical Klebsiella Isolates by Fourier Transform Infrared Spectroscopy and Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/30135233 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6204683},
volume = {56},
year = {2018}

}
@article{DiPilato2016,
abstract = {Sequencing of the blaKPC-positive strain Proteus mirabilis AOUC-001 was performed using both the MiSeq and PacBio RS II platforms and yielded a single molecule of 4,272,433 bp, representing the complete chromosome. Genome analysis showed the presence of several acquired resistance determinants, including two copies of blaKPC-2 carried on a fragment of a KPC-producing plasmid previously described in Klebsiella pneumoniae.},
author = {{Di Pilato}, Vincenzo and Chiarelli, Adriana and Boinett, Christine J. and Riccobono, Eleonora and Harris, Simon R. and D'Andrea, Marco Maria and Thomson, Nicholas R. and Rossolini, Gian Maria and Giani, Tommaso},
doi = {10.1128/genomeA.00607-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Di Pilato et al. - 2016 - Complete genome sequence of the first KPC-type carbapenemase-positive Proteus mirabilis strain from a bloodstr.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {3},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of the first KPC-type carbapenemase-positive Proteus mirabilis strain from a bloodstream infection}},
volume = {4},
year = {2016}
}
@article{Das2015,
abstract = {The present research work reports the whole genome sequence analysis of Pseudomonas aeruginosa strain N002 isolated from crude oil contaminated soil of Assam, India having high crude oil degradation ability. The whole genome of the strain N002 was sequenced by shotgun sequencing using Ion Torrent method and complete genome sequence analysis was done. It was found that the strain N002 revealed versatility for degradation, emulsification and metabolizing of crude oil. Analysis of cluster of orthologous group (COG) revealed that N002 has significantly higher gene abundance for cell motility, lipid transport and metabolism, intracellular trafficking, secretion and vesicular transport, secondary metabolite biosynthesis, transport and catabolism, signal transduction mechanism and transcription than average levels found in other genome sequences of the same bacterial species. However, lower gene abundance for carbohydrate transport and metabolism, replication, recombination and repair, translation, ribosomal structure, biogenesis was observed in N002 than average levels of other bacterial species.},
author = {Das, Dhrubajyoti and Baruah, Reshita and {Sarma Roy}, Abhijit and Singh, Anil Kumar and {Deka Boruah}, Hari Prasanna and Kalita, Jatin and Bora, Tarun Chandra},
doi = {10.1016/j.ygeno.2014.12.006},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Das et al. - 2015 - Complete genome sequence analysis of Pseudomonas aeruginosa N002 reveals its genetic adaptation for crude oil degrad.pdf:pdf},

issn = {10898646},
journal = {Genomics},
keywords = {Bioremediation,Crude oil,Genome,Lista{_}Filtrada,Pseudomonas aeruginosa},
mendeley-tags = {Lista{_}Filtrada},
month = {mar},
number = {3},
pages = {182--190},
publisher = {Academic Press Inc.},
title = {{Complete genome sequence analysis of Pseudomonas aeruginosa N002 reveals its genetic adaptation for crude oil degradation}},
volume = {105},
year = {2015}
}
@article{Conlan2016,
abstract = {Here, we report the genome sequence of a blaNDM-1-positive Klebsiella pneumoniae AATZP isolate cultured from a perirectal surveillance swab collected upon admission of a patient to the NIH Clinical Center in 2014. Genome sequencing of this isolate revealed three plasmids, including one carrying the blaNDM-1 gene encoding resistance to carbapenems.},
author = {Conlan, Sean and Lau, Anna F. and Palmore, Tara N. and Frank, Karen M. and Segre, Julia A. and {NISC Comparative Sequencing Program}},
doi = {10.1128/genomeA.00664-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Conlan et al. - 2016 - Complete genome sequence of a Klebsiella pneumoniae strain carrying blaNDM-1 on a multidrug resistance plasmid.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {4},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of a Klebsiella pneumoniae strain carrying blaNDM-1 on a multidrug resistance plasmid}},
volume = {4},
year = {2016}
}
@article{Chuanchuen2001,
abstract = {Triclosan is an antiseptic frequently added to items as diverse as soaps, lotions, toothpaste, and many commonly used household fabrics and plastics. Although wild-type Pseudomonas aeruginosa expresses the triclosan target enoyl-acyl carrier protein reductase, it is triclosan resistant due to expression of the MexAB-OprM efflux system. Exposure of a susceptible (mexAB-oprM) strain to triclosan selected multidrug-resistant bacteria at high frequencies. These bacteria hyperexpressed the MexCD-OprJ efflux system due to mutations in its regulatory gene, nfxB. The MICs of several drugs for these mutants were increased up to 500-fold, including the MIC of ciprofloxacin, which was increased 94-fold. Whereas the MexEF-OprN efflux system also participated in triclosan efflux, this antimicrobial was not a substrate for MexXY-OprM. Pseudomonas aeruginosa is a clinically significant pathogen, particularly in immunocompromised hosts (36). Infections caused by this

