

Germplasm understanding

- * germplasm gathering and genotyping with anonymous markers
- * structure analysis and identification of reference samples
- * assessment of linkage disequilibrium

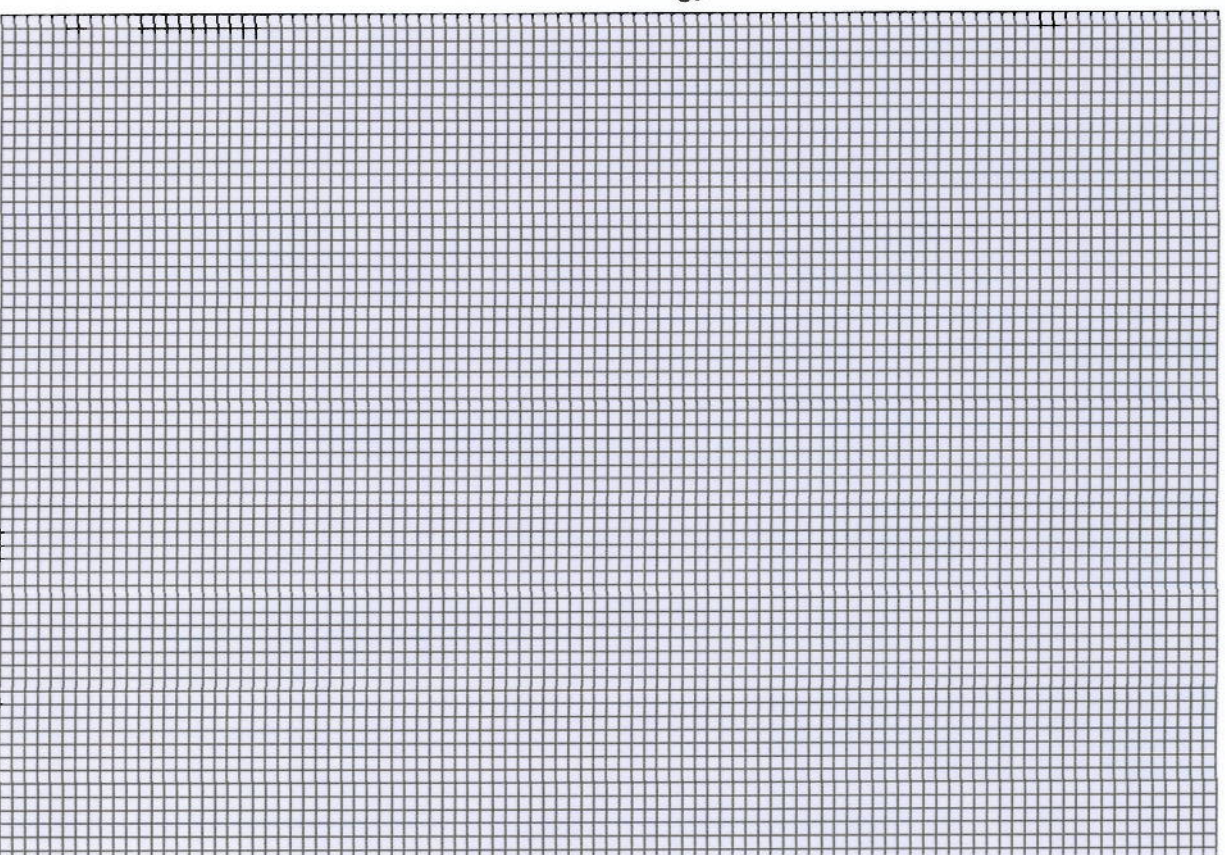
Methodological studies/capacity consolidation

