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# Editorial: Microbiota and mitochondria: Impact on cell signaling, physiology, and disease

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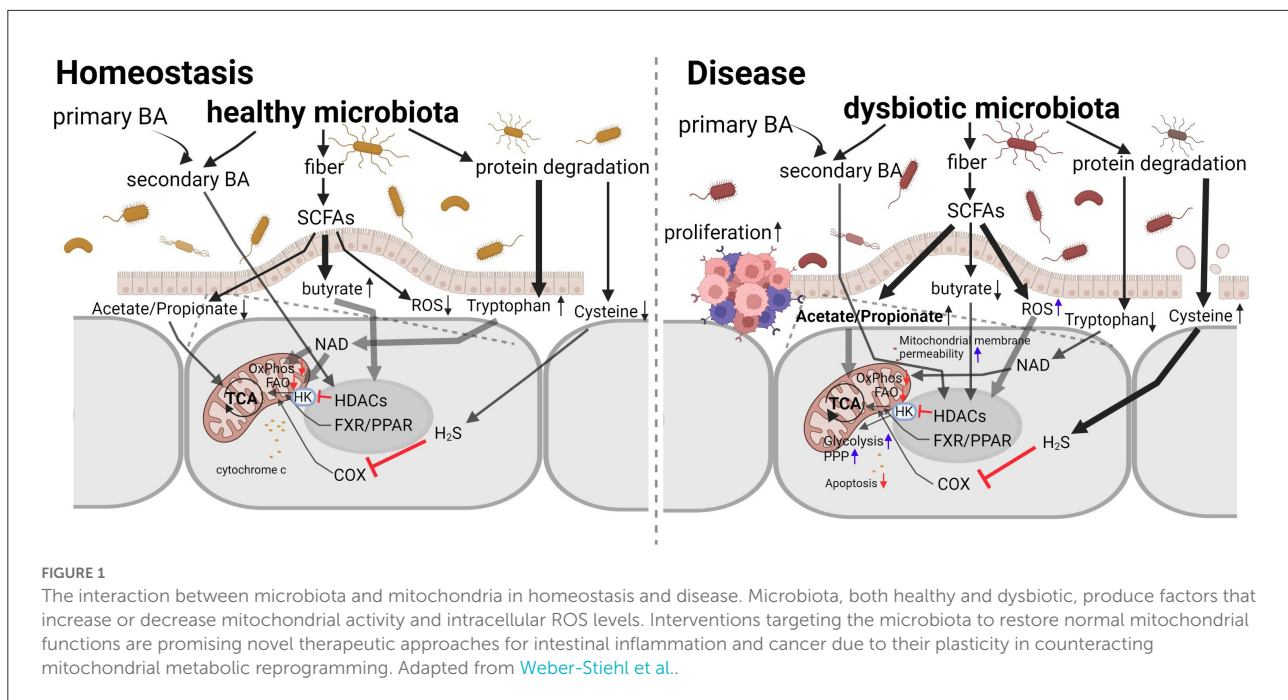
## Editorial on the Research Topic

[Editorial: Microbiota and mitochondria: Impact on cell signaling, physiology, and disease](#)

The mitochondrion is an organelle of endosymbiotic origin that is central to the cell's energy production, contributing to cellular signaling and homeostasis. Higher eukaryotes have external symbionts, comprising their so-called microbiome, consisting primarily of bacteria found in various body surfaces, such as the mouth, skin, lungs and gut. Advances in the sequencing technology and the facile characterization of host bacteria at the species and even the gene level provide associations between microbiota profiles and diseases, including diabetes, obesity (Karlsson et al., 2013), neurodegenerative (Sarkar and Banerjee, 2019) and autoimmune diseases (Opazo et al., 2018). For instance, mitochondria exhibit reduced oxidative phosphorylation in the setting of diabetes and reduced plasticity in insulin-resistant subjects (Szendroedi et al., 2011). Also, in neurodegenerative diseases like Alzheimer's or Parkinson's, mitochondria show impaired bioenergetics (Knott et al., 2008).

Given that mitochondria likely evolved from ancient bacteria (Labbé et al., 2014), it is plausible that microbiota interact with the mitochondria of their host cells. A central factor may be reactive oxygen species (ROS), serving as a nexus of a microbiota-mitochondria crosstalk (Ballard and Towarnicki, 2020). However, the exact mechanisms of this communication remain unclear.

A PubMed search in September 2022 using the terms "microbiota and mitochondria" resulted in 382 papers (including 145 reviews), 80% of which were published within the last five years. This reflects that the precise high-throughput study of microbiota, mitochondria and their metabolites is only recently popularized.



Host mitochondria can affect the gut microbiome *via* ROS ([Yardeni et al., 2019](#)). Microbiota, in turn, can produce metabolites, such as short-chain fatty acids and secondary bile acids, which can alter the expression of genes, for example Pgc-1 $\alpha$ , that regulate mitochondrial biogenesis and function ([Clark and Mach, 2017](#)). Hence, the crosstalk between microbiota and mitochondria is bidirectional and relatively hard to study, as it involves intimate host, microbe, and metabolite interactions ([Figure 1](#)).

In this Research Topic (RT), we welcomed basic, translational, and clinical research studies on microbiota with emphasis on delineating the signal transduction pathways and crosstalk between microbiota and mitochondria and the effects of this interaction on physiology and related diseases. A pertinent paper ([Weber-Stiehl et al.](#)) published in this issue provides a very useful perspective on the interactions between intestinal microbiota and the mitochondria of enterocytes. There is evidence that intestinal microbiota metabolites and metabolic byproducts, such as short-chain fatty acids, butyrate, acetate and propionate, and secondary bile acids, as well as the amino acids, tryptophane and cysteine, facilitate a balanced mitochondrial function. Under intestinal inflammation, this interaction is altered, leading to a vicious cycle that perpetuates the inflammatory state and predisposes to cancer.

The impact of host metabolism is also illustrated in an interesting research paper describing differences in vaginal bacterial communities between estrus and non-estrus in giant pandas ([Yue et al.](#)). Specifically, species of the genera

*Streptococcus*, *Escherichia*, and *Bacteroides* were significantly increased in the vagina of giant panda during estrus, providing a link between the reproductive hormonal state of estrus and vaginal bacterial composition. Further research may determine if carbohydrate and galactose metabolic pathways highly enriched in estrus pandas are related to the mitochondrial function ([Aguer et al., 2011](#)).

Along the same lines, this topic includes a translational research article describing distinct microbiota profiles in the placenta of pregnant women with premature rupture of membranes (PROM) or gestational diabetes mellitus (GDM) ([La et al.](#)). This study, along with others associating mitochondrial membrane damage with PROM ([Fortunato and Menon, 2001](#)) and mitochondrial dysfunction with GDM ([Fisher et al., 2021](#)), encourages further research on microbiota profiles associated with these pathologies and the role of mitochondrial function.

A deeper understanding of the interactions between mitochondria and microbiota is necessary to link microbial and host metabolism in health and disease mechanistically. Research similar to the works described in this RT may stimulate further investigation in this area and pave the way for biochemical studies focusing on the interplay between microbiota and mitochondria.

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## Author contributions

All authors have contributed substantially and equally to the article and approved the manuscript for publication.

## Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships

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