

Recently novel strategies based on the use of RNA interference (RNAi) are rising up in the crop protection scenario. Spray-induced gene silencing (SIGS) is a potential strategy for plant disease management, whereby nucleotide sequence-specific double-stranded RNA (dsRNA) can be sprayed onto a crop and it could represent a potential alternative to conventional fungicides. SIGS could give rise to transient silencing without producing genetically modified organisms (GMO) neither requiring transformation method for plants. Nevertheless, the instability of naked dsRNA sprayed on plants is a major challenge towards its practical application. To overcome this limiting aspect, nanocarriers for dsRNA delivery can be used to extend its stability and durability. We previously shown that topical application of a *BcBmp3*-dsRNA construct mediated both *in vitro* and *in vivo* knockdown of *B. cinerea* transcripts on *Lactuca sativa*. Our dsRNA construct was loaded on non-toxic, degradable, layered double hydroxide clay nanosheets for a sustained release on the leaf surface under ambient conditions. We prepared LDH by a modified non-aqueous method and the *BcBmp3*-dsRNA/LDH optimal ratio was assessed by the gel retardation assay. Lettuce plants were sprayed with either water, LDH, or *BcBmp3*-dsRNA/LDH complex on day 0. *B. cinerea* was inoculated using a conidial suspension 7 days after spray treatment. A significant reduction of gray mould severity was observed as assessed by a rating scale and by calculating the McKinney index. Our results suggest a possible development of SIGS approach for the management of *B. cinerea* disease, although further experiments are needed to fully understand this potential.

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Microbiome composition provides a powerful tool to elucidate the epidemiology of postharvest diseases of apples

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Apple fruits are susceptible to postharvest rots caused by different fungal genera. Some emerging diseases, such as white haze and dry lenticel rot, result in reducing fruit quality and their epidemiology is poorly understood. In recent years, metabarcoding has been extensively used to characterize microbial complexity in apple fruit, based on cultivar, tissue and phenological phase. In this work, we sequenced the ITS2 and V4 regions for both epiphytic and endophytic samples of apple cultivars ‘Opal’ and ‘Ambrosia’ to investigate the composition of fungal and bacterial communities, at different developmental stages in the orchard, at storage and shelf-life. Bioinformatic analyses of sequencing data showed significant differences in alpha diversity in the endophytic and epiphytic fungal and bacterial communities in the two apple cultivars. The differences were particularly pronounced for the fungal community samples from similar tissues over the same time points. Compositional and disease incidence data indicate that *Golubevia* spp. is the main causal agent of white haze and its presence in fruit tissue became significant from September. *Ramularia* spp., the causal agent of dry lenticel rot, is shown to have a relatively high abundance early during fruit development as part of endophytic microbiota, suggesting the earlier presence in the fruit tissue. This finding provides interesting information about the epidemiology of some postharvest pathogens, which is important to develop adequate management strategies for apple fruit pathogens.

Improvement of nutraceutical value of parsley (*Petroselinum crispum*) upon field applications of beneficial microorganisms

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Parsley (*Petroselinum crispum*) is an important aromatic herb that has gained importance in food and cosmetic industry, and it is used as medicinal plant due to the presence