*Czech J. Genet. Plant Breed., 40, 2004 (4): 134–136*

# SHORT COMMUNICATION

# Characterisation of Genetic Diversity in ICARDA Core Collection of Cultivated Barley (*Hordeum vulgare* L.)

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**Abstract**: Out of the total accessions of cultivated barley, held at ICARDA, a subset core collection consisting of 153 accessions originating from different countries was established. Genetic diversity of the core collection was studied using AFLP markers. The accessions were grouped into different geographic sub-regions and the total genetic variation was estimated using Popgene software. Genetic distance matrix was computed and hierarchical unrooted tree was performed using Phylip software package. Our results demonstrate that the AFLP markers were highly informative and were useful in generating a meaningful classification of the cultivated barley that we determined as a subset of core collection.

**Keywords**: barley; *Hordeum vulgare* L.; genetic diversity; AFLP markers

Barley was one of the first crops to be cultivated and is considered one of the major crops in the world. In order to optimise breeding to genetically improve barley for different purposes, it is important to assess genetic diversity among and within the species which would allow for more accurate estimates of gene pool variation. Furthermore, the genetic diversity of the crop plants may be decreasing, and that could create a problem. To elucidate whether such a problem exists and to alleviate the consequences if it does, it is critical to have a better understanding about the genetic diversity.

Cultivated barley, *Hordeum vulgare* L., is widely distributed over the eastern Mediterranean region and the western Asian countries (CWANA). The cultivated subset core collection investigated in this study and representing the geographical distribution of *Hordeum vulgare* was analysed using Amplified Fragment Length Polymorphism (AFLP) to assess the geographical pattern of genetic diversity.

## MATERIAL AND METHODS

***Plant material***. The core collection, a total of 153 accessions was collected from thirteen countries. The ICARDA subset core collection was selected from the entire *H. vulgare* collection held at the center to represent the species diversity across its geographical distribution area. Three plants were analysed per accession.

***AFLP analysis***. Total DNA was extracted from 50 mg of fresh leaves of each individual plant using the modified CTAB method. Approximately 500 ng of total DNA per sample was used for AFLP reaction. Three primer combinations were used for all of the 450 samples. Bands were scored manually and visually within a range from 100 bp to 300 bp.

***Statistical analysis***. To evaluate the genetic diversity within and among populations, Phylip and Popgene softwares were used. The total gene diversity of cultivated barley originated from different countries was estimated, which was partitioned into the mean of allelic variations within the *Hordeum vulgare* from diverse countries.

## RESULTS

The three primer combinations gave highly informative patterns that were polymorphic among individuals within and between the cultivated barley accessions. A total of 165 AFLP's markers were detected for all three-primer pair combinations and the percentage of polymorphic loci was equal to 92%.

To assess the relationship of the accessions listed in different regions, consensus tree was calculated (Figure 1).

The barley landraces from Morocco were the most diverse (Table 1), followed by the populations from Oman and Iran. The populations from Turkey, Egypt, Syria, Yemen and Iran showed intermediate genetic diversity. The third group represent the populations from Algeria, Tunisia, Yemen and Jordan. The lowest genetic variation was for barley landraces from Cyprus and Uzbekistan.

## DISCUSSION

Landraces of barley are known to offer rich sources of genetic variations for the crop improvement. The accessions from Morocco were found to be more genetically diverse. This result corroborates that one revealed by agro morphological characterisation where great genetic variations exist between and within landraces for different characters. The same observation is valid for the populations from Oman. Barley landraces from Uzbekistan were found to be genetically very distinct from the rest of the populations. Barley landraces from Cyprus and Oman were closely related to those from Yemen

