

Friday, 18th September



Generation Challenge Programme
Annual Research Meeting
20–23 September 2009
Laico L'Amitié Bamako Hotel
Bamako, Mali

AGENDA FOR PARALLEL SESSIONS

Monday, 21st September 2009

1030–1215

Bamako, Mali

Parallel activities on (i) Cereals research–diversity and (ii) Legumes research development

Groups, facilitators and rooms	Cereals research–diversity Facilitator: <i>Jean Christophe Glaszmann</i> Room: <i>Union Africaine 1</i>	Legumes research development Facilitator: <i>Carmen de Vicente</i> Room: <i>Union Africaine 2</i>
Time		
1030–1045	Connecting performance under drought with genotypes through phenotype associations in rice (<i>A Kumar</i>)	Drought tolerance and disease resistance improvement in groundnut: An update on progress (<i>V Vadez</i>)
1045–1100	Interspecific hybridisation for the exploitation of genetic diversity in rice (<i>A Ghesquiere</i>)	Accelerating development and use of genomic and genetic resources in chickpea to improve its crop productivity in Asia and sub-Saharan Africa (<i>RK Varshney</i>)
1100–1115	Genomic dissection of tolerance to drought stress in landrace barleys from Syria and Jordan (<i>J Russell</i>)	Improving common bean productivity for drought environments in Eastern and Southern Africa (<i>M Blair</i>)
1115–1130	Large-scale phenotyping for drought tolerance gene discovery in wheat (<i>D Mullan</i>)	New breeding approaches and trait discovery for cowpea improvement enabled by high-throughput genotyping platforms (<i>J Ehlers</i>)
1130–1145	Phenotyping sorghum reference set for drought tolerance—Year 1 progress (<i>H Upadhyaya</i>)	Next generation sequencing and genotyping technologies applied to legume germplasm and reference mapping populations (<i>D Cook</i>)
1145–1200	Origin and evolution of aluminum tolerance in sorghum (<i>J Magalhães</i>)	Fresh seed dormancy of short duration peanut: latest advances (<i>O Ndoye</i>)
1200–1215	Discussion	Discussion

Monday, 21st September 2009 (cont'd...)

1330–1500

Bamako, Mali

Group discussions/meetings I (in parallel)

Participants are free to join one of the following sessions (90 minutes each):

1. Panel discussion on data curation, standards and quality (*E Arnaud*)

Room: Union Africaine 1

Presentations (10mins maximum):

- Passport and SSR datasets in the GCP Central Registry: issues related to management of quality (*Theo Van Hintum*)
- Validation of GCP SSR genotyping data: revisiting the process (*Claire Billot*)
- Quality phenotyping data (*Ruaraidh Sackville-Hamilton*)
- Geospatial metadata: the process for the developing internationally standardised metadata; importance of geospatial metadata for environmental analysis (*Glenn Hyman*)
- Biocuration: Its importance in data quality and role in standardizing data – will be an overview of data curation processes and available tools, particularly using Ontology. Outputs of the Biocuration Meeting, March 2009, Germany (*Rosemary Shrestha*)

Objectives

A large amount of data is being generated by GCP partners. All necessary GCP tools and services must be maintained and further developed to facilitate access to GCP quality data sets. Data templates, ontology, Central Registry and data-quality reports are all inter related outputs that support the delivery of quality products to the public audience. Quality of the data in terms of its scientific accuracy is checked as part of the research protocol within each research institute, but the process is not often documented. At the data-provider level, the process of data-quality checking must be improved, or better yet standardised for each data type.

1. What are the bottlenecks encountered by Biocurators with GCP data and what solutions can be applied?
2. How to build and sustain a curation community involving PIs for the GCP data sets and ensure peer reviewing? Example of the Biocuration Society.
3. What criteria can be applied to define the 'quality data' for breeders? For the GRSS?
4. What metadata for GCP data ?

The objective of the session is to look at the quality checks performed this year or needed, at applied solutions and get researchers' involvement in the process. Theo van Hintum will give an overview of issues he observed regarding the quality of the data sets in the GCP Central Registry. Despite the use of templates for uploading passport and SSR data, it appeared that many of the data sets are still of limited use because of lacking meta information; if it is unclear what material was genotyped or what markers were used, the marker scores do not have much value. The largest improvement can be made on the basis of plain common sense by asking the question: can an outside user understand what has been done and what came out? Apart from the quality control

issues, the GCP Central Registry will have to about procedures regarding version management and the provision of meta-data.

This session should serve as preparation for the Data clinic session on Thursday when the helpdesk team will show uploading and formatting of the data sets, including the phenotyping wizard. The Ontology session on Thursday will also be a part of the quality data in follow up to this session.

