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Understanding the Metabolic Processes that Shape the Adaptation of *Escherichia Coli* to the Mammalian Gastro-Intestinal Tract

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Many microbes colonise the gut establishing interactions with their host and their nutritional environment. Studying genetics and metabolism brought about the drive and potential to engineer communities to promote health and improve industrial processes. However, structuring artificial communities in predictable ways is underdeveloped. We studied *Escherichia coli*'s genetic targets and physiological mechanisms during gut colonization and adaptation and how metabolic environment microbiota complexity shape these processes.

We introduced a tractable *E.coli* K-12 in mice Germ-free or with polymicrobial communities. Whole Genome Sequencing identified potential adaptive targets. Here, we established phenotypic assays as well characterizing effects of key mutations and metabolomics was performed with 1H-NMR of intestinal contents. Genes for sugar alcohol metabolism (gat) was the only target common to both mouse models, evidencing specificity. Facing complex microbiota *E.coli* targeted use of sugar alcohols (*srlR, kdgR*) and anaerobic respiration (*dcuB, focA*) [1] whereas alone, we observed instead mutations pointing to increased ability for amino acid use (*lrp, dtpB, alaA*). Mutations selected correlated dinamically with metabolomics: our results fit the model whereby other microbiota members scavenge oxygen and breakdown complex sugars, limiting *E.coli* to anaerobically respire simple by-product carbon sources. In the opposing scenario (functional absence) improved amino acid use are favoured colonisation factors.

Through experimental evolution we gained insight on shaping *E.coli*'s metabolic traits through genetic engineering to colonise specific host environments. This work also highlights the versatility of E.coli as potential biotic sensor.

[1] Barroso-Batista, J. et al. The first steps of adaptation of *Escherichia coli* to the gut are dominated by soft sweeps, 2014.

Biography:

Miguel has been working at one of the main research institutes in Portugal, Gulbenkian Institute for Science, a relatively large, multidisciplinary Molecular biology center focused mostly on fundamental science. Here, he has developed his project with a scientific article in preparation, having attended various conferences and also shared his knowledge through several scientific poster presentations. With a sound training on Molecular Microbiology acquired ever since he started his Masters, Miguel has also had the opportunity to develop various complementary skills such as omics techniques in sample processing and manual curation of Metabolomics and metagenomics datasets; Accredited training in Animal use, handling & welfare in experimentation, including extensive use of Gnotobiology techniques with rodents; As well as basic bioinformatics skills with interest in further integrating them on future work. When he is not trying to answer existential questions or doing actual research work, he enjoys getting lost in mountains and Rock climbing.

Finally, Miguel is very keen on transitioning from academia to academia-to-industry research allocation, particularly in the environmental/agro-forestry industries fueled by his early experiences during training in Agronomics (Animal Production Engineering Bachelors) at the Agronomy Superior Institute of Lisbon.

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