

Global Population Genetics and Phylogeny of *Spongospora subterranea* f.sp. *subterranea* the Cause of Powdery Scab of Potato

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Spongospora subterranea f. sp. *subterranea* (*Sss*) is a soilborne biotrophic protozoan pathogen, which causes powdery scab of potato (*Solanum tuberosum*). This is an economically important disease, causing severe losses in all types of potato production, and in most potato growing regions of the world. *Sss* is capable of long term survival (many years) by producing aggregations of thick walled resting spores in sporosori. The resting spores are resistant to treatments commonly used to control soilborne plant diseases, making it very difficult to control powdery scab. To control the disease, resistant potato cultivars are important. Usually breeders screen new germplasm lines against a range of pathogen strains representing the known genetic diversity to select for the most durable resistance. In the case of *Sss*, currently this type of screening is not possible, because little is known about its genetic structure and diversity of the pathogen, and its life cycle is not completely understood.

Plant pathogens are capable of constant adaptation to changes in agricultural ecosystems. Locally occurring virulent pathogen mutants can infect plants in monocultures, increasing in frequency through selection and rapidly spreading over large areas and continents. Effective control strategies must therefore target pathogen populations rather than individuals. Knowledge on the population genetic structure of a pathogen can help to determine which factors play major roles in pathogen evolution, and how these evolutionary forces interact to determine the genetic composition and evolutionary potential of pathogen populations in agricultural ecosystems.

The present research aims to determine the amount and geographical distribution of genetic variation among and within collections the of *Sss*. Specific microsatellite markers were obtained and applied to field populations of the pathogen from each continent. The actin and ITS regions of the *Sss* genome were sequenced, to examine the pathogen's evolutionary history, and potential to evolve.

In this study, the distribution of genetic diversity within and among populations was analyzed to identify patterns of migration and to expose the underlying structures of recombination. Recombination frequency was analyzed using statistical tests, which can detect deviations from the expected frequencies which lead to gametic disequilibrium (or linkage disequilibrium). Additionally, the common presence of rare alleles was used to calculate recent and historical gene flow between and among populations from many different worldwide locations.

Our results consistently showed that world populations generally have low genetic diversity, in contrast to South American populations, which have significantly greater diversity.

Furthermore, there is only little recombination and no evidence of historic or recent migration. Of the worldwide populations, only collections from Malta are an exception, because these seem to be closely related to South American Sss, a result which we still have to examine in greater detail.

The findings are consistent with historic and recent trade maps and with results already obtained for other potato pathogens, such as *Phytophthora infestans* (potato late blight) or *Burkholderia solanacearum* (black leg of potato). All show little diversity worldwide and a much greater diversity in South America. Our hypothesis is that the origin of Sss is most likely to be South America, and that quarantine measures should to be taken to avoid further introductions of Sss from South America to the world. Introduction of new pathogen strains might lead to greater diversity, more recombination and to more virulent pathotypes causing increased disease.

This study is the first thorough population genetic characterization of a plasmodiophorid pathogen, and provides new information on the global population structure of *S. subterranea* f.sp. *subterranea* infecting potato.