

An abstract graphic on the left side of the slide features several circles in shades of teal and pink, connected by thin, light-colored lines that create a network-like structure.

GENOME ANALYSIS: *Neisseria* *meningitidis*

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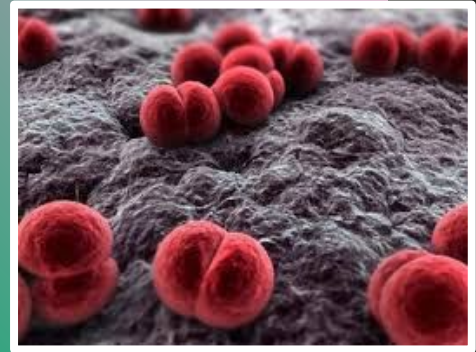
Introduction

Neisseria Meningitidis

Gram Diplococci bacteria
highly similar to gonococci
equipped with different
virulence factors to persist
systematically

Goal:

Identification of genes that
promote those virulence
factors in this species



Methods

SPAdes

ABYSS

**Prokka
(v.1.14.6)**

**FastANI
(v.1.34)**

BlastN

Genome Assemblers

Focuses on
small genomes
like prokaryotes

Greater suited
towards Eukaryotic
assembly due to
longer sequence
reads

**Gene
Annotator for
specific gene
function**

Determines levels
of relatedness
across species
based on
nucleotide identity

**Aligns nucleotide
sequences to
find similar
species related
to the reference**

Results (SPAdes vs. ABySS)

All statistics are based on contigs of size ≥ 500
"Total length (≥ 0 bp)" include all contigs).

ABySS

Assembly	assembly-scaffolds
# contigs (≥ 0 bp)	459
# contigs (≥ 1000 bp)	71
# contigs (≥ 5000 bp)	61
# contigs (≥ 10000 bp)	47
# contigs (≥ 25000 bp)	26
# contigs (≥ 50000 bp)	12
Total length (≥ 0 bp)	2192604
Total length (≥ 1000 bp)	2117273
Total length (≥ 5000 bp)	2081184
Total length (≥ 10000 bp)	1974717
Total length (≥ 25000 bp)	1608517
Total length (≥ 50000 bp)	1064322
# contigs	85
Largest contig	201878
Total length	2127124
GC (%)	51.66
N50	50375
N90	13514
auN	66021.5
L50	12
L90	42
# N's per 100 kbp	128.15

All statistics are based on contigs of size ≥ 500
"Total length (≥ 0 bp)" include all contigs).

SPAdes

Assembly	scaffolds
# contigs (≥ 0 bp)	142
# contigs (≥ 1000 bp)	53
# contigs (≥ 5000 bp)	46
# contigs (≥ 10000 bp)	34
# contigs (≥ 25000 bp)	24
# contigs (≥ 50000 bp)	15
Total length (≥ 0 bp)	2144857
Total length (≥ 1000 bp)	2116054
Total length (≥ 5000 bp)	2092576
Total length (≥ 10000 bp)	2003699
Total length (≥ 25000 bp)	1822849
Total length (≥ 50000 bp)	1509711
# contigs	69
Largest contig	230895
Total length	2126697
GC (%)	51.63
N50	88099
N90	19398
auN	92894.2
L50	9
L90	29
# N's per 100 kbp	47.49

Results (Blastn)

