

S1-O8. RNA-Seq in *Betula* species: Berlin – Bordeaux collaboration contributes to the first assessment of the birch virome. Artemis Rumbou¹, Thierry Candresse², Armelle Maraix², Sebastien Theil², Maria Landgraf¹, Susanne von Bargaen¹, Carmen Büttner¹

¹Humboldt-Universität zu Berlin, Division Phytomedicine, Lentzeallee 55/57, 14195 Berlin, Germany

²UMR 1332 BFP, INRA, Univ. Bordeaux, 33882 Villenave d'Ornon, France

The scientific exchange aimed to contribute to the investigation of the birch virome initiated at the Phytomedicine laboratory, Berlin. It was intended to analyse RNA-Seq data from birch samples, some originating from symptomatic trees affected by the “birch leaf-roll disease”, and some from non-symptomatic trees. It was also aimed to determine the taxonomic classification of the new viruses and to complete the genomic information missing from the novel viral genomes. The visit was performed at the laboratories of INRA Bordeaux and lasted one week - from 26th to 30th October 2015.

NGS data processing and analysis were performed using CLC Genomics Workbench. Standard PCR reactions, 5'RACE-PCR and Long-Distance-PCR assays were performed to complete the genome sequences. The analyses led to the genomic characterization of a novel virus strongly associated with the disease, which represents a new member in the genus *Badnavirus*, family *Caulimoviridae*, and is the first badnavirus found to infect birch. The novel virus is tentatively named as Birch leaf roll-associated virus (BLRaV) and the new findings have been published (Rumbou et al., 2018). Furthermore, the birch virome of five different trees was characterized and different patterns of viral infections were determined. Interestingly, the virus complex observed in each sample exhibits a high diversity in viral species and virus variants. Among the identified viruses, a novel carlavirus was characterized, which was tentatively named as Birch carlavirus (BiCV) and its full-length genomic sequence has been deposited in the GenBank database (Rumbou et al., publication under preparation).

The scientific visit in Bordeaux, apart from allowing gaining new results, offered the opportunity to establish a close collaboration among the scientists involved. This network built thanks to the COST Action FA 1407 – DIVAS sustains a creative communication in order to prepare further common publications and to proceed with recent HTS dataset analyses.

Rumbou A, Candresse T, Maraix A, Theil S, Landgraf M, Von Bargaen S, Büttner C, 2018:

RNA-Seq in *Betula* species: Berlin – Bordeaux collaboration contributes to the first assessment of the birch virome.

Oral Presentation: **S1-O8.**

COST-DIVAS Meeting "HTS Technologies for the study and diagnostic of plant viruses",
26.-30.11.2018, Université de Liège, Belgium, p. 24

