# Genetic Structure and diversity in Hordeum vulgare species

J. Comadran, J Russell, W Thomas, F van Eeuwijk, S Ceccarelli, S Grando, AM Stanca, L Cattivelli, E Francia, T Akar, A Al-Yassin A Benbelkacem, M Karrou, H Ouabbou, J Bort, J-L Araus, A Pswarayi and I Romagosa.

Scottish Crop Research Institute, Invergowrie, Dundee DD2 5DA Scotland.

#### Introduction

Improvement of stable crop performance under drought conditions is a slow, laborious and difficult task for plant breeders due to the extremely complex genetic basis of yield, the complexity of drought, and the diversity of drought tolerance strategies developed by the plants, involving a large number of genes and processes. Conventional QTL studies cannot account for all these complexities as they are based upon single pair crosses.

This study is therefore based on diverse barley germplasm, DBG, representing distinct geographic regions from around the Mediterranean rim and elsewhere. The DBG takes advantage of recombination in several backgrounds over many generations to identify and confirm candidate genomic regions associated with yield and drought.

### **Materials**

50 EST and genomic molecular markers and 4 chloroplast molecular markers have been used to screen diversity and analyze population structure of a collection of the DBG, comprising 192 barley genotypes.



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#### **Genetic diversity**

Considering all the germplasm assayed with the SSR set, there are 435 alleles with an average of 8.7 per locus. Diversity values range from 0 to 0.915 with an average of 0.605.

Comparing diversity values between landraces and cultivars (84 and 104 samples respectively), we can observe a decrease of diversity with 7.35 and 6.58 alleles per loci for landraces and cultivars respectively.

## Population structure

Population substructure needs to be investigated to avoid false associations likely to be related to different time periods or geographic areas. Different approaches have been used to investigate population structure prior to any association test. Four Chloroplast SSRs have been genotyped on the DBG, and their maternal inheritance is important to the understanding of population substructure.

Five main groups can be distinguished within the DBG: North Mediterranean Spring and Winters, East Mediterranean, Turkish accessions, and South Mediterranean that appears to be spring 6 rows but they seem to be relatively diverse in terms of origin.



STRUCTURE software was used to estimate membership coefficients and assign accessions to inferred clusters.

#### Phenology

Chromosomes 6H and 7H emerged from preliminary analyses as important regions for drought tolerance. Amazingly, 50 markers were enough to detect regions with stable QTL effects on yield.



In order to correct for the effects of vernalization, diversity on VRN-1 and VRN-2 has been screened on the DBG, as well as different genes that control photoperiod requirement.

#### Future

A number of candidate genes emerging from expression studies, particularly those identified under stress regimes, are being genotyped on the DBG using SNPs and CAPs molecular markers.