



Generation Challenge Programme

CULTIVATING PLANT DIVERSITY FOR THE RESOURCE-POOR

2008

Project abstracts



Generation Challenge Programme

Project abstracts

July 2008

Generation Challenge Programme (GCP)

Hosted by CIMMYT

(Centro Internacional de Mejoramiento de Maíz y Trigo;
the International Maize and Wheat Improvement Center)

Mailing address:

Apdo Postal 6641

06600 Mexico, DF Mexico

Physical address:

Km 45 Carretera México-Veracruz

El Batán, Texcoco, México, CP 56130

Tel: +52 55 5804 2004

Fax: +52 55 5804 7558

Email: generationcp@cgiar.org or info@generationcp.org www.generationcp.org

to allow recording of easy-to-score characteristics. The rice founder lines will be phenotyped in the Philippines at one irrigated and one rainfed lowland trial site over the next two years (one wet and one dry season). S1 families will be available for selective phenotyping during Year 2. Within the duration of the project, we will concentrate on highly heritable traits that do not require extensive replicated trials and that are not influenced greatly by intra-plot heterogeneity.

The founder lines, samples from each population, and bulks of selfed progenies will be genotyped with a set of genome-wide markers to validate their population structure. It is planned to use a low-cost oligo-chip to generate whole-genome graphical genotypes anchored to the rice physical map, building on the rice SNP project (<http://www.oryzasnp.org/>). This will provide 300-500 well-spaced polymorphic markers for any pair of parental lines.

Though developing the diverse MAGIC populations can be cumbersome and challenging, once these populations are developed, they will become immortal resources for breeding and genetics research, in general, and for fine mapping of multiple QTLs for multiple traits in rice, in particular. The advanced recombinant lines may also be used in product development – either being used directly as released varieties or being used as parents for developing novel rice populations with wider genetic base.

Acknowledgment: We thank Ian Mackay and Collin Cavanagh for discussion and active collaboration in this project.

39. G4008.02: Phenotyping sorghum reference set for drought tolerance

January 2008–December 2010

Principal Investigator

Hari Upadhyaya, ICRISAT, h.upadhyaya@cgiar.org
International Crops Research Institute for the Semi-Arid Tropics
(ICRISAT), Patancheru, 502324, India, Phone: 91-040-30713071 (extension 2333)

Collaborating institutions and scientists

- ICRISAT India: V Vadez, CT Hash, and L Krishnamurthy
- ICRISAT, Mali: F Rattunde and E Weltzein-Rattunde
- ICRISAT, Kenya: MA Mgonja
- UAS–Dharwad: PM Salimath
- KARI: CK Karari
- National Plant Genetic Resources Centre, Arusha, Tanzania: W Ntundu
- IER: M Diourte
- ISRA–CERAAS, Thiès, Senegal: N Cisse

Drought is one of the most important yields reducing abiotic constraint worldwide. It is proposed to evaluate sorghum reference germplasm set (360 of the 384 reference set accessions), selected based on the genotyping information of composite collection (41 SSR loci data on 3372

accessions), for post-flowering drought tolerance. In the first year, the reference set will be characterised for morpho-agronomic traits to classify accessions into distinct flowering and plant height groups at ICRISAT locations in India, Mali, and Kenya. In the second year, these subgroups will be evaluated for post-flowering drought tolerant traits at three ICRISAT locations (as above). In addition, they will also be evaluated at ICRISAT Patancheru, India for seed micronutrients (Zn and Fe) under varying water regimes (stressed vs unstressed conditions) to identify seed micronutrient dense lines. In third year, selected reference set accessions and stay-green QTL introgression lines will be evaluated for water uptake under stressed conditions in PVC tubes (2.0-m long and 25-cm diameter), and for the proportion of water used prior/after anthesis. In the same year, the most promising post-flowering drought tolerant reference set accessions and stay-green QTL introgression lines will be multilocally evaluated for post-flowering drought tolerance at ICRISAT and NARS locations in India and Africa. In addition to evaluating for post-flowering drought tolerance traits, additional data will be collected on grain/stover yield and component traits to identify lines that are better able to maintain normal growth/yield processes under stress. It is proposed to evaluate this select group of materials in the fourth year (subject to GCP provides funds) at NARS locations to generate additional data on the performance of post-flowering drought tolerant lines. At the completion of project, we will have a better understanding of post-flowering drought tolerance in sorghum, the traits associated with post-flowering drought tolerance, and a range of post-flowering drought tolerant sorghum lines for use in crop improvement programmes.

40. G4008.03: Precision phenotyping of the GCP spring wheat reference sample for drought

January 2008–December 2010

Principal Investigator

Susanne Dreisigacker, CIMMYT, sdreisigacker@cgiar.org

Apdo. Postal 6-641, 06600 Mexico, D.F., Mexico, Phone: +52 55 5804 2004,

Fax: + 52 55 5804 7558

Collaborating institutions and scientists:

- CIMMYT: Matthew Reynolds, Yann Manes, Karim Ammar, Tom Payne, Hans-Joachim Braun, Jose Crossa, M Warburton, M Zaharieva
- INRA–Morocco: Rachid Dahan
- CIMMYT–Iran in collaboration with the Dryland Agricultural Research Institute: MR Jalal Kamali

Global genetic resources provide a fundamental source for further crop improvement. The GCP Subprogramme 1 aims to characterise the diversity of crop germplasm collections held by the CGIAR and its partners. This characterisation includes an assessment of the genetic structure of the collections as well as the phenotypic variation associated with that structure. The ultimate goal is to provide access to sources of genetic diversity that may supply genes and alleles involved in key agricultural traits, especially stress tolerance. During the last three years, 3000 wheat accessions provided by major germplasm banks were characterised by CIMMYT and collaborators with 50 SSR markers for the development of reference samples including accessions maximizing neutral genetic diversity. In the first year of this project we will build up a seed stock for