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Gut microbiome signatures of nursing home residents carrying Enterobacteria Producing Extended-spectrum β-lactamases

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Background.

The prevalence of extended beta-lactamase producing Enterobacteriaceae (ESBL-E) has been constantly increasing over the last decades. These microorganisms that have acquired broad antibiotic resistance are now common human pathogens. Changes in the gut microbiome, induced by antibiotics or other drugs, enable expansion of these microorganisms, but the mechanisms are not yet fully understood.

Objective.

We investigated taxonomic and functional characteristics of the gut microbiome of nursing home residents carrying ESBL-E using metagenomics.

Methods.

- 144 residents living in two different nursing homes.
- All fecal samples were screened for ESBL-E
- Gut microbiome was characterized using shallow shotgun metagenomic DNA sequencing.

Plateforme BiRD Nantes

Main results.

Ten nursing home residents were colonized by ESBL-E, namely Escherichia coli, Klebsiella pneumoniae and Enterobacter cloacae species, and were compared to non-carriers individuals.

Biodiversity.

We found that ESBL-E carriers had an alteration in within-sample diversity.

Species biodiversity

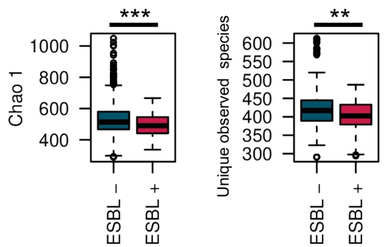

Figure 1. Alpha-diversity indices in gut microbiomes of ESBL-E carriers, based on species, is decreased when compared to non-carriers

Taxonomic signature.

Using a bootstrap algorithm, we found that the gut microbiome of ESBL-E carriers was depleted in butyrate-producing species and enriched in succinate-producing species.

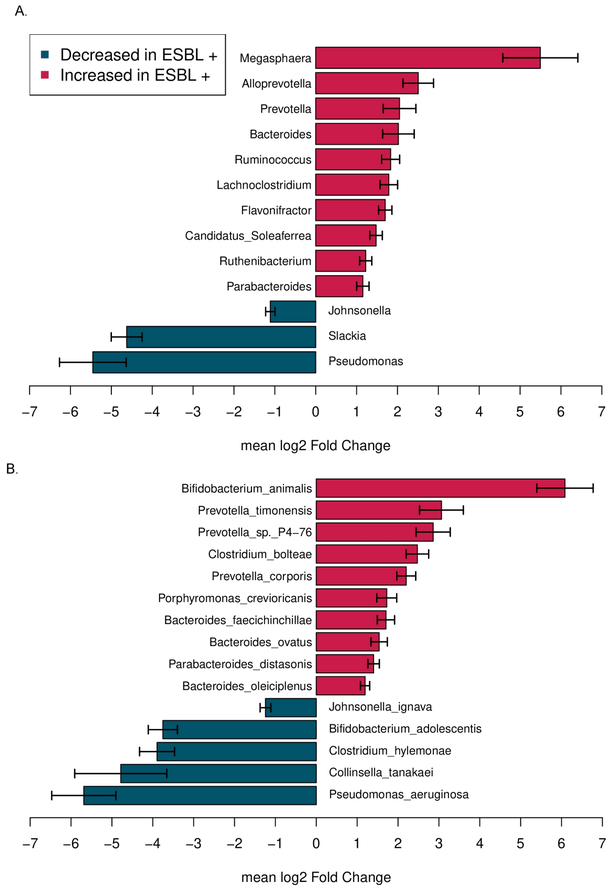

Figure 2. Microbes that differentiate ESBL-E carriers and non-carriers at genus level (2.A) and species level (2.B), using DESeq2 with bootstrap iterations.

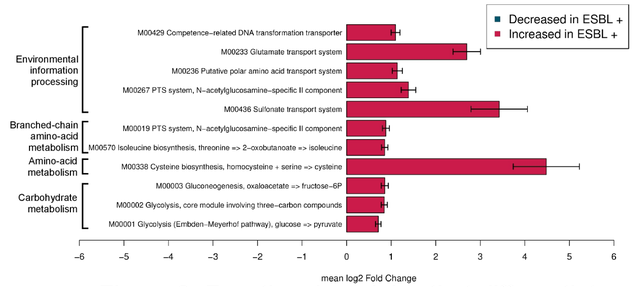

Figure 3. Functional modules that differentiate ESBL-E carriers and non-carriers using DESeq2 with bootstrap iterations.

Functional signature.

The gut microbiome of ESBL-E carriers was upregulated for pathways involved in intracellular pH homeostasis compared to non-carriers individuals.

Several energy metabolism pathways were overexpressed in ESBL-E carriers suggesting a greater ability to metabolize multiple microbiota-derived nutrients.

Analyse of CAZymes revealed an over-expressed mucin degradation activity suggesting an increased availability of host-derived sugar which could facilitate post-antibiotic expansion of enteric pathogens

Conclusions.

The gut microbiome of ESBL-E carriers in nursing homes harbors specific taxonomic and functional characteristics, conferring an environment that enables Enterobacteriaceae expansion. Tailored shifts in the gut microbiome could be a tool to prevent gut colonization by antimicrobial-resistant microorganisms in this at-risk population.