- * genotyping
- * phenotyping

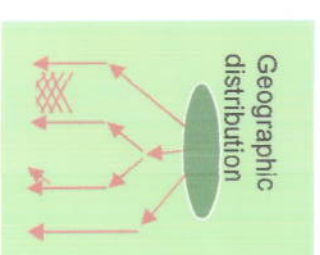
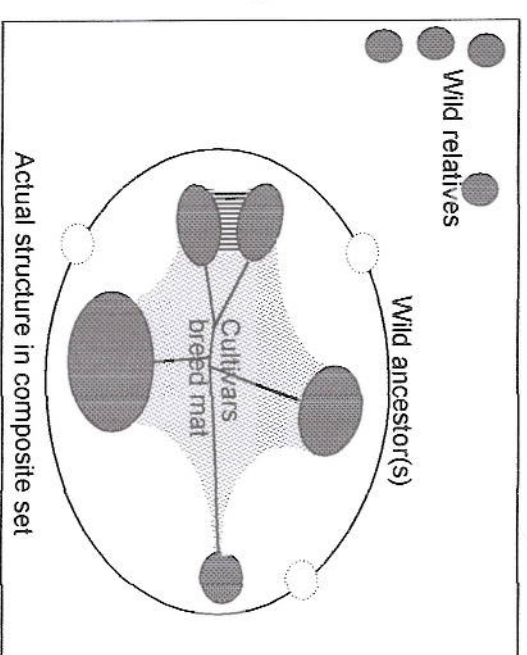
Broadening the genetic base

- * introgressing useful alleles
