ARCHAEA ASSOCIATED WITH
THE PORCINE ILEUM OF WEANED PIGS

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ABSTRACT

The porcine digestive tract harbors copious bacterial flora which plays an important role in digestion. While much is now known about the eubacterial diversity present, little is known about the prevalence and diversity of Archaea. The aim of this project was to determine the diversity of the archaeal microflora present in the ileum using 16S rDNA sequences as indicators of diversity. Two five week old weaned pigs were chosen at random. Genomic DNA was extracted from ileal lumen and the PCR was done with Archaea-specific primers A571F and UA1204R. Amplicons were cloned in pGEM-T Easy, transformed into *E. coli* JM109 and white colonies selected at random. The DNA sequences were checked for chimeras using the Pintail program. After authentication, sequences were aligned using ClustalW and grouped according to relatedness into a phylogenetic tree. The sequences of the closest related known species were also added to the tree. All archaeal amplicons were related to methanogens and no chimeras were found. Some of the PCR amplicons were not of archaeal origin; however, some sequences indicated pig or human DNA, showing that the primer set was not specific for Archaea. Those sequences were not included in the tree. The result positioned the sample sequences into three clusters. Cluster One grouped closely with *Methanobrevibacter ruminantium*, Cluster Two with *M. sp. ZA-10* and SM9 and *M. gottschalkii*, and Cluster Three with *M. smithii* strain PS. These results indicate that the Archaea present in the ileum of young pigs are largely members of the genus *Methanobrevibacter*. 