

PROJECT TITLE

Role of DNA methylation variation in Barley Powdery Mildew resistance

CONSORTIUM

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SUMMARY OF THE REPORT

Powdery mildew is a ubiquitous threat for field-grown barley. While many spring cultivars carry dominant Mildew resistance locus o (MLO) loci, this is not the case for currently used winter barley varieties [1]. Therefore identifying additional loci or pathways for powdery mildew resistance is of critical importance.

Recent work has highlighted the role of DNA methylation in modulating resistance to pathogen attack [2] in many different plant species including wheat and barley [3], [4].

To clarify the role of DNA methylation in disease resistance we propose to take advantage of an existing world-wide panel of 120 barley landraces from USDA core collection for which in addition to existing genotyping and climate of origin data [5], we have recently generated whole genome bisulfite sequencing (WGBS) data (Dubin et al., unpublished).

In this project we quantified variation in susceptibility to the barley powdery mildew fungus *B. graminis* f.sp. *Hordei* in the population. Here we show that the signalSCREEN platform identified extensive variation in susceptibility to PM (powdery mildew) within this population. We also found that this variation was correlated with growth habit and the climate from which the accessions originate, and is thus a promising approach for investigating variation in PM susceptibility in this population.