2. Panel discussion–Continuous evolution of marker systems: where we would like to be? (RK Varshney)

Room: Union Africaine 2

Panelists: *David Bertioli, Brazil; Doug Cook, USA; Hei Leung, Philippines; Andy Paterson, USA*

Background

Molecular markers are important genetic tools for genetic analysis and breeding applications. Molecular markers research first began in the 1980s, starting with isozyme markers which were soon replaced by RFLPs in the late 80s and early 90s. RFLP markers were used to develop the first generation genetic maps for several important species, and provided the concept of comparative genomics in species of several taxa. Subsequently, the invention of PCR led to the development of mainly RAPD, SSR and AFLP marker systems or their derivatives. However, SSR markers were found and considered to be the markers of choice for plant breeding applications. As a result, SSR markers were developed in larger numbers and integrated into genetic maps in almost all important crop species.

Accumulation of sequence data in the public domain, due to the establishment of genome/transcriptome sequencing projects as well as advances in gene expression analysis (eg, microarray) triggered the development of SNP and SFP marker systems, and several crop communities have either already developed large-scale SNP genotyping platforms or are working in that direction. Another important class of molecular markers that is generic and doesn't need the availability of sequence data is the DArT, with several crop species already enjoying the availability of DArT arrays.

As such, it is evident that there has been a continuous evolution of marker systems throughout the last 25 years or so. This poses an important question to plant breeders, who, in turn, frequently ask their colleagues involved in genetics/genomics research the question: “How soon we will have another marker system?” Or: “How long do I have to wait to have a more advanced marker system available for my breeding experiments?”

In view of above, this sessions will be used to discuss the following questions:

1. Which marker system is good for breeding applications at present?
2. Are non-SNP marker systems looking likely to become outdated? If so, how soon?
3. Have we already reached the peak of evolution for marker systems? Or might another marker system become available soon? If so, what it will be? And for how long will we continue to develop new marker systems?
4. Are we moving towards sequencing-based genotyping (SBG) instead of marker-based genotyping in breeding?

To discuss the above-mentioned issues, we have a panel of eminent scientists and experts in molecular marker research. Each panelist will introduce the topic (focusing on different marker systems) in 5–7 minutes (with/without powerpoint slides).

3. Brainstorming: How to standardise information management in the MBP
(*G McLaren*)

Room: Union Africaine 3

This session will consider the problem of standardising information management across crops and breeding projects to the extent that common workflows, laboratory interfaces, bar coding equipment, hand-held devices and analytical tools can be used. We will consider the following questions amongst others:

- Are legacy information management systems a constraint to adopting modern breeding technologies?
- Does molecular breeding raise new requirements for information management which are not catered for by legacy information systems?
- How can new information management applications be added to existing systems to fill gaps required by modern breeding technologies?
- How can common analytic tools be used across diverse information systems?

The goal of the discussion is to guide service providers and developers of the Molecular Breeding Platform in establishing procedures and practices for helping users to upgrade their information management to accommodate modern breeding technologies and analytical tools.

4. Brainstorming: From good science to good payoffs–Improving the targeting, effectiveness and efficiency of crop improvement investments (*S Wood*)

Room: Banquet 2

Driving questions:

- (a) How do research managers, including the GCP management team, satisfy themselves and others that, if successful, their research investments can deliver the expected benefits to the expected beneficiaries? What such information provides the best support for advocacy and fund-raising?
- (b) What data, tools and analysis are available to help obtain relevant information about; smallholder farmers and households, their preferences and constraints, existing patterns of production systems and production constraints (including drought), and the potential impacts of cutting edge GCP science?
- (c) How might better information and analysis guide the design of more cost-effective R&D investments? For example how can better methods of site and systems characterisation across countries and continents be used to design more rapid and effective breeding and dissemination strategies?
- (d) What is the risk to good and successful GCP science investments if national breeding, seed systems, extension services and farmers themselves do not have the capacity to use GCP technologies appropriately and successfully? How can those capacities be assessed?

Format: 5–6 presentations each of 7–8 minutes to leave maximum time for questions, sharing of experiences and indentifying potential issues of sufficient importance for follow-up information-sharing and action.

