

Generation Challenge Programme

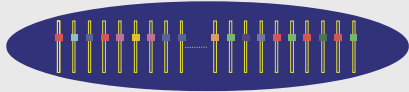
Subprogramme 1

Genetic diversity of global genetic
resources

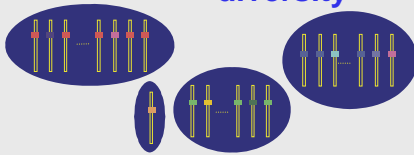
*Activities,
achievements after 1.5 year
and perspectives*

SP1

Germplasm diversity



Molecular diversity



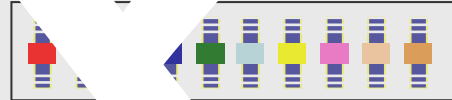
Phenotyping

Heritability

Association studies

Integration in plant breeding

SP4



SP3

Genetic mapping

X

Comparative genomics

Identify candidate genes

Physiology

Functional genomics

ESTs

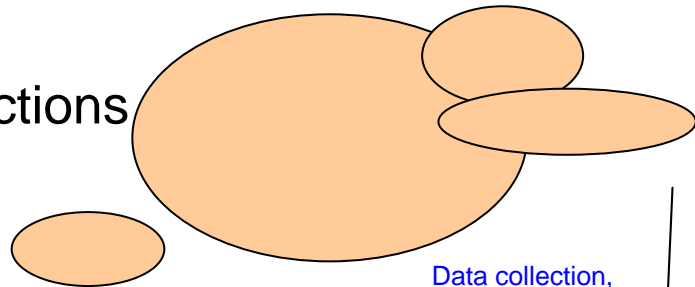


KO mutants

DNA chips

Main activities in year 1

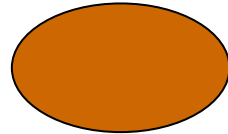
Various collections



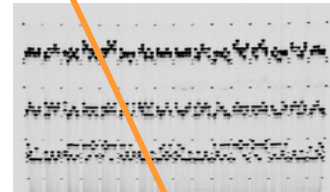
Data collection,
Analysis

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

Core sample (10%, up to 3000)



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

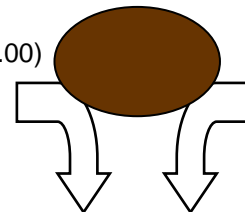


Marker development
Genotyping,
Sampling

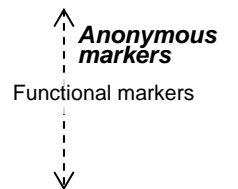
Reference sample (.00)



