Flax is a valuable crop plant and one of the few crops that gives two types of products – fibre and oil. However, flax cultivation is constantly limited by various environmental stresses, with fungal infections causing the greatest yield losses. One of those pathogenic fungi is *Fusarium oxysporum* f. sp. *lini* (Foln), which causes *Fusarium* wilt in flax.

Better understanding of the interactions between the plant and the fungus during infection may enable more effective protection of crops against pathogens. It is important not only to understand the plant's defense mechanisms but also the pathogenic mechanisms of the fungus, as an evolutionary "arms race" keeps ongoing in the crop fields. For every resistance protein in the plant, the fungus will respond with its own protein that aids the infection. An example of such fungal protein is Secreted In Xylem (SIX), with 14 families detected in other fungi of the *Fusarium oxysporum* species. These small proteins are secreted in the plant's xylem during infection. They play a crucial role in pathogenicity and the fungus's ability to overcome host plant resistance. The presence of different sets of SIX genes also allows the classification of *F. oxysporum* into races. In the case of *F. oxysporum* f. sp. *lini*, the SIX genes present in the genome and their function during flax infection have not been fully investigated.

The project will analyze the genomic sequences of *F. oxysporum* f. sp. *lini* to identify all present SIX genes. Additionally, the expression of these genes will be examined at different stages of flax infection. Their role in pathogenicity will then be experimentally tested by silencing of SIX genes in *F. oxysporum* f. sp. *lini* and analyzing the impact of these changes in the flax infection process. Environmental strains of *F. oxysporum* f. sp. *lini* from Polish flax fields will also be studied to check their pathogenicity. Sets of SIX genes in their genomes will be identified and compared. This will help understand whether variations in SIX genes in different strains of *F. oxysporum* f. sp. *lini* affect their pathogenicity.

The implementation of the project will contribute to better understanding of the pathogenic mechanisms of *F. oxysporum* f. sp. *lini*, which in the long term may help in developing more effective methods of protecting flax against *Fusarium* wilt. Additionally, detecting differences between sets of SIX genes in environmental strains of *F. oxysporum* f. sp. *lini* may enable their classification into races, increasing knowledge about the environmental diversity of this pathogen.