

Diversity of Bovine Rumen Methanogens *In Vitro* in the Presence of Condensed Tannins, as Determined by Sequence Analysis of 16S rRNA Gene Library

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Molecular diversity of rumen archaeal populations from bovine rumen fluid incubated with or without condensed tannins was investigated using 16S rRNA gene libraries. The predominant order of rumen archaea in the 16S rRNA gene libraries of the control and condensed tannins treatment was found to belong to a novel group of rumen archaea that is distantly related to the order *Thermoplasmatales*, with 59.5% (15 phylotypes) and 81.43% (21 phylotypes) of the total clones from the control and treatment clone libraries, respectively. The 16S rRNA gene library of the control was found to have higher proportions of methanogens from the orders *Methanomicrobiales* (32%) and *Methanobacteriales* (8.5%) as compared to those found in the condensed tannins treatment clone library in both orders (16.88% and 1.68% respectively). The phylotype distributed in the order *Methanosarcinales* was only found in the control clone library. The study indicated that condensed tannins could alter the diversity of bovine rumen methanogens.

Keywords: condensed tannins, methanogens, bovine rumen fluid, rumen archaeal diversity, gene library