Speakers:

- Stanley Wood: *The generation of strategic targeting and impact information for the new CGIAR strategy and A review of relevant data and tools* (Two presentations).
- Steve Waddington: *Lessons from the GCP Constraints Analysis study on potential traits and implications for GCP design and potential impacts.*
- Carlos Tovar: *Designing a capacity assessment study for GCP.*
- Godfrey Asumugha: *The use of focus group discussions to help assess the capacity of national systems to use GCP technologies.*
- Glenn Hyman: *The use of site characterisation and homologue tools in improving the effectiveness of GCP breeding strategies.*

END OF MONDAY PARALLEL SESSIONS

Tuesday, 22nd September 2009

FIELD TRIPS

Departure: 08.00 hrs from hotel lobby

Packed lunches will be provided for all participants

Facilitator: *Griselda Marquez*

The following options will be on offer:

Option 1

- Visit **Sanankoroba, Marako** and **Dialakoroba** villages; sites include IER sorghum and maize experimentation, first guinea race sorghum hybrid seed production in farmers' fields and maize seed production with one of the first private companies in Mali.
- Lunch at the Campement "Woloni", on the shore of the lake.
- In **Selingue**, a perimeter for irrigated rice will be visited, which may include a walk along the lake.
- Visit will be led by Abdoulaye Diallo (sorghum breeder) and Ntji Coulibaly (Head of Maize Programme, IER).
- Max distance to site (ie. Distance of the furthest of the three villages from Bamako): 150km

Option 2

- Visit the villages around **Siby**; focus will be on farmers' experimentation with sorghum varieties and legume crops (including groundnut, cowpea and soybean); this trip will also include a visit to a farmer seed producers cooperative.
- Picnic lunch at a natural arch
- Possible visit to a traditional iron ore smelter may be included, time permitting

- Visit will be led by Dr Eva Weltzien (sorghum breeder, ICRISAT), Dr Sidi Bekaye Coulibaly (sorghum breeder, IER–Cinzana), and Mamadou Coulibaly (Association des Organizations Paysannes Professionnelles [AOPP]).
- Max distance to site (ie. Distance of the furthest of the villages from Bamako): 80km

Option 3

- Visit **Tioribougou, Mamabougou** and **Kolokani** villages; focus will be on cereal farmer marketing groups and their experimentation with improved technologies, as well as farmer-managed groundnut variety testing, seed production and integrated aflatoxin management.
- Upon returning to Bamako the group will visit a sorghum and pearl millet processing enterprise in Bamako.
- The visit will be led by Dr. Mamourou Diourte (Head of Sorghum Programme, IER) and Awa Traore (Scientific Officer, ICRISAT–Mali).
- Max distance to site (ie. Distance of the furthest of the three villages from Bamako): 158km

Option 4

- Visit the IER **Sotuba** research station, near Bamako; focus will be on sorghum breeding research, including CP-funded projects. The AGRA-funded experimentation with maize, cowpea, rice, millet and sorghum will be included.
- Possibility of visiting the ICRISAT/IER GIS laboratory.
- Picnic lunch in the garden of the national museum, and guided tour of the museum afterwards.
- Visit will be led by Dr. Niaba Teme (geneticist) and Abocar Toure (sorghum breeder).
- Approx. distance to site: 7km

Option 5

- Visit the ICRISAT research station at **Samanko**, near Bamako; focus will be on groundnut breeding, aflatoxin management and sorghum breeding research for the Sudanian zone, including GCP-funded experimentation.
- The visit will include an overview of AVRDC experimentation with vegetables in Mali, and ICRAF's collection of *Zizyphus*, and *Moringa* ssp.
- Picnic lunch at Samanko research station, followed by a visit to the Bamako Handcrafts market.
- Visit will be led by Dr. Fred Rattunde (sorghum breeder) and Dr. Bonny Ntare (groundnut breeder).
- Approx. distance to site: 20km

END OF FIELD TRIP OPTIONS

Wednesday, 23rd September 2009

1045–1230

Bamako, Mali

Parallel activities on (i) *Cereals research–breeding* and (ii) *Clonally-propagated crops*

Groups, facilitators and rooms	Cereals research–breeding Facilitator: <i>Xavier Delannay</i> Room: <i>Union Africaine 1</i>	Clonally-propagated crops Facilitator: <i>Carmen de Vicente</i> Room: <i>Union Africaine 2</i>
Time		
1045–1100	Improving salinity tolerance in rice, progress in QTL mapping and marker-assisted backcrossing (<i>A Ismail</i>)	Genetic and genomic resources for sweet potato improvement (<i>R Schafleitner</i>)
1100–1115	Candidate genes in the major QTL Phosphorus uptake 1 (<i>Pup1</i>) and marker-assisted breeding of <i>Pup1</i> rice varieties (<i>S Heuer</i>)	A cassava physical map for genome-wide SNP discovery (<i>P Rabinowicz</i>)
1115–1130	Major QTLs for grain yield under drought: fine mapping and MAB (<i>A Kumar</i>)	Progress in developing the potato DArT and its use in the potato genome sequencing efforts (<i>B Sagredo</i>)
1130–1145	QTL validation in introgression line populations of common wheat (<i>R Jing</i>)	Cassava breeding community of practice: A partnership in modern breeding and product delivery for Africa (<i>E Okogbenin</i>)
1145–1200	Bridging together molecular techniques, genetic resources and breeding of wheat in Morocco (<i>N Nsarellah</i>)	<i>Musa</i> genomics: past, present and future (<i>N Roux</i>)
1200–1215	Efficient use of known major gene and QTL information in plant breeding (<i>JK Wang</i>)	Sweetpotato, SPVD resistance and molecular marker development for SPVD resistance (<i>W Gruneberg</i>)
1215–1230	Discussion	Discussion

Wednesday, 23rd September 2009 (cont'd...)

