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Engineering the Plant Microbiota to Protect against Diseases

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The physiology and growth of plants are strongly influenced by their associated microbiomes. In turn, the composition of the plant microbiota is flexible, responding to the environment and the state of the host and raising the possibility that it can be engineered to benefit the plant. However, technology for engineering the structure of the microbiome is not yet available. Here we show that glutamic acid reshapes the plant microbial community and enriches populations of *Streptomyces*, a functional core microbe in the strawberry anthosphere. Similarly, in the tomato rhizosphere, treatment with glutamic acid increased the population sizes of *Streptomyces* as well as those of Bacillaceae and Burkholderiaceae. At the same time, diseases caused by species of *Fusarium* were significantly reduced in both habitats. Plant resistance-related genes were not activated, suggesting that glutamic acid modulates the microbiome community directly, rather than activating the host's own protective mechanisms. Much is known about the structure of plant-associated microbial communities, but less is understood about how the community composition and complexity are controlled. Our results demonstrate that the intrinsic level of glutamic acid in planta is associated with the composition of the microbiota, which can be modulated by the external supply of a stimulant such as glutamic acid.