

Identifying possibly novel sources of antimicrobial resistance in uncultivated bacterial and archeal metagenome-assembled genomes

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Abstract

Antimicrobial resistance (AMR) is a global threat to human health. Efforts to prevent the spread of AMR rely on surveillance of possible AMR determinants. Using phylogenetics to highlight potential sources of AMR could guide researchers in choosing organisms for phenotypic resistance testing. A systematic way of classifying AMR gene variants is important in comparing these phylogenetic relationships. In this study, the phylogenetic neighborhoods of several named AMR genes are characterized by their diversity, spread, and potential for discovering possibly novel AMR variants. Canonical sequence data from the Comprehensive Antibiotic Resistance Database (CARD) was used to query CARD prevalence data, NCBI sequence data, and draft quality metagenome assembled genomes (MAGs) from various uncultivated bacterial and archeal sources (UBAs). Genes which were potentially associated with mobile colistin resistance (MCR) were found in the UBA sources. New Delhi beta-lactamases (NDM), *Klebsiella pneumoniae* carbapenemases (KPC), and OXA beta-lactamases were not found to be represented in the UBAs, [TODO: “gradient of the AMR trees”] [TODO: conclusion: lots of novelty that cannot be accommodated by existing nomenclature schemes?]

Introduction

Antimicrobials are substances that can halt the growth of and/or kill microorganisms [1](#). An important part of the microbial adaptive process is the ability to adapt to pressure from antimicrobial agents within the environment. This ability allows microbes to continue to live and grow in the presence of antimicrobial compounds. This is known as antimicrobial resistance (AMR) <https://www.cdc.gov/drugresistance/about.html>. The abuse and misuse of antimicrobials has led to increasing levels of AMR within clinical settings [2](#).

The spread of AMR is a growing global health crisis. AMR within pathogenic microbes is a threat to our treatment of infectious diseases, reducing the efficacy of antibiotics, allowing for prolonged and more severe infections, and increased mortality [3](#). The European Centre for Disease Prevention and Control estimates that 25,000 people die per year due to infections related to AMR [4](#), with reports showing the annual cost to combat AMR infections in just the USA alone to be between \$21 billion and \$34 billion [5](#).

Microbes can be intrinsically resistant to AMR or acquire resistance via lateral gene transfer [6](#). These mechanisms allow for the constant change of the resistome, making determining the scope of AMR within both pathogenic and non-pathogenic bacteria difficult [2](#). To impede the spread of AMR the World Health Organization (WHO) created an action plan which emphasizes the need to strengthen the knowledge and surveillance of AMR. An important aspect of this research is to examine the spread of AMR between environmental and clinical samples url: <https://www.who.int/antimicrobial-resistance/global-action-plan/en/>. Characterization of many AMR genes is currently being done through curated databases. The Comprehensive Antibiotic Resistance Database (CARD) is an example of one of these curated databases. CARD contains reference data pertaining to the genes, proteins and mutations involved in AMR. CARD allows for the identification of resistance genes within a genome using the Resistance Gene Identifier (RGI). [2](#).

AMR genes which have been verified experimentally are present in the CARD database. Upon discovery, these AMR determinants are classified into various AMR families, some of which are based on phenotypic properties, and some based on sequence variation. The nomenclature is usually an acronym representing the mechanism of resistance, along with a numerical value to distinguish variants. Each sequence, determined to be novel by some arbitrary criteria, is assigned a new number. Sequences are further sub-categorized when the sequence similarity is high, and as much as a single amino acid difference has given rise to a newly named determinant. This system for classification has the potential to be misleading when conducting AMR research. AMR families could appear to have a

large amount of diversity, when in reality, sequences are closely related, and only a small number are actually distinct. Additionally, sequences which are not homologues, could potentially be classified in the same family, simply based on their function. This is a problem when attempting to characterize the AMR determinants by sequence similarity. [TODO: analogy to multi-locus sequence typing?]

These curated databases also contain a large amount of information on the resistomes that are most commonly studied, especially those pertaining to *Staphylococcus aureus*, *Escherichia coli*, *Klebsiella pneumoniae*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*. These pathogens are multi-drug resistant and are the leading cause of hospital acquired infections [2](#). Most antibiotics have no efficacy on these infections and are therefore treated with carbapenems or polymyxins [4](#).

Carbapenems are broad spectrum beta-lactam antibiotics typically used to treat life threatening, high risk, and multi-drug resistant bacterial infections. beta-lactamase producing bacteria have difficulty degrading carbapenems when combined with beta-lactamase inhibitors making them effective treatments against pathogens with multi-drug resistance [4](#). However, there has been a recent emergence of resistance to these antimicrobials, presenting a new threat to public health. One way microbes can develop carbapenem resistance is through the acquisition of carbapenamase genes. [4](#). Three main carbapenamase genes of concern are *Klebsiella pneumoniae* carbapenemase (KPC), New Delhi metallo-beta-lactamase (NDM) and OXA beta-lactamases [4](#).

Carbapenamases are classified as one of four classes (A-D) based on their molecular structure [8](#). Class A, C, and D both use a serine residue to hydrolyze beta-lactam antibiotics [9](#). KPC genes are a part of class A. Many variants of KPC are spreading and being discovered, however carbapenamases within this class are more rare than the other three classes [4](#). Class D contains the OXA family of beta-lactamases. Unlike KPC and NDM, this family is characterized by phenotype rather than genotype. This family is characterized by specific hydrolases that can hydrolyze oxacillin and cloxacillin, with the enzyme being poorly inhibited by clavulanic acid <https://card.mcmaster.ca/ontology/36026>. This results in a low amount of sequence homology within the family. A subset of this family, OXA-48 possesses carbapenem hydrolyzing activity [10](#). The OXA-48 subfamily consists of five variants: OXA-48, OXA-162, OXA-163, OXA-181, OXA-204, and OXA-232 [11](#). Class B beta-lactamases are metalloenzymes that use a zinc active site to hydrolyze beta-lactam antibiotics. The NDM gene is classified as a class B beta-lactamase [4](#).

When pathogens become resistant to carbapenems, the last line of defense is colistin. Colistin is a polymyxin antibiotic. Polymyxins act via disrupting membrane permeability [12](#). Colistin is limited to a last line defense against carbapenem resistant infections due to its neurotoxic and nephrotoxic effects [12](#). Despite its already limited use, mobilized colistin resistance (MCR) have been discovered [13](#). Due to the emergence of resistance to many last-line antibiotics, it is important to characterize the total diversity and spread of these resistance determinants.

