

Microbiota and Host Nutrition across Plant and Animal Kingdoms

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Plants and animals each have evolved specialized organs dedicated to nutrient acquisition, and these harbor specific bacterial communities that extend the host's metabolic repertoire. Similar forces driving microbial community establishment in the gut and plant roots include diet/soil-type, host genotype, and immune system as well as microbe-microbe interactions. Here we show that there is no overlap of abundant bacterial taxa between the microbiotas of the mammalian gut and plant roots, whereas taxa overlap does exist between fish gut and plant root communities. A comparison of root and gut microbiota composition in multiple host species belonging to the same evolutionary lineage reveals host phylogenetic signals in both eukaryotic kingdoms. The reasons underlying striking differences in microbiota composition in independently evolved, yet functionally related, organs in plants and animals remain unclear but might include differences in start inoculum and niche-specific factors such as oxygen levels, temperature, pH, and organic carbon availability.

Physiological Functions of the Vertebrate Gut and Plant Roots

The vertebrate gut and plant roots evolved independently in animal and plant kingdoms but serve a similar primary physiological function in nutrient uptake (Figure 1). One major difference between plant and animal nutritional modes is their distinct energy production strategy. Plants are autotrophs, producing their own energy through photosynthesis (carbohydrate photo-assimilates), while animals rely entirely on the energy originally captured by other living organisms (heterotrophs). Long-distance transport mechanisms ensure the distribution of carbohydrate photo-assimilates from chloroplasts in leaves to all other body parts, including roots. Nutrient acquisition by roots to support plant growth is therefore almost exclusively limited to uptake of mineral ions and water from soil. In contrast, the mammalian gut has evolved to facilitate the uptake of simple sugars, amino acids, lipids, and vitamins in addition to ions. It is typically compartmentalized into sections with low microbial biomass in which the products of host enzymatic activity are absorbed (i.e., the human small intestine, SI) and a section for the uptake of microbe-derived fermentation products (human large intestine or hindgut, LI).

A significant fraction of the soil nutritive complement and of the dietary intake remains unavailable for plants and animals, respectively, and this defines their dietary constraints. Critical

nutrients for plant growth and productivity in soil are nitrogen and phosphorus. However, plant roots can absorb only inorganic nitrogen and orthophosphate (Pi), although phosphorus is abundant in soil both in inorganic and organic pools. Pi can be assimilated via low-Pi-inducible (high-affinity) and constitutive Pi uptake systems (low-affinity) (Lambers et al., 2008; López-Arredondo et al., 2014). Plant species adapted to neutral or higher soil pH, and more aerobic soils have a preference for nitrate and deploy two nitrate uptake and transport systems that act in coordination. By contrast, plants adapted to low pH (reducing soil) as found in forests or the arctic tundra appear to assimilate ammonium or amino acids (Maathuis, 2009). Similarly, a fraction of normal human dietary intake remains undigested and therefore non-bioavailable (fiber). These non-digestible components include plant cell wall constituents such as cellulose, hemicellulose, xylan, and pectin, and certain polysaccharides such as β -glucan, inulin, and oligosaccharides that contain bonds that cannot be cleaved by mammalian hydrolytic enzymes (Tunland and Meyer, 2002).

Plant roots and animal guts are colonized by diverse microbial classes, including bacteria and archaea, fungi, oomycetes, as well as viruses (Table 1). These communities can be regarded as the host's extended genome, providing a huge range of potential functional capacities (Berendsen et al., 2012; Gill et al., 2006; Qin et al., 2010; Turner et al., 2013). Here we focus on