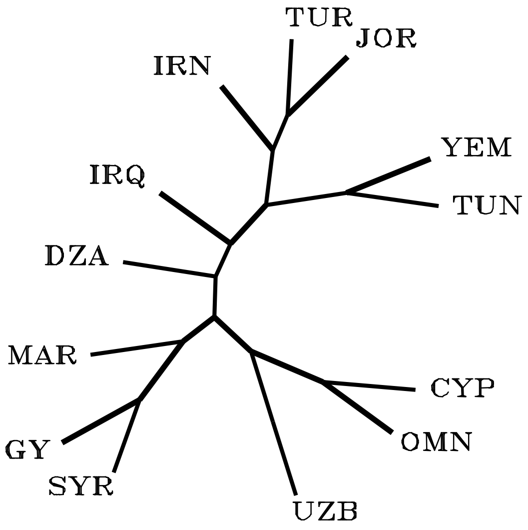

Figure 1. Unrooted phylogentic tree reporting AFLP based genetic relationships among barley countries

Table 1. Summary of statistical analysis

| Countries | No. populations | Nei's gene diversity | No. polymorphic loci | % polymorphic loci |
|---|---|---|---|---|
| Morocco (MAR) | 27 | 0.218 | 145 | 88 |
| Oman (OMN) | 7 | 0.187 | 104 | 63 |
| Iran (IRN) | 13 | 0.174 | 102 | 62 |
| Egypt (EGY) | 4 | 0.161 | 85 | 51 |
| Syria (SYR) | 21 | 0.154 | 121 | 73 |
| Turkey (TUR) | 27 | 0.150 | 126 | 76 |
| Jordan (JOR) | 7 | 0.125 | 80 | 49 |
| Tunisia (TUN) | 5 | 0.128 | 94 | 57 |
| Yemen (YEM) | 8 | 0.120 | 102 | 62 |
| Cyprus (CYP) | 3 | 0.117 | 56 | 34 |
| Uzbekistan (UZB) | 3 | 0.106 | 67 | 41 |
| Iraq (IRQ) | 3 | 0.097 | 49 | 30 |
| All |  | 0.198 | 151 | 92 |

and Tunisia as well as to those from Syria and Egypt. The populations from Algeria and Iraq were relatively distant from the rest of the landraces. The results of this study suggest that the genetic variation in ICARDA *H. vulgare* subsp. *vulgare* subset of the core collection is geographically structured, however, a major part of the genetic diversity is within the geographical subregions.

## References

Badr A., Muller K., Schafer-Pregl R., El Rabey H., Effgen S., Ibrahim H.H., Pozzi C., Rohde W., Salamini F. (2000): On the origin and domestication history of barley (*Hordeum vulgare*). Mol. Biol. Evol., **17**: 499–510.

Chabane K., Valkoun J. (2002): Evaluation of genetic diversity of barley (*Hordeum vulgare* L.) from Ethiopia, Eritrea and Yemen using AFLP markers. In: Al-Shaji Y.A., Sidhu J.S., Saleem M., Guerinik K. (eds): Biotechnology Applications for the Arid Regions. Kuwait Institute for Scientific Research (KISR), Kuwait: 173–179.

Allaby R.G, Brown T. A (2003): AFLP data and the origins of domesticated crops. Genome, **46**: 448–453.

Received for publicaion August 2, 2004
Accepted after corrections October 1, 2004

## Abstrakt

Chabane K., Valkoun J. (2004): **Charakteristika genetické diversity v „core“ kolekci ječmene (***Hordeum vulgare* L.**) genové banky ICARDA**. Czech J. Genet. Plant Breed., **40**: 134–136.

Z celkového počtu vzorků ječmene uchovávaných v genové bance ICARDA byl vybrán základní soubor 153 vzorků pocházejících z různých zemí. Genetická diversita „core“ kolekce byla sledována pomocí AFLP markerů. Přírůstky byly roztříděny podle geografických subregionů a celková genetická variace byla stanovena použitím softwaru Popgen. Byla vypočítána matrice genetické vzdálenosti (genetic distance matrix) a byl sestaven genetický diagram (hierarchical unrooted tree) při použití souboru Phylip software. Výsledky prokázaly, že AFLP markery mají vysokou informativní hodnotu a umožňují účelnou klasifikaci v kolekci ječmene.

**Klíčová slova**: ječmen; *Hordeum vulgare* L.; genetická diversita; AFLP markery

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