

## Genomics Approaches to Analysis of Genetic Adaptation to Climate in Barley

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Wild barley (*Hordeum spontaneum*) represents a significant genetic resource for crop improvement in barley (*Hordeum vulgare*) and for the study of the evolution and domestication of plant populations. Genomics tools are now available for analysis of large number of barley genes. We have developed, genotyping, SAGE (White *et al.*, 2006) and microarray tools for these analyses. However as a model example we have also focused on two genes, the *Isa* gene (Bundoock and Henry, 2004) that has a putative role in plant defense against biotic stress and the genes encoding betaine aldehyde dehydrogenase (BAD) associated with abiotic stress tolerance (Bradbury *et al.*, 2005). We found that the *Isa* gene was expressed in the maternal tissues of the seed (Furtado *et al.*, 2003). We identified 16 Single Nucleotide Polymorphisms (SNPs) in the coding region of the *Isa* locus of 189 wild barley accessions from 8 sites that were characterized for 16 ecogeographical variables (Cronin *et al.*, 2007). The pattern of SNP suggested a large number of recombination events within this gene and 7 amino acid substitutions were present in the coding region. Highly significant correlations were found between diversity at the *Isa* locus and key water variables - evaporation, rainfall, humidity and latitude. The association is evident at both a local and regional level. These results are consistent with the possibility that inhibition of the plant's own  $\alpha$ -amylase by BASI may be a novel plant defense function. Study of the promoter and coding region of this gene indicate evolution of function at both levels. More recent work has extended these findings by examining variation in the betaine aldehyde dehydrogenase (BAD) genes in these samples.

### Keywords

Wild barley, genetic diversity, climatic adaptation

### Analysis of wild barley populations

Wild barley (*Hordeum spontaneum*) is a key genetic resource for barley improvement. The diversity of wild barley has been assessed using molecular markers and more recently by analysis of the variation in the sequences of some genes. We have recently investigated the impact of the environment on gene diversity of wild populations. Samples were collected from a range of environments with different soil types, aspects and rainfall.

## **Genomics tools**

The growing availability of DNA sequence data, genetic maps and transcriptome analysis tools such as microarrays for barley provide the tools for analysis of diversity in gene sequence and expression in barley populations. For example, White *et al.* (2006) reported analysis of more than 150000 SAGE tags from malting barley that have been used to design microarrays for analysis of gene expression in barley. This allows the monitoring of differences in expression of large numbers of barley genes.

## **Analysis of specific genes**

Several specific genes have been sequenced in plants from these populations. These include genes likely to be involved in both biotic and abiotic stress tolerance in the plants.

### ***Isa***

The bifunctional amylase/subtilisin inhibitor (BASI) protein encoded by the *Isa* gene is involved in defense of the seed against pathogens. The protein was found to have separate domains responsible for the inhibition of  $\alpha$ -amylase and bacterial subtilisin. This gene was found to be expressed in the pericarp (Furtado *et al.*, 2003). The gene has been shown to be at a site of high levels of recombination in barley, including an example of recombination between alleles in wild and cultivated barley populations (Bundock and Henry, 2004). Diversity at this locus was found to be higher at sites with more limited water (Cronin *et al.*, 2007). The response of the plant to varying abiotic stress in this case results in increased diversity of biotic stress genes due to the impact of the environment on the diversity of fungi in the soil.

### **BAD**

The gene encoding betaine aldehyde dehydrogenase (BAD) is associated with stress tolerance in plants (Bradbury *et al.*, 2005a and b). We have found that the fragrance of rice is associated with a deletion in BAD2 in rice. We have now examined the variation of this gene in wild barley populations. The loss of function of BAD 2 has been found to result in fragrance in rice. BAD 1 may be more important in stress tolerance in plants. The diversity of both of these genes has now been analysed in wild barley populations.

## References

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