

Molecular analysis of adhesive substances in *Pasteurella multocida*

A *Pasteurella multocida* adhéziójában szerepet játszó struktúrák molekuláris vizsgálata

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Pasteurella multocida is a member of the normal flora of mucosal surfaces and a widely distributed pathogen of many animal species. Molecular bases of pathogenesis and protective immunity against *P. multocida* infections are far from fully understood. Putative virulence determinants like outer membrane proteins, iron uptake and acquisition proteins, sialidases, toxins and various adhesins may play a part in these mechanisms. Adhesins have a crucial role in mediating colonization and invasion of the host. Thus, their presence on the bacterial surfaces and their morphological variability usually correlate with virulence.

The aim of our study was to characterize the molecular diversity of some earlier detected adhesive appendages, like auto transporters (*hsf1,2*), filamentous haemagglutinin (*pfhB1,2*) and fimbrial structures (tight adherence macromolecular transport system, type IV pili), in *P. multocida* strains using with data generated by direct and next generation sequencing. The different types of adhesives have a role in various stages and sites of infection. The filamentous haemagglutinins and autotransporters are essential for initial colonization of trachea while the Tad system and P4T are involved in biofilm initiation and development promoting bacterial persistence in the lower respiratory tract.

Lack of proper annotation of most *P. multocida* genomes in the GenBank, the PM70 and multiple alignment (progressiveMauve algorithm) of other genomes (36950, NH06, 3480, X73, P1059) were used as a reference for selection of adequate genes from our assembling genomes. Exception of *pfhB2*, both of structural and functional genes of the above mentioned structures were detectable in all strains. The functional genes presented allele differentiations in various rates. The supporting of these results comparison of further gene sequences from different strains are needed. Detection and studying of these characteristic sequence variances we obtain useful information about structural changing of adhesins of strains possessing different adhesive features and the results yield targets for prediction of virulence.

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