

**GCP ARM 2009**  
**Brainstorming II—Weds 23<sup>rd</sup> Sep (1345-1515)**  
**The future of molecular breeding**  
**Xavier Delannay (Minutes taken by Humberto Gomez)**

Introduction –G. Atlin–

High density genotyping is becoming very cheap allowing the application of more intense/dense marker assisted breeding. Thus instead of tracking QTLs and single individual plants, as research units, breeders may concentrate their work on marker-trait associations basing the decision making on alleles and haplotypes.

Comments 1<sup>st</sup> round:

Hary

For less studied crops, actions may be needed to find/assign breeding values that individual alleles can make to yield and adaptation. A large part of the genetic variability found in the germplasm collections is not represented in the breeders active populations

H. Gomez

Suggest if MAGIC populations + high density genotyping may assist in finding new genetic variation and to put it within the breeders reach, while at the same time assign breeding values to the alleles.

Fred

Indicates that due to GXE the process is not going to be straightforward.

G. Atlin

Instead of creating new populations, just put on top of the current breeding materials the high density genotyping and carry on from there.

Comments 2<sup>nd</sup> round:

After a quick introduction

T. Hash

Indicates that low cost + high density genotyping would allow moving the experimental unit from single plant to alleles.

However, instead of thousands of markers he would prefer a few hundred well positioned ones. His view is that it will be more advantageous to work with larger numbers of plants in order to apply higher selection pressures. He would rather use the minimum cost effective number of markers and the larger possible number of plants.