- * producing resolutive populations

Markers



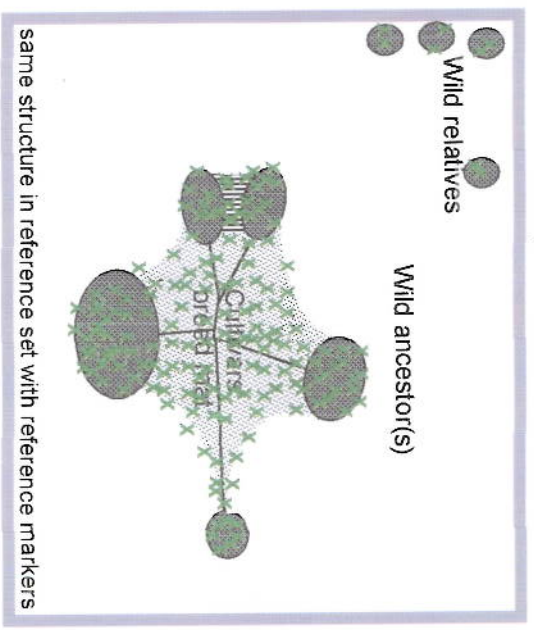
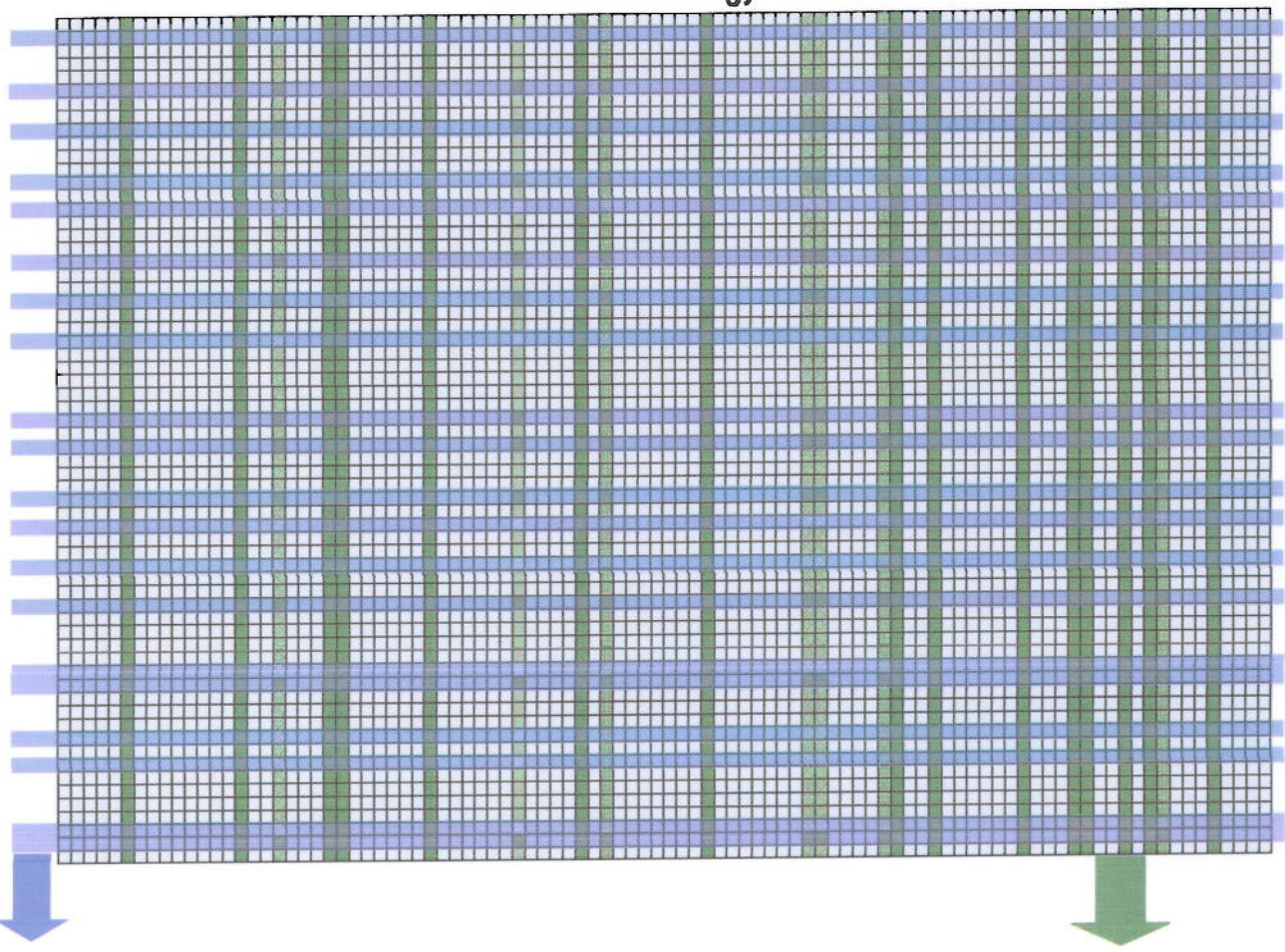
Accessions



