

Investigating the German hop virome

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Germany has more than 20,600 hectares of hop-cultivated area and is the second biggest hop producer in the world. Many pests and pathogens threaten hop production. These can cause severe reduction in hop yield and quality.

In summer 2019, citrus bark cracking viroid (CBCVd) was detected for the first time in Germany. CBCVd is known as a pathogen of citrus plants that causes mild and often tolerated infections of different *Citrus* species, whereas it causes massive damages to hop plants.

The project “HopfenViroid” is addressing practical and scientific questions regarding CBCVd. As a part of this project, high-throughput sequencing (HTS) is being applied to investigate the viral diversity in German hop fields. In 2021, we have started with a pilot study, and 90 samples were collected from three fields in Hallertau (Southern Germany). The samples were collected from fields where CBCVd was detected previously. The samples from each field contained: 10 hop samples, 10 non-hop plants within the field, and 10 non-hop outside the field. Samples were pooled and double-stranded RNAs extracted as a viral and viroid enrichment approach (Gaafar and Ziebell 2020) followed by Illumina sequencing. Bioinformatic analysis was performed with Geneious Prime software (version 2022.1.1). Raw reads were normalized and *de novo* assembled. Assembled contigs were mapped to a local database of virus and viroid sequences downloaded from NCBI. All identified viruses and viroids in hops across the three fields were previously described as hop pathogens. In 2022, this study has been extended to cover three different hop-growing locations in Germany. A comprehensive understanding of the viral diversity in German hops is expected by the end of this study.