Descriptions		Graphic Summary	Alignments	Taxonomy								
Sequences producing significant alignments					Download	Select columns	Show	100				
<input checked="" type="checkbox"/> select all 100 sequences selected					GenBank	Graphics	Distance tree of results	MSA Viewer				
	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession			
<input checked="" type="checkbox"/>	Neisseria sp. Marseille-Q6792 genome assembly_chromosome: contig00001	Neisseria sp. Marseille-Q6792	5112	20448	100%	0.0	99.24%	2024518	QW969598.1			
<input checked="" type="checkbox"/>	Neisseria cinerea strain ATCC 14685 23S ribosomal RNA gene_complete sequence	Neisseria cinerea	5103	5103	100%	0.0	99.17%	2890	NR_121917.1			
<input checked="" type="checkbox"/>	Neisseria cinerea strain FDAARGOS_871 chromosome_complete genome	Neisseria cinerea	5098	20394	100%	0.0	99.13%	1832901	CP065726.1			
<input checked="" type="checkbox"/>	Neisseria cinerea strain NCTC10294 genome assembly_chromosome: 1	Neisseria cinerea	5098	20394	100%	0.0	99.13%	1832904	LS483369.1			
<input checked="" type="checkbox"/>	Neisseria polysaccharea strain M18661 chromosome_complete genome	Neisseria polysaccharea	5098	20369	100%	0.0	99.13%	2024930	CP031325.1			
<input checked="" type="checkbox"/>	Neisseria polysaccharea strain ATCC 43768 chromosome_complete genome	Neisseria polysaccharea	5098	20260	100%	0.0	99.13%	2024350	CP181243.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae isolate 632_2023 genome assembly_chromosome: 1	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2228442	QZ004876.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain FQ82 chromosome_complete genome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2217835	CP034018.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 10239 chromosome_complete genome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2223679	CP098474.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain FQ04 chromosome_complete genome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2217528	CP034028.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae NCCP11945_complete genome	Neisseria gonorrhoeae NCCP11945	5084	20330	100%	0.0	99.03%	2232025	CP001050.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 2010C02-038 chromosome_complete genome	Neisseria gonorrhoeae	5084	20333	100%	0.0	99.03%	2163486	CP131641.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 10743 chromosome_complete genome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2227249	CP106805.1			
<input checked="" type="checkbox"/>	Neisseria macacae ATCC 33926 chromosome_complete genome	Neisseria macacae ATCC 33926	5084	20339	100%	0.0	99.03%	2801968	CP094241.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain NCTC13800 genome assembly_chromosome: 1	Neisseria gonorrhoeae	5084	20326	100%	0.0	99.03%	2226638	LT906472.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain WHO G genome assembly_chromosome: 1	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2167361	LT591898.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 9035 chromosome_complete genome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2223133	CP104546.2			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 1137292 chromosome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2228866	CP107273.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 9458 chromosome_complete genome	Neisseria gonorrhoeae	5084	20339	100%	0.0	99.03%	2233050	CP098476.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain 2004S05-027 chromosome_complete genome	Neisseria gonorrhoeae	5084	20320	100%	0.0	99.03%	2226346	CP131645.1			
<input checked="" type="checkbox"/>	Neisseria gonorrhoeae strain RIVM0610_complete genome	Neisseria gonorrhoeae	5084	20326	100%	0.0	99.03%	2229240	CP019466.1			

Results (FastANI)

Original Genome	Ref Genome	ANI%	Aligned Fragments	Total Fragments
Spadesout/sc affolds.fasta	neighbors/gonor rhoeae.fna	95.08	604	681
Spadesout/sc affolds.fasta	neighbors/polys accharea.fna	94.31	581	681

Gene Identifications Using Prokka

Gene	Feature ID	Function	Virulence Factor Relevance
pilE	ODNGKOGP_00526	Production of pilin protein	Major subunit for Type IV pili to attach to epithelia
lldD	ODNGKOGP_01508	Produces Lactate dehydrogenase	Allows for the production of nutrients as a growth factor in anaerobic conditions
igA	ODNGKOGP_00112	Produces igA protease	Significant for mucosal colonization in both nasopharynx and cervical pathways

Conclusions/Review

- Identification of varying virulence factors of *Neisseria Meningitidis*
- Confirmation of the selected bacteria through genome analysis done using genome software (SpAdes, Prokka, etc.)
- Denoting of similarities in genome alignments of other species of *Neisseria*