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Role of metabolic adaptation in regulation and expression of virulence in *Escherichia coli* strains.

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Escherichia coli is a normal inhabitant of the gut microbiota. However, *E. coli* is also a highly versatile bacterium with considerable pathogenic potential that is implicated in enteric infections and extraintestinal infections such as neonatal meningitis and septicemia. Numerous highly versatile and highly competitive pathogenic and commensal strains of *E. coli* belong to phylogenetic group B2, the prevalence of which is increasing in developed countries. Comprehensive understanding of the intestine-*E. coli* interaction is a major issue for human or animal health and nutrition, as well as for the basic knowledge of the functioning of gut microflora. The general aim of our project is to understand how the adaptation of *E. coli* to the environmental conditions found in the gut can favour its implantation, and also what are the physiological bases that determine the expression of the specific traits of each strain, including fitness and virulence factors. To reveal the key players in the global adaptation to changes in carbon nutrition, large-scale analysis – i.e. transcriptomics, proteomics, metabolomics and fluxomics – are combined to modelling approaches to detail the dynamic response of the bacteria during changes in carbon nutrition that are representative of life in the colon. The dynamic response will be linked to the functional phenotype (i.e. implantation and persistence in the gut). In addition, the link between metabolic adaptation and virulence will be investigated. This work should provide new orientations in terms of preventive nutrition and therapeutics.

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