bacterium are difficult to treat due to its many intrinsic and acquired antibiotic resistances. Intrinsic resistance is mostly attributable to the expression of several multi-drug resistance (MDR) efflux systems. The P. aeruginosa ge-nome (35) contains structural genes for at least 12 resistance nodulation type efflux systems, of which only 4, i.e., MexAB-OprM (27), MexCD-OprJ (26), MexEF-OprN (13), and MexXY (1, 21, 38), have been characterized. Exposure to selected substrates can select for their upregulated or constitu-tive expression (13, 14, 26, 38). 2-Hydroxyphenylethers are a class of compounds that exhibit broad-spectrum antimicrobial activity. Triclosan is the most potent and widely used member of this class (2, 5) and is used in hand soaps, lotions, toothpastes, and oral rinses, as well as in fabrics and plastics. It was long thought to act as a nonspecific "biocide" (29), but recent biochemical and genetic studies have shown that triclosan acts on a defined bacterial target in the fatty acid biosynthetic pathway, enoyl-acyl carrier protein (ACP) reductase (FabI) (7, 9, 10, 12, 18, 20) or its homolog InhA in mycobacteria (18). Some bacteria possess triclosan-resistant enoyl-ACP reductase homologs (FabK), and to date P. aeruginosa is unique among gram-negative bacteria in that it possesses both triclosan-sensitive and-resistant enzymes (8). Alterations in FabI active-site residues confer resistance to triclosan (9, 10, 20). Of particular concern is that such amino acid changes selected by exposure to triclosan lead to cross-resistance with other antimicrobial agents (9), including clinically used front-line drugs, since some mutations leading to triclosan resistance in Mycobacterium smegmatis also caused resistance to isoniazid (18). Moreover, triclosan is a substrate of a multidrug efflux pump in clinical and laboratory Esche-richia coli strains (19). We have recently shown that P. aerugi-nosa strain PAO1 is intrinsically resistant to triclosan by virtue of expression of the MexAB-OprM efflux pump (32), and the same is true for all strains of this species tested to date (our unpublished results). While the contribution of antibiotic exposure to development of MDR due to efflux pump expression has clearly been documented in vitro and in vivo, little is known about antiseptic resistance mechanisms (30) and their possible contribution to MDR. In this paper we present results that triclosan is a substrate for multiple P. aeruginosa efflux pumps and that it is capable of selecting not just for mutants resistant to this particular antiseptic but, perhaps more importantly, also for MDR bacteria. MATERIALS AND METHODS Bacterial strains, culture conditions, and molecular biology techniques. The bacterial strains used in this study are shown in Table 1. Unless otherwise noted, bacteria were grown at 37°C in Luria-Bertani (LB) medium or on LB agar (31) or in Mueller-Hinton broth (MHB; Difco, Detroit, Mich.). For plasmid maintenance , P. aeruginosa media were supplemented with 200 g of carbenicillin/ml. Unmarked efflux pump-negative mutants were derived using a previously described Flp/FRT recombinase technology (11). The sources for the mutant alleles were pPS952 for (mexAB-oprM) (32), pPS1008 for (mexCD-opJ) (derived by deletion of a 6,138-bp region encompassing three ClaI fragments from pKMJ002 [26]), and pPS1128 for (mexXY) (derived by deletion of a 2,868-bp DNA fragment encompassing several SalI-XhoI fragments from pAMR-1 [38]). The chromosomal deletions were verified by PCR and genomic Southern analyses. Standard molecular biology methods were used (31). Plasmid pKMM128 is pAK1900 (28) expressing oprM (16). Antimicrobial susceptibility testing. MICs were determined by the twofold broth

microdilution technique according to National Committee for Clinical Laboratory Standards guidelines (22) or by the E-test system and the protocols provided by the supplier (AB Biodisk, Piscataway, N.J.) (ciprofloxacin and tet-racycline only).},
author = {Chuanchuen, Rungtip and Beinlich, Kerry and Hoang, Tung T and Becher, Anna and Karkhoff-Schweizer, Roxann R and Schweizer, Herbert P},
doi = {10.1128/AAC.45.2.428-432.2001},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Chuanchuen et al. - 2001 - Cross-Resistance between Triclosan and Antibiotics in Pseudomonas aeruginosa Is Mediated by Multidrug Effl(2).pdf:pdf},
journal = {Am Soc Microbiol},
number = {2},
pages = {428--432},
title = {{Cross-Resistance between Triclosan and Antibiotics in Pseudomonas aeruginosa Is Mediated by Multidrug Efflux Pumps: Exposure of a Susceptible Mutant Strain to Triclosan Selects nfxB Mutants Overexpressing MexCD-OprJ Downloaded from}},
url = {http://aac.asm.org/},
volume = {45},
year = {2001}
}
@article{Chi2019,
abstract = {Klebsiella pneumoniae is a gram-negative, opportunistic pathogen, and a common cause of healthcare-associated infections such as pneumonia, septicemia, and urinary tract infection. The purpose of this study was to survey the occurrence of and characterize K. pneumoniae in different environmental sources in a rural area of Shandong province, China. Two hundred and thirty-one samples from different environmental sources in 12 villages were screened for extended-spectrum {\ss}-lactamase-(ESBL)-producing K. pneumoniae, and 14 (6{\%}) samples were positive. All isolates were multidrug-resistant and a few of them belonged to clinically relevant strains which are known to cause hospital outbreaks worldwide. Serotypes, virulence genes, serum survival, and phagocytosis survival were analyzed and the results showed the presence of virulence factors associated with highly virulent clones and a high degree of phagocytosis survivability, indicating the potential virulence of these isolates. These results emphasize the need for further studies designed to elucidate the role of the environment in transmission and dissemination of ESBL-producing K. pneumoniae and the potential risk posed to human and environmental health.},
author = {Chi, Xiaohui and Berglund, Bj{\"{o}}rn and Zou, Huiyun and Zheng, Beiwen and B{\"{o}}rjesson, Stefan and Ji, Xiang and Ottoson, Jakob and Lundborg, Cecilia St{\aa}lsby and Li, Xuewen and Nilsson, Lennart E.},
doi = {10.3389/fmicb.2019.00211},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Chi et al. - 2019 - Strains of extended-spectrum {\ss}-lactamase-producing klebsiella pneumoniae occurring in environmental sources in a rur.pdf:pdf},
issn = {1664302X},
journal = {Frontiers in Microbiology},
keywords = {Environment,Extended-spectrum {\ss}-lactamase,Feces,Klebsiella pneumoniae,Lista{_}Filtrada,Multilocus

