Review Article

The Multikingdom Microbiome: Composition, Communication, and Collective Impact

Holistic Microbiome Review

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Abstract

The concept of a "microbiome" has evolved from a census of bacteria to a holistic framework encompassing the complex community of Bacteria, Archaea, Eukarya, and viruses, their collective genomes, and their dynamic interactions within an environmental niche. This review synthesizes current knowledge on the composition and function of multikingdom microbiomes. We begin by defining the modern microbiome, detailing the distinct roles of its cellular constituents from the Three Domains of life. We then explore the critical regulatory influence of the virome, focusing on bacteriophages. The review further examines the sophisticated chemical communication networks, such as quorum sensing, that enable microbial communities to coordinate behavior. Finally, we address the "biomass paradox" how these minuscule organisms, through their immense collective genetic potential and integrated activity, exert macroscopic influences on host physiology and global biogeochemical cycles. Understanding this intricate ecosystem is fundamental to advancing fields from medicine to environmental science.

Keywords: microbiome, microbiota, virome, archaea, quorum sensing, bacteriophage, host-microbe interactions, microbial ecology

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Introduction:

1. Redefining the Microbiome

A paradigm shift in biology has recast our view of individual organisms, from autonomous entities to complex ecosystems or "holobionts." Central to this concept is the **microbiome**—the full complement of microorganisms, their genes, and their metabolites in a specific environment (Marchesi & Ravel, 2015). While early research equated the microbiome largely with bacteria, contemporary understanding recognizes it as a multispecies consortium involving members from all domains of life and acellular viruses. This community functions not as a random assembly but as an integrated metabolic network that profoundly influences the health of its host, whether a human, plant, or an entire environmental habitat like soil or ocean (Lynch & Pedersen, 2016).

This review aims to deconstruct the multikingdom microbiome. We will explore the taxonomic and functional identities of its cellular members (Bacteria, Archaea, microbial

Eukarya), the regulatory role of viruses, the mechanisms of intra- and inter-kingdom communication, and conclude by synthesizing how this collective, despite its microscopic scale, achieves monumental functional significance.

2. The Cellular Players: The Three Domains of Life

All cellular organisms belong to one of three domains, a classification based on fundamental genetic and biochemical differences (Woese et al., 1990). Each domain contributes uniquely to microbiome structure and function.

2.1. Bacteria: The Metabolic Powerhouses

As prokaryotes with peptidoglycan cell walls, bacteria are often the most abundant and studied members of microbiomes. Their immense metabolic diversity allows them to occupy myriad niches. In host-associated contexts, such as the mammalian gut, they are primary agents of dietary fiber fermentation, vitamin synthesis, immune system priming, and colonization resistance against pathogens (Sender et al., 2016). Their rapid replication and horizontal gene transfer make them dynamic and adaptable components of the ecosystem.

2.2. Archaea: The Specialists and Methanogens

Once considered extremophiles, archaea are now known to inhabit moderate environments, including the human gut and ocean. Though prokaryotic, they are phylogenetically distinct from bacteria, featuring ether-linked lipids in their cell membranes. A key functional group within host microbiomes are the methanogenic archaea (e.g., *Methanobrevibacter smithii*), which consume bacterial fermentation end-products (hydrogen and carbon dioxide) to produce methane. This activity improves the overall efficiency of microbial digestion by stabilizing redox conditions (Cavicchioli et al., 2019).

2.3. Eukarya: The Predators, Decomposers, and Partners

Microbial eukaryotes—including fungi, protists, and microscopic animals—add critical functional layers. Fungi (yeasts and molds) are master decomposers, breaking down complex polymers like chitin and cellulose. In soil, mycorrhizal fungi form symbiotic networks with plant roots, extending their nutrient uptake capacity. Protists range from beneficial algae to pathogenic amoebas and predatory ciliates that shape bacterial community structure through grazing (Parfrey et al., 2011). Their inclusion is essential for a complete ecological picture of any microbiome.

3. Viruses: The Unseen Regulators of the Ecosystem

The **virome**, comprising bacteriophages (phages), archaeal viruses, and eukaryotic viruses, is the most abundant genetic entity in any microbiome. Viruses are not merely pathogens but essential drivers of microbial ecology and evolution.

