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Sommario/riassunto	<p>All parts of our body having communication with the external environment such as the skin, vagina, the respiratory tract or the gastrointestinal tract are colonized by a specific microbial community. The colon is by far the most densely populated organ in the human body. The pool of microbes inhabiting our body is known as "microbiota" and their collective genomes as "microbiome". These microbial ecosystems regulate important functions of the host, and their functionality and the balance among the diverse microbial populations is essential for the maintenance of a "healthy status". The impressive development in recent years of next generation sequencing (NGS) methods have made possible to determine the gut microbiome composition. This, together with the application of other high throughput omic techniques and the use of gnotobiotic animals has greatly improved our knowledge of the microbiota acting as a whole. In spite of this, most members of the human microbiota are largely unknown and remain still uncultured. The final functionality of the microbiota is depending not only on nutrient availability and environmental conditions, but also on the interrelationships that the microorganisms inhabiting the same ecological niche are able to establish with their partners, or with their potential competitors. Therefore, in such a competitive environment microorganisms have had to develop strategies allowing them to cope, adapt, or cooperate with their neighbors, which may imply notable changes at metabolic,</p>

physiological and genetic level. The main aim of this Research Topic was to contribute to better understanding complex interactions among microorganisms residing in human microbial habitats. All parts of our body having communication with the external environment such as the skin, vagina, the respiratory tract or the gastrointestinal tract are colonized by a specific microbial community. The colon is by far the most densely populated organ in the human body. The pool of microbes inhabiting our body is known as “microbiota” and their collective genomes as “microbiome”. These microbial ecosystems regulate important functions of the host, and their functionality and the balance among the diverse microbial populations is essential for the maintenance of a “healthy status”. The impressive development in recent years of next generation sequencing (NGS) methods have made possible to determine the gut microbiome composition. This, together with the application of other high throughput omic techniques and the use of gnotobiotic animals has greatly improved our knowledge of the microbiota acting as a whole. In spite of this, most members of the human microbiota are largely unknown and remain still uncultured. The final functionality of the microbiota is depending not only on nutrient availability and environmental conditions, but also on the interrelationships that the microorganisms inhabiting the same ecological niche are able to establish with their partners, or with their potential competitors. Therefore, in such a competitive environment microorganisms have had to develop strategies allowing them to cope, adapt, or cooperate with their neighbors, which may imply notable changes at metabolic, physiological and genetic level. The main aim of this Research Topic was to contribute to better understanding complex interactions among microorganisms residing in human microbial habitats.
