**“Characterizing the pangenome of probiotic candidate *Roseburia intestinalis*”.**

**Basics about *Roseburia intestinalis*:**

a [saccharolytic](https://en.wikipedia.org/wiki/Saccharolytic" \o "Saccharolytic), [butyrate](https://en.wikipedia.org/wiki/Butyrate" \o "Butyrate)-producing bacterium first isolated from human faeces (2002)

- anaerobic

- [gram-positive](https://en.wikipedia.org/wiki/Gram-positive" \o "Gram-positive)

- non-sporeforming

- slightly curved rod-shaped

- [motile](https://en.wikipedia.org/wiki/Motile" \o "Motile) by means of multiple subterminal [flagella](https://en.wikipedia.org/wiki/Flagellum" \o "Flagellum)

**Why important?**

β-Mannans are plant cell wall polysaccharides that are commonly found in human diets (more specifically they are widely used in food as thickening, stabilizing, and gelling agents[27](https://www.nature.com/articles/s41467-019-08812-y" \l "ref-CR27" \o "Yamabhai, M., Sak-Ubol, S., Srila, W. & Haltrich, D. Mannan biotechnology: from biofuels to health. Crit. Rev. Biotechnol. 36, 32–42 (2016).) (glucomannan and galactomannan. They are found in the endospermic tissue of nuts (homopolymeric mannan), coffee beans, coconut palm, tomato, and legume seeds (galactomannan) and play vital roles in the cell wall structure and as storage polysaccharides in plants). *R. intestinalis* is a primary degrader of this dietary fiber and this metabolic capacity could be exploited to selectively promote key members of the healthy microbiota using β-mannan-based therapeutic interventions.

More specifically it expresses two loci conferring metabolism of β-mannans.

It plays an important role in the control of gut inflammatory processes, amelioration of atherosclerosis and in the maturation of the immune system, primarily through the production of butyrate.

(Butyrate is an important nutrient for colonocytes, as well as a

signalling molecule with a central role in cell differentiation and apoptosis).

**Where it is located in the organism?**

*Roseburia* spp., together with *Faecalibacterium prausnitzii* and *Eubacterium rectale*, constitute a group of dominant butyrate-producing Firmicutes, estimated to account for 7–24% of the total bacteria in the healthy human colon. Interest in *Roseburia* spp. has increased with reports that the abundance of these bacteria is reduced in individuals affected by inflammatory diseases and colorectal cancer. Complementary studies have shown that *Roseburia* spp.. *R. intestinalis* preferentially colonizes the mucin layer and this intimate association to the host may contribute to the local level of butyrate available for the colonic epithelial cells[22](https://www.nature.com/articles/s41467-019-08812-y" \l "ref-CR22" \o "Nishino, K. et al. Analysis of endoscopic brush samples identified mucosa-associated dysbiosis in inflammatory bowel disease. J. Gastroenterol. 53, 95–106 (2018).). This species appears to be a specialist able to grow only on a few glycans and has been recently shown to be a prominent xylan degrader in vitro and in the healthy human colon

**Phylogenetic analysis**

- Phylogenetic analysis indicated that the most closely related species are Eubacterium rectale, Eubacterium oxidoreducens and Roseburia cecicola, (2002).

*- Roseburia intestinalis* is a species of [Bacteria](https://eol.org/pages/288) in the family [Lachnospiraceae](https://eol.org/pages/7764).

(only one attribute on the Encyclopedia of Life - EOL)

<https://eol.org/pages/7764> -->map of the family it belongs

The strains of this family (but maybe of no interest, if it very diverse) that have been sequenced come mostly form South America then Australia and then Western Europe.

<https://eol.org/pages/98341> -> map of its genus (= Roseburia)

Most of them were on Europe (=34) and then south America (=25) and Honolulu (=24) ?

<https://www.itis.gov/servlet/SingleRpt/SingleRpt?search_topic=TSN&search_value=965681#null> --> detailed taxonomy of species, there is no geographic info on division or origin of the species.

**General on pangenomes - genomes:**

**Completeness of a genome: Frequently, the completeness of a species’ gene catalog is measured using a set of marker genes that are expected to be present. This expectation can be defined along an evolutionary gradient, ranging from highly conserved genes to species-specific genes**.

A simple approach is common to all reported measures of completeness ([Figures 1B](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5006709/figure/fig1/" \t "/home/maria/Documents\\x/figure) and [​and1C).1C](https://www.ncbi.nlm.nih.gov/pmc/articles/PMC5006709/figure/fig1/" \t "/home/maria/Documents\\x/figure)). First, one measures the size of the assembled genome (i.e., total assembly length) or the gene space (i.e., the number of genes), in the following referred to as the “observed.” Second, one selects a reference to define the expected genome size or gene space, here referred to as the “expected.” To define the expected genome size, both physical measurements (e.g., nuclear weight) and computational methods that analyze the sequence space (such as k-mer spectra) should be used. Furthermore, to define the expected gene space, one can rely on evolutionary conservation and use the gene space of related species as reference (interspecies comparisons).Alternatively, one can define a species-specific measure of the gene space by transcriptome or EST sequencing in the species itself (intraspecies comparisons;

References:

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* Duncan SH, Hold GL, Barcenilla A, Stewart CS, Flint HJ. Roseburia intestinalis sp. nov., a novel saccharolytic, butyrate-producing bacterium from human faeces. Int J Syst Evol Microbiol. 2002 Sep;52(Pt 5):1615-1620. doi: 10.1099/00207713-52-5-1615. PMID: 12361264.
* **<https://eol.org/pages/976983> (Encyclopedia of Life)**
* **<https://www.itis.gov/servlet/SingleRpt/SingleRpt?search_topic=TSN&search_value=965681#null>**

**<https://bacdive.dsmz.de/strain/6366> (available sequences of strains)**

* Veeckman, E., Ruttink, T., & Vandepoele, K. (2016). Are We There Yet? Reliably Estimating the Completeness of Plant Genome Sequences. *The Plant cell*, *28*(8), 1759–1768. <https://doi.org/10.1105/tpc.16.00349> (on completeness of genomes)