

**PROJECT TITLE**

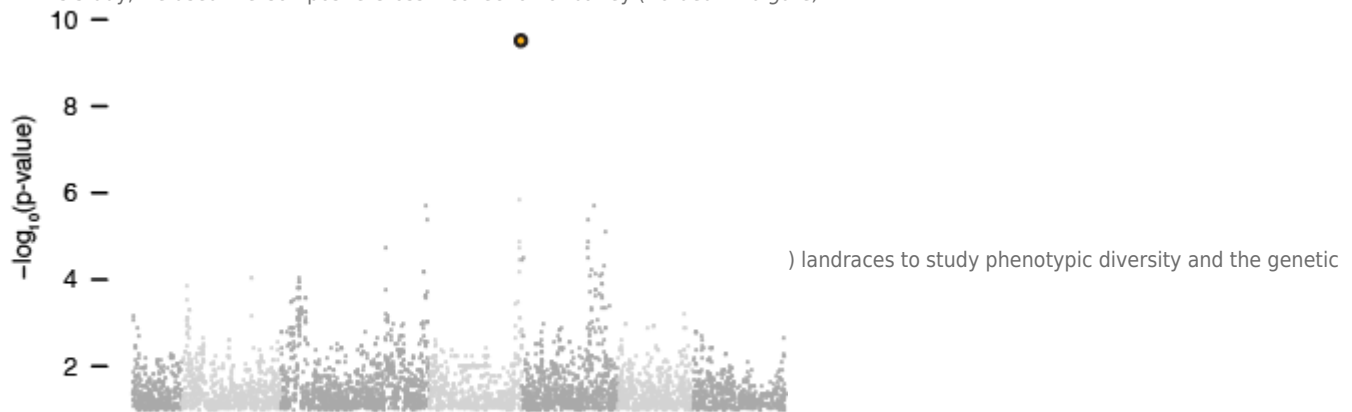
The Phenotypic Basis Of Barley (*Hordeum vulgare*) Success In a Ninety Year Long Competition Experiment

**CONSORTIUM**

P 1	Claude Becker		
P 2	Daniel Koenig		

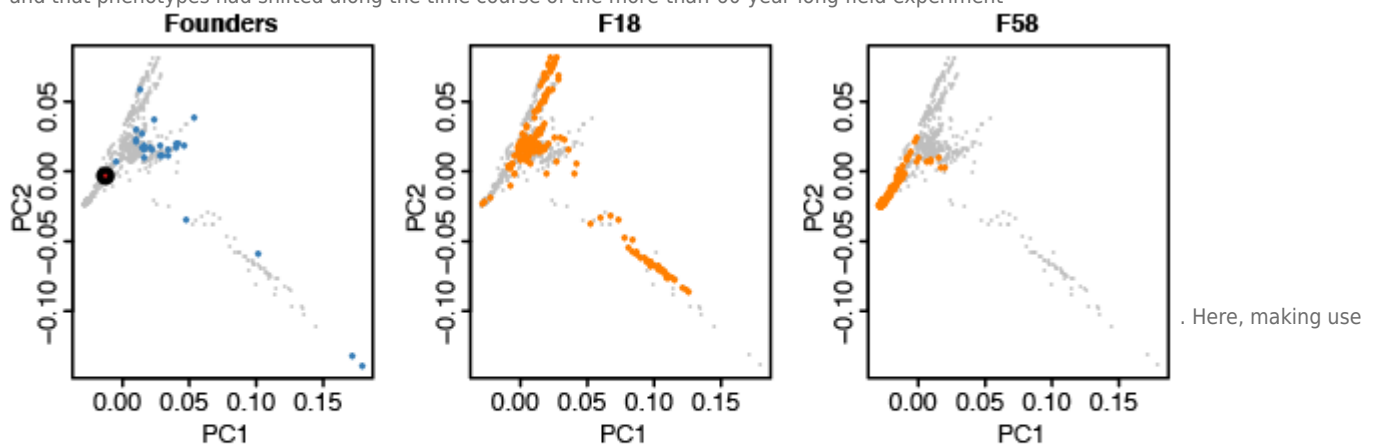
# SUMMARY OF THE REPORT

In this study, we used the Composite Cross II collection of barley (*Hordeum vulgare*;



**Figure 1. Genome-wide association analysis of flowering time using the CCII-core. The data point marked in orange is significant after Bonferroni correction.**

basis of phenotype/genotype associations. Previous experiments had shown a substantial degree of phenotypic diversity among CCII lines, and that phenotypes had shifted along the time course of the more-than-60-year-long field experiment



**Figure 2. Principle component (PC) analysis of genetic diversity in the CCII-core. All samples plus the founding lines are shown in grey in each plot. The left plot shows founder diversity (blue) and highlights the Californian landrace, Atlas (red). Much of the founding diversity remains after 18 generations of evolution (middle, orange), but a limited number of haplotypes similar but not identical to Atlas remain after 58 generations.**

of the large APPC facility at IPK Gatersleben, we collected phenotypic data of over 400 traits on a daily basis along the complete life cycle of the plant. The experiment included 160 CCII progeny lines as well as the parental landraces. In the near future, these data will be combined with available genomic data to map the genetic variants underlying phenotypic diversity.