Contribution ID : **37** Type : **Oral**

Vitamin B_{12} Accumulation in Duckweed Emerges from a Cooperative, Environmentally Responsive Microbiome

mercoledì 30 settembre 2026 09:15 (15)

Vitamin B_{12} is synthesized exclusively by bacteria and archaea, yet duckweeds accumulate bioavailable B_{12} despite lacking the capacity to produce or use it. We asked how this function is organized within the duckweed microbiome, and whether cultivation conditions could enhance it. Bioavailable B_{12} was detected across rooted and rootless duckweed genera, and in additional aquatic plants. Among 16 B_{12}-containing duckweed haplotypes spanning seven species, endophyte composition varied markedly, but neither community structure nor predicted B_{12}-biosynthesis potential tracked host taxonomy; distinct microbiomes converged on the same function. In the rootless species Wolffia globosa, the endosphere formed a host-filtered community in which a subset of bacteria encoded complete or near-complete cobalamin pathways; most co-occurring taxa instead carried partial pathways, precursor-salvage genes, or cobamide-remodeling capacity. Network analysis linked putative producers to salvagers, and endophytic genomes carried fewer biosynthetic genes than related planktonic strains, suggesting adaptation to metabolic interdependence over autonomous production. Experimental manipulation confirmed that B_{12} production is a community-level trait. Epiphytic Rhizobium and Caulobacter isolates produced B_{12} in culture, but co-cultivation with duckweed did not increase plant B_{12} and instead disrupted plant–microbiome performance. Cobalt supplementation, by contrast, increased bioavailable B_{12} up to fivefold without cost to growth, and reshaped endophyte composition, diversity, and core-community membership in species-specific ways. Our results show that B_{12} accumulation in duckweed is an emergent property of a cooperative, environmentally responsive microbiome, not the output of a single producer. This positions duckweed as a tractable model for cobamide-mediated microbial interactions and a promising platform for microbiome-guided B_{12} biofortification.

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Scientific Session

Microbiome & Interactions

Keywords

B_{12} biosynthesis Metabolic interdependence Endophytes

References

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Session Classification : Microbiome & Interactions I