Step 1. Molecular variation (e.g. SSRs) enables description of germplasm structure

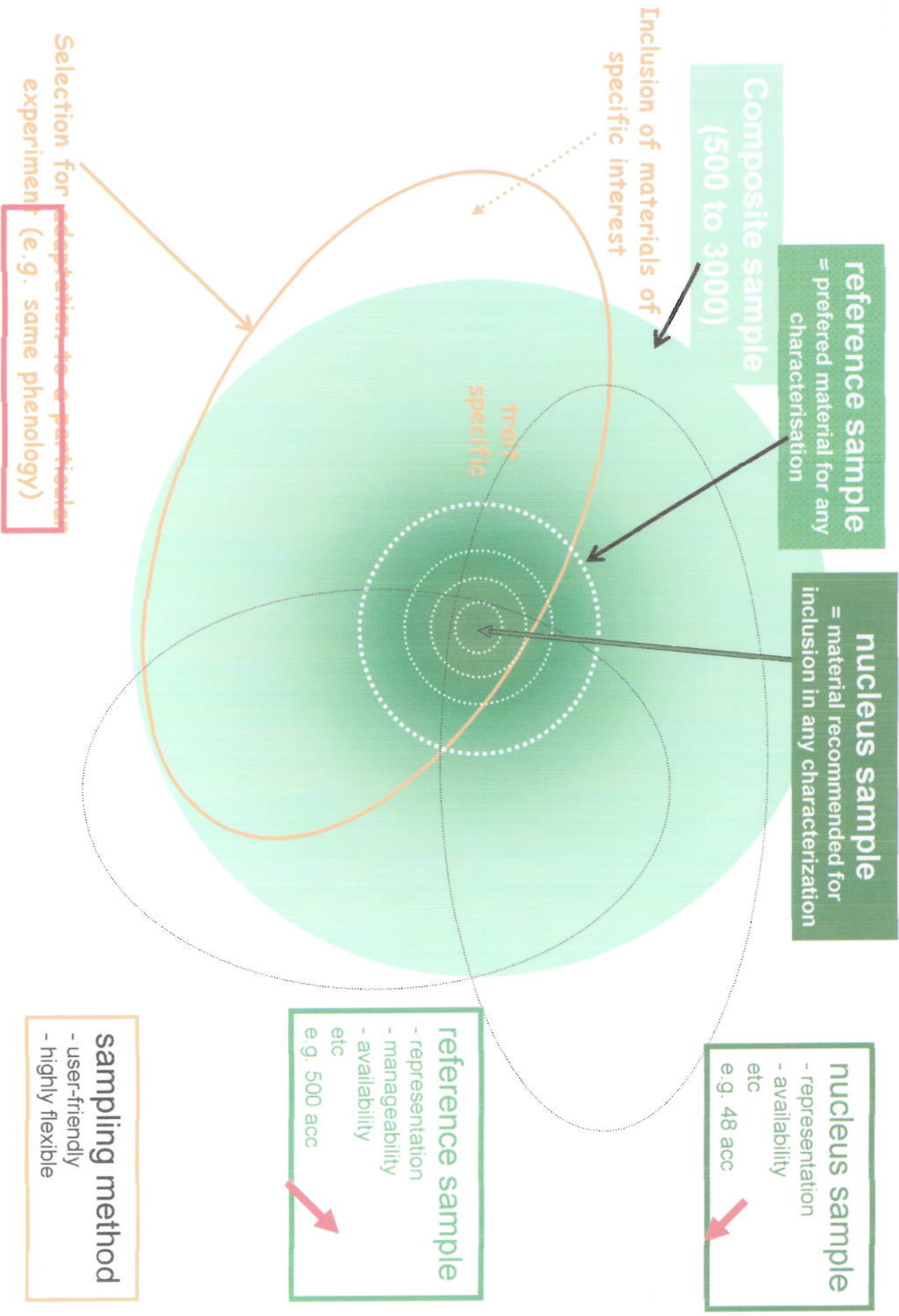
Markers

Accessions



same structure in reference set with reference markers

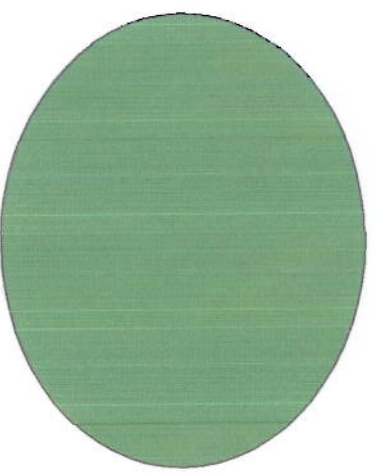
reference markers



Selection of materials for a particular characterisation

Homogeneous

Representative

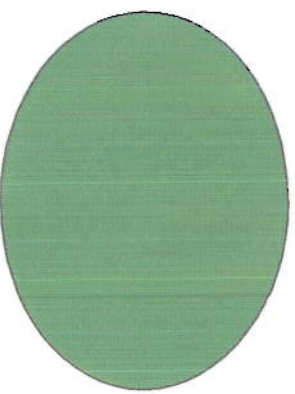


Association

detection
refinement
proof

Homogeneous

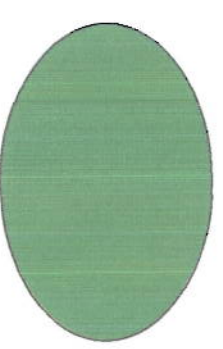
Representative



reinforcing evidence

(proven)
allele comparison

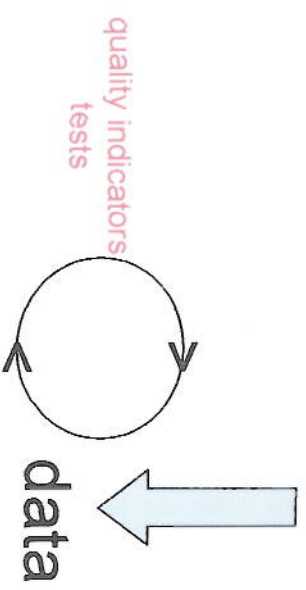
Homogeneous
Representative



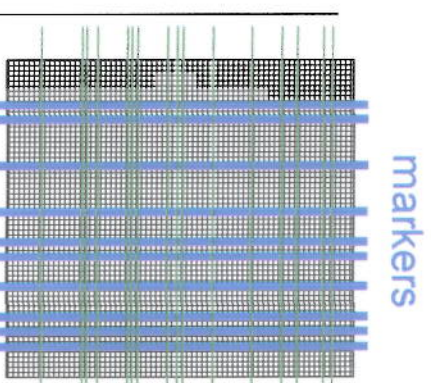
diversity description
& exploration

maize vs yam

project

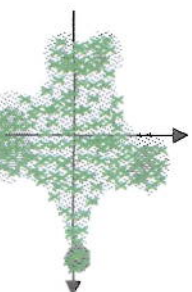


accessions



data matrix, PI, Lab/Institute

labelled reference markers
(marker kit?)



labelled reference sample

'representative' + ...

validation

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Generation
Tapping Nature's Diversity for Humanity

Creation of an improved understanding of the structure of the diversity for the major world food crops

- 1.1. Structure of genetic resources for the most advanced crops (tier-1) accurately described (including tools) and summarized in a reference sample
- 1.2. Structure of genetic resources for the less advanced crops (tiers2 and 3) accurately described (including tools) and summarized in a reference sample
- 1.3. Seed of reference germplasm readily available for all crops
