



GCP: Barley Technical Report (May 2006-October 2006)

GCP Project Number: #01a

Project Name: Completing genotyping of composite germplasm set of barley

Principle Investigator: Drs. J. Valkoun, S. Grando and M. Baum (ICARDA)

Collaborators: Chinese Academy of Agricultural Science (CAAS), Dr. Zhang Jing,

Item	Subtotal
CAAS	65.000
ICARDA	55.000
Overhead 18%	9.900
	129.900

Report: technical update October 2006

The Generation Challenge Program barley composite set consists of the following germplasm: *H. vulgare* ssp. *spontaneum* (15%) The barley wild progenitor is represented by 445 accessions, 65 % of this total are original accessions from GRU collection missions. Hyper-arid, arid and semi-arid collection sites represent 1%, 20% and 63% of the total, respectively. The set originate from 20 countries and collection sites belong to 58 ecological clusters. **Landraces (65%):** Landraces are a major part of the set with 1935 accessions. A significant part (20 %) is original material collected by ICARDA. Hyper-arid, arid and semi-arid collection sites are present with 3%, 33% and 43%, respectively. The landrace set originates from 85 countries and 78% is of CWANA origin. Collection sites belong to 255 ecological clusters. **Improved germplasm (20%):** This category includes cultivars, unfinished breeders' materials and genetic stocks, which represent 13%, 6% and 1% of the CP barley set, respectively.

Analysis of 3000 accessions of barley with the 50 SSR has been carried out. A high level of genetic variability was observed. The number of alleles detected by the SSR markers varied (from 7 alleles for HVHVA1 to 33 alleles for SCSSR3907) and between accessions. The frequency of alleles varied also between SSR loci. (Figure 1).

