

## Assessing the role of *Pasteurella multocida* putative adhesion factors in fowl cholera

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Fowl cholera caused by *Pasteurella multocida* is a contagious disease that affects most of the avian species and leads to significant economic losses in domestic poultry breeding worldwide. The course of infection can be either acute or chronic. In acute infections, the clinical signs are often restricted only to the observation of sudden death. In chronic infections, the spectrum of clinical signs is rather wide, and it may affect the limb joints, the comb, the oviduct, the respiratory tract, the wattles, and the subcutaneous tissue of the head. Diverse virulence traits could explain the different clinical outcomes of the infection.

All bacterial infection begins with the process of colonization. Thus, adhesion to mucosal epithelial cells is an important virulence attribute of bacterial pathogens. This ability depends on the expression of adhesive molecules or structures, called adhesins. The aim of our study was to detect and characterise the putative adhesins of *P. multocida*, like *fimA* (fimbriae), *hsf-1*, -2 (autotransporter adhesins), *pfhA* (filamentous haemagglutinin), *tadD* (nonspecific tight adherence secretion system, secretin protein), and *ptfA* (subunit of type 4 fimbriae). Fifty-two field strains of *P. multocida* were involved in the study isolated from different avian hosts representing both forms of infection and, and type strains of somatic serotype 1, 3, and 4 were used for reference. The *fimA* and *hsf-2* were present in all strains, but the occurrence of other genes (*hsf-1*, *pfhA*, and *tadD*) showed great variety. Eight combinations of virulence genes could be detected within the tested population. Notably, the *tadD* gene was observed hardly in any other strains than A:1 serotype which were mostly responsible for acute form of the disease and could be characterized with A allele type of *ptfA* as well. This result revealed that the *tad* locus-bearing widespread colonization island was not frequent among the avian *P. multocida* strains as it predicted from the published genome sequence data (originating mainly from mammals).

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