- 1.4. Local assessment of linkage disequilibrium in the genome of rice conducted
- 1.5. Global assessment of linkage disequilibrium in the genome of rice conducted
- 1.6. Linkage disequilibrium assessed across several legumes along conserved gene stretches
- 1.7. Detailed analysis conducted of maize diversity after migration out of America
- 1.8. Methodology developed for resampling genetic diversity in large germplasm collections

Development of a range of flexible HTP genotyping techniques accessible in reference laboratories

- 1.9. DArT's validated as a genome-wide molecular characterization technology
- 1.10. EcoTILLing assessed as a gene-targeted molecular characterization technique
- 1.11. Methodology developed to assess SNPs with effect on allele expression (Non Coding SNPs)
- 1.12. Database on allele diversity at candidate genes across species developed

Establishment and implementation of a scientific and organizational framework to describe tolerance to drought

- 1.13. A database on field-proven drought tolerant and drought susceptible genotypes established
- 1.14. Set of phenotyping facilities in Brazil made accessible for GCP germplasm evaluation
- 1.15. A crop and whole-plant modeling framework developed to support assessment of tolerance to drought
- 1.16. Phenotyping capacity accessible to the GCP is inventoried
- 1.17. Drought-related phenotyping of specific populations with high quality molecular information implemented/Support service consolidated

