PrimedPlant: Priming for increased disease resistance in *Hordeum vulgare*

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The primed state is a unique physiological state, induced in plants upon a priming stimulus. Subsequently, if compared to a naïve plant, a primed plant is able to respond faster and stronger to a challenging stress. Therefore, priming is an efficient strategy for the plant to protect itself against pathogens.

The knowledge of priming and induced resistance is currently based mainly on the model plant *Arabidopsis thaliana*. Our *PrimedPlant* project's aim is to expand the expertise on priming in barley (*Hordeum vulgare*), as one of the economically most important cereals.

Different stimuli are able to cause and promote the primed state of a plant: *e.g.* chemical compounds or beneficial microorganisms. Previous research showed that bacterial quorum sensing molecules, like the *N*-acyl homoserine lactone (AHL) oxo-C14-HSL, are natural inducers of the primed state. The Gram-negative bacterium *Ensifer meliloti* which is known as root-nodule symbiont in legumes produces oxo-C14-HSL.

Here we investigate the ability of barley to face the challenge against the powdery mildew causing fungus *Blumeria graminis* f. sp. *hordei* upon priming induced by oxo-C14-HSL, produced by *E. meliloti*.

In this setting the priming capacity of different spring barley cultivars is investigated. For this purpose, two reference cultivars (Golden Promise and Morex) and based on their genetic distance, five cultivars from the spring barley GENOBAR collection (BCC768, BCC1589, BCC1415, BCC436 and HOR7985) were selected.

The infection rate and priming capacity was assessed phenotypically, employing a detached leaf assay. The selected cultivars showed differences regarding their resistance to powdery mildew and responded differently to the priming stimulus. Additionally, in order to localize and analyze the plant defense reaction, the production of reactive oxygen species in the leaves was visualized *via* DAB staining. As a second approach, a luminometer-based assay was used to quantify the generation of reactive oxygen in leaves.

Furthermore, we plan to investigate the changes in gene expression upon priming and a triggering stimulus *via* MACE (Massive Analysis of cDNA Ends). This approach should result in detailed understanding of the priming process in barley. In addition, these data will be used to identify marker genes for priming in barley, to further analyze the cultivar-dependent impact of priming on the transcriptional level *via* qPCR.

In the future this information should be used to improve resistance of barley and other economically relevant cereals and to identify promising breeding targets.