Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008 Project abstracts

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Generation Challenge Programme (GCP)
Hosted by CIMMYT
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the International Maize and Wheat Improvement Center)

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COMMISSIONED PROJECTS

Subprogramme 1: Genetic diversity of global genetic resources

23. G4005.01.03 (1c): Completing genotyping of composite germplasm set of sorghum

January 2005−December 2006, no-cost extension to September 2008

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Collaborating institutions and scientists

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Context: This project was designed to establish a composite germplasm set of circa 3000 accessions of wild and cultivated sorghum, determine the population structure of this using approximately 50 SSR marker loci distributed across all 10 linkage groups of the genome of cultivated *Sorghum bicolor*, and based on this information develop a reference germplasm set of sorghum for use in allele mining and linkage disequilibrium mapping. This was completed in 2007. Due to difficulties in getting the required genome coverage with publicly available SSR markers, additional markers were developed and an additional set of 40 of these have been used in 2008 to validate the population structure of the sorghum reference germplasm set.

Findings and implications: The population structure of the GCP sorghum reference germplasm set, which was originally determined based on allelic variation detected by 41 SSR primer pairs, was largely validated when independently assessed using a set of 40 additional EST-SSR primer pairs developed at ICRISAT from publicly available EST sequence information. This new set of EST-SSRs offers genome coverage comparable to the initial set of 41 SSRs (mostly genomic SSRs) that were used for genotyping the sorghum composite germplasm set. The new set of EST-SSRs detected a total of 362 alleles across the 384-entry sorghum reference germplasm set, with 2.1% missing data. Individual primer pairs detected 3 to 38 alleles, and had PIC values ranging from 0.13 to 0.94. Importantly, heterozygosity levels detected by these new EST-SSR primer pairs were generally low, averaging 0.038 and ranging from a low of 0.003 to a maximum of 0.106, suggesting that most detect single loci.

As in the earlier analysis completed in 2007, diversity analysis based on allelic variation across the 40 new EST-SSR markers indicates the margaritiferum sub-group within the guinea race is distinct and more closely related to wild sorghums than to the other cultivated sorghums studied, suggesting once again that this group represents an independent domestication event. Landrace germplasm exhibited population substructure

based on geographic origin and this was further characterised within racial groups (five basic races and ten hybrid races). Race kafir (largely from Southern Africa) was distinct. Accessions of the durra, caudatum and guinea races each formed distinct geographic subgroups. Race bicolor was more structured than in the original analysis, with two clusters of East African origin, one of which grouped with bicolor accessions having passport data indicating a North American origin (which in turn suggests that the latter are originally from East Africa).

This additional marker genotyping has doubled the density of SSR marker genotyping of the GCP sorghum reference germplasm set, and largely validated the population structure of this set. The combined results will benefit sorghum research programmes globally, and ultimately sorghum producers and consumers around the world. The implications of this work are that the GCP sorghum reference germplasm set is sufficiently diverse that it can serve as a suitable panel for linkage disequilibrium mapping, and/or as an entry to global sorghum germplasm collections when seeking variation in any trait of interest, provided that the phenological diversity present in this germplasm set is not so great that it interferes with phenotyping of other traits of interest.

Work remaining: Submitting the final project report and drafting journal article manuscripts for publication.

24. G4005.01.04 (1d): Completing genotyping of composite germplasm set of chickpea

January 2005−December 2005; no-cost extension to October 2007

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Collaborating institutions and scientists

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Composite collection

ICRISAT and ICARDA jointly developed a composite collection of 3000 accessions (Upadhyaya et al. 2006), which consists of 1956 accessions of the ICRISAT core collection (Upadhyaya et al. 2001), 709 accessions from ICARDA, 39 advanced lines/cultivars, 35 accession with distinct morphological variants, 20 accessions from wild *Cicer* species (*C. reticulatum* and *C. echinospermum*), and 241 trait-specific (resistance to biotic and abiotic stresses, early maturity, multi-seeded pods, double podded, large-seed, high seed protein, nodulation and responsive to high input conditions) accessions. Biologically, it represents 80% land races, 11% advanced lines/cultivars, 1% wild species, and 8% accessions of unknown biological status or geographic origin. This composite collection has been molecularly profiled using 50 SSRs in high throughput assay (ABI3700).