Phenotyping



Genotyping



Step 3. Association studies



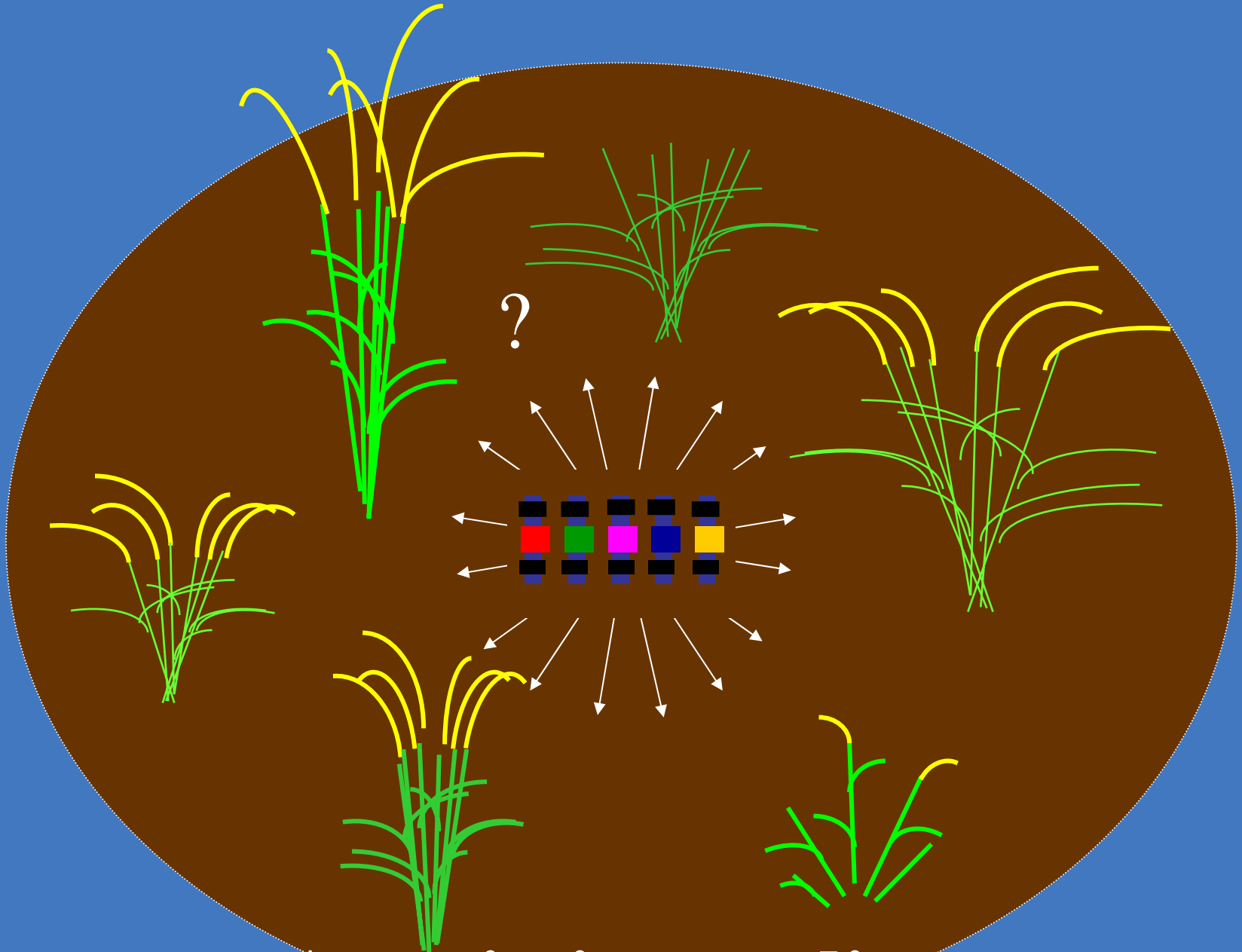
genes/alleles tagged for marker-assisted breeding

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

Expected outputs

- A good understanding of the germplasm diversity structure of the major food crops
- Reference samples for integrating future characterization efforts in order to resolve trait components, genetic control and allelic diversity
- Easy-to-use marker systems for classifying any new germplasm in relation to reference samples representative of global diversity
- A community of trained scientists with access to tools and facilities

Crop	Lead institution and partners	year start – end	Core sample genotyping target N acc. x N loci
Rice	IRRI-CAAS-CIAT-WARDA-Agropolis	2004-2005	3000 x 50
Maize	CIMMYT-CAAS-IITA-Agropolis	2004-2005	1775 x 50
Wheat	CIMMYT-CAAS-ICARDA-Agropolis	2004 – 2006	(2600 + 400) x 50
Sorghum	ICRISAT-Agropolis-CAAS	2004 – 2006	(700 + 2300) x 50
Barley	ICARDA-CAAS	2004 – 2006	(500 + 2500) x 50
Common bean	CIAT-EMBRAPA	2004-2005	3000 x 50
Cowpea	IITA	2004-2005	2000 x 50
Chickpea	ICRISAT-ICARDA	2004 – 2006	286 + 2714
Cassava	CIAT-EMBRAPA-IITA	2004-2005	3000 x 36 + DArTs
Potato	CIP	2004-2005	1000 x 50
Musa	IPGRI-IITA-Agropolis	2004-2005	960 x 50
Finger millet	ICRISAT	2005-2006	1000 x to be det'd
Groundnut	ICRISAT-EMBRAPA	2005-2006	1000 x 20
Pigeon pea	ICRISAT	2005-2006	1000 x 20
Lentil	ICARDA	2005-2006	1000 x 30
Yam	IITA	2005-2006	350 x 20
Coconut	Agropolis	2005-2006	1000 x 22
Sweet potato	CIP	2005-2006	500 x 50
Pearl millet	ICRISAT	2006	to be determined



