Plant specialized metabolites constitute an unusually large group of structurally diversified compounds that contribute to the interactions of plants with the environment, including plant immunity. Of note, the phylogenetic occurrence of particular plant secondary products is frequently restricted to particular lineages, such as a family or genus. Primarily, particular specialized metabolites have been proposed to act in plant immunity based on their antimicrobial activities. In addition, experimental evidence suggested that apart from directly inhibiting pathogen growth some of these compounds can act as signalling molecules that control different conserved in the plant kingdom immune-related processes including cell wall reinforcement, stomata closure and programmed cell death. It has been shown that particular specialized metabolites restrict pathogen growth at clearly defined infection stages. Some of them control entry (penetration) of pathogens into plant tissue while some others can restrict spread of the pathogen from initially colonized cells. However, it is not clear to which extend this is defined by temporal and spatial expression patterns of genes encoding respective biosynthetic enzymes, and to which extend by unique properties of particular metabolites. Strikingly, in different plant species the same immune functions can be fulfilled by structurally different secondary metabolites. This is not surprising for metabolites that act as antimicrobials; however, rather difficult to explain for compounds that are supposed to act as signaling molecules controlling immune responses conserved in the plant kingdom.

In this project we would like to investigate to which extend spatial and temporal production patterns, and host genetic background determines function of particular specialized metabolites that are derived from the aromatic amino acid tryptophan. The investigated compounds will include indole-type phytoalexins produced by plants representing cabbage family (Brassicaceae), benzoxazinone glucosides produced by many grasses including maize, and serotonin that is also produced by selected members of the grass family including rice and wheat. To check functions of these compounds we will use defined mutants of the model plant Arabidopsis (cabbage family) that are depleted from their native defensive metabolites and consequently are highly susceptible to infection. We will engineer the mentioned above biosynthetic pathways in these mutants using specific regulatory sequences supporting production of respective enzymes at strictly defined stages of infection. Subsequent analysis of susceptibility of obtained transgenic lines will answer the questions (i) to which extend “foreign” metabolites can overtake the function of native compounds in plant immunity and (ii) to which extend precise function of particular compounds depends on their spatial and temporal production patterns.

Results obtained in this project will expand our fundamental knowledge on the function of specialized metabolites in plant immunity. This in turn will be of significance for future crop cultivation and protection strategies. Our results may facilitate rational breeding of varieties of crop plants representing cabbage and grass plant families with specialized metabolite profiles optimal for plant immunity. In addition, they can give basis for rational metabolic engineering of specialized metabolites with function in plant defense.