

Talking roots: a genotype-specific interactive dialogue between endophytic bacteria and wild and domesticated rice revealed by multi-omics

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Plant-microbe interactions are crucial for plant health and productivity, and root exudates play a central role in shaping these associations. Here, we investigated the bidirectional transcriptional and hormonal dialogue between rice and two endophytic plant growth-promoting bacteria using an integrated multi-omics approach.

We exposed *Enterobacter asburiae* RCA24 and *Kosakonia sacchari* RCA25 to root exudates from three rice genotypes: two cultivated varieties (*Oryza sativa* cv. Baldo and Vialone Nano) and the wild ancestor *Oryza rufipogon*. Bacterial RNA-seq revealed genotype-by-genotype interactions: *E. asburiae* RCA24 was able to distinguish between *O. sativa* varieties, and *K. sacchari* RCA25 responded more strongly to *O. rufipogon* exudates. Functional annotation highlighted differential expression of genes involved in central metabolism, stress response, and signal transduction among the cultivated and wild rice genotypes, suggesting that domestication has reduced the stimulatory capacity of rice exudates on beneficial microbes.

Hormonomic profiling of root exudates revealed genotype-specific phytohormone signatures. Gibberellins showed strong differentiation (PERMANOVA $R^2=0.53$, $p=0.006$), with GA_9 characterizing Baldo (956 pmol/L) and GA_{51} dominating *O. rufipogon* (577 pmol/L). Auxin profiles exhibited moderate genotypic variation ($R^2=0.39$, $p=0.034$).

To assess reciprocal effects, we also analyzed the rice transcriptome following bacterial colonization. The analysis revealed that bacterial colonization triggered tissue- and genotype-dependent responses. For *E. asburiae* RCA24, 3,813 differentially expressed genes were observed in Baldo stems, while for *O. rufipogon*, limited transcriptional responses were recorded.

Overall, these findings highlight the reciprocal and genotype-specific transcriptional crosstalk between rice and endophytic bacteria, demonstrating that *O. rufipogon* may be a reservoir of traits that could be exploited to optimize rice-microbe interactions that promote plant growth for sustainable agriculture.