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Potential cobalamin-producing *Wolffia globosa*-associated microbiome

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Potential cobalamin (vitamin B12)-producing *Wolffia globosa*-associated bacteria were investigated through shotgun metagenomic sequencing analysis. Taxonomic classification assigned microbiomes consisting of 5 phyla, 8 classes, 36 families, and 68 genera. High-quality metagenome-assembled genomes (MAGs) were assigned to *Allorhizobium* sp., *Alsobacter* sp., *Bosea* sp., *Bradyrhizobium huaxiensis*, *Brevundimonas* sp., *Methylophilus* sp., *Microbacterium* sp., *Mycobacterium* sp., *Neoroseomonas marina*, *Nevskia* sp., *Novosphingobium* sp., *Phenylobacterium* sp., *Pseudonocardia carboxydovorans*, *Rhizobium* sp., *Rhizorhabdus* sp., *Roseomonas* sp., *Sphingomonas* sp., and *Xanthomonas sontii*. Functional annotation across all MAGs revealed potential pathways related to aromatic compound degradation, cofactor and vitamin metabolism, serine and threonine metabolism, nitrogen metabolism, and other carbohydrate metabolic processes. Several MAGs contained complete modules of cobalamin biosynthesis including *hem*, *cob*, *cbi* genes responsible for corrin ring synthesis, cobalt transport, lower-ligand formation, and final cobalamin assembly. Interestingly, the definitive molecular marker for active B12 production, *bluB*, was identified in several MAGs. Subsequently, eight bacterial genera were isolated using culture dependent methods and three novel species have been proposed. Co-cultivation experiments are underway to understand the associated B12 production of *W. globosa* holobionts.

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References

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