

Justification for tackling scientific problems by the proposed project results presumably from the urgent need of understanding genome-wide adaptation of European F.g. s.s. FHB of wheat and barley is a major disease in Europe, with F.g. s.s. being the main causal agent. Notably, F.g. s.s. was recently ranked fourth in a top 10 fungal plant pathogen list. FHB not only directly affects the grain production but also poses a severe threat to plant, animal, and human health due to the accumulation of mycotoxins on kernels and wheat products. Current state of knowledge lacks data on evolutionary processes and genomic features contributing to population divergence of F.g. s.s. outside North America. The innovative nature of the planned research results from uncovering population structure and identification of genomic targets of selection within European F.g. s.s.

We believe that the expected results of the planned studies will have significant impact on the development of the research fields such as phytopathology, plant breeding, fungal genetics and biology, etc. We predict that our planned results will provide previously uncovered insights into evolutionary processes and genomic features contributing to population divergence in F.g. s.s. and will highlight candidate genes for future functional studies of pathogen specialization.

The regional differences in Tri genotype frequency in Europe suggest the existence of substructured meta-population exhibiting presumably evidence of gene flow. We hypothesize that evolutionary trajectory of European population(s) of F.g. s.s. is different from that observed in other geographic locations and more comprehensive confirmation of the above hypothesis could be achieved through identification of more genomic traits characterizing different populations. We hypothesize that European F.g. s.s. consist of single recombining metapopulation consisting of 15ADON genotypes and other co-occupying local populations of 3ADON and NIV producers exhibiting limited gene flow. Co-existence of these populations for sufficient time, but genomic insight is needed to elucidate different evolutionary trajectories taken by these populations. We believe that the results of such studies will provide insights into the evolutionary processes and genomic features contributing to F.g. s.s. population divergence in Europe.

Synthetic fungicides, principally from the azole class, play a prominent role in controlling *Fusaria* in the field. However, variation between *Fusarium* isolates in sensitivity to azoles has been shown. There is a need to better understand the basis of adaptation to azoles in F.g. s.s., given the limited options for effective disease management, and the critical role of azoles in limiting the losses caused by these fungi. We hypothesize that the predomination of 15ADON genotypes in Europe might be associated with the increased resistance to widely used fungicides and/or better adaptation potential to azoles. To confirm it, we will predict degree of adaptation to tebuconazole of a range of European strains. We are going to link these results to genomic data to reveal correlation between the genomic traits and fungicide adaptation. RNA-Seq analysis are also planned to reveal transcriptomic differences between the strains differing in fungicide adaptation.

The goal of the work is to assembly genomes of different F.g. s.s. strains. 105 F. g. s.s. strains from cereal crops recovered all over the Europe, North and South America, Africa and Asia will be included into analyses. The assembled and annotated genomes of F.g. s.s. will be used to achieve the major goals of the planned studies including: detection of SNP (Single Nucleotide Polymorphism), establishment of differences in genome-level demographic structures of European populations of F. g. s.s., detecting selection in fungal populations, comparison of gene content among strains, functional annotation and enrichment analyses, assessing differences in adaptation of fungal strains to tebuconazole and transcriptome analyses.