

Microbiome-mediated metabolic defence

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The destructive panicle disease rice false smut is caused by the biotrophic fungus *Ustilagoideia virens*. Disease-suppressive microorganisms present in rice panicles have now been found to mediate fungal resistance by modulating the metabolism of the host plant.

Plants establish intimate associations with complex communities of microorganisms that contribute to various aspects of plant health, including protection against pathogens¹. Global warming may exacerbate the likelihood of disease outbreaks^{2,3} – particularly panicle diseases such as rice false smut, which is caused by the biotrophic fungal pathogen *Ustilagoideia virens*⁴. Current strategies to combat this disease mostly rely on the use of synthetic fungicides, which pose potential risks to the environment and human health. Manipulation of the plant microbiome has emerged as a sustainable approach to promoting plant health and controlling diseases⁵. Although many studies have focused on the functions of the rhizosphere microbiota, our knowledge of the role of the phyllosphere microbiome is still limited. In *Nature Microbiology*, Liu et al. present a mechanistic understanding of the role of the panicle microbiome in manipulating rice metabolism to confer resistance to rice false smut resistance⁶.

During an outbreak of rice false smut in Zhejiang province, China, Liu and colleagues identified the emergence of a susceptible rice cultivar that displays resistance to *U. virens* infection. The authors initially confirmed that both diseased and disease-suppressive plants experienced the same pathogen pressure. They also verified that the rhizosphere microbial community was indistinguishable between diseased and disease-suppressive plants. However, a distinct panicle microbial community was identified in disease-suppressive plants. The panicles of these plants were enriched with keystone microbial taxa, including the bacterial genera *Lactobacillus* and *Leifsonia* and the fungal genera *Aspergillus*, *Nigrospora* and *Moesziomyces*. On the basis of these findings, Liu et al. hypothesized that these microorganisms could have a role in disease suppression. In addition, a metabolomics survey revealed a higher abundance of branched-chain amino acids (BCAAs) (including leucine, isoleucine and valine) in the panicles of disease-suppressive plants. Therefore, the authors subsequently centred their investigation on elucidating the putative mechanistic connections among the altered BCAA profile, the distinct panicle microbiota community and disease suppression.

Liu et al. found a positive correlation between the presence of keystone microbial taxa and higher levels of leucine (a predominant BCAA) in rice panicles. This correlation was not observed when rice panicles were colonized by non-keystone taxa. Along with elevated BCAA levels, the study showed that expression of a specific BCAA aminotransferase gene (*OsBCAT*) is repressed by these

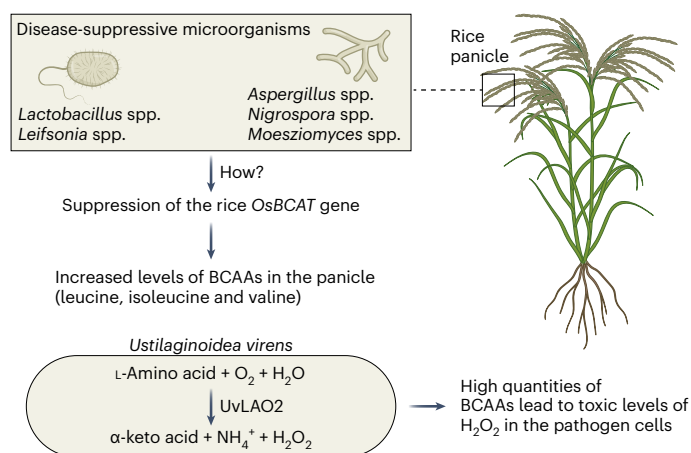


Fig. 1 | The phyllosphere microbiome triggers metabolic defences in rice and suppresses *U. virens* pathogenicity. Keystone microbial taxa that are present in the microbiome of rice panicles can modify host metabolism by repressing the expression of a specific BCAA aminotransferase gene (*OsBCAT*). Higher levels of BCAAs (primarily leucine) are generated in rice panicles of disease-suppressive plants. The catabolism of BCAAs by *U. virens* L-amino acid oxidase (UvLAO2) leads to the overproduction of H₂O₂, which triggers apoptosis-like cell death in the fungus and prevents *U. virens* infection.

key bacteria and fungi. Mutation of *OsBCAT* led to increased leucine levels in rice, which indicates that this gene negatively regulates the production of BCAAs in panicles. However, a central question remained concerning the contribution of BCAAs to disease resistance. This study further demonstrated that BCAAs exert a detrimental effect on *U. virens* cells by triggering apoptosis-like cell death through H₂O₂ overproduction, thereby impairing the pathogenicity of this fungus (Fig. 1). The authors concluded that these key microbial taxa modulate BCAA levels by manipulating *OsBCAT* expression, and thus contribute to disease resistance.

To investigate the applicability of these results in real-world scenarios, the authors conducted field trials across various rice producing-regions of China. Preliminary results indicate a synergistic effect between BCAAs and chemical fungicides that allows a reduction in fungicide dosage by 50%, while maintaining comparable efficacy to higher concentrations of fungicides. A sustainable approach to crop protection that involves the use of BCAA-eliciting microbial agents or the application of exogenous BCAAs could thus greatly contribute to reducing our reliance on chemical fungicides.

To date, several studies have shown that many plant-associated microorganisms can confer disease resistance¹. However, much of this research remains descriptive and leaves the precise mechanisms that underlie the effects of the phyllosphere microbiome on plant health relatively unexplored. The study conducted by Liu et al. represents a notable exception by providing mechanistic insights

into the involvement of the panicle microbiota in plant protection. Despite their substantial efforts, how exactly these protective microorganisms suppress the expression of the *OsBCAT* gene to modulate BCAA levels in rice panicles remains an open question. Microbial pathogens are well-known for their ability to interfere with host immunity and metabolism through specialized effector proteins and metabolites⁷. Although emerging research indicates that non-pathogenic members of the microbiota can also modulate their plant hosts^{8,9}, the molecular mechanisms that are involved in this process are still largely unknown.

Plant microbiome research is transitioning from descriptive surveys to mechanistic and causative studies. Recent studies have revealed examples of both direct (by microbiome–pathogen interactions) and indirect (by microbiome–plant interactions) disease protection mediated by the microbiome¹⁰. The study by Liu et al. exemplifies how disease-suppressive microorganisms can act indirectly to confer disease resistance through the manipulation of the metabolism of their host. In the future, it will be interesting to explore the limits of the mechanism discussed in this paper and investigate whether microbiota-mediated modulation of BCAA levels can also confer resistance against fungal pathogens in other plant species.

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Competing interests

The authors declare no competing interests.