Clubroot is a plant disease occurring in different crops like oilseed rape, cabbage, and cauliflower, **and is becoming a major problem for growers in Poland, Germany, Canada and many other countries because reductions in the yields of affected crops, in the most severe cases, can reach up to 90%**. The main symptom of this disease is an amorphous growth and thickening of the roots known as galls which interfere with the uptake of water and nutrients from the soil. One of the best solutions to control this disease is to grow resistant plant varieties that can restrict the pathogen growth and survive in infested fields. Unlike the immune system of humans and vertebrate animals, plants cannot develop immunity to pathogens but need to inhereit it, which means that is important to have parentals resistant to Clubroot, in order to produce seeds that possess the same characteristic. To identify which variants present in the DNA of the resistant plants may be responsible for the resistance to Clubroot, we should compare the DNA sequences of varieties of the same species of plant, in order to associate sequences or genes that are predominantly present in the resistant varieties and absent in the susceptible ones. Through these kinds of comparisons, some segments of DNA have been identified and used in breeding programs to produce resistant plant varieties; however, recent studies of the pathogen populations suggest they are evolving to overcome this resistance.

It is thought that the best solution to prevent this disease is to develop new resistant plant varieties using newly identified parentals, and at the same time, **it is also important to improve our understanding of how the plants may be defending themselves from *Plasmodiophora brassicae*. In order to elucidate how the plants can recognize the presence of the pathogen and activate a defense response, our research group performed a genetic association study with a plant named Arabidopsis or Thale cress, that is affected by Clubroot disease as well.** Arabidopsis is the most important plant in the research community and is one of the most studied plants around the world, because of its size, speed of growth and some genetic characteristics that are desirable for genetic studies. Moreover, there are plenty of freely available tools and germplasm that allow performing genetic studies much faster and with much more precision than in any other flowering plant and most of the biological concepts developed initially in Arabidopsis had been extended or transferred to other economically important plants.

As a result of the mentioned studies, we identified the sequence of a gene that we called *RPB2* (Resistance to *Plasmodiophora brassicae* 2), which is very similar to other molecules involved in plant immunity described before. Despite our evidence strongly associating *RPB2* with resistance, only the inactivation of this gene in resistant Arabidopsis plants will provide us the necessary information to confirm that this gene is responsible for resistance to Clubroot. In order inactivate or knock down the function of *RPB2*, we will use a methodology for genome editing known as CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats/ CRISPR associated protein), this methodology, which has been developed in the last 8 years, is extensively used to create very precise modifications in the DNA, including the deletion of small fragments, that might help us to inactivate the function and in consequence confirm the role of *RPB2* in the resistance to Clubroot disease. This confirmation would be an exciting development that would open up many new avenues for future experiments looking into how Arabidopsis is recognizing *Plasmodiophora brassicae* and launching its immune response. **Additionally, we want to establish if there is a genetic interaction between our *RPB2* and the previously identified gene *RPB1* by inactivating both genes together.**

With the expected results of our project, we want to better understand how the plants can defend against Clubroot and generate knowledge that could be used to improve the searching of resistant plants and production of varieties with more durable resistance.