sequence typing,Pulsed-field gel electrophoresis,Water,Whole-genome sequencing},
mendeley-tags = {Lista{_}Filtrada},
number = {FEB},
publisher = {Frontiers Media S.A.},
title = {{Strains of extended-spectrum {\ss}-lactamase-producing klebsiella pneumoniae occurring in environmental sources in a rural area of China by using whole-genome sequencing}},
volume = {10},
year = {2019}
}
@article{Chen2019,
abstract = {The outbreak of carbapenem-resistant Klebsiella pneumoniae is a serious public health problem, especially in the neonatal intensive care unit (NICU). Fifteen K. pneumoniae strains were isolated from 7 neonates during June 3 to 28, 2017 in an NICU. Antimicrobial susceptibility was determined by the Vitek 2 system and microbroth dilution method. Multilocus sequence typing (MLST) and pulsed-field gel electrophoresis (PFGE) were used to analyze the genetic relatedness of the isolates. Whole-genome sequencing and gene function analysis were performed to investigate pathogenicity and drug resistance and screen genomic islands. Three clones of K. pneumoniae were identified from 7 neonates: 7 strains of ST37, 7 of novel ST3006, and 1 of ST1224. Gene sequencing showed that the kpn1343 (ST37) strain harbored 12 resistance genes (OXA-33, TEM-1, SHV-11, AAC (6')-IId, AAC (3)- IIa, AAC (6')-Ib-cr, catB3, arr-3, sul1, oqxB, oqxA, CRP, and catB3) and included 15 genomic islands and 205 reduced virulence genes. The kpn1344 (ST3006) strain harbored 4 antibiotic-resistant genes (TEM-1, CTX-M-3, vgaC, and CRP) and included 19 genomic islands and 209 reduced virulence genes. MLST and PFGE showed that 15 strains of K. pneumoniae were divided into 3 groups with a high level of homology. ST1224 (kpn1362) was isolated on June 28, 2017, which was 10 days after the last isolate (kpn1359, June 18, 2017); thus, we speculated that ST1224 was not the clone that caused the outbreak. This co-outbreak of K. pneumoniae involved 2 clones: ST37 and ST3006. ST37 carried the multidrug-resistant genes, such as OXA-33, TEM-1, and SHV-11, and ST3006 was a novel K. pneumoniae ST typing. Whole-genome sequencing may be an effective method for screening bacterial-resistant genes and their functions. Abbreviations: CARD = Comprehensive Antibiotic Resistance Database, MLST = multilocus sequence typing, NICU = neonatal intensive care unit, PCR = polymerase chain reaction, PFGE = pulsed-field gel electrophoresis, PHI = pathogen-host interaction.},
author = {Chen, Dongjie and Hu, Xinlan and Chen, Falin and Li, Hongru and Wang, Daxuan and Li, Xiaoqin and Wu, Changsheng and Li, Ning and Wu, Shaolian and Li, Zhen and Chen, Liqing and Chen, Yusheng},
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file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Chen et al. - 2019 - Co-outbreak of multidrug resistance and a novel ST3006 Klebsiella pneumoniae in a neonatal intensive care unit A re.pdf:pdf},
issn = {15365964},
journal = {Medicine (United States)},
keywords = {Co-outbreak,Klebsiella pneumoniae,Multidrug resistance,Neonatal intensive care unit,Whole-genome sequencing},
number = {4},

