## Assembly and structure of root-associated microbiomes involved in strawberry health and nutrition

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## Background

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Manipulation of root-associated microorganisms is a promising alternative to reduce agrochemical inputs and the environmental impacts associated to the management of crop biotic and abiotic stressors. For this, understanding the factors that drive the assembly of beneficial microbiomes is essential. Plants recruit microorganisms from the soil environment to the soil immediately around the roots (rhizosphere) which then may colonize the roots (endosphere) providing the last barrier of plant defense against pathogens. Strawberry cropping systems rely heavily on soil fumigants for the reduction of potentially devastating soil-borne pathogens. Restrictions in pesticide use have fostered robust breeding efforts aimed at improving strawberry cultivar tolerance to soil-borne fungal pathogens. Several cultivars exist that are tolerant to some of the major diseases, yet the resistance mechanisms are still unknown. Objective

Here we assessed how strawberry cultivars showing different vigor and resistance against pathogens, recruit microorganisms from the soil environment.

We hypothesized that the endosphere and rhizosphere have distinct microbial communities which are shaped over time due to the influence of the surrounding soil after the plants are transplanted. This process is altered in the presence of soil borne pathogens to trigger resistance mechanisms.

ated through sieving of	· Lyophilization Grinding	<ul> <li>Illumina MiSeq</li> <li>Sequencing of targete</li> <li>V4 region of the 16S</li> <li>rRNA</li> </ul>
ts uning of ts with 10% ach solution autoclaved er to isolate osphere roorganisms	<ul> <li>DNA isolation in roots, rhizosphere and bulk soil using Quiagen Powerlizer PowerSoil kit</li> </ul>	<ul> <li>Reads summarized to Amplicon Sequence Variants (ASVS), filtered for chimeric sequences using DADA2</li> <li>SILVA database used for taxonomy identification</li> </ul>



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