Sequencing the genome of a European *Diplocarpon coronariae* strain

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Diplocarpon coronariae ((Ellis and Davis) Wöhner and Rossmann) is a fungal pathogen that causes apple blotch disease and occurs in meadow orchards as well as in organic and integrated fruit cultivation. The fungus has spread in Europe since the last 15 years. Only a few information is known about the biology and pathogenicity of the organism. A valuable source on infection mechanisms can be provided e.g. by genome sequences. Recently, the sequence of a Chinese isolate (NL1) of *D. coronariae* was published. The sequence information of this strain indicates that secondary metabolites such as toxins and inhibitor proteins play a role in host colonization. Currently, no sequence of a European isolate exists.

In this study we sequenced a *D. coronariae* strain (Fu0034) obtained from Dresden, Germany. After isolation from an infected leaf and cultivation on PCDA media, the DNA was isolated from grown mycelia after three weeks. The DNA was sequenced with an Illumina NovaSeq sequencer (NovaSeq 6000 S4 PE150 XP). 21,037,227 raw reads were obtained. After cleaning and mapping of high quality reads a total of 94.1% reads were aligned to the reference genome NL1 with 91x coverage. GATKs Haplotype caller detected 477,451 variants (445,890 SNP, 31,561 InDel). A consensus sequence of Fu0034 was calculated with the software bcftools consensus using the variant information and the reference sequence NL1. The final draft of Fu0034 contained 589 contigs with a total length of 50,283,537 bp and a N50 of 231,484 bp. The BUSCO analysis on genome completeness resulted in 98.4%.

The results of this study provide a basic tool for studying the genome structure, and sequence variation of a European pathotype from the apple blotch pathogen *D. coronariae.* Future analysis like structural and functional genome annotation will give deeper insights into the pathogen biology and host colonization mechanisms.