UBA datasets, and databases such as NCBI, and CARD prevalence data, contain data which could better characterize the phylogenetic neighborhoods of these AMR determinants, improving AMR surveillance. UBA datasets could better diversify samples, by querying against under-sampled genomes. The CARD prevalence data, provides an expansion to the canonical variants, and would find many relevant sequences. NCBI serves as a good source of many other possible sequences. Coupling RGI predictions of the UBA metagenomes with phylogenetic analysis of the predicted AMR genes enables the possibility to discover previously unseen AMR diversity in genomes not yet analyzed for AMR, and provides insight into the diversity of AMR across non-clinical samples.

Methods

AMR Prediction

Materials

A data-set of 7903 draft quality MAGs which were recovered from the Sequence Read Archive by Parks [14](#) were used for this analysis. These genomes were chosen specifically because they were likely to be from lineages which were under-sampled. Environmental and non-human gastrointestinal samples were the main focus of these samples.

RGI version 5.0 with CARD database version 3.02 [2](#) was run on the contigs of the 7903 MAGS with the inclusion of loose, perfect, and strict hits.

CARD prevalence data version 3.0.4 ("based on sequence data acquired from NCBI on 28-Feb-2019, analyzed using RGI 4.2.2 (DIAMOND homolog detection) and CARD 3.0.1") was used to query the UBA data. [TODO: Other versions of software]

Obtaining reference sequences

32 canonical MCR sequence variants, 14 canonical NDM sequence variants, 6 canonical OXA-48-like sequence variants, and 18 canonical KPC sequence variants (see Table S1) as indicated by CARD for the , were obtained from the CARD database.

In the case of OXA beta-lactamase, only OXA-48-like genes were used for analysis. The OXA family is characterized by phenotype rather than genotype, and results in a low amount of sequence homology within the family. The phenotype of OXA-48 results from carbapenem hydrolyzing activity [10](#). This subfamily of OXA contains homologous sequences suitable for this study. Incorporating other subfamilies of OXA proved to be too cumbersome.

Additional putative AMR gene family sequences were accumulated by querying the CARD prevalence data. The prevalence data was translated to a BLAST database. The CARD canonical sequences from each family were used to perform a multiple query BLASTP against the prevalence blast database with a e-value threshold and query coverages shown in Table [1](#)

Many of the sequences are nearly identical, thus they were further processed by clustering with CD-HIT at a minimum sequence identities indicated also in Table [1](#)

The CARD canonical sequences were also used to perform a multiple query BLASTP against the NCBI non-redundant database blast database with a e-value threshold, and query coverage indicated in Table [1](#)

For simplicity in identifying the taxonomic history of the non-redundant hits, MULTISPECIES sequences were removed from the analyses. There are many highly sampled taxa and genes in the non-redundant database. To balance the distribution, and reduce the size of the non-redundant sequence set, CD-HIT was used to cluster the data as per table [1](#).

Sequences possibly containing AMR gene prediction data for each gene family was produced by filtering RGI output based on the its association with the search strings for each determinant in Table [1](#) The filtered data were translated to a blast database. The CARD canonical sequences were used to perform a multiple query BLASTP against this UBA blast database with a e-value threshold and query coverage in Table [1](#).

Table 1: [TODO: fill in the actual values] e-value, query coverage, and cluster percentage used for

each AMR family experiment for the prevalence, ncbi non-redundant, and UBA databases.

A. MCR phosphoethanolamine transferase		B. NDM beta-lactamase		C. OXA beta-lactamase		D. KPC beta-lactamase	
Tree	LG+I+G4	Tree	LG+I+G4	Tree	LG+I+G4	Tree	LG+I+G4
e-value_p	1e-160	e-value_p	1e-160	e-value_p	1e-160	e-value_p	1e-160
e-value_n	1e-160	e-value_n	1e-160	e-value_n	1e-160	e-value_n	1e-160
e-value_u	1e-160	e-value_u	1e-160	e-value_u	1e-160	e-value_u	1e-160
coverage_p	98	coverage_p	98	coverage_p	98	coverage_p	98
coverage_n	98	coverage_n	98	coverage_n	98	coverage_n	98
coverage_u	98	coverage_u	98	coverage_u	98	coverage_u	98
clustering_p	N/A	clustering_p	N/A	clustering_p	N/A	clustering_p	N/A
clustering_n	N/A	clustering_n	N/A	clustering_n	N/A	clustering_n	N/A
clustering_u	N/A	clustering_u	N/A	clustering_u	N/A	clustering_u	N/A

Redundant results for the prevalence, NCBI, and UBA queries were filtered from these BLASTP results by retrieving only the longest sequence for each uniquely labeled result.

Phylogenetic analysis

To compare the phylogenetic relationship of only the putative sequences, the sequences from the CARD prevalence data were concatenated to one multi-FASTA format file with the canonical sequences. These the concatenated amino acid sequences were aligned with MAFFT-LINSI. The aligned sequences were trimmed by trimal using the automated1 option. IQ-TREE was then used to build a bootstrapped tree with -bb 1000 with the G+I+G4 model of substitution.

For the overall comparison of sequences, the filtered sequences from NCBI non-redundant data, CARD prevalence data, UBA data were all concatenated to one multi-FASTA format file with the canonical sequences. These the concatenated amino acid sequences were aligned with MAFFT-LINSI. The aligned sequences were trimmed by trimal using the automated1 option. IQ-TREE was then used to build a bootstrapped tree with -bb 1000 with the G+I+G4 model of substitution. All leaves of the trees were labeled with as much taxonomic information as possible for each rank, based on information from metadata [TODO: supplemental].

Results

Phylogenetic analysis of putative MCR sequences

The phylogenetic relationships of the CARD canonical sequences, and the CARD prevalence sequences involving the MCR family were investigated to show the phylogenetic relationship of only the putative MCR sequences without the noise of additional sequences. A total of 87 genes, an out-group, the 32 canonical sequences, and the 54 prevalence sequences (clustered as per Table 1), were selected for analyses. The tree in Figure 1 shows several distinct clades. Each MCR variant forms its own clade. MCR-1, MCR-2, and MCR-6 form a clade, appearing to more closely related to one another than with

the other MCR family members. This clade is also closely related to the ICR-Mc clade. ICR-Mc [15](#) is another phosphoethanolamine transferase which confers colistin resistance.

