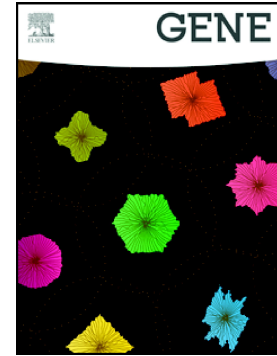


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Pan-genomic approach shows insight of genetic divergence and pathogenic-adaptation of *Pasteurella multocida*

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Abstract

Pasteurella multocida is a gram-negative, non-motile bacterial pathogen, which is associated with chronic and acute infections as snuffles, pneumonia, atrophic rhinitis, fowl cholera and hemorrhagic septicemia. These diseases affect a wide range of domestic animals, leading to significant morbidity and mortality and causing significant economic losses worldwide. Due to the interest in deciphering the genetic diversity and process adaptive between *P. multocida* strains, this work aimed was to perform a pan-genome analysis to evidence horizontal gene transfer and positive selection among 23 *P. multocida* strains isolated from distinct diseases and hosts. The results revealed an open pan-genome containing 3,585 genes and an accessory genome presenting 1,200 genes. The phylogenomic analysis based on the presence /absence of genes and islands exhibit high levels of plasticity, which reflects a high intraspecific diversity and a possible adaptive mechanism responsible for the specific disease manifestation between the established groups (pneumonia, fowl cholera, hemorrhagic septicemia and snuffles). Additionally, we identified differences in accessory genes among groups, which are involved in sugar metabolism and transport systems, virulence-related genes and a high concentration of hypothetical proteins. However, there was no specific indispensable functional mechanism to decisively correlate the presence of genes and their adaptation

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