publisher = {Lippincott Williams and Wilkins},
title = {{Co-outbreak of multidrug resistance and a novel ST3006 Klebsiella pneumoniae in a neonatal intensive care unit: A retrospective study}},
volume = {98},
year = {2019}
}
@article{Chavda2016,
abstract = {Knowledge regarding the genomic structure of Enterobacter spp., the second most prevalent carbapenemase-producing Enterobacteriaceae, remains limited. Here we sequenced 97 clinical Enterobacter species isolates that were both carbapenem susceptible and resistant from various geographic regions to decipher the molecular origins of carbapenem resistance and to understand the changing phylogeny of these emerging and drug-resistant pathogens. Of the carbapenem-resistant isolates, 30 possessed blaKPC-2, 40 had blaKPC-3, 2 had blaKPC-4, and 2 had blaNDM-1 Twenty-three isolates were carbapenem susceptible. Six genomes were sequenced to completion, and their sizes ranged from 4.6 to 5.1 Mbp. Phylogenomic analysis placed 96 of these genomes, 351 additional Enterobacter genomes downloaded from NCBI GenBank, and six newly sequenced type strains into 19 phylogenomic groups-18 groups (A to R) in the Enterobacter cloacae complex and Enterobacter aerogenes Diverse mechanisms underlying the molecular evolutionary trajectory of these drug-resistant Enterobacter spp. were revealed, including the acquisition of an antibiotic resistance plasmid, followed by clonal spread, horizontal transfer of blaKPC-harboring plasmids between different phylogenomic groups, and repeated transposition of the blaKPC gene among different plasmid backbones. Group A, which comprises multilocus sequence type 171 (ST171), was the most commonly identified (23{\%} of isolates). Genomic analysis showed that ST171 isolates evolved from a common ancestor and formed two different major clusters; each acquiring unique blaKPC-harboring plasmids, followed by clonal expansion. The data presented here represent the first comprehensive study of phylogenomic interrogation and the relationship between antibiotic resistance and plasmid discrimination among carbapenem-resistant Enterobacter spp., demonstrating the genetic diversity and complexity of the molecular mechanisms driving antibiotic resistance in this genus. IMPORTANCE Enterobacter spp., especially carbapenemase-producing Enterobacter spp., have emerged as a clinically significant cause of nosocomial infections. However, only limited information is available on the distribution of carbapenem resistance across this genus. Augmenting this problem is an erroneous identification of Enterobacter strains because of ambiguous typing methods and imprecise taxonomy. In this study, we used a whole-genome-based comparative phylogenetic approach to (i) revisit and redefine the genus Enterobacter and (ii) unravel the emergence and evolution of the Klebsiella pneumoniae carbapenemase-harboring Enterobacter spp. Using genomic analysis of 447 sequenced strains, we developed an improved understanding of the species designations within this complex genus and identified the diverse mechanisms driving the molecular evolution of carbapenem resistance. The findings in this study provide a solid genomic framework that will serve as an important resource in the future development of molecular diagnostics and in supporting drug discovery programs.},

author = {Chavda, Kalyan D and Chen, Liang and Fouts, Derrick E and Sutton, Granger and Brinkac, Lauren and Jenkins, Stephen G and Bonomo, Robert A and Adams, Mark D and Kreiswirth, Barry N},
doi = {10.1128/mBio.02093-16},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Chavda et al. - 2016 - Comprehensive Genome Analysis of Carbapenemase-Producing Enterobacter spp. New Insights into Phylogeny, Populatio.pdf:pdf},
issn = {2150-7511},
journal = {mBio},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {jan},
number = {6},
pmid = {27965456},
publisher = {American Society for Microbiology},
title = {{Comprehensive Genome Analysis of Carbapenemase-Producing Enterobacter spp.: New Insights into Phylogeny, Population Structure, and Resistance Mechanisms.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/27965456 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5156309},
volume = {7},
year = {2016}
}
@article{Cella2017,
abstract = {Carbapenems resistant Enterobacteriaceae infections are increasing worldwide representing an emerging public health problem. The application of phylogenetic and phylodynamic analyses to bacterial whole genome sequencing (WGS) data have become essential in the epidemiological surveillance of multi-drug resistant nosocomial pathogens. Between January 2012 and February 2013, twenty-one multi-drug resistant K. pneumoniae strains, were collected from patients hospitalized among different wards of the University Hospital Campus Bio-Medico. Epidemiological contact tracing of patients and Bayesian phylogenetic analysis of bacterial WGS data were used to investigate the evolution and spatial dispersion of K. pneumoniae in support of hospital infection control. The epidemic curve of incident K. pneumoniae cases showed a bimodal distribution of cases with two peaks separated by 46 days between November 2012 and January 2013. The time-scaled phylogeny suggested that K. pneumoniae strains isolated during the study period may have been introduced into the hospital setting as early as 2007. Moreover, the phylogeny showed two different epidemic introductions in 2008 and 2009. Bayesian genomic epidemiology is a powerful tool that promises to improve the surveillance and control of multi-drug resistant pathogens in an effort to develop effective infection prevention in healthcare settings or constant strains reintroduction.},
author = {Cella, Eleonora and Ciccozzi, Massimo and {Lo Presti}, Alessandra and Fogolari, Marta and Azarian, Taj and Prosperi, Mattia and Salemi, Marco and Equestre, Michele and Antonelli, Francesca and Conti, Alessia and Cesaris, Marina De and Spoto, Silvia and Incalzi, Raffaele Antonelli and Coppola, Roberto and Dicuonzo, Giordano and Angeletti, Silvia},
doi = {10.1038/s41598-017-03581-4},

