

Genomics and Informatics working group

Summary of discussion and plans

1. Data Management

- Create an INTEGRATED depository of the genotype and linked phenotype data to be updated real-time (Benyamin, Vincent, Varma).
- Use templates in developed systems, and formats easily downloadable into breeding, statistics, and genomics packages (Kassaye).

2. Population Genetics

- Sequence new Jens' populations → pooled GBS.
- Move on with the analyses of 'genetic load' in domesticated genome as compared to the 'wild genome'.
- Include the analyses of new PacBio and optical mapping data to incorporate structural variation.

3. Optimizing crosses

- Analyze data from Bunyamin & Abdullah & Jens to guide crosses .
- Speciation: analyses of reproductive incompatibilities between echinospermum & cultivated → to illuminate potential advanced generations incompatibilities between ret & cultivated.

4. Functional Annotation

- Improve genome annotation by incorporating available transcriptomic data.
- Get Judith's data (5' capped – seq).
- Develop allele-imbalance analyses in F1 (and following generation crosses) to evaluate molecular dominance of cultivated / wild alleles (Doug, Susan, Vincent).

5. i-Plant

- Develop a process-based phenotypic-physiological model for chickpea development (aka Walsh, Wild & others approaches, new collaboration of Vincent & Sergey groups?).
- Use Approximate Bayesian Computation to fit the model to the multitude of phenotypic data for numerous genotypes obtained in several environments.
- Test model predictions, if verified, it should become a nice deliverable (also, check IMAG).