

Bullet points from Genomics Discussion

“Integrating genomics, phenotyping
and genetics: knowledge driven
breeding”

2 years

- Community practice:
 - combine protocols for phenotyping across labs (post-computational: data normalizations, machine learning);
 - provide guidelines for designs and sample sizes;
- Annotation of ~270 wilds using pop. gen. tools, emphasis onto functional annotations of genes and variants in the 26;
- Sharing pipelines for GWAS among recombinant populations and cross-validations.

5 years

- Characterize 26 wild species for as many traits as possible and share the data;
- Integrating the platforms of breeding and association analysis;
- Interactively use new breeding data to dynamically adjust models;
- Develop predictions based on individuals markers and genome-based information (for marker-assisted and genomic selection);

10 years (we assume we have complete set of deliverables)

- More complex, epistatic terms for continuous improvement;
- Multi-trait optimization of chickpea as a crop; combine accomplishments of different groups on specific traits to developed fully optimized plants given;
- Extend the platform we developed for a range of grain legumes.