

Plant parasitic nematodes are responsible for substantial crop loss in Polish and in global agriculture worth of 100 billion Euro annually. They infect many plants important in food and biofuel production, in particular: potato, beet root, maize, soybeans and rapeseed. The nematodes feed on roots leading to water and nutrients deficiency, and indirectly, creating an entry point for other pathogenic organisms. The nematodes induce development of specialized feeding structures for larvae and adults called syncytia. Their development involves fundamental genetic and metabolic reprogramming, as well as attenuation of defense response. The ultimate effect of this reprogramming is synthesis of proteins having specific functions which in turn may be fine-tuned by post translational modifications, including phosphorylation.

With spectacular progress in mass spectrometry based protein identification methods and quite few reports on protein dynamics and their phosphorylation in nematode infected plants we plan to study proteome dynamics in Potato Cyst Nematode (PCN) induced syncytia on tomato roots in different time points. Previous studies of parasite-host plant interactions, in which our team participated, show gene expression dynamics on transcriptional level, assuming it reflects changes in protein activity as well. We want to verify this simplified image in our experiments. They will lead to the discovery of new, key processes in the nematode pathogenesis or at least broaden the current knowledge. In addition proteins of nematode and host plant will be studied in parallel. Very important is the proper selection of our experimental model: PCN and tomato. PCN is a persistent, very difficult to control pathogen of solanaceous crops in Poland, being on the quarantine list. Tomato, on the other hand, is a very important crop plant, quite easy to work with in the lab and closely related to a potato. Very important advantage of this experiments is they focus on susceptible and resistant to PCN tomato lines what will allow to follow processes linked with resistance genes. These studies will result in identification of new targets for future breeding of crop plants with broad nematode resistance. Importantly such molecular breeding may involve modern targeted mutagenesis, which is much less controversial method than classical recombinant DNA techniques. Long lasting and broad pathogen resistance, not limited to certain pathotypes, is a key element of integrated biomass production, gold standard in agriculture of all developed countries.

Submitted project uses the most advanced tools used in genomics and proteomics which are based on the whole genome sequences and allow to study dynamics of thousands of proteins. Applicant's team has experience in this type of research what can be proven by publication record, established collaborations as well as the advanced computer hardware and fully laboratory. The applicants are collaborators of the international scientific networks and are aware of current progress in related fields of research. This project raises an issue not only important for the Polish agriculture but fosters international collaboration. Summing up, analyzing qualitative and quantitative proteome of tomato and PCN at different stages is a basic research project with a huge potential to transform the knowledge to the new strategies for improving crop resistance.