1345–1515

Bamako, Mali

Group discussions/meetings II (in parallel)

The four meetings listed below will be divided into three sessions of 30 minutes each.

Participants will be encouraged to move to a new session after each 30 minutes, allowing participation in three sessions in total.

1. Brainstorming: What do breeders want from the next generation information system (*G Davenport*)

Room: Union Africaine 1

The purpose of this discussion is to get a better idea of what breeders are expecting from the platform. The outputs will be (1) a list of tools/functionalities requested by breeders; (2) the minimum information sets for effective marker-assisted breeding.

Flowcharts for the key breeding methods used in user cases

Can we group the user cases into a few large categories?

The key information required to support breeding

- Raw data vs. derived intermediate information
- What is the role of genomics information?
- What is the key information used for making crossing decision?
- What is the key information used for making selection decision at different stages of a breeding programme?

A wish-list of the needed decision-making tools for marker-assisted recurrent backcrossing (MARB), marker-assisted gene pyramiding (MAGP), marker-assisted recurrent selection (MARS), and genomic selection (GS)

Stand-alone tools vs. tools as integral components of the information network and workflow system

- Expected outputs from these tools
- What options for selection criteria computation are most needed?
- Is genetic simulation tool needed? Should it be part of the Platform?
What are the expected outputs?
- Are economic evaluation functions required?
- Explore opportunities for marker-assisted breeding
- At which stages of a breeding programme MAS is/will be conducted?
- How are the marker information used?

2. Brainstorming: The future of molecular breeding (*X Delannay*)

Room: Union Africaine 2

This session will explore with the participants potential new applications of molecular breeding technologies that could further enhance the efficiency of breeding programmes in the long run, taking advantage of recent advances in high-density genotyping and next-generation sequencing. We will be looking at the next stage beyond the bi-

parental MARS projects that are starting to be implemented across various GCP crops. Examples of such applications that will be discussed are:

- High-density genotyping applications
- Genomic selection
- Multiparental populations
- Selection indices under genome wide and for multiple environments

We aim to identify important new applications that the GCP should start getting involved in and should help implement in key crops to complement current efforts.

3. Brainstorming: Environmental profiling of cultivar trial sites in multi-environment trials (*Glenn Hyman*)

Room: Union Africaine 3

This session will discuss tools and methods for environmental data to support experimental designs of cultivar trials at a site and in multi-environment trials (MET). The session will discuss some basic tools to acquire and analyse climate data. These include online tools and weather generators. We have developed some tools to estimate the probability of water stress throughout the growing season. Some examples will be discussed for Challenge Initiative sites. The session will also include analysis of a large number of sites to help design an efficient strategy for testing. Some designs may want several similar sites as well as different ones to represent the full environmental range of the cultivar. We will demonstrate software for assessing site similarity. The session will also discuss how you can participate in GCP's trial network and in other non-GCP initiatives.

4. Brainstorming: Training for applied molecular breeding (*C de Vicente*)

Room: Banquet 2

The benefits of molecular breeding tools and modern breeding methods that exploit these tools have been sufficiently proven in the private seed sector, but plant breeders in the public sector, particularly in developing countries, have had limited or no experience in applying tools now available.

In its second phase, GCP will focus on fostering modern breeding with the expectation of increasing the efficiency of breeding programmes and as a consequence speeding up the development of new crop cultivars considered basic for food security in the developing world.

This session will invite participants to identify and express training needs to become proficient in applied modern breeding. The plan is not so much to focus on specific topics, but to help design the outline and specifications for a high-quality course or suite of courses covering the molecular breeding pipeline.

The outline should list topics based on questions such as:

- How are approaches (breeding methods/plans and data analysis) different between self- and cross-pollinated species?
- What are the considerations to opt for a breeding approach depending on the

- trait(s) the programme is focusing on?
- What considerations need to be accounted for in determining what generations to genotype and phenotype?
 - How to decide the number of families and population sizes needed for the various breeding methods?
 - When to decide for a design with bi-parental populations vs. one with multi-parental populations?

The aim of this training is to provide whatever knowledge and expertise plant breeders need in order to embark with confidence in the modern approaches in which they are now engaged through GCP projects.

END OF WEDNESDAY PARALLEL SESSIONS

PARALLEL SESSION AGENDA ENDS