

Pathogenic microorganisms attacking plants developed smart strategies to interfere with host defense system. To this aim, many of them deliver a specific set of proteins, called effectors, directly into plant cells. The effectors usually target critical components of plant defense response. Therefore elucidation of the mode of action of an effector, not only contributes to understanding of the virulence mechanisms but may provide evidence of novel aspects of host protein function.

Our previous studies showed that HopBF1, an effector secreted by some *Pseudomonas syringae* strains inactivates HSP90 chaperone by transferring a phosphate group to the highly conserved serine residue. This leads to inhibition of the ATPase activity of HSP90 resulting in cell death. Observable characteristics of plants transiently expressing HopBF1, allow us to assume that inhibition of HSP90 activity affects also small RNA machinery in the cell. We hypothesize that HopBF1 may interfere with small RNAs' loading into ARGONAUTE (AGO) proteins since this process requires ATPase activity of HSP90. Therefore in a series of experiments, we would like to compare small RNA (miRNAs and siRNAs) profiles and transcriptomes of plants in response to HopBF1. We are also going to analyze miRNAs and siRNAs bound to AGO1 and AGO4 proteins, respectively upon local HopBF1 expression. The next question we pose relates to identity of the signal that transmits information from the leaf, where HopBF1 is expressed to the upper leaves. We will also check, which physiological processes are disturbed in those upper leaves. In our studies we employ new generation sequencing techniques, advanced bioinformatics tools as well as plant biology techniques.

We expect, that results from this project will contribute to the deeper understanding of mechanism of action of the proteins belonging to HopBF1 family and thereby will shed a new light on the function of host cellular machinery. Since HopBF1-like proteins are produced not only by bacteria attacking plants, our studies may lead to unraveling of general virulence mechanisms.