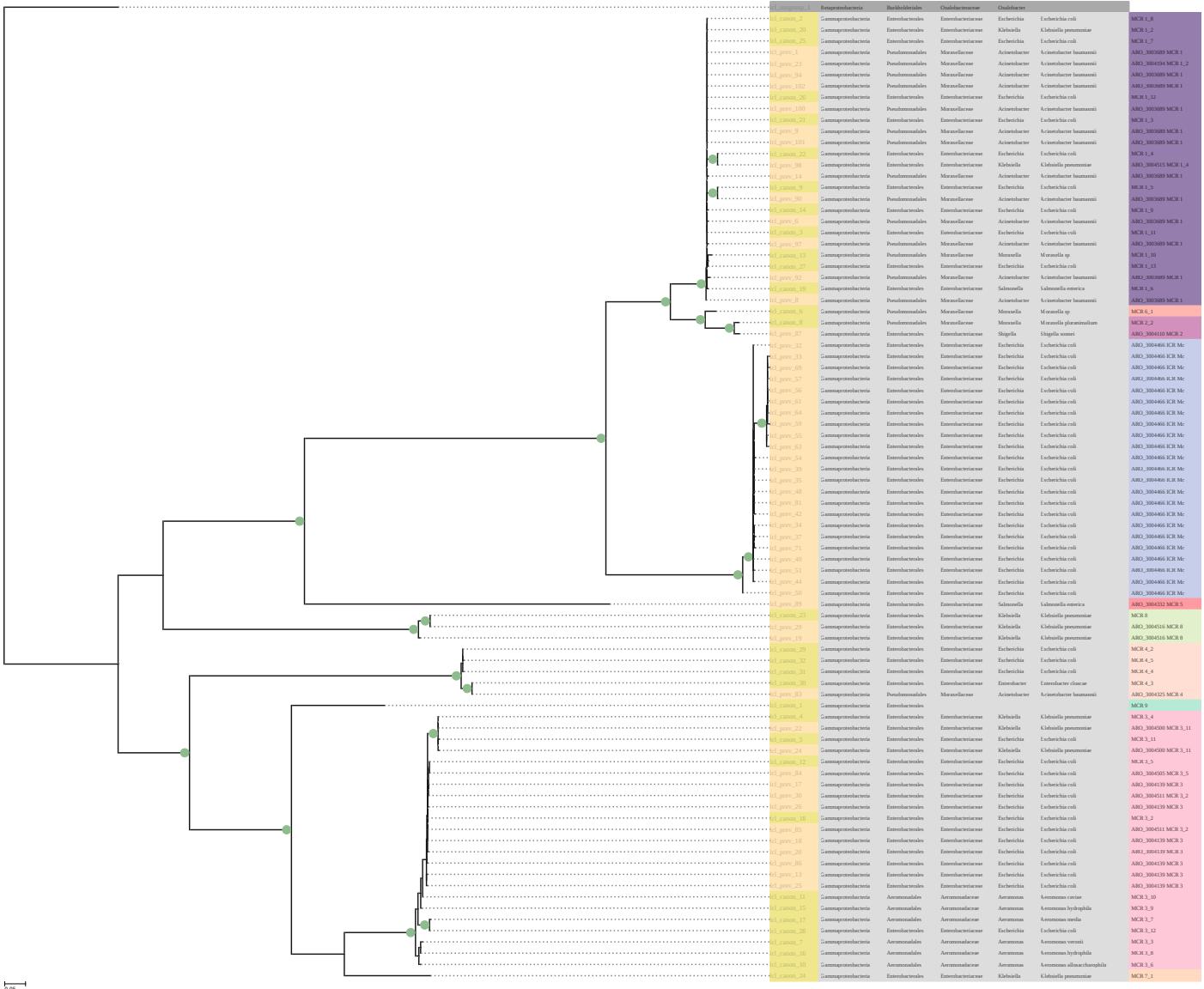
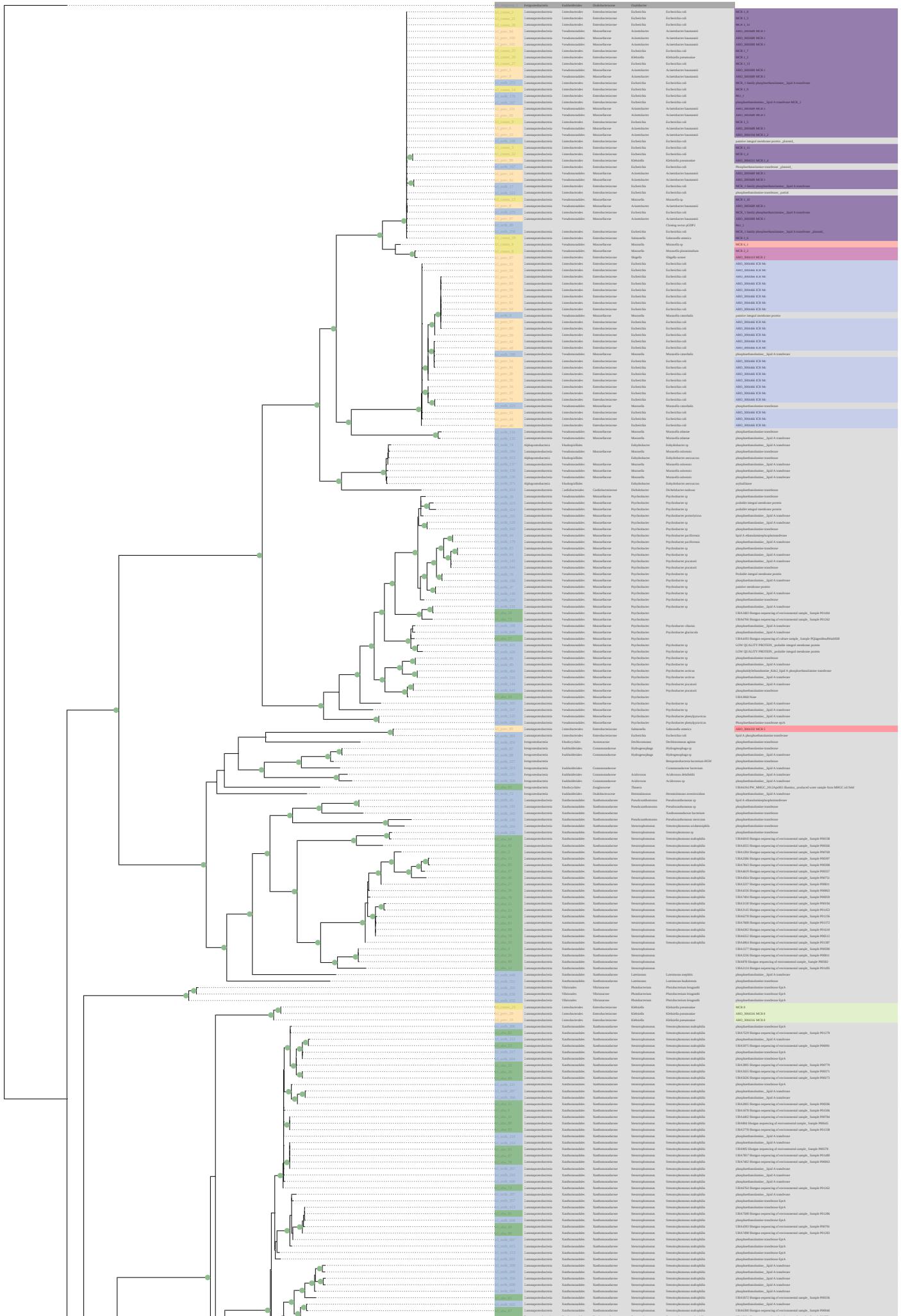
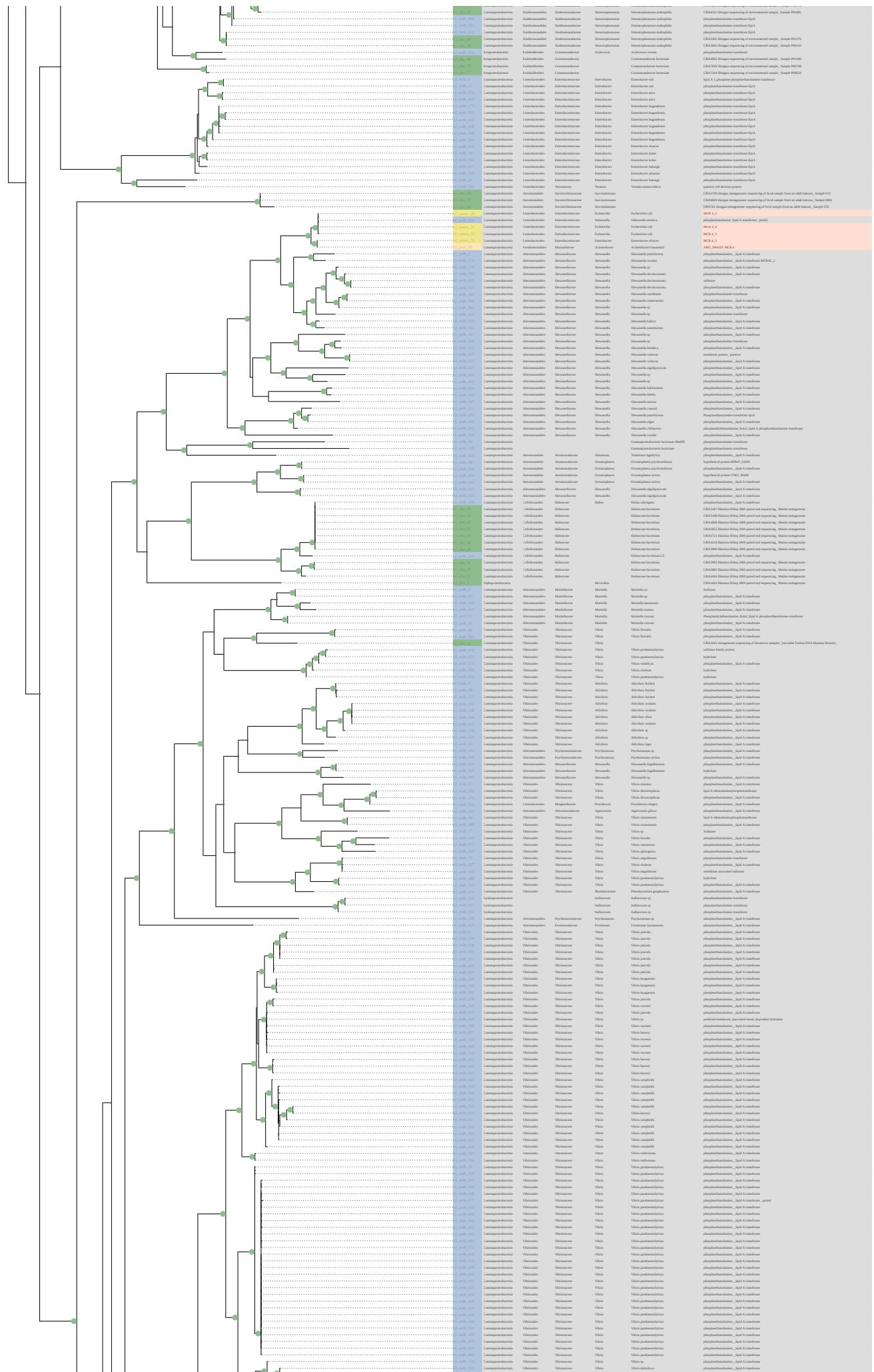


