COMPARATIVE GENOME OF TWO STRAIN *MORAXELLA CATARRHALIS* USING IN SILICO ANALYSIS

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ABSTRACT

Moraxella catarrhalis can cause otitis media and exacerbations of chronic obstructive pulmonary disease in human. Here we describe the comparison between two publicly available genomes of two strain of M.catarrhalis using computational analysis to obtain genomic features between them. Comparative genomic analysis were carried out using available tools in public domain websites. The aim of this study was to investigate the differences and similarities between two strains by comparing their genomic sequences. The results indicated that may be used to offer better understanding M.catarrhalis lifestyle.

Keywords: *Moraxella catarrhalis; In Silico; Comparative genome analysis*

INTRODUCTION

Comparative genome analysis is a branch of biology that studies the comparison between two different genomes. This approach can be used to study the bacterial lifestyle, virulences and host pathogen interaction. This analysis is based on the hypothesis that an important biological order has sustainable properties [1].

Moraxella catarrhalis is human-restricted respiratory tract pathogen. This pathogen cause otitis media and exacerbations of chronic obstructive pulmonary disease [2]. M. *catarrhalis* strain BBH18 (formerly known as RH4 strain) is the first completely assembled genome sequence of this species [2]. The BBH18 was isolated from blood of an infected patient [2]. Wherease, M. *catarrhalis* strain CCRI-195ME was isolated from the middle ear of sick children with otitis media [3].

MATERIAL AND METHOD

Strain genome were downloaded from NCBI (National Center for Biotechnology Information) at www.ncbi.nlm.nih.gov/genome. Genome features of each strain was obtain from NCBI. BLAST Genome was used to analyze genome stability. The genomes sequences of the two strains were subjected to wgVISTA at genome.lbl.gov/vista/index.shtml [4] to identify conserved region between sequences. Phylogenetic tree was built using Mega7 [5] with bootstrap 1000.

RESULTS AND DISCUSSION
Genome features
Genome features comparison can be seen in Table 1. Both genome features have no significant difference. However, M. *catarrhalis* strain CCRI-195ME has a plasmid. This plasmid contains 44 predicted open reading frames (ORF) [3].

Whole genome alignment

BLAST Genomes was used to analyze genome stability. Both strain share 99% identities (173843/174937) with 141/174937 gaps. Based on the genomic information, M. *catarrhalis* strain BBH18 has 343 predicted ORFs while M. *catarrhalis* strain CCRI-195ME has 377 predicted ORFs.

Conserved region was analysis using wgVista. Based on wgVISTA analysis, several regions in the genomes alignment were identified as divergent region (Figure 1). ORFs that located in those region were analyzed further to predict the protein content using Blastp (Table 2).

Phylogenetic analysis

In this phylogenetic analysis, we used five available M. *catarrhalis* genome data in NCBI. Phylogenetic tree was built based on 16S rRNA gene sequences. 16S rRNA gene sequences were extracted from the genomes based on NCBI's annotation. Figure 2 show M. *catarrhalis* strain BBH18 was closer to 25239, FDAARGOS 213, and 25240 strain than CCRI-195ME.

CONCLUSION

In this report, M. *catarrhalis* strain BBH18 and CCRI-195ME genome were compared with each other. Both strain share several similarity and difference that makes each strain unique. We hope through this comparative genome analysis can contribute to gain deeper understanding of M. *catarrhalis* lifestyle.

ACKNOWLEDGEMENTS

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Table 1 Genome features of M. *catarrhalis* strain BBH18 and CCRI-195ME

