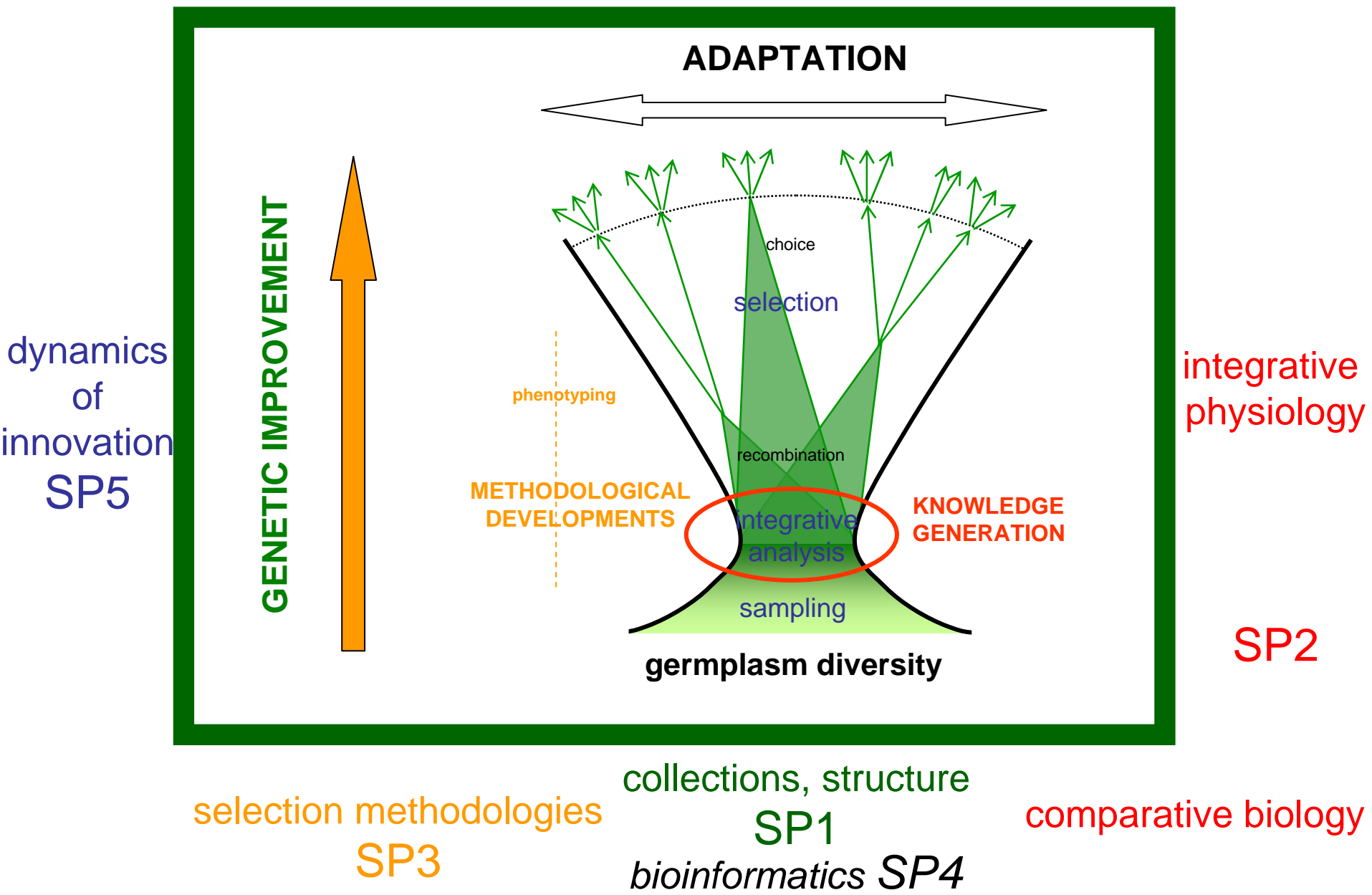


SP1 perspective

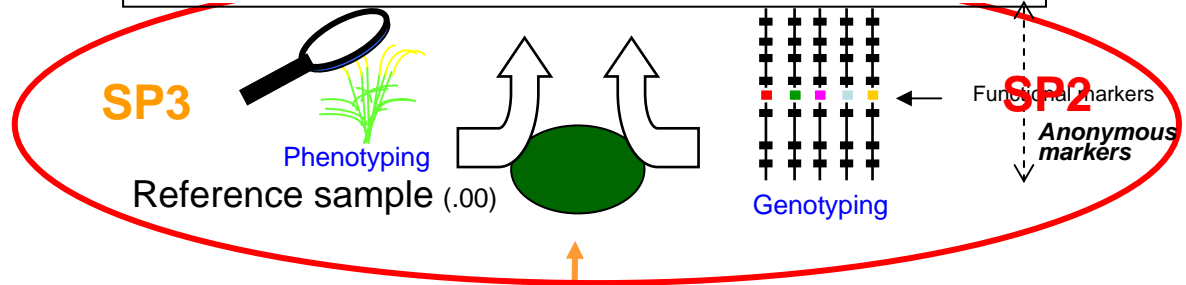
day 1



Step 3.
Association studies



genes/alleles tagged for marker-assisted breeding

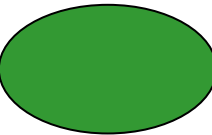


**Step 2: from molecular data
sampling the core sample
to produce a reference sample
for integrated characterisation
and evaluation efforts**



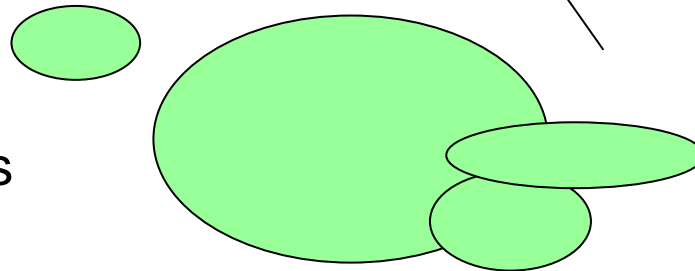
**Step 1: from passport information,
sampling global resources
to produce a core sample**

Composite sample
(10%, up to 3000)



Data collection,
Analysis

Various collections



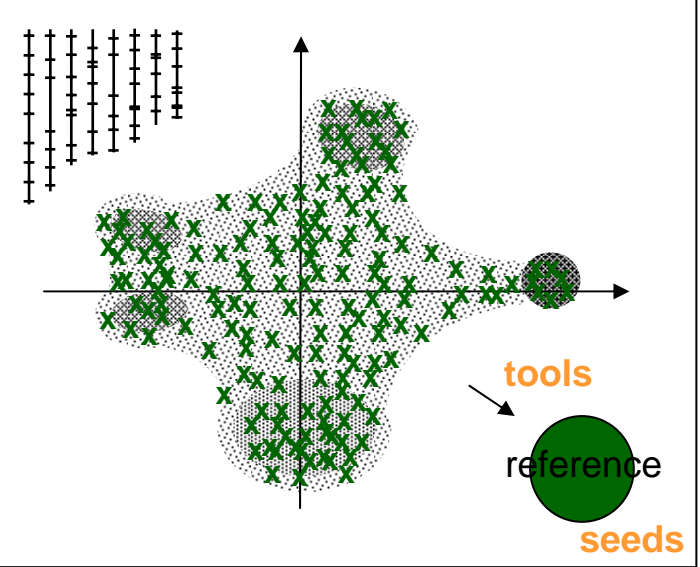
Three steps to elaborate reference collections