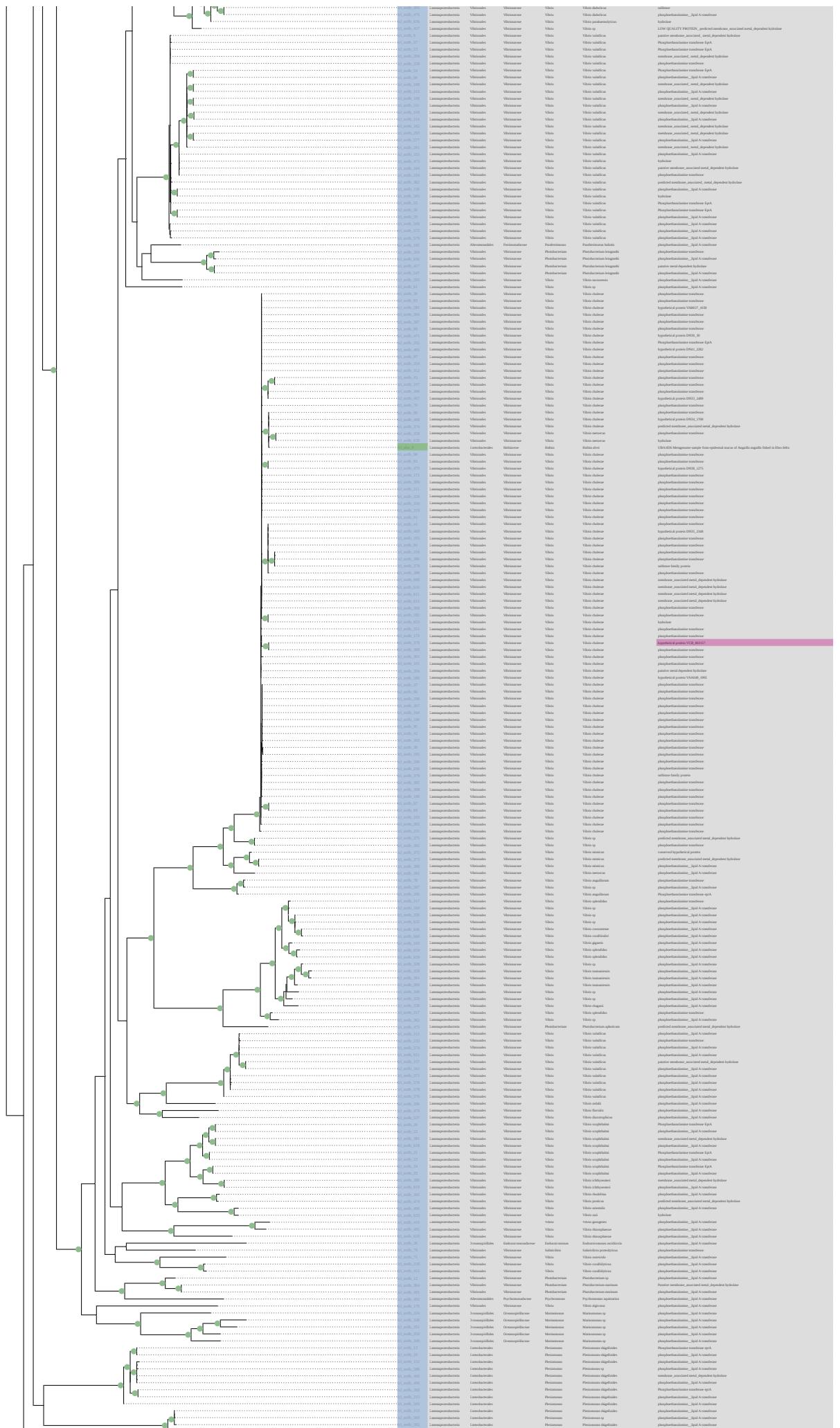
Figure 1: Phylogenetic relationship of 32 canonical (labels prefixed with lcl_canon_ in yellow), 54 prevalence (labels prefixed with lcl_prev_ in tan) MCR family sequences, and an outgroup from Betaproteobacteria (lcl_prev_ in tan) Each MCR variant is coloured based on its primary numerical value.

