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Differentiation of porcine wild-type lactobacilli strains, with ERIC-PCR and PFGE band patterns included in polyphasic taxonomy

E. Bolado-Martínez, E. Acedo-Félix

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Probiotic administration is an alternative to antibiotic supplementation in pig management. However, potential probiotic microorganisms included in foods must be well defined and correctly named, on the basis of a valid taxonomic system. The aim of the present study was to analyze band patterns generated by the polymerase chain reaction (PCR) amplification of enterobacterial repetitive intergenic consensus sequences (ERIC-PCR), obtained from porcine wild-type *Lactobacillus* strains, as a rapid alternative for genotypic characterization in polyphasic taxonomy. In the present study 36 porcine wild-type *Lactobacillus* strains were analyzed by polyphasic taxonomy which included API 50 CHL system, ERIC-PCR, and pulsed field gel electrophoresis (PFGE) band analysis, after digestion with *XbaI* or *SpeI* restriction enzymes. Polyphasic taxonomy discriminated among 23 strains of *Lactobacillus reuteri*, 12 strains of *Lactobacillus salivarius* and one strain of *Lactobacillus mucosae*. None of the tested methods was able to reliably resolve the three selected species of lactobacilli at a strain level. However, results improved considerably when ERIC-PCR results were combined with phenotypic characterization, and those results were comparable to the taxonomy that included PFGE.

Keywords:

Lactobacillus, porcine lactobacilli phenotypic characterization; genotypic characterization

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Contact

Ing. Gabriela Vladyková Executive Editor (Editoria publication)

e-mail: cjas@cazv.cz Ing. Kateřina Kheilová Executive Editor (submis: editorial system) e-mail: cjas@af.czu.cz

Address

Czech Journal of Animal . Czech Academy of Agricu Sciences Slezská 7 120 00 Praha 2 Czech Republic

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