

PREDICTIVE MICROBIAL BIOMARKERS FOR IDENTIFYING PREMATURE INFANTS MOST LIKELY TO BENEFIT FROM A CLINICAL INTERVENTION

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application claims the benefit of priority to U.S. provisional application number 62/986,271 (filed March 6, 2020), the contents of which are incorporated by reference herein in their entirety.

FIELD OF INVENTION

[0002] The described invention relates generally to gut microbial colonization and gut microbial community types in preterm infants.

BACKGROUND OF THE INVENTION

[0003] The human microbiota consists of 10-100 trillion symbiotic microbial cells harbored by each person, primarily bacteria in the gut, while the human microbiome consists of the genes these cells harbor. [Ursell, LK et al., “Defining the human microbiome.” *Nutr. Rev.* (2012) 70 (Suppl. 1) S38-S44.] These microbial cells, and their genetic material, live with humans from birth, and every individual has a unique mix of species. This relationship is important for nutrition, immunity and effects on the brain and behavior, and has been implicated in a number of diseases where the disease is caused by a disturbance in the normal balance of microbes or where the disturbance is another downstream consequence of the disease. The interaction between the human microbiota and the environment is dynamic, meaning that microbial communities are constantly being transferred between surfaces, and that a dynamic interaction exists between environmental microbiota and different human body sites. There is increasing evidence that individuals actually share a core microbiota, with vastly different sets of microbial species yielded very similar functional molecular interactions, reactions and relation networks for metabolism, genetic information processing, environmental information processing, cellular processes, and organismal systems referred to as KEGG pathways.

Where gut bacteria originate

[0004] Mode of delivery has been shown to influence the newborn microbiome, with the microbiome of newborns delivered by cesarean section characterized by a lack of strict anaerobes and the presence of facultative anaerobes. [DiBartolomeo, ME and Claud, MC. “The