in order to mine genes, alleles and markers

MTP SP1 section ("project 1")

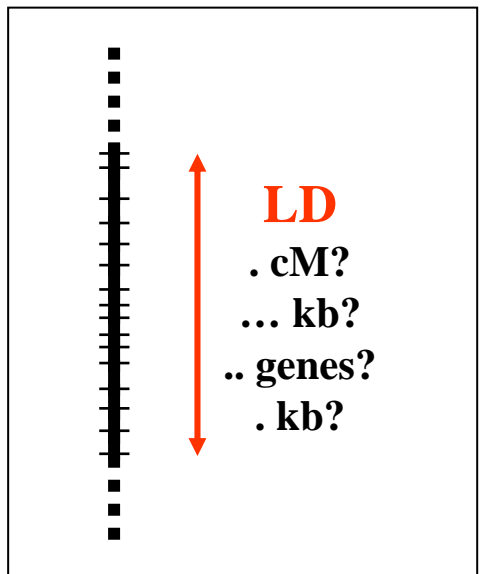
- 1. Creation of an improved understanding of the structure of the diversity for the major world food crops**
- 2. Development of a range of flexible HTP genotyping techniques accessible in reference laboratories**
- 3. Establishment and implementation of a scientific and organizational framework to describe tolerance to drought**
- 4. Identification of favourable genetic factors (i.e., potential genes or genome segments) and superior alleles (or haplotypes) through association studies**
- 5. Development of novel populational approaches for relating genotypes to phenotypes**

