



## Modelling of potato immune signalling response

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Infection of a plant by a pathogen initiates a complex interaction between both players involved, leading to changes in the complex signalling network, which result in gene activity changes and reprogramming of the cell metabolism. A systems biology approach was adopted for the purpose of modelling complex biological processes in order to understand the mechanisms and dynamics involved in potato plant defense following the infection with potato virus Y (PVY).

A qualitative model of potato plant defence signalling network (PDS) was constructed (Miljkovic et al., 2012), describing the biosynthesis and signal transduction pathways for three crucial phytohormones involved in plant defence: salicylic acid (SA), jasmonic acid (JA) and ethylene (ET). The prior knowledge from literature was expanded with information on the viral and plant component interactions, protein-protein interactions and protein-DNA interactions in plant *Arabidopsis*.

The resulting robust qualitative model offers new insights into the plant-virus interaction by expanding the knowledge on critical components of plant defence signalling, thus producing novel hypotheses to be tested in the wet lab. First efforts of dynamical modelling of the selected ethylene model sub-component were already performed, indicating the importance of protein degradation efficiency to obtain biologically relevant representations of network responsiveness.