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Plant Biology

The seed's hidden arsenal: using bacteria to defend against disease

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ABSTRACT

Crop diseases are currently on the rise worldwide due to changes in global climate and farming techniques. We have discovered what is hidden in the cereal plants' seeds, and how it makes them more resistant to infection by bacterial pathogens. This opens up a new way to improve disease resistance or sustainable agricultural production.

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Stable cereal production plays an important role in maintaining a food supply for the world's growing population. However, seed-borne bacterial diseases can limit crop production and quality. This has been aggravated in recent decades by changes in both the global climate and modern farming techniques. Chemicals have typically been used to prevent disease, but manipulation of the plant itself has been deemed to be a promising and more environmentally friendly alternative. While disease resistance has been thought to be determined primarily by a plant's innate immune system, recent evidence has also shown that a plant can host microbiota, like fungi or bacteria, that affect the plant's growth, development, and health. But can the plant's disease resistance be shaped by these resident microbiota? And if so, can this be passed on? These intriguing questions remain to be explored.

By observing a variety of rice seeds from different geographic locations, we observed that rice seedlings of the same cultivar (Zhongzao 39) can be separated into disease-resistant and -susceptible groups in a controlled environment. Distinct seedlings of this cultivar were shown to withstand infection by *Burkholderia plantarii*, a toxin-producing seed-borne bacteria, known as a pathogen.

Classically, the relationship between host plants, pathogens and environmental conditions (a 'disease triangle') determines whether a pathogen can successfully infect its host plant. But if, in this recent study, we use the same cultivar, the same pathogen, and the same controlled environment, why did we have disease-resistant and -susceptible groups? We were able to exclude the impact of microbiota from the seed surface, and so we hypothesized that microbiota inside the seeds themselves might be responsible for the distinctive occurrence of disease resistance.

To test our hypothesis, we analyzed the rice seed microbiota, and found that the bacterial genus *Sphingomonas* was more common in the disease-resistant seeds. *Sphingomonas melonis* was then obtained from disease-resistant seeds by simulating infection by the pathogen. We found that it was the key agent sustaining the disease-resistant phenotype and could also confer disease resistance to the disease-susceptible plants. More interestingly, *Sphingomonas melonis* was shown to be passed down through three successive plant generations while maintaining its beneficial function.

We were also curious as to how *Sphingomonas melonis* confers the disease resistance. We found a small chemical molecule secreted by *Sphingomonas melonis*, anthranilic acid, was able to interfere with pathogen infection. To prove anthranilic acid was important, we located the main gene in *Sphingomonas melonis* that controls anthranilic acid biosynthesis and knocked it out. The modified *Sphingomonas melonis* lost the ability to produce anthranilic acid, and we found that it could no longer confer disease resistance.

We then aimed to find out how anthranilic acid counteracts the pathogen infection. We found that anthranilic acid was able to block the pathogen signaling pathway, which is needed for the pathogen to infect the plant.

But could we control *Sphingomonas melonis*? Is it affected by the environment? If so, how could we make sure the rice takes it up? Answering these questions was very important to understand how the host and its microbiota develop. We searched for clues in carefully collected climate data and local archives about soil properties and chemical use. Fortunately, we found that while chemical use was a highly prevalent agricultural practice in these rice production areas, the actual chemicals applied did differ. We analyzed different soils and found that the *Sphingomonas melonis* population increased in regions that were exposed to certain herbicides. We then ran simulations that showed that *Sphingomonas melonis* enters rice after applying a specific herbicide mixture. This could help the rice to thrive under these conditions, while simultaneously improving the host's health.

Our overall findings reveal that the resident microbiota hidden in plant seeds can provide disease resistance that is passed from generation to generation. Moreover, our study may help develop alternative strategies to breed crops for disease resistance. Finally, improving our understanding of the how host plants and their seed microbiota evolve together in response to their environment might provide promising solutions for crop production threatened by prevalent bacterial diseases.