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

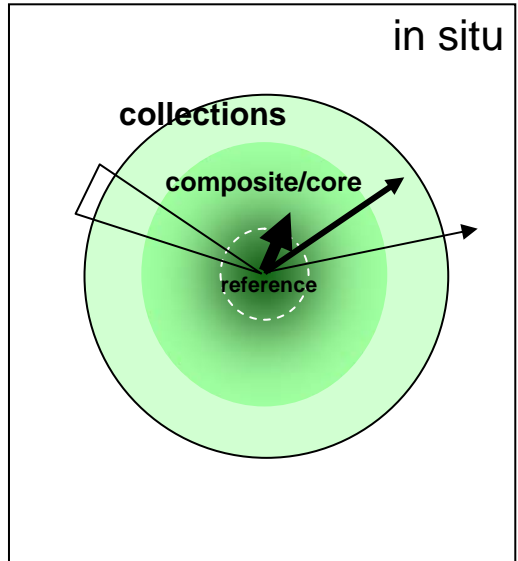
- 1.1. Structure of genetic resources for the most advanced crops (tier-1) accurately described (including tools) and summarized in a reference sample *
- 1.2. Structure of genetic resources for the less advanced crops (tiers2 and 3) accurately described (including tools) and summarized in a reference 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



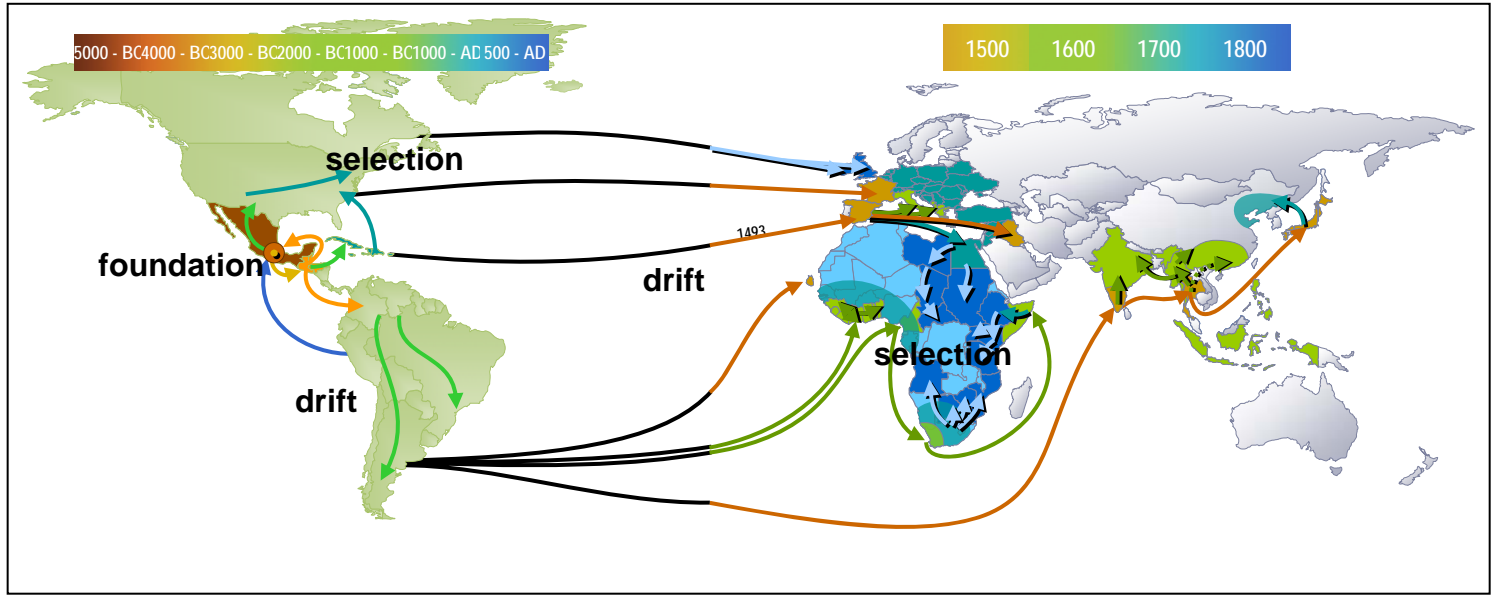
sampling, distributing



calibrating



mining



monitoring history, drift vs selection

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