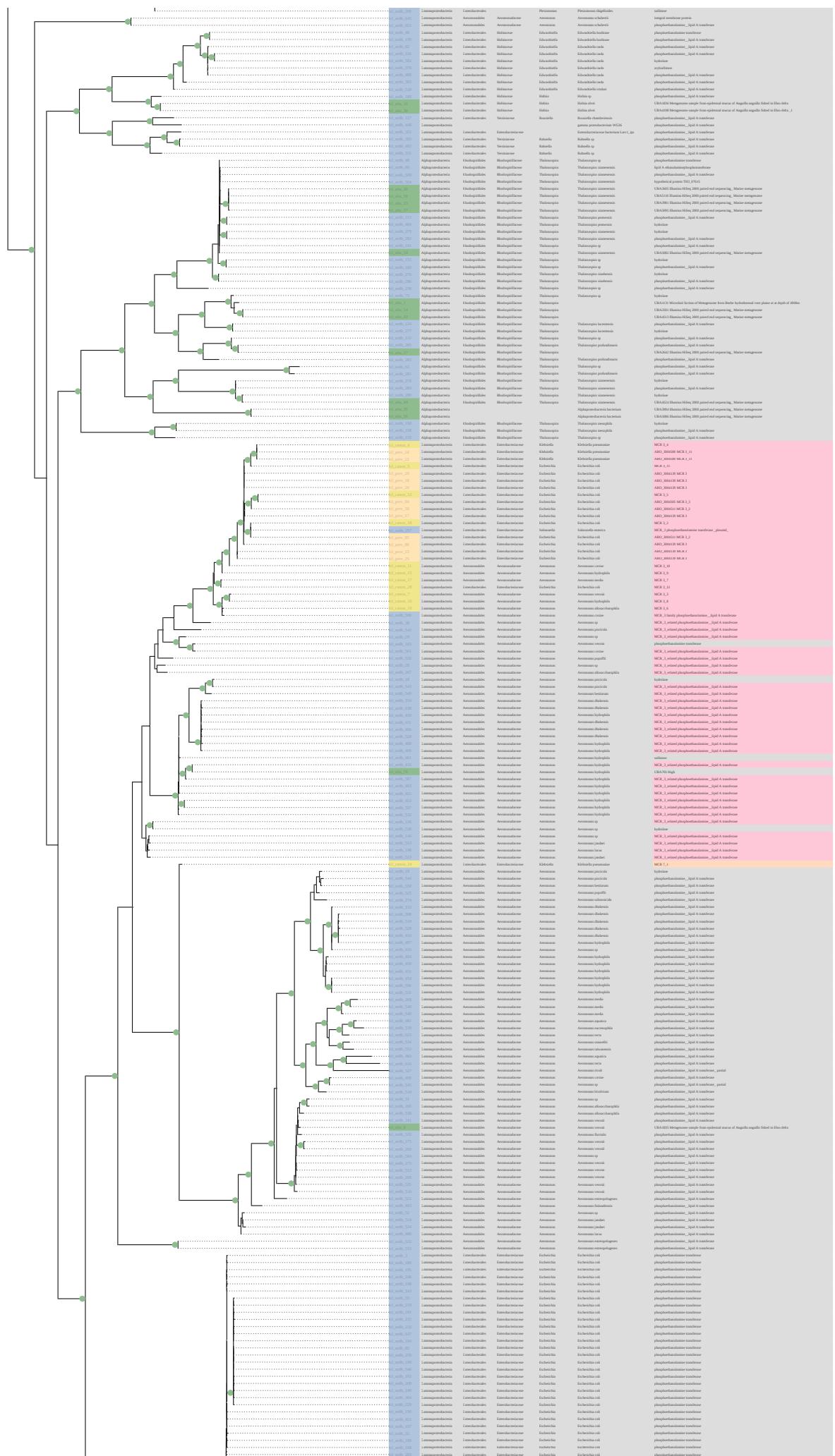
Sequences from the NCBI non-redundant data were added to the analysis to be compared with the canonical and prevalence sequences. This resulted in a total of 409 sequences for subsequent analysis, all labeled as phosphoethanolamine lipid A transferase genes, where 104 hits were labeled as MCR family genes.

