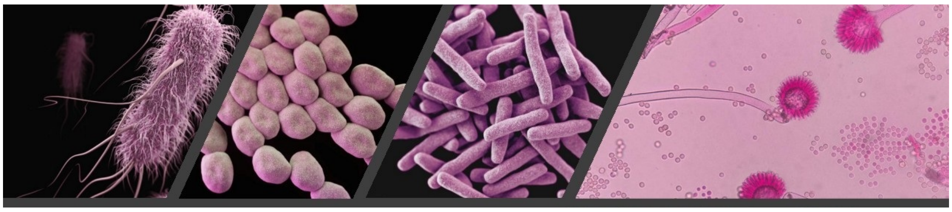

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Usefulness of Metagenome-Assembled Genomes (MAGs) for the study of pathogen–microbiota interaction in swine dysetenry model

Friday 12 September 2025 14:45 (15 minutes)

This study aims to deepen the mapping of bacteria that may participate in infectious processes as pathobionts, using information obtained from short-read sequencing and the subsequent assembly of genomes from these reads, a method known as metagenome-assembled genomes (MAGs) in an experimental infection model of swine dysentery by Brachyspira hyodysenteriae. Shotgun metagenomic sequencing with Illumina NovaSeq technologywas performed in 112 samples which enabled the reconstruction of 3,735 MAGs. These MAGS were filter by quality and GTDB database annotation, identifying 576 MAGs at the species level. We further explored MAGs from species of interest based on metataxonomic analyses Prevotella pectinovora (9 MAGs), Acetivibrio ethanolgingens (7 MAGs), and Campylobacter hyointestinalis (4 MAGs) Roseburia inulinivorans (1 MAG), all exclusively reconstructed from samples of animals affected by the disease, and in all cases, at least one of the sequences was of high quality. No major virulence genes were detected in the MAGs of these species although several minor factors and resisntace genes were identified. In addition, we observed discrepancies in the taxonomic classification of the specie A. ethanolgignens which in the GTDB database is annotated as "Velocimicrobium ethanolgignens"based on gene markers. In conclusion, the study results reveal the usefulness and discriminatory power of metagenomic assemblies to characterise novel species in disease pathogenesis.

Keywords

Metagenomics, microbiota, pig, B hyodysenteriae

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