

ARM 2009
Brainstorming II (Weds 23rd Sep, 1345-1515)
What do breeders expect for the next generation information system?
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Minutes taken by Arlett Portugal

A. Data needed to be stored

- cleaned raw data
- summarized data
- description
- SNP data –
- field data (raw data and summarized data from statistical analysis; field map)
- field map – will help you to find why some data are stranded
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- pedigree data
- what kind of tool to be developed? - tools that breeders can use
- how does the breeder do it now? - Excel application, CIMMYT (statistician receives the data and analyzed data)
- There are a lot of data during the breeding process; it might not be needed but eventually that data might help to efficiently handle the breeding because they d

B. What information needed for cross creation?

- background and foreground
 - genetics maps, QTL information
 - hybrid material produced by private sector (parents of the materials coming from outside source)
 - genomics sequence (pulling the info one at a time; markers for a specific region – what are the possible markers that are there?)

C. Information for the selection

- field data
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D. Breeding strategies (by task, by crops, by use cases, or by methods?)

- recombination, MARS or parental selection
- in the public, there is no system that handles population improvement
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In the next generation system, what will be the building platform?

Inbreeding	Outbreeding
Pure line breeding	
- simple	- composite
- double	- synthetic
- triple cross	Hybrids

Clonal – potatoes, apple, cassava	

The tools that need to be developed is based on how your crops will be developed?
 Are they diploid? Polyploidy?
 Self-pollinated

First phase is to provide the system (ICIS) that we have now.
 Second phase is meant to improve to make it more user-friendly and to add another functionalities.

Second Group Tools

- Gary: free statistical software that does mix-model (cropstat)
- Pedigree management (ability to manage pedigree information)
- Manual to move the data pedigree info into the system like a boot camp
- Cleaning the pedigree information is a great tasks
- Fred: looking into the state of the art, there is a need to mix-model software but it is indeed a state-of-the-art; there is a need to have a team of programmers to cope with the changes in the technology of the molecular breeding.
- GenStat has multi-location analysis tool and it is free;
- Is simulation tool a necessity? Predicts haplotypes from crosses and genes; the platform can provide the data needed by simulation tool. The connectivity from the data is necessary. Flabjack is used as the intermediate way to connect with the data. Simulation test data are needed
- Timeliness of the availability of the data.
- Is the platform web-based? The breeder needs an application that they can run in their computer, which is not depended on the internet. A web-based portal will still be available for querying.
- ICIS does not generate the field design. On the fly analysis of the data can be good. However, across study retrieval of the data will be the one available. A simple analysis of the data can be good.
- The data entry should be easy.
- An easy-to-use standalone application with a data consolidation facility that will be available in the public.
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Third Group

- The responsibility of the breeding platform is to provide the training and the development but not the curation
- Do you see the need for simulation tool? The pedigree management, field trial are the major needs.
- How are the genotyping data used? Primarily to find markers to use, for selection?

- Coefficient of parentage is also necessary
- Presence of gene in a selection; that particular SNP or allele is associated with this parent etc.
- Crop-specific databases up and running;
- What kind of data? Genotype by location data can be useful for what parents to cross in a particular area.
- Are genomics data necessary?
- Compatibility of the platform with what exists or being used like the size of the Illumina chips. A platform that will handle millions of data might be under utilized at this point. Some options about few markers with few traits can already be very useful. Major genes that you want to be integrated can be the start for consideration and not to get involved with many traits or genes.

Clonal breeding

- For the pedigree management, family which code was assigned, all materials that fall under a code has same parents;