microbiomes are yet to be investigated. Considering that microbes such as fungi can also synthesize SeNPs, it would be interesting to determine whether there is any interaction between these cross-kingdom organisms that may, in the long run, influence the biosynthesis of these particles or bridge the signaling pathways between bacteria and plants.

Taken together, a combination of various techniques with microbial applications in plant science will ensure sustainable agriculture and improve crop performance. The concert of the plant microbiome, directed by the nano-boosting microbes and SeNPs, promises a harmonious and prosperous future for agriculture.

ACKNOWLEDGMENTS

This work was supported by the National Key R&D Program of China (2022YFA1304400 to K.T.), the National Natural Science Foundation of China (32250710139 and 32170298 to K.T.), and HZAU-AGIS Cooperation Fund (SZYJY2021007 to K.T.).

DECLARATION OF INTERESTS

The authors declare no competing interests.

REFERENCES

1. Bais, H.P., Weir, T.L., Perry, L.G., Gilroy, S., and Vivanco, J.M. (2006). The role of root exudates in rhizosphere interactions with plants and other organisms. Annu. Rev. Plant Biol. *57*, 233–266. https://doi.org/10.1146/annurev.arplant.57.032905.105159.

2. Trivedi, P., Leach, J.E., Tringe, S.G., Sa, T., and Singh, B.K. (2020). Plant–microbiome interactions: from community assembly to plant health. Nat. Rev. Microbiol. *18*, 607–621. https://doi.org/10.1038/s41579-020-0412-1.

3. Singh, N.A., Narang, J., Garg, D., Jain, V., Payasi, D., Suleman, S., and Swami, R.K. (2023). Nanoparticles synthesis via microorganisms and their prospective applications in agriculture. Plant Nano Biology *5*, 100047. https://doi.org/10.1016/j.plana.2023.100047.

4. Lowry, G.V., Giraldo, J.P., Steinmetz, N.F., Avellan, A., Demirer, G.S., Ristroph, K.D., Wang, G.J., Hendren, C.O., Alabi, C.A., Caparco, A., et al. (2024). Towards realizing nano-enabled precision delivery in plants. Nat. Nanotechnol. *19*, 1255–1269. https://doi.org/10.1038/s41565-024-01667-5.

5. Wei, L., Liu, J., and Jiang, G. (2024). Nanoparticle-specific transformations dictate nanoparticle effects associated with plants and implications for nanotechnology use in agriculture. Nat. Commun. *15*, 7389. https://doi.org/10.1038/s41467-024-51741-8.

6. El-Badri, A.M., Hashem, A.M., Batool, M., Sherif, A., Nishawy, E., Ayaad, M., Hassan, H.M., Elrewainy, I.M., Wang, J., Kuai, J., et al. (2022). Comparative efficacy of bio-selenium nanoparticles and sodium selenite on morpho-physiochemical attributes under normal and salt stress conditions, besides selenium detoxification pathways in Brassica napus L. J. Nanobiotechnology *20*, 163. https://doi.org/10.1186/s12951-022-01370-4.

7. Hussein, H.G., El-Sayed, E.-S.R., Younis, N.A., Hamdy, A.E.H.A., and Easa, S.M. (2022). Harnessing endophytic fungi for biosynthesis of selenium nanoparticles and exploring their bioactivities. Amb. Express *12*, 68. https://doi.org/10.1186/s13568-022-01408-8.

8. Sun C., Sun B., Chen L., Zhang M., Lu P., Wu M., Xue Q., Guo Q., Tang D., Lai H. Harnessing biosynthesized selenium nanoparticles for recruitment of beneficial soil microbes to plant roots. Cell Host and Microbe *32*. https://doi.org/10.1016/j.chom.2024.10.015.

9. Züst, T., and Agrawal, A.A. (2017). Trade-offs between plant growth and defense against insect herbivory: an emerging mechanistic synthesis. Annu. Rev. Plant Biol. *68*, 513–534.

10. Alam, H., Khatoon, N., Khan, M.A., Husain, S.A., Saravanan, M., and Sardar, M. (2020). Synthesis of selenium nanoparticles using probiotic bacteria Lactobacillus acidophilus and their enhanced antimicrobial activity against resistant bacteria. J. Clust. Sci. *31*, 1003–1011.

Exploring the early life gut microbiome with MAGIC

Edoardo Pasolli[1,*]
[1]University of Naples Federico II, Department of Agricultural Sciences, Piazza Carlo di Borbone 1, 80055 Portici, Italy
*Correspondence: edoardo.pasolli@unina.it
https://doi.org/10.1016/j.chom.2024.10.019

In this issue of *Cell Host & Microbe*, Peng et al. provide the MAGIC catalog as a resource for studying bacterial and viral diversity of the global gut microbiome in early life. By addressing gaps in geographic and age representation, this database enhances our understanding of early microbiome dynamics.