file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Cella et al. - 2017 - Multi-drug resistant Klebsiella pneumoniae strains circulating in hospital setting whole-genome sequencing and Bay.pdf:pdf},
issn = {2045-2322},
journal = {Scientific reports},
month = {dec},
number = {1},
pages = {3534},
pmid = {28615687},
publisher = {Nature Publishing Group},
title = {{Multi-drug resistant Klebsiella pneumoniae strains circulating in hospital setting: whole-genome sequencing and Bayesian phylogenetic analysis for outbreak investigations.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/28615687 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC5471223},
volume = {7},
year = {2017}
}
@article{Boeckman2019,
abstract = {Klebsiella pneumoniae is an important human pathogen due to the wide range of infections it can cause and its emerging drug resistance. Isolation and characterization of phage infecting K. pneumoniae could be important for future therapeutic applications. Here, we report the complete genome sequence of the T4-like Klebisella pneumoniae myophage Mineola.},
author = {Boeckman, Justin X. and Lessor, Lauren and Gill, Jason J. and Liu, Mei},
doi = {10.1128/mra.00257-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Boeckman et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Myophage Mineola.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {apr},
number = {17},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Myophage Mineola}},
volume = {8},
year = {2019}
}
@article{Bezdicek2019,
abstract = {Studying bacterial population diversity is important to understand healthcare associated infections' epidemiology and has a significant impact on dealing with multidrug resistant bacterial outbreaks. We characterised the extended-spectrum beta-lactamase producing K. pneumoniae (ESBLp KPN) population in our hospital using mini-MLST. Then we used whole genome sequencing (WGS) to compare selected isolates belonging to the most prevalent melting types (MelTs) and the colonization/infection pair isolates collected from one patient to study the ESBLp KPN population's genetic diversity. A total of 922 ESBLp KPN

isolates collected between 7/2016 and 5/2018 were divided into 38 MelTs using mini-MLST with only 6 MelTs forming 82.8{\%} of all isolates. For WGS, 14 isolates from the most prominent MelTs collected in the monitored period and 10 isolates belonging to the same MelTs collected in our hospital in 2014 were randomly selected. Resistome, virulome and ST were MelT specific and stable over time. A maximum of 23 SNV per core genome and 58 SNV per core and accessory genome were found. To determine the SNV relatedness cut-off values, 22 isolates representing colonization/infection pair samples obtained from 11 different patients were analysed by WGS with a maximum of 22 SNV in the core genome and 40 SNV in the core and accessory genome within pairs. The mini-MLST showed its potential for real-time epidemiology in clinical practice. However, for outbreak evaluation in a low diversity bacterial population, mini-MLST should be combined with more sensitive methods like WGS. Our findings showed there were only minimal differences within the core and accessory genome in the low diversity hospital population and gene based SNV analysis does not have enough discriminatory power to differentiate isolate relatedness. Thus, intergenic regions and mobile elements should be incorporated into the analysis scheme to increase discriminatory power.},
author = {Bezdicek, Matej and Nykrynova, Marketa and Plevova, Kristina and Brhelova, Eva and Kocmanova, Iva and Sedlar, Karel and Racil, Zdenek and Mayer, Jiri and Lengerova, Martina},
doi = {10.1371/journal.pone.0221187},
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issn = {1932-6203},
journal = {PloS one},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {8},
pages = {e0221187},
pmid = {31408497},
publisher = {Public Library of Science},
title = {{Application of mini-MLST and whole genome sequencing in low diversity hospital extended-spectrum beta-lactamase producing Klebsiella pneumoniae population.}},
url = {http://www.ncbi.nlm.nih.gov/pubmed/31408497 http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=PMC6692064},
volume = {14},
year = {2019}
}
@article{Becker2018,
abstract = {Background: By using whole genome sequence data we aimed at describing a population snapshot of carbapenemase-producing K. pneumoniae isolated from hospitalized patients in Germany between 2008 and 2014. Methods: We selected a representative subset of 107 carbapenemase-producing K. pneumoniae clinical isolates possessing the four most prevalent carbapenemase types in Germany (KPC-2, KPC-3, OXA-48, NDM-1). Isolates were processed via illumina NGS. Data were analysed using different SNP-based mapping and de-novo assembly approaches. Relevant information was extracted from NGS data (antibiotic resistance

