FUNCTIONAL RELATEDNESS OF BRUCELLA GENOMES

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Abstract: The genus Brucella belong to an aerobic group of Gram-negative cocccobacilli that have the characteristics of being non-motile and non-spore forming on growth media that must contain carbon dioxide for survival of the organisms. On the basis of pathogenecity to humans three important species are classified into Brucella (B.) melitensis, B. abortus and B. suis). Brucella canis affects dogs and is of less importance to humans. These species are differentiated by their growth characteristics of producing urease, an enzyme that breaks down urea, by the production of hydrogen sulfide (H2S), by being sensitive to dyes, by cell wall antigens that may be sensitive to viruses entry (phage sensitivity). The major species are divided into multiple biovars. Infections in humans occur through the portals of the mouth, the conjunctiviae, the respiratory tract and through skin abrasions. Brucellosis is a zoonosis transferred from other animals and their products and result in severe acute febrile infection caused by this genus; it may have usual relapses with focal lesions in bones, joints, genitourinary tract, and other sites. There are seven finished genomes of Brucella genus. We hypothesize that species specific differences exist in the genome sizes and gene complement of finished genomes of Brucella species. Genome Clustering Tool on the Integrated Microbial Genome (IMG) database was used to cluster the seven finished Brucella genomes according to a functional profile called Clusters of Orthologous Groups (COG) of proteins. Two clustering profiles, Hierarchical and Correlation Matrix were generated for the genomes. Brucella suis ATCC 23445 genome had the highest gene count of 3419 while Brucella melitensis abortus 2308 had the lowest gene count of 3102. Brucella suis ATCC 23445 has the highest genome size of 5.8Mb. Brucella ovis ATCC 25840 has the lowest genome size of 3.7Mb. Genomes from the same species belong to the same cluster. A correlation coefficient of 0.90 was observed as the minimal relatedness indicating that all Brucella genomes are closely related in terms of the function encoded in the genomes.

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