

Unraveling the Evolution of Mycoplasma Hominis Through Its Genome Sequence

Authors : Boutheina Ben Abdelmoumen Mardassi, Salim Chibani, Safa Boujemaa, Amaury Vaysse, Julien Guglielmini, Elhem Yacoub

Abstract : Background and aim: Mycoplasma hominis (MH) is a pathogenic bacterium belonging to the Mollicutes class. It causes a wide range of gynecological infections and infertility among adults. Recently, we have explored for the first time the phylogeny of Tunisian M. hominis clinical strains using an expanded MLST. We have demonstrated their distinction into two pure lineages, which each corresponding to a specific pathotype: genital infections and infertility. The aim of this project is to gain further insight into the evolutionary dynamics and the specific genetic factors that distinguish MH pathotypes. Methods: Whole genome sequencing of Mycoplasma hominis clinical strains was performed using Illumina Miseq. Denovo assembly was performed using a publicly available in-house pipeline. We used Prokka to annotate the genomes, Panaroo to generate the gene presence matrix and Jolytree to establish the phylogenetic tree. We used TreeWAS to identify genetic loci associated with the pathotype of interest from the presence matrix and phylogenetic tree. Results: Our results revealed a clear categorization of the 62 MH clinical strains into two distinct genetic lineages, with each corresponding to a specific pathotype: gynecological infections and infertility [AV1]. Genome annotation showed that GC content is ranging between 26 and 27%, which is a known characteristic of Mycoplasma genome. Housekeeping genes belonging to the core genome are highly conserved among our strains. TreeWas identified 4 virulence genes associated with the pathotype gynecological infection, encoding for asparagine-tRNA ligase, restriction endonuclease subunit S, Eco47II restriction endonuclease, and transcription regulator XRE (involved in tolerance to oxidative stress). Five genes have been identified that have a statistical association with infertility, two lipoproteins, one hypothetical protein, a glycosyl transferase involved in capsule synthesis, and pyruvate kinase involved in biofilm formation. All strains harbored an efflux pump that belongs to the family of multidrug resistance ABC transporter, which confers resistance to a wide range of antibiotics. Indeed many adhesion factors and lipoproteins (p120, p120', p60, p80, Vaa) have been checked and confirmed in our strains with a relatively 99 % to 96 % conserved domain and hypervariable domain that represent 1 to 4 % of the reference sequence extracted from GeneBank. Conclusion: In summary, this study led to the identification of specific genetic loci associated with distinct pathotypes in M. hominis.

Keywords : Mycoplasma hominis, infertility, gynecological infections, virulence genes, antibiotic resistance

Conference Title : ICBID 2023 : International Conference on Bacteriology and Infectious Diseases

Conference Location : Amsterdam, Netherlands

Conference Dates : November 06-07, 2023