OCCURRENCE OF VIRULENCE-RELATED GENES AMONG *ENTEROCOCCUS* ISOLATED FROM THE INTESTINAL MICROBIOTA OF WILD BIRDS

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A variety of virulence-associated genetic determinants can be found among enterococcal isolates recovered from human sources, but little is known about their occurrence among animal isolates. These genes encode secreted proteolytic enzymes (*gel*E, *cyl*A, *hyl*), adhesion proteins to eukaryotic cells and surfaces (*esp*, *asa*1, *efa*A, *ace*) and mediators of pheromone expression (*agg*A and *ee*P), that may play important roles in the establishment of enterococcal infections. The aim of the study was to investigate the occurrence of genes related to virulence among *Enterococcus* isolates obtained from the feces of wild birds. A total of 260 isolates were recovered from faecal samples of 113 birds (Accipitriformes, Falconiformes, Cathartiformes and Strigiformes) sent to CETAS-RJ and CRAS-UNESA, during 2013. The isolates were identified, by using both conventional phenotypic and PCR-based testing, as*: E. faecalis* 63.8%; *E. hirae* 16.2%; *E. faecium* 11.5%; *E. gallinarum* 5.4%; *E. casseliflavus* 0.8%; *E. avium* 1.5%; *E. raffinosus* 0.4% and *E. cecorum* 0.4%. The presence of virulence-associated genes was investigated by two multiplex PCR reactions [reaction 1: *asa*1, aggregation sub-stance; *esp*, extracellular surface protein; *cyl*A, cytolysin activator; *gel*E, gelatinase; and *hyl*, hyaluronidase, and reaction 2: *ace*, collagen-binding protein; *agg*A, aggregation substance; *ee*P, pheromone; *efa*A, endocarditis antigen] using primers and conditions previously described. The results of reaction 1 demonstrated that 63.5% of the isolates were positive for *gel*E and 53.5%, 33.8%, 11.9% and 1.1% of them were positive for *asa*1, *cyl*A, *esp*, *hyl*, respectively. Reaction 2 data indicated that 65% of the isolates had the *efa*A gene, 61.5% the ace, 56.5% the *ee*P and 34.2% the *agg*A genes. Moreover, 99.4% of the isolates identified as *E. faecalis* harbored at least two of the virulence-related genes. On the other hand, 96.7% of the isolates identified as *E. faecium*, 69% of those identified as *E. hirae* as well as the single *E. cecorum* and *E. raffinosus* isolates did not present any of the genes investigated. The *hyl* gene predominated among the *E. casseliflavus* and *E. gallinarum* isolates. Our results are in agreement with the literature showing that *E. faecalis* is associated with higher occurrence of virulence-related genes. Such genes can be found in mobile genetic elements, and their presence among enterococcal strains in the gastrointestinal tract of wild birds can lead to the spread of such properties.

Key Words: Avian microbiota, *Enterococcus*, virulence genes

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