
M. PILAR FRANCINO

CV

PARTICIPANT AT:

THE HUMAN MICROBIOME. PRESENT STATUS AND FUTURE PROSPECTS

**July, 2nd-3rd, 2015, Barcelona**

M. Pilar Francino, Head, Genomics and Health Area, Valencian Region Foundation for the Promotion of Health and Biomedical Research (FISABIO)-Public Health, Valencia, Spain.

Background in Biology (BSc in Biology, National University of Mexico (UNAM), PhD in Ecology and Evolutionary Biology, University of Rochester, New York). Her main research areas are evolutionary genomics, microbial ecology, and the human microbiome. Her current work focuses on understanding the development of the gut microbiota, from the transmission of microbes from mother to offspring to the overall process of microbial succession and community assembly during early life. To this goal, her research group analyzes the taxonomic composition, coding capabilities and gene expression patterns of the gut microbial community at different stages during infancy, as well as the relationships of these features with health. She is a member of the International Human Microbiome Consortium (IHMC), the Genomic Standards Consortium (GSC), the Global Microbial Identifier (GMI) initiative and the Spanish Biomedical Research Consortium for Epidemiology and Public Health (CIBERESP), and belongs to several scientific societies: American Society of Microbiology, Society for Molecular Biology and Evolution, Spanish Society of Evolutionary Biology and Catalan Society of Biology.

B-DEBATE IS AN INITIATIVE OF:



M. PILAR FRANCINO**ABSTRACT**

PARTICIPANT AT:

**THE HUMAN
MICROBIOME. PRESENT
STATUS AND FUTURE
PROSPECTS****July, 2nd-3rd, 2015, Barcelona**

M. Pilar Francino, Head, Genomics and Health Area, Valencian Region Foundation for the Promotion of Health and Biomedical Research (FISABIO)-Public Health, Valencia, Spain.

The Gut Microbiota in Mother and Infant

Gut microbiota development involves a complex process of succession that impacts life-long health through early interactions with metabolism and immunity. New results support the notion that bacteria reach the fetal gut in utero, in a process influenced by various maternal factors with likely consequences for the child's health. After birth, the individual patterns of gut colonization in healthy infants vary greatly, but, overall, two distinct phases of succession can be defined, separated by the introduction of solid foods. This change causes the loss of many rare taxa, but the number of core genera shared by all infants increases substantially and novel functions become common in the metagenome. Throughout the first year of life, there is an overarching directionality of change towards the taxonomic and functional composition of the maternal microbiota, although succession is not complete by the one-year mark. Taxon co-occurrence and co-abundance analyses reveal the progressive development of an ecological network similar to that of the adult. Remarkably, a substantial fraction of positive associations are established between genera belonging to the same taxonomic groups, suggesting that related taxa have similar competitive abilities or that they have coevolved to occupy finely subdivided and complementary niches, potentially enabling cooperation.

B-DEBATE IS AN INITIATIVE OF:

