

In Asia and the Middle East camelid husbandry represents an increasingly popular market. The role of camels in the more arid regions of the world is becoming more prominent as they are discovered to be an economic alternative to traditionally raised livestock, and they are well suited to the climate. Camels are pseudoruminants, possessing a three-chambered stomach, and like their ruminant cousins are host to a variety of microorganisms, including methane producing archaea called methanogens. Methanogen research has been conducted on a variety of livestock species due to their significant methane emissions, but camel methanogens have not yet been investigated. This study identified methanogens found in the hindgut of four Bactrian camels (*Bactrianus camelus*), from two different zoos, Potter Park Zoo in Lansing, MI and Southwick Zoo in Mendon, MA. A 16S rRNA gene library was constructed for each zoo, and the resulting clones were sequenced and identified to determine their closest relative. In total, 108 clones were analyzed; 55 from the Southwick library and 53 from the Potter Park library. Approximately 98% of the clones from the Potter Park library and 96% of the clones from Southwick library were identified as members belonging to the genus *Methanobrevibacter*. This is consistent with findings showing that *Methanobrevibacter* phylotypes are dominant in most ruminant species. According to Shannon Index and Libshuff analysis, the two libraries showed significant differences in diversity ($p < 0.05$) and composition ($p < 0.0001$), respectively. Two OTUs were found in both libraries, whereas two OTUs were found only in the Southwick library and seven OTUs were found only in the Potter Park library. Further studies are warranted to properly assess the foregut and colonic methanogens from these pseudoruminants.