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Sommario/riassunto	<p>The human intestine is home of an almost inconceivable large number of microorganisms. The human gut microbiota can therefore be pictured as an organ placed within a host organism. The human gut microbiome, which in total may contain &gt;100 times the number of genes present in our genome, endows us with functional features that we did not have to evolve ourselves. It is recognized that intestinal microbiota plays an important role in human health and disease. In fact, gut bacteria other than metabolize dietary components, may play complex roles such as modulation of the immune system and in reduction of gut infections. Variations in the presence and/or abundance of certain components of the intestinal microbiota have repeatedly been observed in patients that suffer from atopic diseases, inflammatory bowel disease, Crohn disease, ulcerative colitis, infectious colitis, colon cancer and diabetes. In this context, bifidobacteria represent one of the most common bacterial members of the human gut microbiota. Bifidobacteria are anaerobic, Gram-positive, irregular or branched rod-shaped bacteria that are commonly found in the gastro-intestinal tracts (GIT) of humans, especially during the first stages of life and most animal and insects. Bifidobacterial fluctuations seem directly associated with health effects and for these reasons they are being exploited as health-promoting or probiotic bacteria. However, despite the extensive commercial exploitation of bifidobacteria as probiotic bacteria, little is known about their impact</p>

or dependency on other members of the human gut microbiota or on their host. Genome analyses have highlighted the existence of gene repertoires encoding products that are responsible for the adaptation of bifidobacteria to the human intestine and intense research efforts at international level are ongoing to understand the molecular details of these interactions. Specifically, the molecular interactions that are presumed to exist between bifidobacteria and the human host, as well as interactions between different residents of intestinal microbiota are the main topic of bifidobacterial research communities.

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