The phylogeny in Figure 2 shows that the MCR 3 clade branches with MCR-9. This MCR-3 and MCR-9 clade is separated by a large amount diversity from the MCR 1,2,4,5, and 8 clades. [TODO: reword based on new figure]









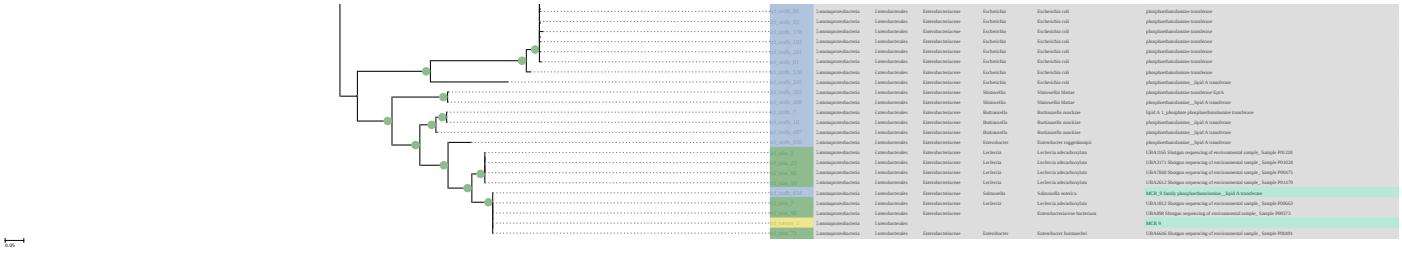


Figure 2: Phylogenetic relationship of 32 canonical (labels prefixed with `Icl_canon_` in yellow), and 54 prevalence (labels prefixed with `Icl_prev_` in tan) MCR family sequences, 595 NCBI non-redundant sequences (labels prefixed with `Icl_prev_` in blue), and 91 UBA sourced sequences (labels prefixed with `Icl_prev_` in green). Each MCR variant is coloured based on its primary numerical value. If the sequence is not reported to be MCR family it is coloured in grey.

Phylogenetic analysis of UBA sequences with RGI-CARD

RGI produced 1457246 results AMR determinants under the loose cutoff from the UBA data, 7171 for the strict cutoff, and 310 for the loose cutoff. It was hoped that phylogenetic analysis could find AMR determinants would be found in under the loose criterion that may have been missed by RGI-CARD. The UBA BLAST results were included in the phylogeny in Figure 2 for the analysis. The diversity between clades, swathes of which are not reported to be in the MCR family, contain multiple sources from UBAs. The remainder of the analysis deals with relationships which are deemed to be interesting based on the locations of the UBAs between MCR family clades.

MCR-5, MCR-1,2,6 clades

The MCR-5, MCR1,2,6 clades shown in figure ?? share, with 100 bootstrap support, a common ancestor. Branching between these two clades, as a descendant to this ancestor, is a clade of Psychrobacter species bacteria. This clade includes two hits from the non-redundant database, and two hits from the UBA data. According to the Parks [14](#) data, the identity of these samples are, UBA3068, A Psychrobacter sp., sampled from Oil polluted marine microbial communities from Coal and Oil in Point Santa Barbara, California, USA and, UBA4193, a Psychrobacter sp, sampled from the New York City MTA subway samples. The quality information for these sequences, shown in Table ??, shows that UBA3068 is near complete, while UBA4193 is only partial. It is encouraging to see that even with the quality difference, these two sequences branch in the expected clade. Psychrobacter [16](#) is a Genus is widespread and includes many cold adapted bacteria, it is an opportunistic pathogen, and has been found sometimes be a cause of infections in humans, animals, and fish. Many new species of Psychrobacter have been discovered in cold climates [17](#). Some of the species have been shown to be resistant to colistin, like Psychrobacter vallis ps. nov. and Psychrobacter aquaticus ps. nov. [18](#) and is sister to [TODO: display new tree such that Acinetobacter is shown]

MCR-3 clade

A single result, UBA705, which the Parks data [14](#) reports as a Comparative metagenome analyses of anode-associated microbial communities developed in rice paddy field-soil microbial fuel cells, is reported to be Aeromonas hydrophilia. This present within the clade alone with several other canonical and non-redundant Aeromonadaceae. Aeromonas hydrophilia is a species which has been found to have an MCR-3 gene. Again, even though qualities vary (Table ??), the sequences branch in the expected location.

MCR 3,9 clade

This clade contains 8 UBAs from the loose CARD hits under the given constraints, and several NCBI non-redundant hits not reported as MCR family genes. 7 Loose hits for MCR in a /Leclercia/ adecarboxylata branch within this clade, branching closely with the NCBI non-redundant MCR9. These

/Leclercia/ branch below the common ancestor of MCR-9 and MCR-3 which are well supported. The /Leclercia/ UBAs were all sampled from New York City MTA subway samples Metagenome. Acinetobacter is another opportunistic pathogen [19](#) which is becoming resistant to many antimicrobials.

MCR Alignment

TODO: inspect alignment to see if any positions have lots of entropy placeholder figure

Phylogenetic analysis of NDM

The phylogenetic relationships of the NDM family were investigated. The 14 canonical sequences were used to query the same databases as in the phylogenetic analyses of MCR.

