

Potential functional profile of the bacterial community present in a browse-fed goat digestive tract



Vera Guerra¹; Igor Tiago³; Catarina Coelho²; João Nunes¹; Lúgia O. Martins⁴; António Veríssimo³

¹Association BLC3 - Technology and Innovation Campus, Centre Bio R&D Unit, Oliveira do Hospital, Portugal

²Centre for Neuroscience and Cell Biology, University of Coimbra, Coimbra, Portugal

³Centre for Functional Ecology, University of Coimbra, Coimbra, Portugal

⁴ITQB-NOVA- Institute of Chemical and Biological Technology António Xavier- Nova University of Lisbon, Lisboa, Portugal

email: vera.querra@blc3.pt

Background and aim:

The high complexity of chemical composition of plants has hampered its use as feedstock in bio-based industries¹. Goat digestive tract microbiota are specialized in degradation of plant compounds, and is considered a promising source for plant degrading enzymes. It is well known that the type of feed intake by the animal shapes the goat microbiota and the functional profile of the microbial communities². Nevertheless the use of next generation sequencing techniques to predict the functional microbial diversity in goat's digestive tract are scarce. This study describes, for the first time, the potential functions of the bacterial community found in the digestive tract of a goat (*Capra hircus*) browsing free on native shrubby vegetation of the Centre Inner Region of Portugal. It is part of a more vast investigation focused in the identification of bacterial-plant-degrading enzymes present in the digestive tract of the goat and in their potential utilization in the biotechnology industry.

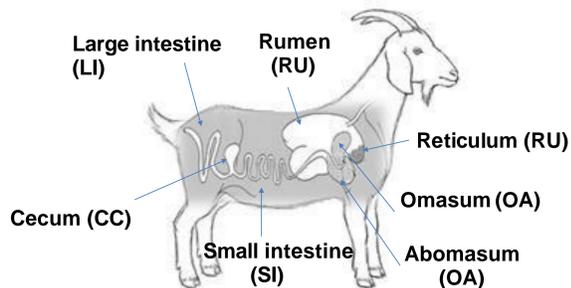


Fig.1 Illustration of goat's digestive tract and sampling locations Adapted from <https://thekebun.wordpress.com/2008/09/07/the-digestive-system-of-the-goat/>, 2017.12.04.

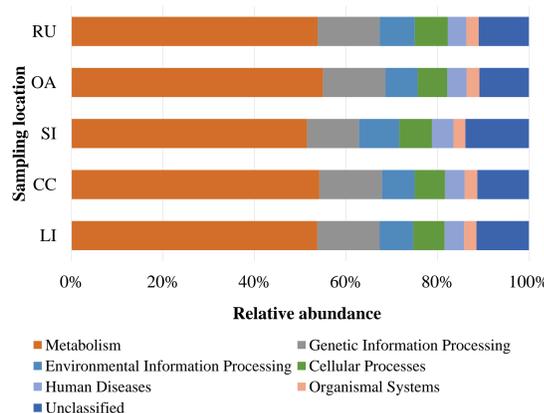
Methods:

Metagenomic DNA was extracted from the microbial communities present in the goat's digestive content in the rumen, omasum-abomasum, small intestine, cecum and large intestine. The predicted bacterial functions were determined by analyzing the metabarcoding 16S rRNA Illumina tags results with PICRUST (Phylogenetic Investigation of Communities by Reconstruction of Unobserved States) v.2.0. The functional predictions were classified into KEGG (Encyclopedia of Genes and Genomes) pathway at level 1, 2, 3 and 4.

Results:

Forty-seven gene families were predicted across the goat's digestive tract. Predominantly, the gene families were assigned to functions on metabolism (55-51.5%). The most prevalent metabolic pathways were related to carbohydrates (13.7-14%) and amino acids (9.1-10.8%) metabolism. Concerning carbohydrate metabolism, samples RU and OA presented less dissimilarity due to the abundance of genes implicated on glyoxylate and dicarboxylate metabolism in both digestive tract regions (data not shown). The same was verified between the samples CC and LI due high abundance of gene implicated on glycolysis/gluconeogenesis. SI displayed distinct functional pattern from the remaining samples, given the major occurrence of genes on starch and sucrose metabolism.

Functional distribution at KEGG Level 1



Top 10 functional distribution at KEGG Level 2

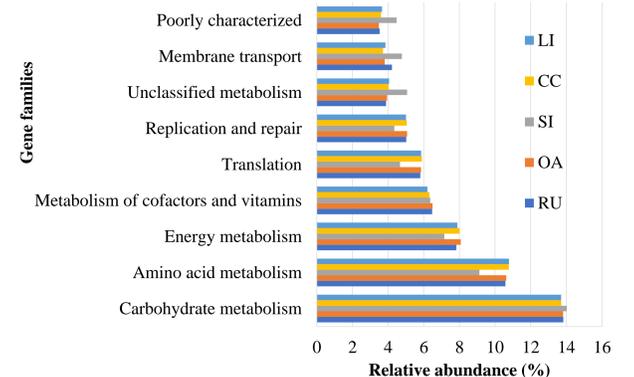


Fig.2 Relative abundance of the bacterial predicted functions across the goat's digestive tract annotated to KEGG Level 1 and 2.

Top 10 predicted enzymes involved on carbohydrate metabolism

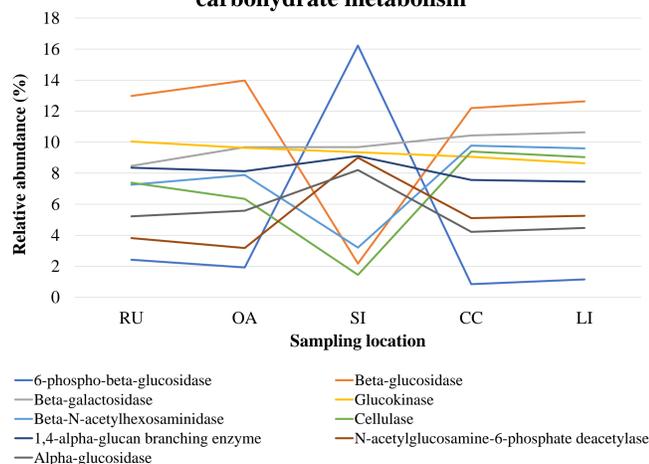


Fig.3 Relative abundance of the dominant predicted bacterial enzymes related with carbohydrate metabolism across the goat's digestive tract.

Results:

A total of 105 enzymes with participation on carbohydrate metabolism were predicted in all regions of the goat digestive tract, mainly glycoside hydrolases (GH) thus, playing a key role in plant degradation. In SI 6-phospho-beta-glucosidase (16.2%) was the most abundant, while in the remaining regions was Beta-glucosidase (12.2-14%).

Conclusions:

The high abundance of predicted functions related to carbohydrate metabolism compared to amino acid metabolism suggests a major contribution of carbohydrate fermentation as a main source of energy for the bacterial community. Concerning the carbohydrate pathways, the functional diversity observed across the goat's digestive tract suggests a correlation to the variation of the physiological and biochemical conditions and carbon type availability³. Adjacent digestive regions with less dissimilar conditions displayed less dissimilar functions. Furthermore the abundance of functions related to carbohydrate metabolism in all the digestive tract regions as well as the prediction of genes coding for enzymes with participation on plant fiber digestion, shows the decisive importance of the bacterial community on host nutrition and highlights the potential of the microbiome as source of plant degrading enzymes for biotechnological applications.

References:

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