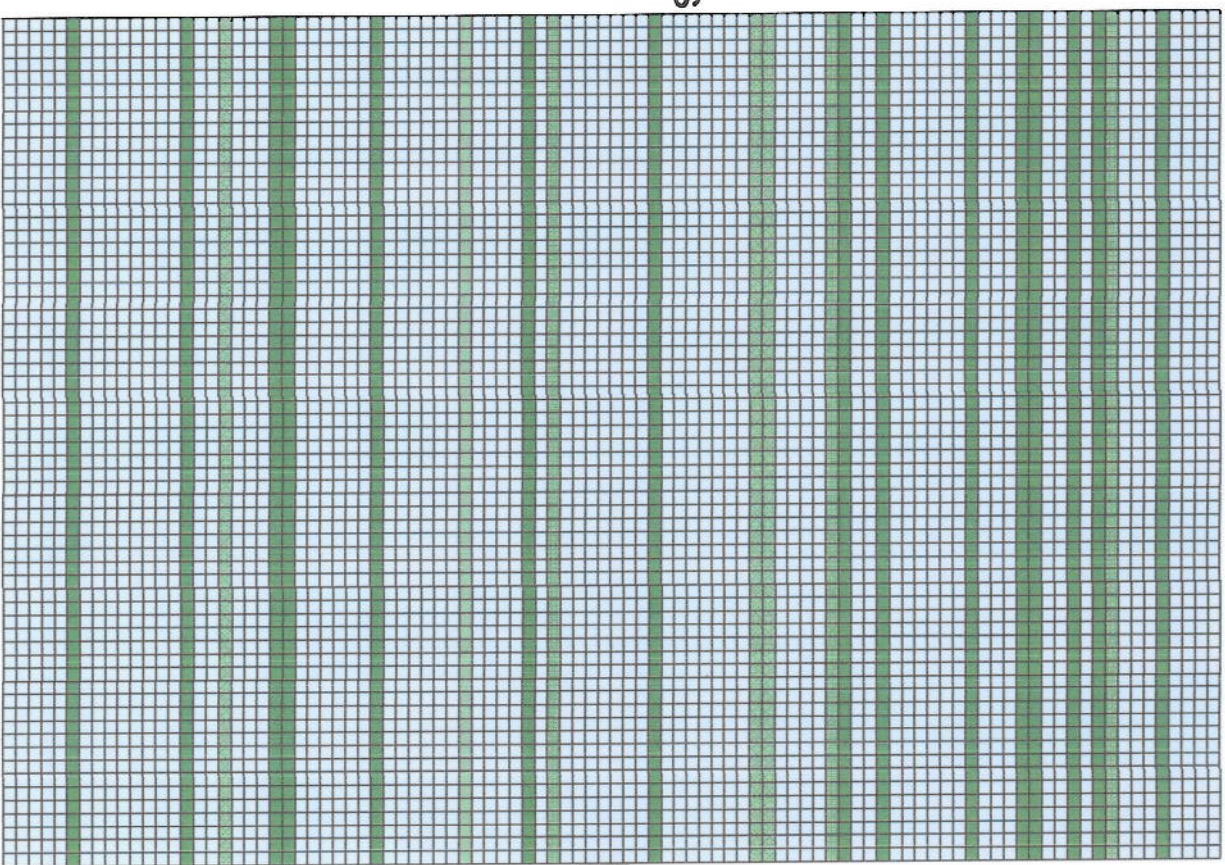
Identification of favourable genetic factors (i.e., potential genes or genome segments) and superior alleles (or haplotypes) through association studies

- 1.18. Favourable genetic factors for drought tolerance in maize identified
- 1.19. Favourable genetic factors for drought tolerance in rice identified
- 1.20 (pending). Favourable genetic factors for stress tolerance in four legume species identified

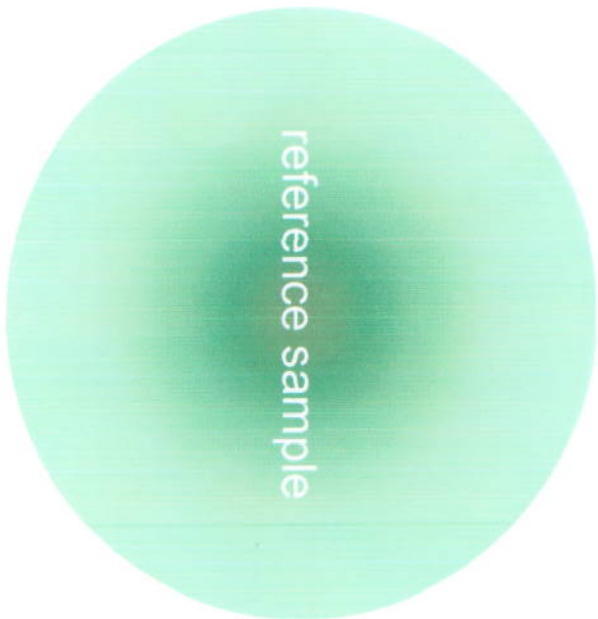
Development of novel populational approaches for relating genotypes to phenotypes

- 1.21. Ecogeographic/genetic clines related to drought identified for selection pattern analysis
- 1.22. Populations for multiple allelic segregation developed through intercrossing
- 1.23. Linkage disequilibrium and patterns of selection in the genome of sorghum used for mapping useful genes
- 1.24. Diversity patterns in the genome of sweet potato used for mapping useful genes in relation to heterosis
- 1.25. Base broadened of current crop diversity in rice using related species
- 1.26. Base broadened of current crop diversity in rice using interspecific bridges with African rice
- 1.27. New alleles introgressed from wide crosses using crop wild relatives in barley

Markers



Accessions



Step 2. Molecular variation is a useful basis for selection of diversity-rich subsamples