determinants, wzi gene/cps type, virulence genes). NGS data from the present study were also compared with 238 genome data from two previous international studies on K. pneumoniae. Results: NGS-based analyses revealed a preferred prevalence of KPC-2-producing ST258 and KPC-3-producing ST512 isolates. OXA-48, being the most prevalent carbapenemase type in Germany, was associated with various K. pneumoniae strain types; most of them possessing IncL/M plasmid replicons suggesting a preferred dissemination of bla OXA-48 via this well-known plasmid type. Clusters ST15, ST147, ST258, and ST512 demonstrated an intermingled subset structure consisting of German and other European K. pneumoniae isolates. ST23 being the most frequent MLST type in Asia was found only once in Germany. This latter isolate contained an almost complete set of virulence genes and a K1 capsule suggesting occurrence of a hypervirulent ST23 strain producing OXA-48 in Germany. Conclusions: Our study results suggest prevalence of "classical" K. pneumonaie strain types associated with widely distributed carbapenemase genes such as ST258/KPC-2 or ST512/KPC-3 also in Germany. The finding of a supposed hypervirulent and OXA-48-producing ST23 K. pneumoniae isolates outside Asia is highly worrisome and requires intense molecular surveillance.},
author = {Becker, Laura and Kaase, Martin and Pfeifer, Yvonne and Fuchs, Stephan and Reuss, Annicka and von Laer, Anja and Sin, Muna Abu and Korte-Berwanger, Miriam and Gatermann, S{\"{o}}ren and Werner, Guido},
doi = {10.1186/s13756-018-0352-y},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Becker et al. - 2018 - Genome-based analysis of Carbapenemase-producing Klebsiella pneumoniae isolates from German hospital patients, 20.pdf:pdf},
issn = {20472994},
journal = {Antimicrobial Resistance and Infection Control},
keywords = {Hypermucoviscous,Hypervirulent,K1 capsule,KPC,Lista{_}Filtrada,OXA-48,ST23,ST258},
mendeley-tags = {Lista{_}Filtrada},
month = {may},
number = {1},
publisher = {BioMed Central Ltd.},
title = {{Genome-based analysis of Carbapenemase-producing Klebsiella pneumoniae isolates from German hospital patients, 2008-2014}},
volume = {7},
year = {2018}
}
@article{Becker2018a,
abstract = {Extended-spectrum β-lactamase (ESBL) producing Klebsiella pneumoniae pose an important threat of infection with increased morbidity and mortality, especially for immunocompromised patients. Here, we use the rise of multidrug-resistant K. pneumoniae in a German neurorehabilitation center from April 2015 to April 2016 to dissect the benefit of whole genome sequencing (WGS) for outbreak analyses. In total, 53 isolates were obtained from 52 patients and examined using WGS. Two independent analysis strategies (reference-based and -free) revealed the same distinct clusters of two CTX-M-15 producing K. pneumoniae clones (ST15, n = 31; ST405, n = 7) and one CTX-M-15 producing Klebsiella quasipneumoniae strain (ST414, n = 8). Additionally, we determined sequence variations associated with antimicrobial resistance phenotypes in single isolates expressing carbapenem and

colistin resistance, respectively. For rapid detection of the major K. pneumoniae outbreak clone (ST15), a selective triplex PCR was deduced from WGS data of the major outbreak strain and K. pneumoniae genome data deposited in central databases. Moreover, we introduce two novel open-source applications supporting reference genome selection (refRank; https://gitlab.com/s.fuchs/refRank) and alignment-based SNP-filtering (SNPfilter; https://gitlab.com/s.fuchs/snpfilter) in NGS analyses.},
author = {Becker, Laura and Fuchs, Stephan and Pfeifer, Yvonne and Semmler, Torsten and Eckmanns, Tim and Korr, Gerit and Sissolak, Dagmar and Friedrichs, Michael and Zill, Edith and Tung, Mei Lin and Dohle, Christian and Kaase, Martin and Gatermann, S{\"{o}}ren and R{\"{u}}ssmann, Holger and Steglich, Matthias and Haller, Sebastian and Werner, Guido},
doi = {10.3389/fmicb.2018.00322},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Becker et al. - 2018 - Whole genome sequence analysis of CTX-M-15 producing Klebsiella isolates allowed dissecting a polyclonal outbreak.pdf:pdf},
issn = {1664302X},
journal = {Frontiers in Microbiology},
keywords = {CTX-M-15,ESBL,Lista{_}Filtrada,NGS,Outbreak analysis,Strain typing},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
number = {FEB},
publisher = {Frontiers Media S.A.},
title = {{Whole genome sequence analysis of CTX-M-15 producing Klebsiella isolates allowed dissecting a polyclonal outbreak scenario}},
volume = {9},
year = {2018}
}
@article{Becker2015,
abstract = {We report here the genome sequence of a multidrug-resistant Klebsiella pneumoniae strain, which caused an outbreak in a neonatal ward in 2011. The genome consists of a single chromosome (5,278 kb) and three plasmids (362 kb, 5 kb, and 4 kb).},
author = {Becker, Laura and Bunk, Boyke and Eller, Christoph and Steglich, Matthias and Pfeifer, Yvonne and Werner, Guido and N{\"{u}}bel, Ulrich},
doi = {10.1128/genomeA.00742-15},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Becker et al. - 2015 - Complete genome sequence of a CTX-M-15-producing Klebsiella pneumoniae outbreak strain from multilocus sequence t.pdf:pdf},
issn = {21698287},
journal = {Genome Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
number = {4},
publisher = {American Society for Microbiology},
title = {{Complete genome sequence of a CTX-M-15-producing Klebsiella pneumoniae outbreak strain from multilocus sequence type 514}},
volume = {3},
year = {2015}

