

## **Investigations of fungi as potential cause of sea buckthorn dieback in Northern Germany**

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Sea buckthorn, *Hippophae rhamnoides*, is a diecious, hard wooded shrub, which is grown in North-East Germany. The berries are characterized by high contents of vitamin c and antioxidants. Therefore, applications are pharmaceuticals, cosmetics and food products like juices or marmalades. Further, wild plants grown along the coastline of the Baltic Sea are of relevance for erosion protection and also form an important habitat and food source for various insects and animals. Since 2015, reports on the occurrence of sea buckthorn dieback, both in wild plants and plantations, have been accumulating, leading to serious ecological and economic consequences. Up to now, the cause of the plant death remains unexplained.

A joint project, HippRham, started in November 2020. It was established investigate the cause of sea buckthorn dieback and to develop practical control strategies. The project partners are Landesforschungsanstalt für Landwirtschaft und Fischerei Mecklenburg-Vorpommern (LFA), Landesamt für Landwirtschaft, Lebensmittelsicherheit und Fischerei Mecklenburg-Vorpommern (LALLF), and JKI/OW. Our focus will be on fungi in context of sea buckthorn dieback. In addition, phytoplasmas and viruses will also be subject of investigations. A culture-dependent isolation approach and a culture-independent sequencing approach will be used to study the fungal community. Later, inoculation experiments are planned. So far, a total of 185 fungi have been isolated from root and shoot material of different varieties and origins. ITS-PCR and Sanger-Sequencing will be applied for identification. In addition, a method for DNA extraction from sea buckthorn plants was established.

In prior work, total nucleic acids were extracted from leaf samples of symptomatic plants and analyzed by high-throughput sequencing (NextSeq). A total of 2 x 36,498,078 reads were generated and *de novo* assembly resulted in 120,723 contigs. Blast analyses of contigs gave hits to a mycovirus, botrytis cinerea mitovirus 2 (RdRp gene), and black currant leaf chlorosis associated virus (50 – 75 % identity). Next steps will be to determine the complete sequence of both potential viruses.