Comparative genomics of *Spongospora subterranea* f. sp. *subterranea* isolates for effector mining

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Breeding potato varieties resistant to *Spongospora subterranea* f. sp. *subterranea* (*Sss*) is impaired by phenotyping methods, which can give variable results due to environmental conditions, inoculum instability, and isolate-specific tolerance/resistance in host lines. Screening based on effector response ("effectoromics") could replace difficult phenotyping assays, and has been used to identify *R* genes in potato that confer resistance to *Phytophthora infestans* and *Synchytrium endobioticum*. Effectoromics relies on potential effectors identified in predicted secretomes. For *Sss*, however, no specific effector signatures are known. This study aims to identify new effectors and corresponding signatures, and select secretome genes which could have resulted from previous *Solanum*/*Sss* interactions and are under diversified selection pressure. To capture the required genomic diversity for selection, *Sss* genomic DNA was prepared from sporosori from more than 20 different isolates originating from 15 countries across five continents. These samples were assessed for *Sss* DNA proportions using Taqman-qPCR, and were subjected to Illumina paired-end sequencing. Initial comparison of the isolates showed at least two groups, one being very different from the current reference genome (SSUBK13), as indicated by regions that were either highly polymorphic or absent in this group when mapped to the reference. To help assemble polymorphic regions through *de novo* assemblies, two isolates representing the two groups were selected for long-read Nanopore sequencing. Characteristics of their assemblies will be described, including insights into genome-wide diversity. There is potential to develop an *Sss* pangenome knowledge base as a resource for plant pathology and potato breeding research.