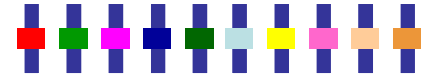
Association studies

Association studies

genotyping

LD analysis

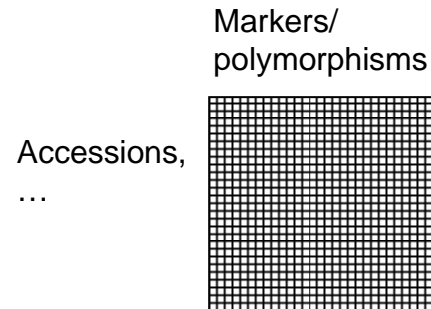
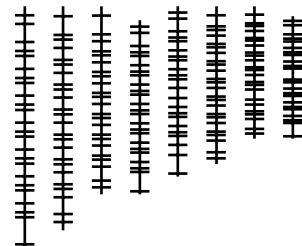
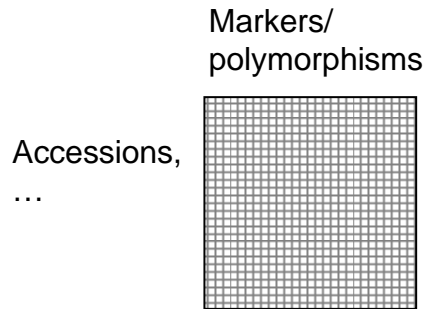
phenotyping



Objectives

NOW

SOON

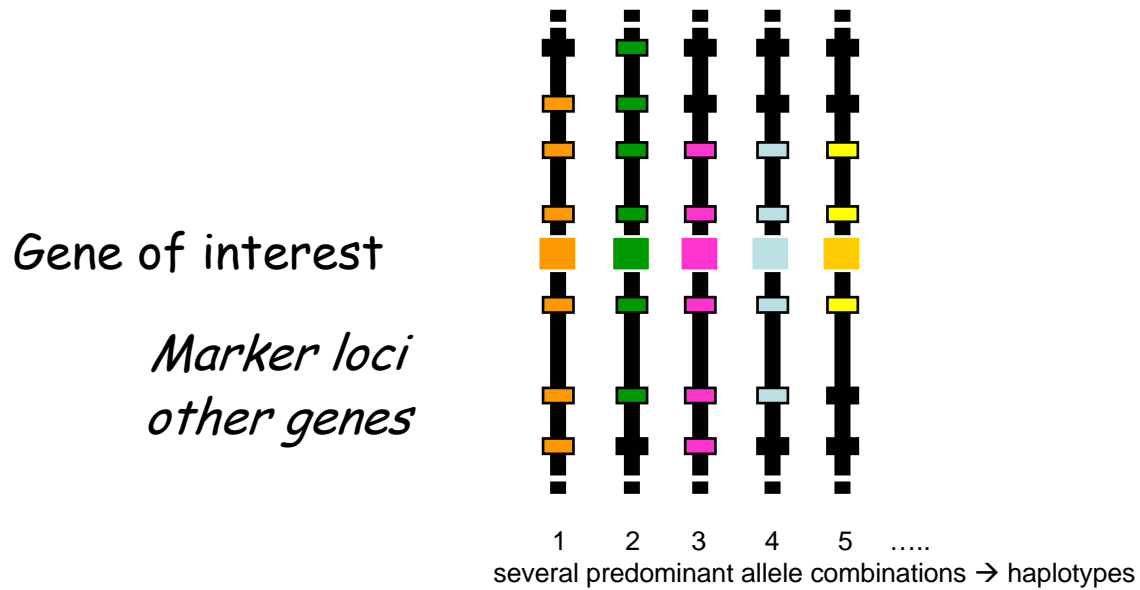


Association studies

genotyping

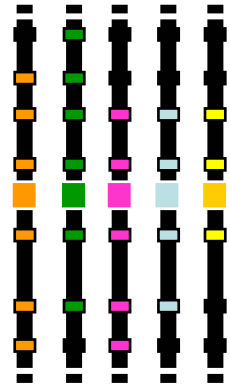
LD analysis

phenotyping



Linkage disequilibrium (LD)