}
@article{Bae2012,
abstract = {We report the complete genome sequence of Pseudomonas aeruginosa siphophage MP1412, which displays synteny to those of P. aeruginosa phages M6 and YuA. However, the presence of two homing endonucleases of the GIY-YIG family is unique to MP1412, suggesting their unique role in the phage life cycle of the bacterial host.},
author = {Bae, H.-W. and Chung, I.-Y. and Sim, N. and Cho, Y.-H.},
doi = {10.1128/jvi.01403-12},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Bae et al. - 2012 - Complete Genome Sequence of Pseudomonas aeruginosa Siphophage MP1412.pdf:pdf},
issn = {0022-538X},
journal = {Journal of Virology},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {17},
pages = {9537--9537},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Pseudomonas aeruginosa Siphophage MP1412}},
volume = {86},
year = {2012}
}
@article{AshokKumar2020,
abstract = {Vibriosis is regarded as an important disease of penaeid shrimps affecting larvae in hatcheries. Among the Vibrio species, Vibrio parahaemolyticus, Vibrio vulnificus, Vibrio furnissii, Vibrio campbellii, Vibrio harveyi, Vibrio alginolyticus, and Vibrio anguillarum are often associated with diseases in finfish and shellfish of brackishwater ecosystem. Accurate species differentiating methods for the organisms present in an ecosystem are required for precise classification of the species and to take steps for their management. Conventional methods like 16s rRNA phylogeny and multilocus sequence typing (MLST) have often failed to correctly identify Vibrio species. This has necessitated a comprehensive investigation on methodologies available to distinguish Vibrio species associated with brackishwater aquaculture system. To achieve this, 35 whole genomes belonging to 7 Vibrio species were subjected to phylogenetic analysis based on 16s rRNA gene, MLST genes, single-copy orthologous genes, and single-nucleotide polymorphisms. In addition, genome-based similarity indices like average nucleotide identity (ANI) and in silico DNA-DNA hybridization (DDH) were computed as confirmatory tests to verify the phylogenetic relations. There were some misclassifications occurred regarding phylogenetic relations based on 16s rRNA genes and MLST genes, while phylogeny with single-copy orthologous genes produced accurate species-level clustering. Study reveals that the species identification based on whole genome-based estimates or genome-wide variants are more precise than the ones done with single or subset of genes.},
author = {{Ashok Kumar}, J. and {Vinaya Kumar}, K. and Avunje, S. and Akhil, V. and Ashok, S. and Kumar, Sujeet and Sivamani, B. and Grover, Monendra and Rai, Anil and Alavandi, S. V. and Vijayan, K. K.},
doi = {10.1177/1176934320903288},

file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Ashok Kumar et al. - 2020 - Phylogenetic Relationship Among Brackishwater Vibrio Species.pdf:pdf},
issn = {11769343},
journal = {Evolutionary Bioinformatics},
keywords = {16s rRNA,ANI,MLST single-copy orthologous genes,Vibrio,isDDH,phylogenetics},
publisher = {SAGE Publications Ltd},
title = {{Phylogenetic Relationship Among Brackishwater Vibrio Species}},
volume = {16},
year = {2020}
}
@article{Arabaghian2019,
abstract = {Klebsiella pneumoniae is a Gram-negative organism and a major public health threat. In this study, we used whole-genome sequences to characterize 32 carbapenem-resistant K. pneumoniae (CRKP) and two carbapenem-resistant K. quasipneumoniae (CRKQ). Antimicrobial resistance was assessed using disk diffusion and E-test, while virulence was assessed in silico. The capsule type was determined by sequencing the wzi gene. The plasmid diversity was assessed by PCR-based replicon typing to detect the plasmid incompatibility (Inc) groups. The genetic relatedness was determined by multilocus sequence typing, pan-genome, and recombination analysis. All of the isolates were resistant to ertapenem together with imipenem and/or meropenem. Phenotypic resistance was due to blaOXA-48,blaNDM-1, blaNDM-7, or the coupling of ESBLs and outer membrane porin modifications. This is the first comprehensive study reporting on the WGS of CRKP and the first detection of CRKQ in the region. The presence and dissemination of CRKP and CRKQ, with some additionally having characteristics of hypervirulent clones such as the hypermucoviscous phenotype and the capsular type K2, are particularly concerning. Additionally, mining the completely sequenced K. pneumoniae genomes revealed the key roles of mobile genetic elements in the spread of antibiotic resistance and in understanding the epidemiology of these clinically significant pathogens.},
author = {Arabaghian, Harout and Salloum, Tamara and Alousi, Sahar and Panossian, Balig and Araj, George F. and Tokajian, Sima},
doi = {10.1038/s41598-018-36554-2},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Arabaghian et al. - 2019 - Molecular Characterization of Carbapenem Resistant Klebsiella pneumoniae and Klebsiella quasipneumoniae Isola.pdf:pdf},
issn = {20452322},
journal = {Scientific Reports},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {dec},
number = {1},
publisher = {Nature Publishing Group},
title = {{Molecular Characterization of Carbapenem Resistant Klebsiella pneumoniae and Klebsiella quasipneumoniae Isolated from Lebanon}},
volume = {9},
year = {2019}
}
@article{AcevedoUgarriza2019,