The human gut microbiome has emerged as a key factor of health research. Its composition is implicated in a variety of important physiological processes, ranging from immunity and metabolism to cognitive development and disease susceptibility. Much of our understanding of this complex microbial ecosystem is grounded in research on adult populations. However, early life encompasses a distinct period in the development of the microbiome, during which microbial communities are seeded, grow, and undergo rapid transitions that are linked to host health outcomes.[1] Despite the importance of early composition, most microbiome data available in databases are still derived from adults, which constrains, in part, our abilities to accurately profile the gut microbiota of infants and the virome during early life. Indeed, this study by Peng et al.[2] introduces the Metagenome-Assembled Genome Inventory for Children (MAGIC) as an effort to characterize the bacterial and viral diversity of the child's microbiomes across the world.

Publicly available microbiome reference databases, including the Human Gut Metagenome (HumGut),[3] Unified Human Gastrointestinal Genome (UHGG),[4] and Metagenomic Gut Virus (MGV)[5] catalogs, represent an extraordinary resource for investigations into the adult microbiome. However, their dominance by adult samples creates an important bias that constrains relevance for early-life microbiome research. In this important development phase, the infant microbiome presents unique taxa, interactions, and evolutionary pressures that may not be common to adults. Although a few databases, such as the Early-Life Gut Genomes (ELGG)[6] and Early-Life Gut Virome (ELGV),[7] have been proposed, their sizes and diversities are still not enough to provide comprehensive profiling of bacterial and viral components in infants.

It has been found that the gut microbiome is uniquely characterized in infants, seeded both by maternal transmission and environmental exposure.[8] For example, species from *Bifidobacterium* are remarkably abundant during infancy, influenced by selective pressures from milk oligosaccharides. Infants also have a different virome in their guts. These microbial communities are critical for immune training, metabolic programming, and the establishment of gut resilience. Disruptions in microbiome development during critical windows of early life have been associated with various long-term health outcomes, including obesity, allergies, asthma, and neurodevelopmental disorders. Thus, a strong understanding of the early-life human microbiome is of great interest and could also serve to inform strategies to prevent or reduce the severity of chronic diseases.

Another limitation with the existing databases is geographical bias. Most of the microbiome studies were conducted in high-income countries; their databases are less represented from other countries and continents such as Africa, Asia, and South America. This focus on population diversity is important because studies have shown that factors such as diet, lifestyle, and environmental exposure are drivers in shaping the gut microbiome. Indeed, feces from non-Westernized populations, such as the Hadza hunter-gatherers,[9] present microbial compositions that are quite different from those coming from industrialized populations, a sign of possible impact of lifestyle on microbiome development. Without such diversity, our understanding of global variability in microbiome development and health implications remains incomplete.

The MAGIC database by Peng et al.[2] tries to address these limitations through the integration of samples comprising children aged 0–7 years, including previously underrepresented regions. The resource includes both bulk and viral-like particle-enriched metagenomes, thus allowing comprehensive gut microbiome profiling in early life. The authors leveraged 19,559 publicly available datasets and added 613 newly generated metagenomes from their MOMMY cohort, thus offering a database that spans 34 countries. This geographical diversity will be important in the effort to address the variability of the microbiome across different demographics and socio-economic backgrounds.

The catalog includes 3,299 prokaryotic operational taxonomic units (pOTUs) and 139,624 species-level viral OTUs (vOTUs), most of which have been novel. The authors made significant enhancements in read mapping. More specifically, there was a 6.7% increase in read mapping, mainly in samples coming from low-income countries, hence indicating the probable role in improving microbiome analyses from diverse populations. The resource is also important to describe the vast collection of viral species. Understanding the role of viruses in the gut microbiome, especially during early life, is still challenging.[10] However, evidence indicates that they play a key role in shaping microbial community structure, bacterial evolution, and host health outcomes. Bacteriophages are especially intimate with bacterial populations and may thus influence bacterial diversity. Such an approach in using MAGIC allows researchers to examine relations between the viral and microbial populations in far greater detail; it finally allows for the assessment of how viruses affect infant gut microbial ecology, a critical perspective considering that the developing human virome is understudied in the literature. The MAGIC virome catalog will provide a reference for such studies that allow the characterization of viral dynamics unique to early life and thus enable the detection of potential microbial markers of health and disease.

One important outcome is the identification of 54 candidate keystone species within the early-life microbiome, including several species of *Bifidobacterium*, such as *Bifidobacterium longum* and *Bifidobacterium infantis*. Keystone species are defined as those organisms that have a disproportionate impact on the structure and function of their ecosystem. Such keystone species could facilitate stabilization of the microbial community within the gut of an infant and its resilience, thereby playing a significant role in the establishment of a healthy microbiome. Importantly, MAGIC has shown that the abundance of some of these keystone species relates to health outcomes, such as allergies and atopic dermatitis in children. These findings constitute a critical foundation for further study of microbial therapies and microbiome-targeted interventions in early life.