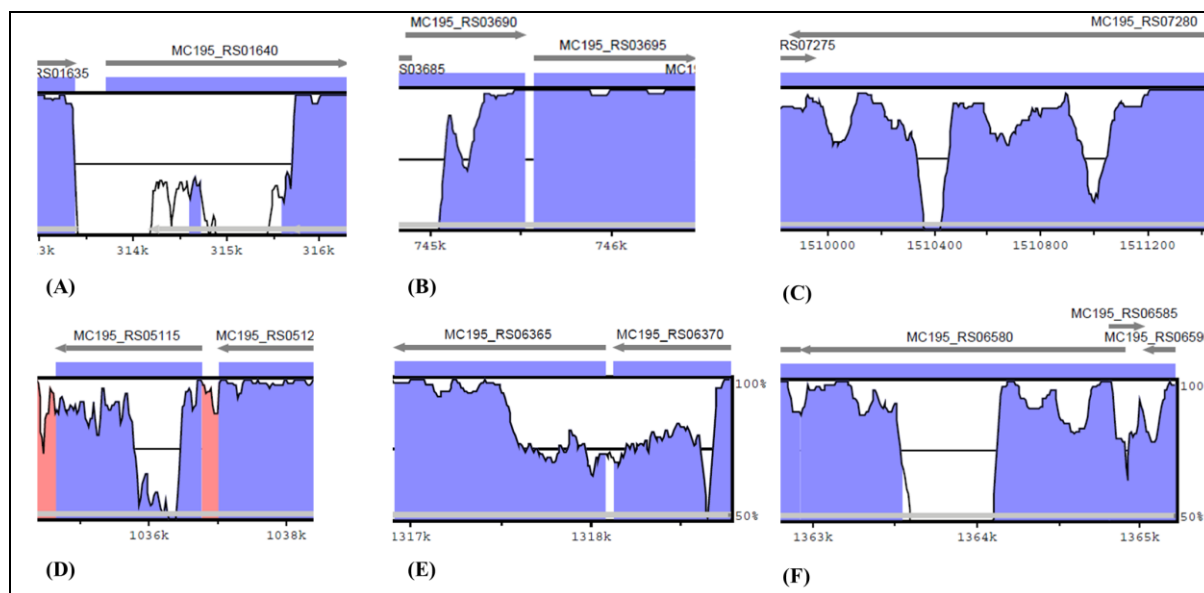| Features	*Moraxella catarrhalis* strain BBH18	*Moraxella catarrhalis* strain CCRI-195ME
Genome size (Mb)	1.86329	1.99439
GC content %	41.70	41.56
Genes	1733	1900
Protein	1622	1775
Ref sequences	NC_014147.1	NZ.CP018059.1
rRNA	12	12
tRNA	50	50
Other RNA	4	4
Pseudogene	45	59
Plasmid	0	1
Clinical details	Blood isolate	Middle ear
Source	Vries, 2010	Tan, 2017

Figure 1 Graphical represent of M. *catarrhalis* strain BBH18 and CCRI-195ME genome analysis using wgVista. Blue colors represent coding sequences. Red colors represent non-coding sequences.

Table 2 Protein encode by ORFs in the divergent region.

ORF	Protein
MC 195_RS01640	ATP-dependent chaperone ClpB
MC195_RS03690	peptidase S24
MC 195_RS07280	transferrin-binding protein
MC 195_RS05115	transferrin-binding protein
MC 195_RS06365	aspartate carbamoyltransferase
MC 195_RS06370	sel1 repeat family protein
MC 195_RS06580	site-specific DNA-methyltransferase
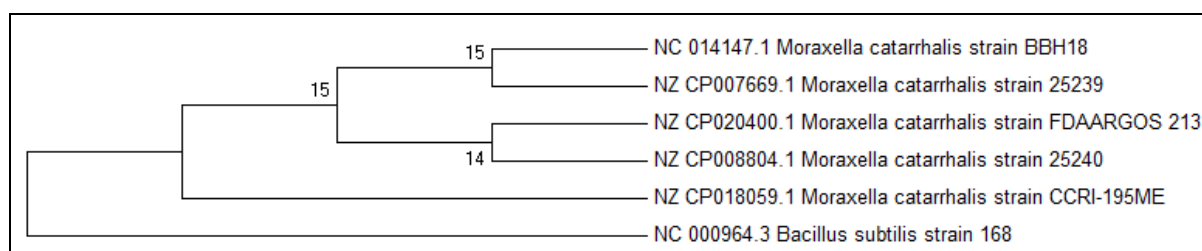
Figure 2 Phylogenetic tree of M. *catarrhalis* 16S rRNA gene sequences.