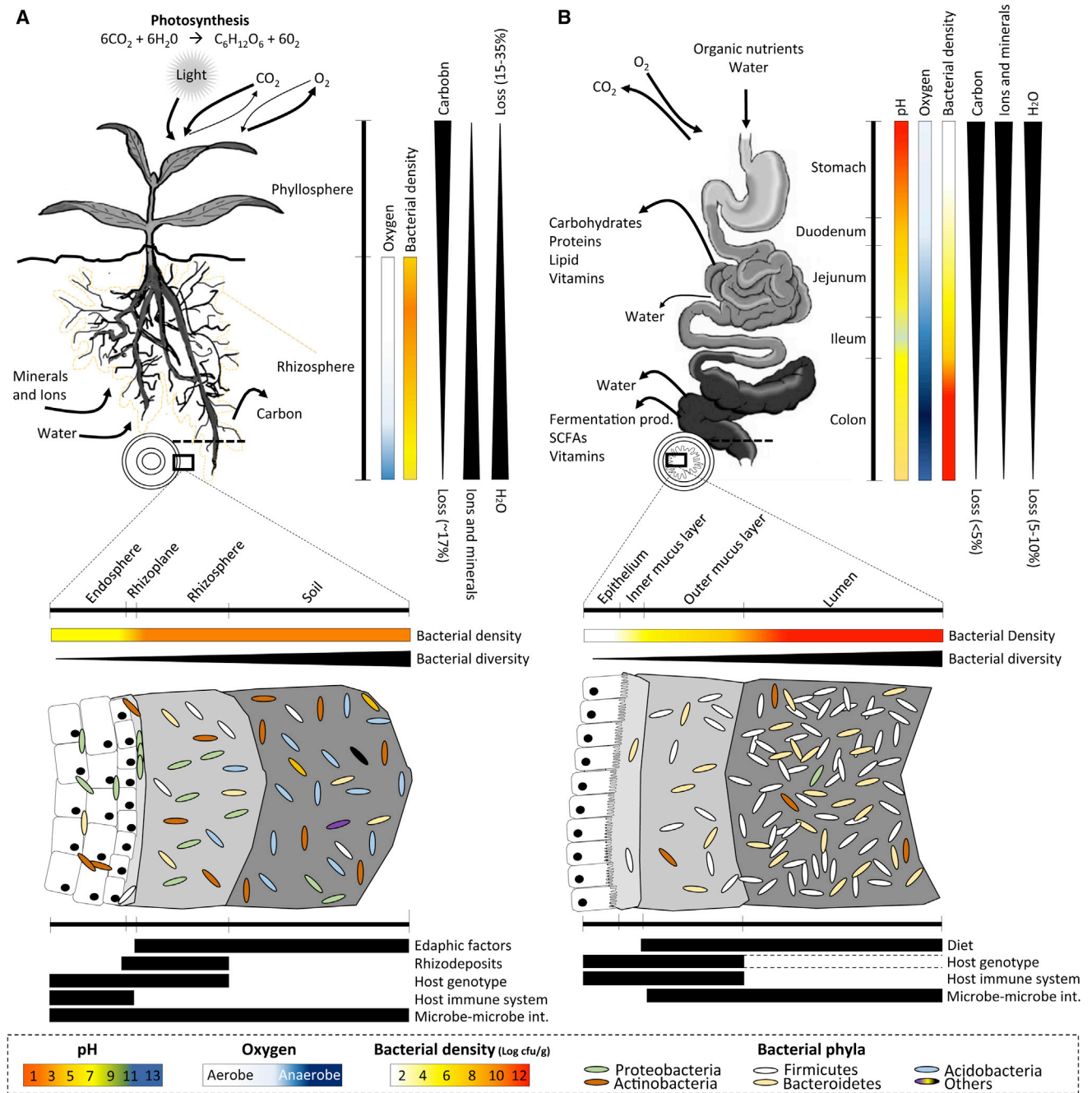


Figure 1. Physiological Functions of the Plant Roots and Human Gut in Nutrient Uptake, Spatial Aspects of Microbiota Composition, and Factors Driving Community Establishment

(A and B) Spatial compartmentalization of the plant root microbiota (A) and the human gut microbiota (B). Upper panels: the major nutrient fluxes are indicated, as well as pH and oxygen gradients in relation with the bacterial density. Lower panels: compartmentalization of the microbiota along the lumen-epithelium continuum in the gut or along the soil-endosphere continuum in the root. For each compartment, the bacterial density, the bacterial diversity, and the major represented phyla are represented for both the gut and the root organs. The main factors driving community establishment in these distinct compartments are depicted with black bars. The gut drawing is adapted from [Tsabouri et al. \(2014\)](#) with permission from the publisher.

bacterial microbiotas because these were shown to form reproducible taxonomic assemblies in animal and plant individuals with well-defined functions.

In plant roots, the microbiota mobilizes and provides nutrients by increasing nutrient bioavailability from soil ([Bulgarelli et al.,](#)

[2013](#)). Non-nutritional functions include increased host tolerance to biotic stresses, e.g., against soil-borne pathogens ([Mendes et al., 2011](#)), and likely abiotic stresses. In addition, the root microbiota can also affect plant fitness by impacting flowering plasticity ([Panke-Buisse et al., 2015](#); [Wagner et al., 2014](#)).

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