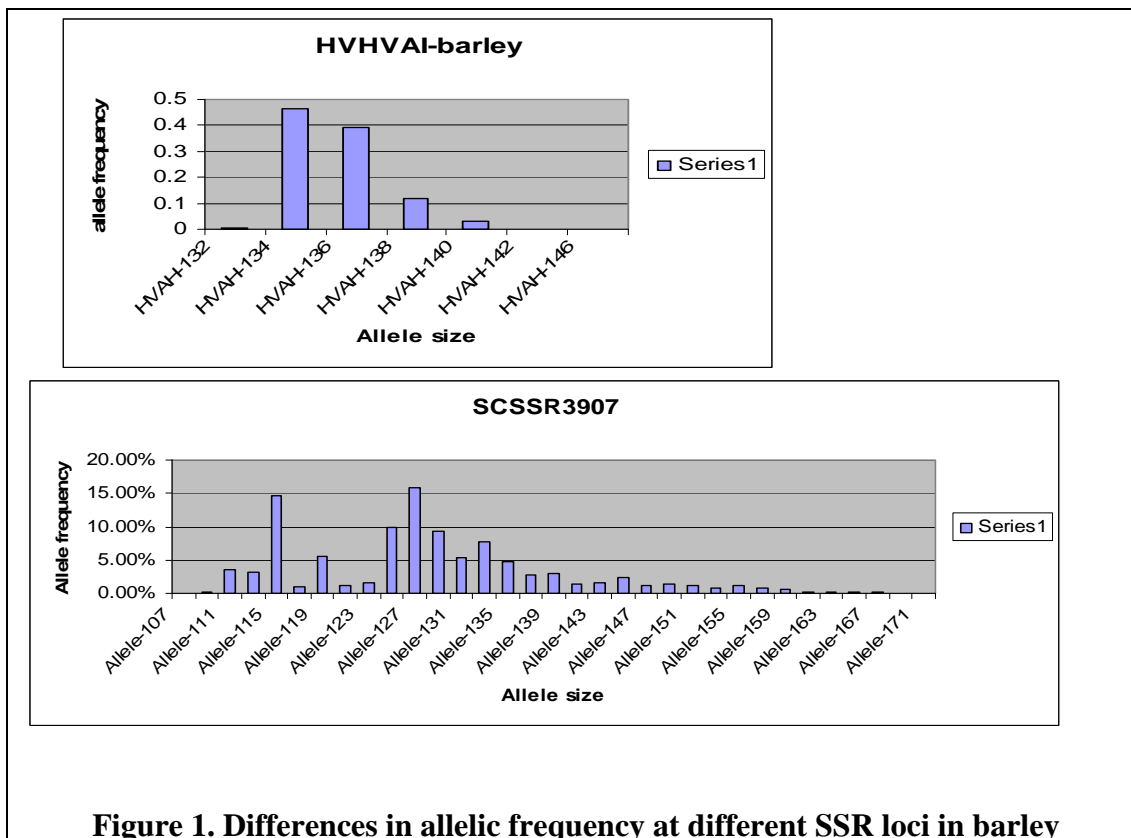


Figure 1. Differences in allelic frequency at different SSR loci in barley

The analysis of data with structure 2.1 (Prichard et al., 2000) allowed the detection of structured genetic variability. The germplasm from different regions was characterized by different allele frequencies. The distribution of genetic variability was divided according to regions. Some regions were very rich in alleles and possessed high levels of genetic diversity. Specific patterns were detected in the different regions demonstrating the presence of region specific alleles. The analysis of the data with DARwin5 (Version 5.0.130) allowed the illustration of genetic dissimilarity between accessions collected from the 85 countries (Fig. 2).

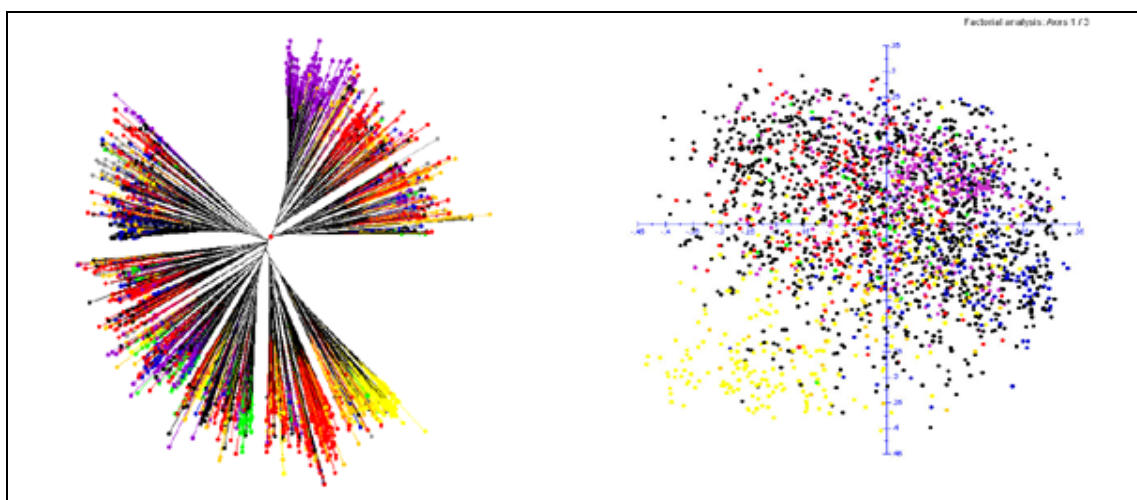


Fig. 2. Illustration of genetic dissimilarity between accessions from different regions (Darwin5).

Based on the genetic diversity of SSR markers, a core collection was developed.

Tangible outputs delivered

1. The analysis of 2692 accessions of barley with 15 SSR primers at ICARDA.
2. The composite collections has been planted for seeds increase and seeds have been collected. Missing accessions need to be re-grown.
3. The Genetic Resource Unit will be provided with a set of the composite collection for reference and future distribution of seeds
4. A core collection has been established (about 300 lines) representing 10% of the whole collection.

Deviations from the work plan

- The genotyping data provided by CAAS differ from the ICARDA data set. More alignments are needed in order to do a combined analysis.
- Not all the accessions that were planted for seed increase produced seeds. Therefore, not all the 3000 accessions of the composite collection will have seeds in the gene bank. This includes 500 accessions (250 from ICARDA: 250 Chinese landraces) that were genotyped in the first year by CAAS for which no seeds were returned. (For accessions produced seeds, we planted at ICARDA 2692 and 2200 produced seeds. For China, 500 accessions analysed first year and seeds were not collected from them)

Data Availability

- Genotyping data on 2692 with 15 SSR carried out by ICARDA is available locally at ICARDA in the GCP data base format. We will deposit these in the central register within the next month.
- Genotyping data on 2500 accessions with 35 SSRs carried by CAAS is locally available at ICARDA in the GCP data base format. However, we will deposit this in the central register once the data format has been improved.

To be carried out until the end of the year:

- Definition of an SSR kit and reference samples based on the available data
- More efforts (CAAS) on aligning the data and combined analysis