abstract = {Bacteriophage Magnus infects Klebsiella pneumoniae , a Gram-negative pathogen whose multidrug-resistant strains are a public health issue. Here, we describe the annotation of the 157,741-bp Magnus genome and its similarity to other myophages.},
author = {{Acevedo Ugarriza}, Laura E. and Michalik-Provasek, Jordyn and Newkirk, Heather and Liu, Mei and Gill, Jason J. and Ramsey, Jolene},
doi = {10.1128/mra.01049-19},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Acevedo Ugarriza et al. - 2019 - Complete Genome Sequence of Klebsiella pneumoniae Myophage Magnus.pdf:pdf},
issn = {2576-098X},
journal = {Microbiology Resource Announcements},
keywords = {Lista{_}Filtrada},
mendeley-tags = {Lista{_}Filtrada},
month = {sep},
number = {39},
publisher = {American Society for Microbiology},
title = {{Complete Genome Sequence of Klebsiella pneumoniae Myophage Magnus}},
volume = {8},
year = {2019}
}
@article{Abril2019,
abstract = {Background: Pseudomonas aeruginosa Sequence Type 235 is a clone that possesses an extraordinary ability to acquire mobile genetic elements and has been associated with the spread of resistance genes, including genes that encode for carbapenemases. Here, we aim to characterize the genetic platforms involved in resistance dissemination in bla KPC-2 -positive P. aeruginosa ST235 in Colombia. Results: In a prospective surveillance study of infections in adult patients attended in five ICUs in five distant cities in Colombia, 58 isolates of P. aeruginosa were recovered, of which, 27 (46.6{\%}) were resistant to carbapenems. The molecular analysis showed that 6 (22.2{\%}) and 4 (14.8{\%}) isolates harboured the bla VIM and bla KPC-2 genes, respectively. The four bla KPC-2-positive isolates showed a similar PFGE pulsotype and belonged to ST235. Complete genome sequencing of a representative ST235 isolate shows a unique chromosomal contig of 7097.241 bp with eight different resistance genes identified and five transposons: A Tn6162-like with ant(2″)-Ia, two Tn402-like with ant(3″)-Ia and bla OXA-2 and two Tn4401b with bla KPC-2. All transposons were inserted into the genomic islands. Interestingly, the two Tn4401b copies harbouring bla KPC-2 were adjacently inserted into a new genomic island (PAGI-17) with traces of a replicative transposition process. This double insertion was probably driven by several structural changes within the chromosomal region containing PAGI-17 in the ST235 background. Conclusion: This is the first report of a double Tn4401b chromosomal insertion in P. aeruginosa, just within a new genomic island (PAGI-17). This finding indicates once again the great genomic plasticity of this microorganism.},
author = {Abril, Deisy and Marquez-Ortiz, Ricaurte Alejandro and Castro-Cardozo, Betsy and Moncayo-Ortiz, Jos{\'{e}} Ignacio and {Olarte Escobar}, Narda Mar{\'{i}}a and {Corredor Rozo}, Zayda Lorena and Reyes, Niradiz and Tovar, Catalina and S{\'{a}}nchez, H{\'{e}}ctor Fabio and Castellanos, Jaime and Guaca-Gonz{\'{a}}lez, Yina Marcela and Llanos-

Uribe, Carmen Elisa and {Vanegas G{\'{o}}mez}, Natasha and Escobar-P{\'{e}}rez, Javier},
doi = {10.1186/s12866-019-1418-6},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/Abril et al. - 2019 - Genome plasticity favours double chromosomal Tn4401b-bla KPC-2 transposon insertion in the Pseudomonas aerugino(2).pdf:pdf},
issn = {14712180},
journal = {BMC Microbiology},
keywords = {Bla KPC-2,Carbapenems,Colombia,Lista{_}Filtrada,Pseudomonas aeruginosa,Resistance,ST235},
mendeley-tags = {Lista{_}Filtrada},
month = {feb},
number = {1},
pages = {45},
publisher = {BioMed Central Ltd.},
title = {{Genome plasticity favours double chromosomal Tn4401b-bla KPC-2 transposon insertion in the Pseudomonas aeruginosa ST235 clone}},
url = {https://bmcmicrobiol.biomedcentral.com/articles/10.1186/s12866-019-1418-6},
volume = {19},
year = {2019}
}
@article{...2012,
abstract = {Lista{_}Filtrada},
author = {undefined ... and Program, NISC Comparative Sequencing},
file = {:C$\backslash$:/Users/Oscar/AppData/Local/Mendeley Ltd./Mendeley Desktop/Downloaded/..., Program - 2012 - Seguimiento de un brote hospitalario de carbapenem-resistente Klebsiella pneumoniae con todo - secuenciaci{\'{o}}n del g.pdf:pdf},
journal = {Science translational ...},
title = {{Seguimiento de un brote hospitalario de carbapenem-resistente Klebsiella pneumoniae con todo - secuenciaci{\'{o}}n del genoma}},
url = {https://stm.sciencemag.org/content/4/148/148ra116.short},
year = {2012}
}