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# MOLECULAR GENOTYPING OF *STAPYLOCOCCUS HYICUS* STRAINS USING REPETITIVE SEQUENCE-BASED PCR

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**Introduction:**

*Staphylococcus hyicus* is a gram-positive bacterium that is considered the cause of exudative epidermitis in pigs. However, it can be isolated from the skin of healthy pigs and other species. A number of phenotypic and genotypic methods have been used to characterize and compare different *Staphylococcus hyicus* strains. However, either their discriminatory ability is low or they are too complex to be used in a routine basis. The repetitive sequence-based PCR (rep-PCR) is a genotyping method that has proven to be relatively easy to perform and to have a high discriminatory power to differentiate strains within species, such as *Staphylococcus aureus* and *Haemophilus parasuis*. The objective of this study was to develop a rep-PCR to genotype strains of *Staphylococcus hyicus*. For this purpose three different sets of primers previously described (ERIC, REP and BOX) were compared. The new protocol was used in a field epidemiological study.

**Results and discussion:**

Twenty *S. hyicus* isolates from a system with endemic exudative epidermitis were genotyped with the three sets of primers mentioned above. The resulting fingerprints were compared using the Bionumerics software and a dendrogram was constructed for each set of primers. ERIC primers were found to be the most appropriate, based on the discriminatory power and on the definition of the obtained fingerprints. The ERIC dendrogram grouped 16 isolates in a major cluster. These isolates which had all been recovered from piglets in the farrowing house and 4 different nurseries of the same company, showed fingerprints with more than 90% similarity among them. The remaining 4 isolates had completely different fingerprints. Therefore, a dominant virulent strain causing disease in different sites of one system was identified.

Also, isolates from lesions on a sow and one piglet, from the environment of the farrowing room and from the autogenous vaccine used in one of the nurseries, were identified as identical to the prevalent strain by ERIC-PCR. On the other hand, another isolate from a piglet with exudative epidermitis and one from the environment of the farrowing room, were found to be new strains in the system.

In this study we adapted the rep-PCR technology to be used in epidemiological studies of S*taphylococcus hyicus* infections. After comparing three sets of primers, we found ERIC-PCR to be more consistent and discriminative. We then applied the technique to a field study, where it proved to be fast and easy and yielded useful information.

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