

## The Microbial Factory Hypothesis: A Bacterial Consortium Drives Bioadhesion in *Posidonia oceanica* Seedlings

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The successful establishment of *Posidonia oceanica* seedlings in dynamic marine sediments critically depends on strong adhesion to substrate particles. As part of the PRIN-PNRR Project "ADHESPO – Exploring the underwater adhesion of *Posidonia oceanica* seedlings: ultrastructural, biochemical and molecular features" (Project Code: P2022TA248, CUP: H53D23007250001), we propose a novel hypothesis that a specific bacterial consortium acts as an essential "microbial factory," synergistically producing, reinforcing, remodeling, and curing a durable, mineral-reinforced bioadhesive at the root-substrate interface. As project results elucidated the role of the arabinogalactan proteins (AGPs) from the plant itself as primary adhesive matrix, the functional role of the associated microbial community remains largely unexplored. Integrating bacterial taxonomic data with functional protein inferences, recent insights into seagrass AGPs, and high-resolution imaging, we constructed a functional model defining a division of labor among five guilds: Architects (Pseudomonadales, Bacillales) excrete exopolysaccharides forming the foundational scaffold; Cement mixers (Desulfobacterales) mediate sulfate reduction, precipitating metal sulfides as natural geochemical cross-linkers; Finishers (Bacteroidales) remodel the matrix via CAZymes, optimizing porosity; Specialists (Corynebacteriales) introduce hydrophobic compounds for adhesion to diverse surfaces; and Syntrophs (Lachnospirales) ferment root exudates to fuel the consortium. Additionally, microbial enzymes (e.g., tyrosinases) are proposed to effect "glue curing" via quinone-mediated covalent cross-linking, analogous to mussel byssus formation. We hypothesize that successful adhesion of *P. oceanica* seedlings is an emergent property of the plant-microbe holobiont, and that disruption of this bacterial consortium leads to a significant decrease in attachment success. This model, developed within the ADHESPO project, establishes a "root pad microbiome" benchmark for comparing substrate designs and assessing microbiome shifts in future restoration efforts.