Distribution of adhesion factors and their impact on the pathogenicity of bovine *Pasteurella multocida* strains in Bovine Respiratory Disease

Boglárka Sellyei, Barbara Ujvari, Krisztián Bányai, Tibor Magyar

Institute for Veterinary Medical Research, Centre for Agricultural Research, Hungarian Academy of Sciences

Bovine Respiratory Disease (BRD) is the most common and costly disease affecting beef and dairy cattle industry all over the world. The economic losses are either direct due to lethal cases, or indirect through additional expenses such as the cost of treatment and lower weight gain and decreased carcass value. For those cattle that survive, the presence of pulmonary lesions at slaughter has been associated with significant reduction in daily weight gain.

The pathogenesis of BRD is complex, involving a number of viruses, bacteria and stress factors. The stressors, combined with the impact on the immune system and viral infections, allow bacteria to invade the lungs. One of the most frequently isolated bacteriological agents is *Pasteurella multocida* in these cases. This organism commonly inhabits the pharynx or upper respiratory tract of most cattle. However, it is not considered as normal flora of the lungs. The inhaled bacteria that attached on the mucus of lower respiratory tract successfully using a wide-range of adhesins, under conditions of impaired pulmonary defences, replicate rapidly and cause pneumonia.

The aim of our study was to detect and characterise the known putative adhesive factors within the bovine *P. multocida* population in Hungary. The studied 39 strains were isolated from diseased animals in different cattle herds and they were earlier characterized with traditional microbiological and general molecular methods and divided into subpopulation considered to contain strains of different virulence. The presence of *ptf*A (subunit of type IV fimbriae), *fim*A (fimbriae), *hsf*-1, 2 (autotransporter adhesins), *tad*D (putative nonspecific tight adherence protein D) and *pfh*A (filamentous haemagglutinin) genes were detected by PCR. The distribution of virulence factors was compared with the strains' recorded diagnostic data. The prevalence of the different genes was various. Whereas the *fim*A was present in all and *hsf*-2, *tad*D, *ptf*A genes in most strains, the occurrence of *hsf*-1 and *pfh*A showed variability. Based on these results, seven combinations of the genes could be detected. These profiles well characterized the delineated main subpopulations. Two of them were dominant. The strains with these latter ones varied in possession of gene encoding filamentous haemagglutinin. The presence of *pfh*A showed significant correlation with diagnostic data. It was associated with pneumonia.

For the discrepancy of virulence, the changes in structures of the virulence factors could also be responsible. Thus detailed study of them is recommended. For the additional characterization of the strains we carried out the sequencing of extended genome region included *tad*D gene. The sequence analysis showed low per cent but characteristic differences between the representative strains. The effect of the changing to the protein structure or function required further investigations.

This research was supported by PD OTKA 101091 and the János Bolyai Research Scholarship of the Hungarian Academy of Sciences.