1.9. DArTs 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

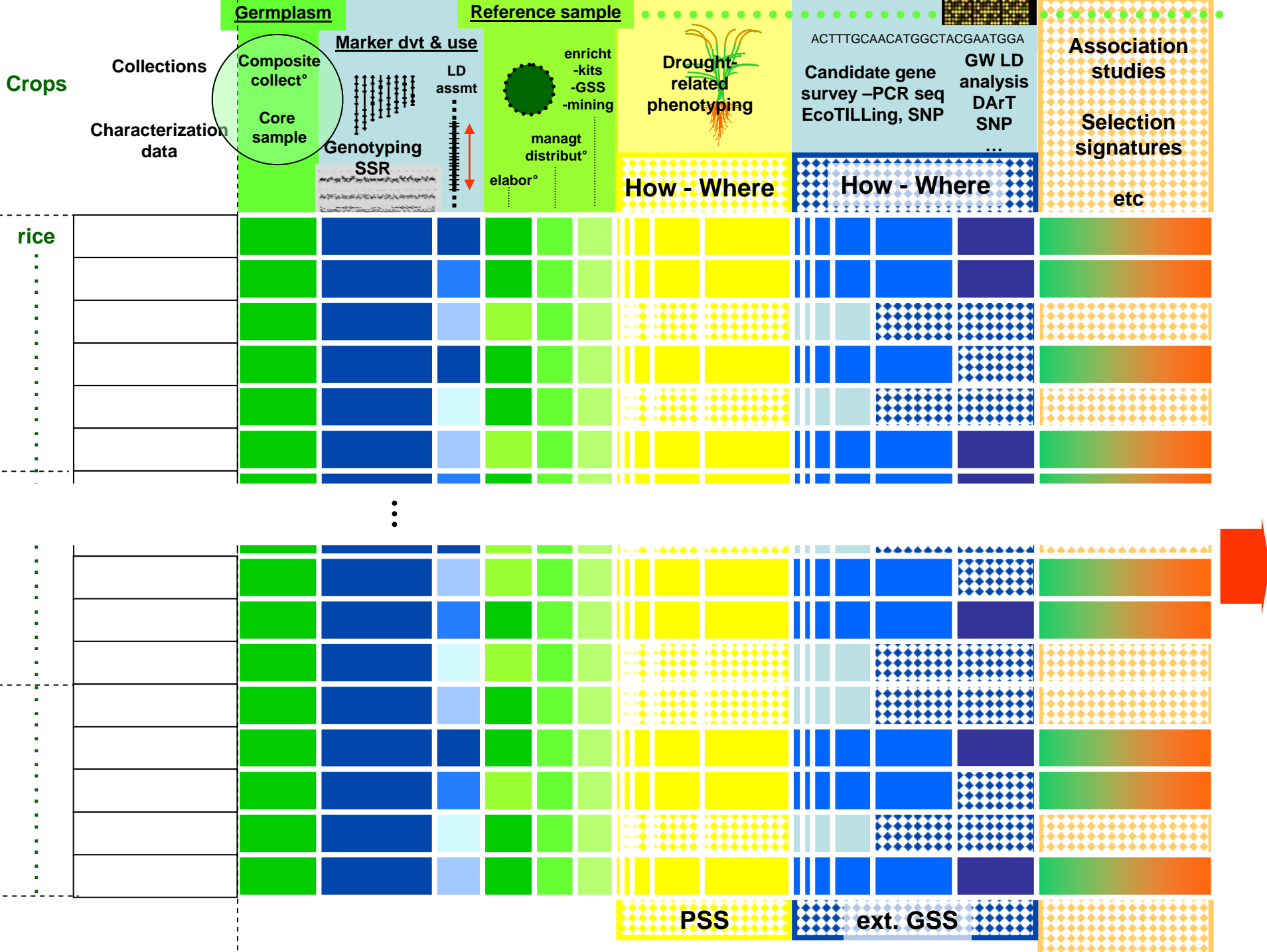
- 1.13. A database on field-proven drought tolerant and drought susceptible genotypes established *
- 1.14. Set of phenotyping facilities in Brazil made accessible for GCP germplasm evaluation
- 1.15. A crop and whole-plant modeling framework developed to support assessment of tolerance to drought
-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

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. 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 *

Brainstorming sessions

Session 1. *Which options for GCP populations development?*

