

BRAINSTORMING SESSION

Group C

Moderated by Theo van Hintum

Feedback from Group C on Genetic Resources

Reporter: Rajeev Varshney

Participants: V. Mahalakshmi, A. Alves, M. Sawkins, L. Beach, P. Herve, S. Sullivan

1. Comparative mapping and comparative genomics is a very potential approach to utilize the existing information from the model species like rice for cereal crops and Medicago/lotus for legume crop species, We also need to generate genetic and genomic resources for orphan crops like millets/sorghum and pigeonpea or cowpea which are really drought tolerant in natural conditions to identify “candidate set of genes” for transferring them to major crop species.
2. From Subprogram 1 of GCP we have already identified set of candidate genes for drought tolerance. Now there is a need to integrate these data from GCP labs or other ARIs and define/identify a most potential candidate set of genes for which can be targeted for mapping across the species and development of molecular markers to implement in breeding.
3. There is a need for CGs to verify the proof of concept Rather we should try to collaborate with ARIs and private companies. We should try to find the ways how CGs can benefit from the experience and results of private companies. Problem is we always assume that they will not share: “Has anybody asked???” **
4. Comparative mapping of legume crops at the genetic level is good enough to establish the synteny and

- development of COS markers based on candidate genes. Probably there is no need to develop physical map for legume crop species. We should try to collaborate with ARIs.
5. There is a need to identify genes for mapping physiological variation within legumes related to stress tolerance.
 6. No need to establish difference platforms for microarray studies for legumes.
 7. In terms of genetic resources there is a need for association mapping. However we need to be careful and clever to define a set of genotypes on the basis of genotyping data for the [1st goal of GCP?]. There is a need to define a good set of candidate genes. Also need to have good phenotyping data in different locations. We can learn from ARIs in this.
 8. Yes, there is a need for generating NILs for drought and other abiotic stress tolerance traits and varieties through MAS.
 9. Our group thinks that we can include fava bean and [lattyrus?] if they can provide some additional information that we do not have now.

****Understanding regulatory variation for candidate genes that contribute to phenotype is a necessity. This should be a task of ARIs. CGs can play a role in this by applying for competitive grants.**