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Engineering in Life Sciences

EDITORIAL

Microbiome research for advancing engineering in life science

Microbiome research has become increasingly prominent, as scientists explore the intricately assembled microbial communities (i.e., microbiota) and their wide-ranging impacts on human systems (e.g., health and foods), environmental sustainability (bioremediation, biogeochemistry, and ecosystem biorestoration, or 3B for Sustainability), and next-generation bioeconomy (i.e., bioenergy, biomedicine, and biomaterials, or 3B for Resources). This burgeoning field has been driven by the widespread adoption of meta-omics methodologies, such as metagenomics, metatranscriptomics, metaproteomics, and metabolomics. In this special issue, we present a compendium of recent human and environmental microbiome studies that elucidate the multifaceted roles of microbial communities and their implications across different domains of research in life sciences and related fields of application.

The gut microbiome stands out as a central player in human health, influencing fundamental physiological processes such as digestion, immunity, and metabolism. Tang et al. delves into the intricate interplay between the gut microbiota and the host epigenome in the context of Non-alcoholic Fatty Liver Disease (NAFLD), shedding light on how microbial factors can modulate gene expression patterns associated with NAFLD pathogenesis [1]. Similarly, Zoghi et al. investigate the association between gut dysbiosis and nutritional imbalances in children, underscoring the potential therapeutic avenues for modulating gut microbiota composition to restore energy homeostasis [2].

Moreover, the symbiotic interplay between flavonoids and the gut microbiota emerges as a promising area of study in maintaining metabolic balance and overall health by Zhou et al. [3]. Flavonoids, abundant in fruits and vegetables, serve as essential dietary components that undergo biotransformation by gut microbes, yielding bioactive metabolites with various health-promoting properties. Understanding this intricate interplay opens new avenues for leveraging dietary interventions to modulate gut microbiota composition and enhance metabolic health (Figure 1).

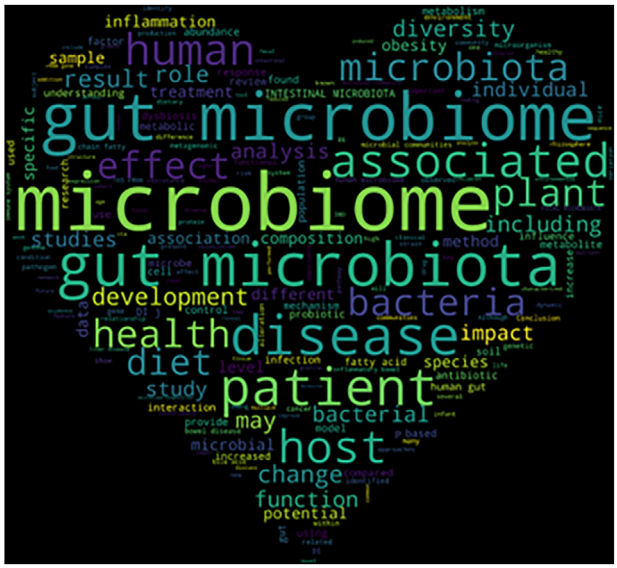

FIGURE 1 A word cloud for microbiome research based on the title and abstract search of 1300+ highly cited papers in Web of Science as of April 14, 2022.

Beyond human health, microbial communities also play critical roles in environmental processes, particularly in the biodegradation of pollutants. Huang et al. leverage meta-omics approaches to uncover the genetic potential of microbial communities in contaminated environments, offering insights into potential bioremediation strategies for mitigating environmental pollution [4].

Furthermore, microbiomes offer promising avenues for bioconversion and biodegradation processes in the context of biotechnology and industrial applications. Zhu et al. investigate the dynamics of microbial consortia during primary sludge and food waste fermentation, revealing insights into how different environmental conditions and additives can modulate fermentation product profiles [5]. The study demonstrates the product plasticity of the microbiome fermentation process and suggests a promising solution for future biowaste valorization. Similarly, Wu et al. examine the effects of varying H_2/CO_2 ratios on

microbial community composition and product distribution, emphasizing the importance of microbial community dynamics in bioprocess optimization [6].

Lastly, Xu et al (2023) showcase the utility of synthetic microbial communities (SynComs) in efficiently managing high-salt and oily food waste through solid-state aerobic biodegradation. Their study highlights the potential of engineered microbial consortia for sustainable waste management and resource recovery [7].

In summary, the studies presented in this special issue underscore the intricate interplay between microbial communities and various aspects of human health, environmental sustainability, and industrial processes. As microbiome research continues to advance, it holds immense promise for addressing pressing societal, environmental, and global sustainability challenges, and fostering innovation across interdisciplinary frontiers underlying the next-generation bioeconomy in the fields of industrial biotechnology, health and medicine, food and agriculture, environmental biotechnology, and bioenergy.

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REFERENCES

1. Tang R, Liu R, Zha H, et al. Gut microbiota induced epigenetic modifications in the non-alcoholic fatty liver disease pathogenesis. *Eng Life Sci*. 2024;24:e2300016.
2. Zoghi S, Sadeghpour Heravi F, Nikniaz Z, et al. Gut microbiota and childhood malnutrition: understanding the link and exploring therapeutic interventions. *Eng Life Sci*. 2024;24:e2300070.
3. Zhou M, Ma J, Kang M, et al. Flavonoids, gut microbiota, and host lipid metabolism. *Eng Life Sci*. 2024;24:e2300065.
4. Huang Y, Hu H, Zhang T, et al. Meta-omics assisted microbial gene and strain resources mining in contaminant environment. *Eng Life Sci*. 2024;24:e2300207.
5. Zhu X, Li P, Ju F. Microbiome dynamics and products profiles of biowaste fermentation under different organic loads and additives. *Eng Life Sci*. 2024;24:e2300216.
6. Wu W, Li Z, Liu G, et al. Regulation on C2-C8 carboxylic acid biosynthesis from anaerobic CO_2 fermentation. *Eng Life Sci*. 2024;24:e2200069.
7. Xu S, Tao L, Wang J, et al. Rapid in-situ aerobic biodegradation of high salt and oily food waste employing constructed synthetic microbiome. *Eng Life Sci*. 2024;24:e2200067.