



## **GCP: Barley Technical Report (November 2005 – May 2006)**

**GCP Project Number:** #01a

**Project Name:** Completing genotyping of composite germplasm set of barley

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**Collaborators:** Chinese Academy of Agricultural Science (CAAS), Dr. Zhang Jing, Dr. Joanne Russell, Scottish Crop Research Institute (SCRI)

Total budget 2006: -

### **Report January – June 2006**

The seeds of 2692 Accessions, representing a barley collection collected from 84 countries, were provided by the International Center for Agricultural Research in the Dry Areas (ICARDA) at Aleppo in Syria and used in this analysis.

We have received data from CAAS on the 35 SSRs loci recently, but were not able to run the analysis prior to this report. The data from CAAS needs to be completed. 500 accessions genotyped by CAAS in the first year, need to be adapted to the data format and included in the analysis.

Using Structure2.1 program (Pritchard et al. 2000), we have analyzed 15 SSR loci data on 2692 of the 3000 accessions of the barley composite collection. The analysis on 15 SSR primers detected a total of 310 alleles, ranging from 7 to 43 alleles with an average of 26.6 alleles per locus and mean PIC (polymorphic information content) value of 0.672362 (ranging from 0.372814 to 0.914002). SSR locus Bmac316, detected the greatest number of alleles (43 alleles) while HVHVAI detected only 7 alleles (see table 1). Detailed analysis for each locus is available and will be incorporated into the database (see SCSSR3907 as example table 2).

Rare alleles are the one, which are present in  $\leq 5\%$  in the population. When 310 alleles detected in the composite collection were grouped into rare or common allele category, there were 252 rare and 58 common alleles at 5% and 172 rare and 138 common alleles at 1%, respectively.

### **Tangible outputs delivered:**

- 2692 Accessions were genotyped with 15 SSR markers
- Single plants from each accession were planted in a greenhouse and seed harvested for about 2000 accessions. In case where no seed was harvested plants were replanted.

### **Deviations from the work plan**

Nil

**Table 1. Number of alleles and the gene diversity at 15 SSR loci determined**

Loci	Chromosome	No. of alleles	Gene diversity
SCSSR15864	7H	21	0.579258834
SCSSR10148	5H	29	0.816028619
SCSSR2306	5H	11	0.671354834
SCSSR25691	3H	16	0.533274004
SCSSR2748	1H	9	0.668369822
SCSSR3907	7H	32	0.914002121
SCSSR5939	5H	17	0.372814448
SCSSR08447	2H	14	0.640349137
SCSSR7970	7H	43	0.665933793
BMAC18	6H	13	0.747358836
BMAC316	6H	43	0.858131925
BMAG382	2H	23	0.683359187
BMAG211	1H	20	0.818979644
HVHVAI	1H	7	0.552136722
HVLTTPPB	3H	16	0.557650141

**Table 2. Fequence of alleles on locus SCSSR3907**

Alleles of Scssr03907	allele freq	%freq	freq2	Classification at 5%	Classification at 1%
3907-1	0.00235	0.2350176	0.0000055	Rare	Rare
3907-2	0.04172	4.1715629	0.0017402	Rare	Common
3907-3	0.03878	3.8777908	0.0015037	Rare	Common
3907-4	0.14689	14.688602	0.0215755	Common	Rare
3907-5	0.00646	0.6462985	0.0000418	Rare	Rare
3907-6	0.06052	6.0517039	0.0036623	Common	Common
3907-7	0.00999	0.9988249	0.0000998	Rare	Rare
3907-8	0.00823	0.8225617	0.0000677	Rare	Rare
3907-9	0.12338	12.338425	0.0152237	Common	Common
3907-10	0.14571	14.571093	0.0212317	Common	Common
3907-11	0.08284	8.2843713	0.0068631	Common	Common
3907-12	0.04113	4.1128085	0.0016915	Rare	Common
3907-13	0.07638	7.6380729	0.0058340	Common	Common
3907-14	0.05523	5.5229142	0.0030503	Common	Common
3907-15	0.03173	3.1727380	0.0010066	Rare	Common
3907-16	0.02879	2.8789659	0.0008288	Rare	Common
3907-17	0.01469	1.4688602	0.0002158	Rare	Common
3907-18	0.01116	1.1163337	0.0001246	Rare	Common
3907-19	0.02174	2.1739130	0.0004726	Rare	Common
3907-20	0.01116	1.1163337	0.0001246	Rare	Common
3907-21	0.01351	1.3513514	0.0001826	Rare	Common
3907-22	0.01528	1.5276146	0.0002334	Rare	Common
3907-23	0.00588	0.5875441	0.0000345	Rare	Rare
3907-24	0.00940	0.9400705	0.0000884	Rare	Rare
3907-25	0.00588	0.5875441	0.0000345	Rare	Rare
3907-26	0.00529	0.5287897	0.0000280	Rare	Rare
3907-27	0.00353	0.3525264	0.0000124	Rare	Rare
3907-28	0.00235	0.2350176	0.0000055	Rare	Rare
3907-29	0.00235	0.2350176	0.0000055	Rare	Rare
3907-30	0.00294	0.2937720	0.0000086	Rare	Rare
3907-31	0.00059	0.0587544	0.0000003	Rare	Rare
3907-32	0.00059	0.0587544	0.0000003	Rare	Rare
Gene diversity					0.9140020

## Appendix