

Complete Genome Sequence of *Spongospora subterranea* from North America

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Obtaining high-quality nucleic acids of *Spongospora subterranea* is difficult due to durability of the sporosori and the obligate pathogen life-style. In this study, root galls were collected from a potato plant ('Russet Burbank'), and Oxford Nanopore long-read sequencing was completed using genomic DNA isolated from sporosori. Illumina short-read sequencing was also completed using genomic DNA from sporosori collected from pustules on tubers from a single commercial potato field in the same region. Polishing long-reads with short-reads resulted in a 31.51 Mb high-quality genome with GC content of 45.7% assembled from 346 scaffolds. The genome was predicted to have 10,325 protein-coding genes, including 321 potential fungal effectors, 700 signal peptide proteins, 135 carbohydrate active enzymes, 1981 KEGG assigned genes, and 2660 COGs. This *S. subterranea* genome resource provides a basis for increased understanding of international populations of the pathogen, and knowledge to assist development of new management strategies for powdery scab and potato mop-top virus of potato.