The genes retained for the phylogeny were the 14 canonical sequences, 3 prevalence sequences ((clustered as per table S3)), 7 non-redundant sequences, 1 UBA sequence, and 1 out-group.

This total of 27 resulted in the phylogeny in Figure 3.

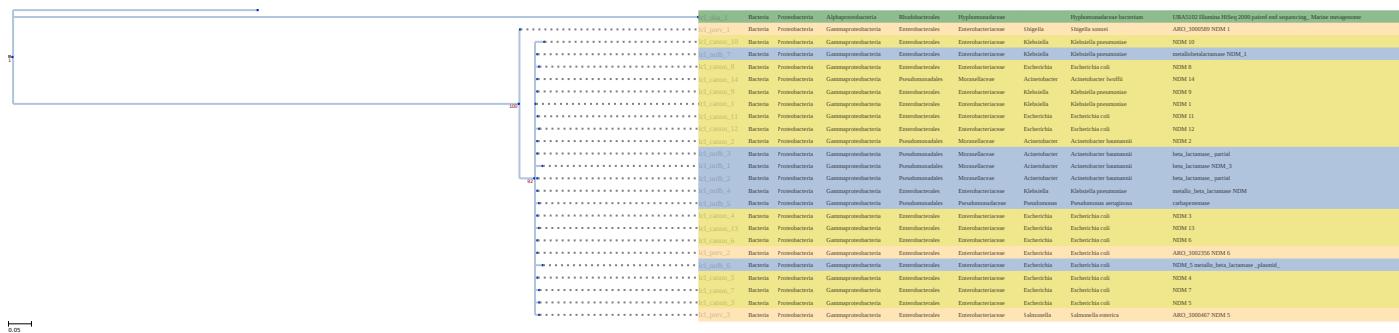


Figure 3: Phylogenetic relationship (lcl_canon) NDM family sequences along with 14 prevalence (lcl_prev) sequences.

The 7 sequences resulting from the NCBI data included 3 genes reported to be NDM-1, NDM-3, and NDM-5. The other 4 genes were reported to be general beta lactamase/carbapenemase hits. These sequences form a closely related multifurcation (due to poor support values) with the prevalence and canonical data. The only phylogenetically resolved gene in this clade was a prevalence hit for NDM-1 found in *Shigella sonnei* representing only itself in the cd-hit cluster. Interestingly other representatives from other purported NDM families are more closely related to each other, including the canonical NDM-1 sequence from *Klebsiella pneumoniae*. The one UBA BLAST result branches far from the clade containing the canonical indicating that under the coverage queried, there are no reasonably detectable NDM homologues in the UBA data. The alignment of this UBA under this relaxed query coverage of 60% is already pushing the limits of a “good alignment”, and reducing this further would produce meaningless results.

Phylogenetic analysis of OXA-48

In investigating the phylogenetic relationship of OXA-48, the result was similar to that of NDM. There were multiple BLAST results for UBA sequences, but the hits were too phylogenetically dissimilar to draw a conjecture about their relationship to the OXA family. 6 canonical sequences, and the 5 prevalence sequences (clustered according to Table S3), 11 non-redundant sequences, and 112 UBA sequences were combined in the phylogeny in Figure 4

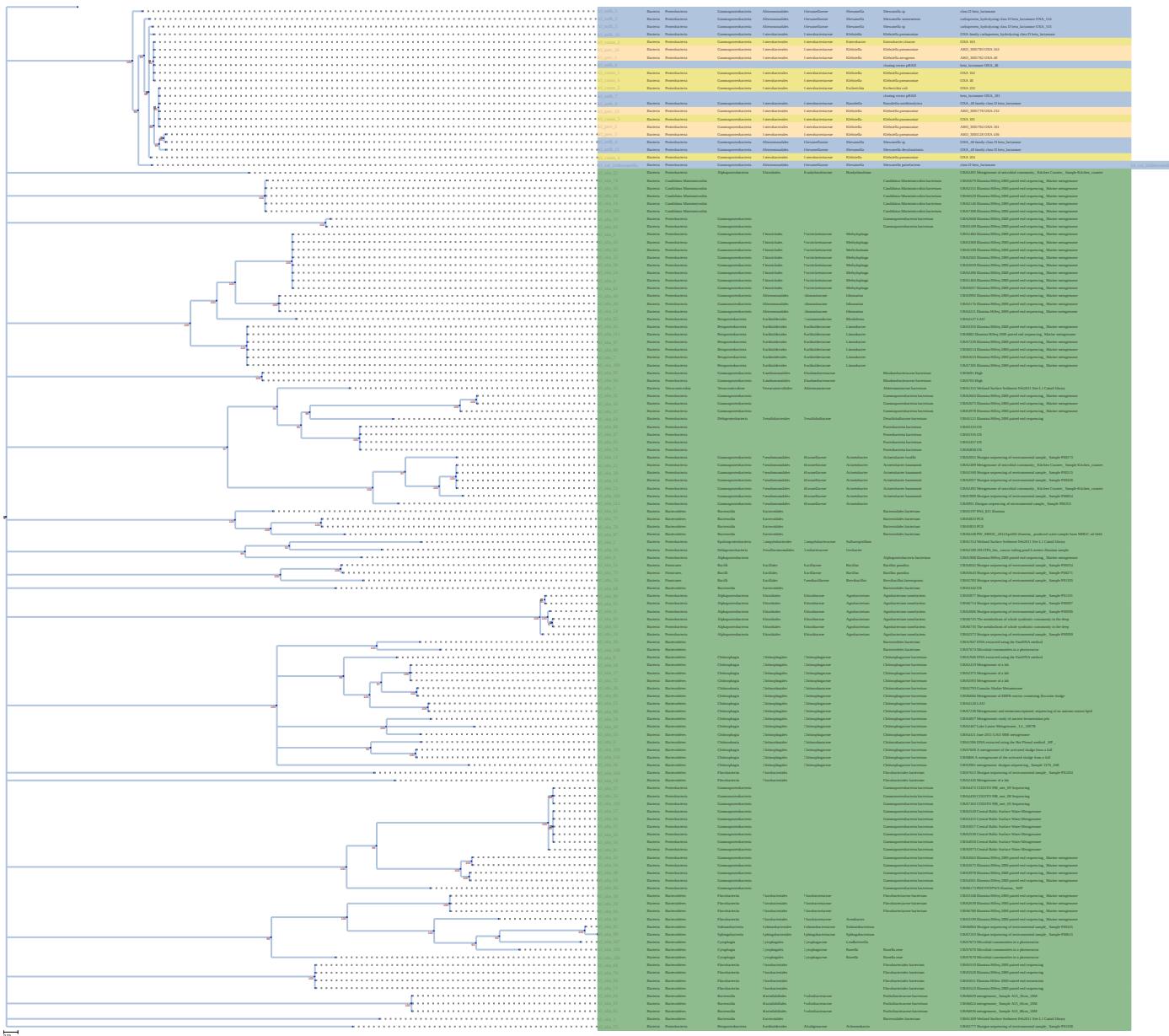


Figure 4: Phylogenetic relationship (lcl_canon) OXA-48 family sequences along with 14 prevalence (lcl_prev) sequences.

