

## **Phylogenetic analysis of the microbial populations in the wild herbivore gastrointestinal tract: insights into an unexplored niche.**

### **Abstract**

At present, there is little information on the phylogenetic diversity of microbial species that inhabit the gastrointestinal tracts of wildlife. To increase understanding in this area, we initiated a characterization of the bacterial diversity in the digestive tracts of three wild African ruminant species namely eland (*Taurotragus oryx*), Thompson's gazelle (*Gazella rufifrons*) and Grant's gazelle (*Gazella granti*), together with a domesticated ruminant species, zebu cattle (*Bos indicus*), and a non-ruminant species, zebra (*Equus quagga*). Bacterial diversity was analysed by PCR amplification, sequencing and phylogenetic analysis of 16S ribosomal DNA (rDNA) sequences. A total of 252 full-length 16S rDNA sequences averaging 1,500 base pairs (bp) in length, and an additional 27 partial sequences were obtained and subject to phylogenetic analysis. Using a 98% criterion for similarity, all except for one of the sequences were derived from distinct phylotypes. At least 24 distinct operational taxonomic units (OTU's) could be identified, with the majority of these sequences representing hitherto uncharacterized species and genera. The sequences were generally affiliated with four major bacterial phyla, the majority being members of the Firmicutes (low G+C Gram-positives) related to the genera *Clostridium* and *Ruminococcus*. By contrast, with earlier studies using 16S rDNA sequences to assess biodiversity in *Bos taurus* dairy cattle, Gram-negative bacteria in the Bacteroidales (*Prevotella*-*Bacteroides* group) were poorly represented. The lack of redundancy in the 16S rDNA dataset from the five African ungulate species, and the presence of novel sequences not previously described from the gastrointestinal tract of any animal species, highlights the level of diversity that exists in these ecosystems and raises the question as to the functional role of these species in the gastrointestinal tract.