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The underlying interactions in rhizosphere micro-ecosystem accelerate the premature senescence of *OsVHA-A1* mutant rice

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Abstract

Abstract Root-pathogen interactions are an important factor accelerating premature senescence of rice, however, few study have addressed the underlying interactions in rhizosphere micro-ecosystem. In this study, the *OsVHA-A1* mutant rice line displayed an early senescent phenotype associated with a special rhizosphere microbiome in contrast to the wild type. Moreover, the pathogen *Gibberella intermedia* had been shown to sharply increase when premature senescence occured in *OsVHA-A1* mutant. Using GC-MS analysis, we found the composition of root exudates from the senescent rice were different from the WT. In addition, transcriptome data revealed that *G. intermedia* preferred using sugars from root exudates that had been generated by fructose and mannose metabolism in the mutant. Furthermore, the *OsVHA-A1* mutant would display cell death in both physiological and molecular levels when suffering from pathogenic infection by *G. intermedia*. However, such fungi showed a weaker virulence for infecting the WT. Finally, *Bacillus* and *Burkholderia* could be used as antagonistic bacteria that could effectively alleviate the early senescent phenotype of *OsVHA-A1* mutant rice thereby improved its grain yield.
Keywords: *OsVHA-A1*, premature senescence, microbiome, *G. intermedia*, GC-MS, transcriptome, sugars, virulence, cell death, antagonistic bacteria

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