3.1. Bacteriophages: Agents of Control and Innovation

Phages exert top-down control on bacterial populations through the lytic cycle, lysing cells and preventing species dominance—a process termed "kill-the-winner" (Shkoporov & Hill, 2019). Perhaps more significantly, they facilitate horizontal gene transfer via transduction. By packaging and transferring host DNA between bacteria, phages can disseminate functional genes, including those for antibiotic resistance, virulence factors, or novel metabolic pathways (e.g., photosynthesis genes in oceans), thereby accelerating microbial adaptation.

3.2. The Eukaryotic Virome and Host Interaction

Eukaryotic viruses within microbiomes, particularly on mucosal surfaces, engage in complex, often persistent, relationships with the host. Their constant presence provides a training stimulus for the innate and adaptive immune systems. Furthermore, some latent viruses can confer indirect benefits to the host, such as protection against bacterial pathogens or modulation of immune responses (Barr, 2017). The virome thus acts as a critical interface between the cellular microbiome and host immunity.

4. Microbial Communication: The Language of Community

Microbiomes exhibit coordinated behaviors akin to multicellular organisms, achieved through sophisticated chemical communication.

4.1. Quorum Sensing (QS): A Census-Based Strategy

QS allows microbes to sense population density and synchronize gene expression. They produce, release, and detect small diffusible autoinducer molecules. Upon reaching a threshold concentration, these molecules trigger a collective behavioral shift, enabling biofilm formation, virulence, bioluminescence, or public good secretion (Whiteley et al., 2017). QS systems are often species-specific but can also facilitate cross-talk between different microbial groups.

4.2. Metabolic Signaling and Cross-Kingdom Dialogue

Communication extends beyond QS. The microbiome is a web of metabolic interactions where the waste product of one organism is the nutrient for another. Key microbial metabolites, such as short-chain fatty acids (SCFAs) like butyrate, serve dual roles: as energy sources and as potent signaling molecules to host intestinal epithelial and immune cells (Fischbach & Segre, 2016). This chemical dialogue is fundamental to host-microbiome symbiosis, influencing processes from inflammation to metabolism.

5. The Biomass Paradox: Integrated Function from Microscopic Parts

The profound influence of microbiomes belies the minute size of their individual members—a phenomenon we term the "biomass paradox."

5.1. Genetic and Metabolic Supremacy

Humans harbor a near 1:1 ratio of microbial to human cells, but the genetic disparity is staggering. The collective microbiome gene catalog (the metagenome) contains millions of genes, dwarfing the ~20,000 in the human genome by orders of magnitude (Qin et al., 2010). This "second genome" provides a vast reservoir of enzymatic functions, enabling hosts to digest otherwise indigestible compounds, synthesize essential vitamins, and metabolize xenobiotics.

5.2. Collective Impact on Host and Planet

The integrated activity of the microbiome confers emergent functions. In humans, it acts as a virtual endocrine organ, producing neurotransmitters and hormones. It is essential for the proper development and function of the immune system. On a global scale, environmental microbiomes are the principal engineers of Earth's biogeochemical cycles. Marine phytoplankton and cyanobacteria produce half of the planet's oxygen, while soil and aquatic microbes drive the carbon, nitrogen, and sulfur cycles that underpin all life (Falkowski et al., 2008). Their cumulative metabolic output is planet-shaping.

6. Conclusion and Future Perspectives

The microbiome is a complex, multikingdom ecosystem where Bacteria, Archaea, Eukarya, and viruses interact through intricate communication networks. Its function arises not from the sum of its parts, but from their integrated, synergistic interactions. Moving beyond a bacterio-centric view is crucial for a complete understanding.

Future research must prioritize holistic, systems-level approaches that capture these cross-domain interactions. Key challenges include developing culturing techniques for uncultivated archaea and eukaryotes, elucidating the functional roles of the "dark matter" of the virome, and mapping the complete metabolite-mediated interactome within the microbiome and with its host. As we unravel this complexity, we open new frontiers for manipulating microbiomes to improve human health, agricultural sustainability, and environmental resilience.

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