

**Title:**

The search for fire blight antagonists: a large-scale survey of apple blossom microbiomes across Switzerland

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**Abstract (300 words maximum):**

Fire blight is a devastating disease of apple trees caused by the bacterium *Erwinia amylovora*, which infects trees through their blossoms. Since the banning of antibiotic applications in 2016, control strategies have become very limited. Applications of microbial antagonists may provide promising alternatives for the development of novel, sustainable control strategies. However, their efficacy is often unreliable with great variations observed across different conditions and years. Besides environmental factors that directly impact the activity of biocontrol agents, variations in efficacy may also result from differences in the native apple blossom microbiomes. Moreover, apple blossom microbiomes, which have not been surveyed across Switzerland, may also represent a source of new biocontrol strains, as shown in a previous study on a single, low-input orchard in Wädenswil. To determine the distribution of the potential fire blight antagonist *Erwinia tasmaniensis* identified in that study, and to characterize the bacterial diversity in apple blossoms in general, a survey was conducted comprising 370 blossom samples from 37 sites across all Swiss apple growing regions. In total, 32'051 bacterial amplicon sequence variants (ASVs), which clustered into 9'530 operational taxonomic units, were recovered. The apple blossom microbiomes were dominated by variable bacterial families including for example Enterobacteriaceae, Pseudomonadaceae, Burkholderiaceae, and Sphingomonadaceae. Five years after the previous study, the dominance of *E. tasmaniensis* was confirmed in the low-input orchard in Wädenswil with relative abundances of 65.7-87.3%. *E. tasmaniensis* was, with more than 1% relative abundance, also among the most abundant taxa in six other sites but did not reach the same dominance. Taken together, these studies show the potential for microbiome surveys to open new avenues in biocontrol development. Further research is required to determine factors structuring the large bacterial diversity revealed in this survey, and to assess effects of the different apple blossom microbiomes on fire blight control.