The OXA-48 prevalence hits added further diversity to the reference OXA-48-like sequences. OXA-436 [20](#) was found, clustered with no other gene, in the prevalence data, and OXA-514 and OXA-515 were found in the non-redundant data.

Phylogenetic analysis of KPC

18 canonical sequences, and the 8 prevalence sequences (clustered according to Table S3), non-redundant sequences, and 7 UBA sequences were combined in the phylogeny in Figure 4. Investigating the phylogenetic relationship of KPC also resulted in UBA sequences which were too distant from the canonical sequences to make a conjecture regarding their relationship to KPC family. In Figure 5 the 7 resulting UBA sequences branch with class A beta-lactamases as reported by the non-redundant BLAST.

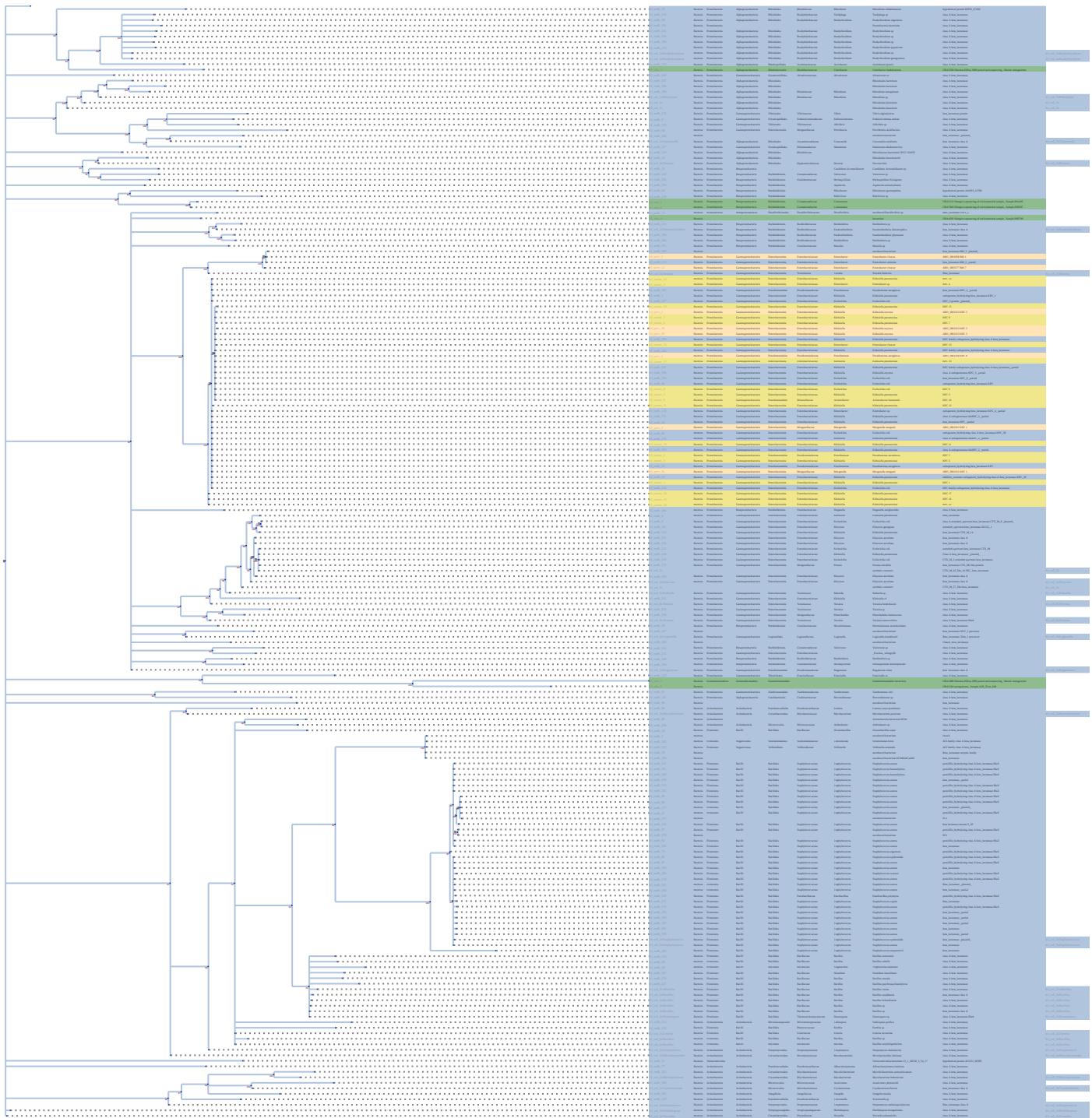


Figure 5: Phylogenetic relationship (lcl_canon) KPC family sequences along with 14 prevalence (lcl_prev) sequences.

Discussion

- TODO: Discuss the following:
 - We found a lot of intermingled MCRs, not so much with the others (plasmids etc.)
 - Why were some UBAs not covered? (plasmids)
 - What should we do with naming, especially as new variants are discovered and fill in the tree?
 - Taxonomic anomalies and how they may be explained
 - There were many clinical samples represented that *did* yeild MCRs, but the recovery could be bad

Conclusion

S1: MCR 3.11, 6.1, 2.2, 3.6, 3.10, 3.5, 1.10, 1.9, 3.9, 3.8, 3.7, 3.2, 3.1, 1.6, 1, 2, 3, 1.2, 1.3, 1.4, 8, 4, 5, 7.1

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