Molecular identification of the bacterial microbiome resident in the hindgut of the North American Beaver (Castor canadensis)

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Abstract

The beaver (*Castor canadensis*) is a prime example of a mammal that has evolutionarily developed advantageous characteristics that allow it to adapt to its environment. One of these adaptations includes the beaver's unique ability to digest bark and wood. The present study examined the bacterial microbiome present in the hindgut of the beaver. The specific objectives of the study were: (i) to identify bacteria that reside in the hindgut and to determine their phylogeny, (ii) to investigate whether the bacterial population structure varies between individuals, and (iii) to compare our findings with previously published reports on the bacterial species residing in other hindgut and foregut fermenters. Fecal samples were obtained from five frozen beavers that had been legally trapped, by a licensed hunter for the Québec Government, from the area around of St-Jean sur Richelieu, Québec. The samples were stored in 70% ethanol until the DNA was extracted from 0.25 g of fecal material from each animal. Microbial DNA from each sample was isolated following the repeated bead-beating plus column (RBB+C) method. DNA was PCR amplified from each animal using the primer set 27F and 519R to amplify only the bacterial V1-V3 region of the 16S rRNA gene. Samples were then sent to Molecular Research DNA (Stilwater, TX) for sequencing. A total of 61,614 sequences were obtained and ranged from 3,762 to 33,114 for the five beavers. Sequence analysis revealed that bacteria belonging to the phyla Firmicutes and Bacteriodetes were the predominant microbes in 3 of the 5 samples. The bacterial population did not vary greatly between individuals. Since Firmicutes and Bacteriodetes make up a large portion of the microbiome of other hind-gut fermenters, such as humans and mice, it can be concluded that the gut microbiome of the beaver agrees with other hind-gut fermenters.