

GCP ARM 2009
Brainstorming I—Mon 21st Sep (1330–1500)

SUMMARY ON PANEL DISCUSSION

“Continuous evolution of marker systems: where we would like to be?”

Organiser: *RK Varshney*

Panelists: *David Bertoli, Brazil; Doug Cook, USA; Hei Leung, Philippines; Andy Paterson, USA and Roland Schafleitner, Peru*

Notes:

Since 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 questions such as: “How soon can we expect to have another marker system?” or: “How long do I have to wait for a more advanced marker system to become available for my breeding experiments?”

In view of above, this session was organised 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 Are non-SNP marker systems looking likely to become outdated?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?

The session was attended by more than 30 participants representing a variety of institutes and countries. A real highlight of the session was the attendance by numerous breeders (or molecular breeders/ geneticists) such as Gary Atlin (maize), Francis Ogonnaya (wheat), Richard Trethowan (wheat), KV Prabhu (wheat), Satish Misra (wheat), Pooran Gaur (chickpea), Arvind Kumar (rice), Jeff Ehlers (cowpea), Marie Noelle Ndjiondjop (rice), Hei Leung (rice), Hari Upadhyaya (groundnut), Emmanuel Okogbenin (cassava), Paul Kimurto (chickpea), Mohd Yasin (chickpea), Nicolas Roux (banana), Joanne Russell (barley), Scott Jackson (soybean) amongst many others, in addition to genomics specialists.

At the start of the session, the panelists presented their views on different marker systems. Following some intense discussions on the above-mentioned issues in the room, the group came to the following conclusions:

- (1) It is difficult to determine which marker system should be considered 'the best', as naturally this would depend on the crop and on intended use.
- (2) Current trends suggest that SNP markers are going to become the markers of choice for breeding applications in the coming years. However, SSR and DArT markers are still useful for several applications in at least some crops (where we still don't have SNP resources).
- (3) Genomics scientists do not need to push technology for use in breeding. There

- was a suggestion from the group that genomics scientists sometimes talk as if they were 'salesmen' for the companies - they should refrain from talking in such a manner. Nevertheless, if technology can help breeders to achieve the same goal in less time and at a lower cost, the community shouldn't have any problem in adoption.
- (4) It seems that sequencing-based genotyping will become feasible in at least some crops such as rice or maize as the community is working hard to get whole genome profiling at just US\$10 per line. Consequently, such advances are going to make a major impact on breeding methodologies. Breeders probably do not need to make larger populations in cases where their selection will be based on whole genome profile data.
 - (5) Breeders should not be swamped with large-scale genome data, but should rather they be given the lines which need to be selected for their breeding programme. As such, there is a need to develop decision support tools (Rajeev mentioned that this is an important component of GCP's Molecular Breeding Platform) so that these can be used to analyse large-scale genotyping data and select the suitable lines. Through SP2–SP4 collaboration, some projects have been initiated to develop appropriate tools for SNP discovery based on next generation sequence data, and possibilities will be explored to develop tools for managing high-throughput genotyping data based on Illumina's GoldenGate assays.
 - (6) Instead of genotyping in breeders' labs, it makes more sense to carry out genotyping on breeding populations from Genotyping Centres as this saves both time and money.
 - (7) Breeders are no longer skeptical about the use of markers in breeding programmes, but are, instead, ready to make use of marker technology in breeding programmes, particularly when they see such opportunities and comparable advantages.
 - (8) Efforts should be made towards data storage and access based on the genotyping and phenotyping data generated so that breeders can have access to old data, helping them to make informed decisions about selection of lines in their breeding programmes.
 - (9) Several colleagues expressed their appreciation to GCP for organising such interactive sessions, rather than Subprogramme-specific parallel sessions, mentioning that this particular session was very informative and useful for both genomics scientists and breeders.
 - (10) GCP should consider hosting a portal/discussion forum to air such issues related to markers, genotyping methodologies, genotyping costs, etc. Such a discussion group should have a moderator (eg, Rajeev) – only then would Panel discussions like the ones held at ARM would have a truly positive impact on the community. We should not forget this once we return to our respective workplaces after this ARM.