

Typing of Nasal Carriage Isolates of *Staphylococcus aureus* from Healthy Horses Using the PCR-RFLP

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Background & Objectives: *Staphylococcus aureus* is an important pathogen that can colonize the nares of different animals. The aim of the present study was to investigate the genetic diversity of 24 *S. aureus* isolates recovered from the nose of healthy horses in Iran by molecular typing based on polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) of the protein A gene (*spa*).

Methods: The polymorphic X region of the *spa* gene was amplified by PCR. The amplicons were then digested with restriction enzyme *Hin6I* and the restriction fragments were resolved by agarose gel electrophoresis.

Results: All isolates gave a single PCR product ranging in size from approximately 1100 bp to 1400 bp. Among 24 *S. aureus* isolates studied, a total of 6 distinct RFLP patterns, designated as A-F, were observed. For the *spa* gene, the lack of amplification was also considered a distinct genotype (G). The genotyping results showed that 9, 1, 4, 4, 1, 4, and 1 isolates belonged to patterns A-G, respectively.

Conclusion: The results of the study suggest that based on *spa* gene RFLP analysis, nares of healthy horses could be a reservoir of several genetic variants of *S. aureus*, with implications in public health.

Keywords: *Staphylococcus aureus*; Horses; Protein A Gene