Population-specific characteristics of these keystone species are also investigated in this study. For instance, the microbial profiles of African children included a different keystone taxa and phage community compared with those from Europe and North America, underpinning the geographic and environmental influences on microbiome composition. Such geographic or regional variation in keystone species may also be related to dietary and other environmental exposures. Whereas in all African samples, MAGIC-unique taxa dominated and were significantly more diverse and richer compared with that of Westernized populations, thus suggesting that early-life non-Westernized microbiomes may harbor unique microbial traits that could inform us about health-promoting microbial configurations.

The most diverse species included in MAGIC is *B. longum* represented by more than 600 MAGs and newly identified gene clusters associated with functions, such as urea utilization. These functional insights also provide the basis for further elucidation of the ecological roles of *Bifidobacterium* species during early life, especially in relation to diet and metabolism. For example, genes encoding proteins of quorum sensing were found in *B. longum*, suggesting the potential of this species for enhanced colonization and biofilm formation in the infant gut. This kind of insight might be useful in the design of probiotics, as strains with a high colonization ability could maintain a more durable presence in the gut microbiome and, thus, may contribute to immune development.

While MAGIC enables new opportunities for microbiome research in early life, further developments may be relevant for the research community. First, this database is primarily focused on cataloging bacterial and viral genomes from DNA. Inclusion of transcriptomic data would provide even more useful information for their use for elucidating functional changes over time. Such databases will allow researchers to perform in-depth investigations into microbial dynamics, keystone species, and strain-level interactions in the developing gut. This can help in advancing our understanding of the influences of the early-life microbiome on long-term health. MAGIC, by capturing microbial diversity across geographical regions, holds potential for advancing basic microbiome science and clinical research for health promotion through microbiome-targeting therapies. In this regard, the MAGIC database is indeed an important example of the general principle of context-specific microbiome research and opens prospects toward studying the complex interactions of microbiomes with human health since life inception.

DECLARATION OF INTERESTS

The author declares no competing interests.

REFERENCES

1. Hickman, B., Salonen, A., Ponsero, A.J., Jokela, R., Kolho, K.L., de Vos, W.M., and Korpela, K. (2024). "Gut microbiota wellbeing index predicts overall health in a cohort of 1000 infants.". Nat. Commun. *15.1*, 8323.

2. Peng, Y., Zhu, J., Wang, S., Zhang, L., Siew, C.N., and Tun, H.M. (2024). A metagenome-assembled genome inventory for children (MAGIC) facilitates early life gut bacteriome and virome studies. Cell Host Microbe *32*, 1–19.

3. Hiseni, P., Rudi, K., Wilson, R.C., Hegge, F.T., and Snipen, L. (2021). HumGut: a comprehensive human gut prokaryotic genomes collection filtered by metagenome data. Microbiome *9*, 1–2. 165.

4. Almeida, A., Nayfach, S., Boland, M., Strozzi, F., Beracochea, M., Shi, Z.J., Pollard, K.S., Sakharova, E., Parks, D.H., Hugenholtz, P., et al. (2021). A unified catalog of 204,938 reference genomes from the human gut microbiome. Nat. Biotechnol. *39*, 105–114.

5. Nayfach, S., Páez-Espino, D., Call, L., Low, S.J., Sberro, H., Ivanova, N.N., Proal, A.D., Fischbach, M.A., Bhatt, A.S., Hugenholtz, P., and Kyrpides, N.C. (2021). Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome. Nat. Microbiol. *6*, 960–970.

6. Zeng, S., Patangia, D., Almeida, A., Zhou, Z., Mu, D., Paul Ross, R., Stanton, C., and Wang, S. (2022). A compendium of 32,277 metagenome-assembled genomes and over 80 million genes from the early-life human gut microbiome. Nat. Commun. *13*, 5139.

7. Zeng, S., Almeida, A., Li, S., Ying, J., Wang, H., Qu, Y., Paul Ross, R., Stanton, C., Zhou, Z., Niu, X., et al. (2024). A metagenomic catalog of the early-life human gut virome. Nat. Commun. *15*, 1864.

8. Grech, A., Collins, C.E., Holmes, A., Lal, R., Duncanson, K., Taylor, R., and Gordon, A. (2021). Maternal exposures and the infant gut microbiome: a systematic review with meta-analysis. Gut Microb. *13*, 1–30.

9. Carter, M.M., Olm, M.R., Merrill, B.D., Dahan, D., Tripathi, S., Spencer, S.P., Yu, F.B., Jain, S., Neff, N., Jha, A.R., et al. (2023). Ultra-deep sequencing of Hadza hunter-gatherers recovers vanishing gut microbes. Cell *186*, 3111–3124.e13.

10. Liang, G., and Bushman, F.D. (2021). The human virome: assembly, composition and host interactions. Nature Reviews Microbiology *19*, 514–527.