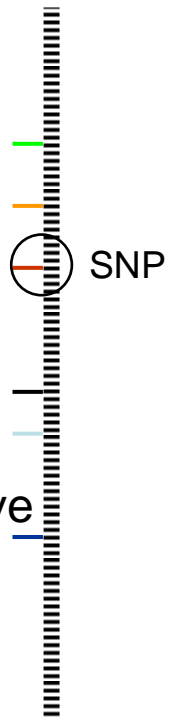
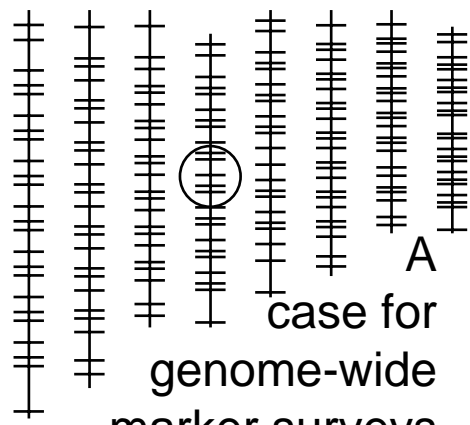
Tagging strategies and extent of linkage disequilibrium



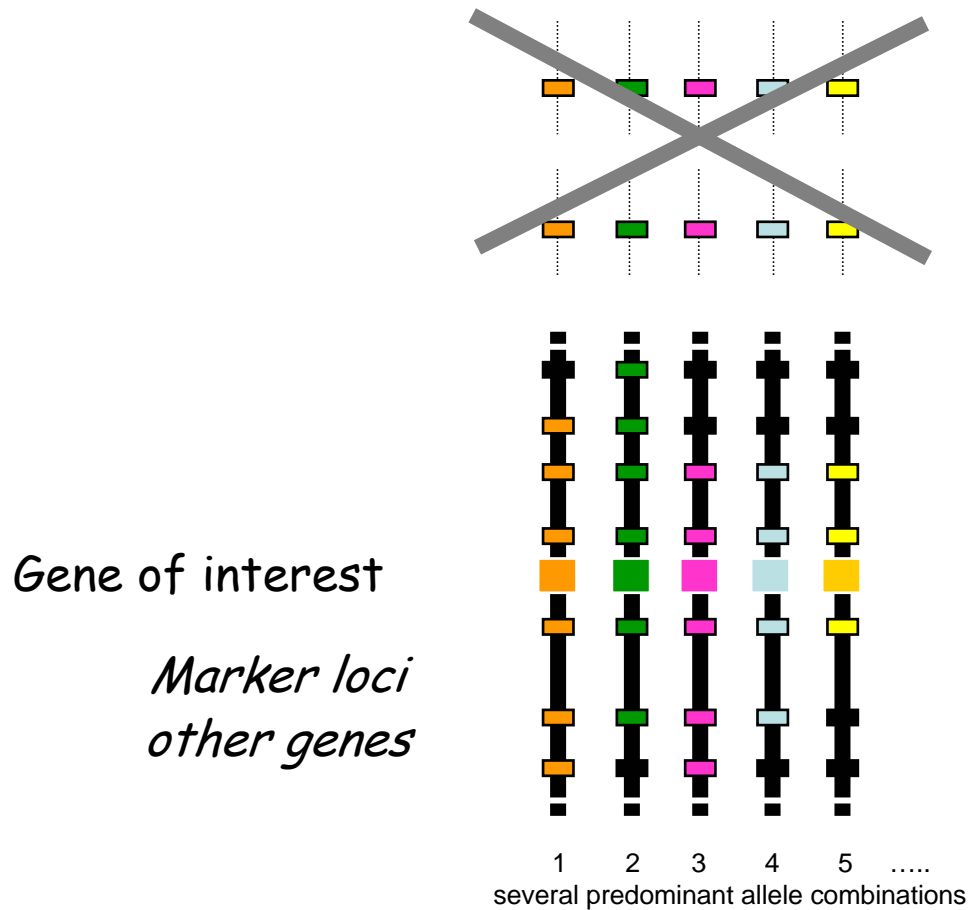
. cM
... kb
.. genes

← ?

Extensive LD



Cases for intensive gene-targetted surveys

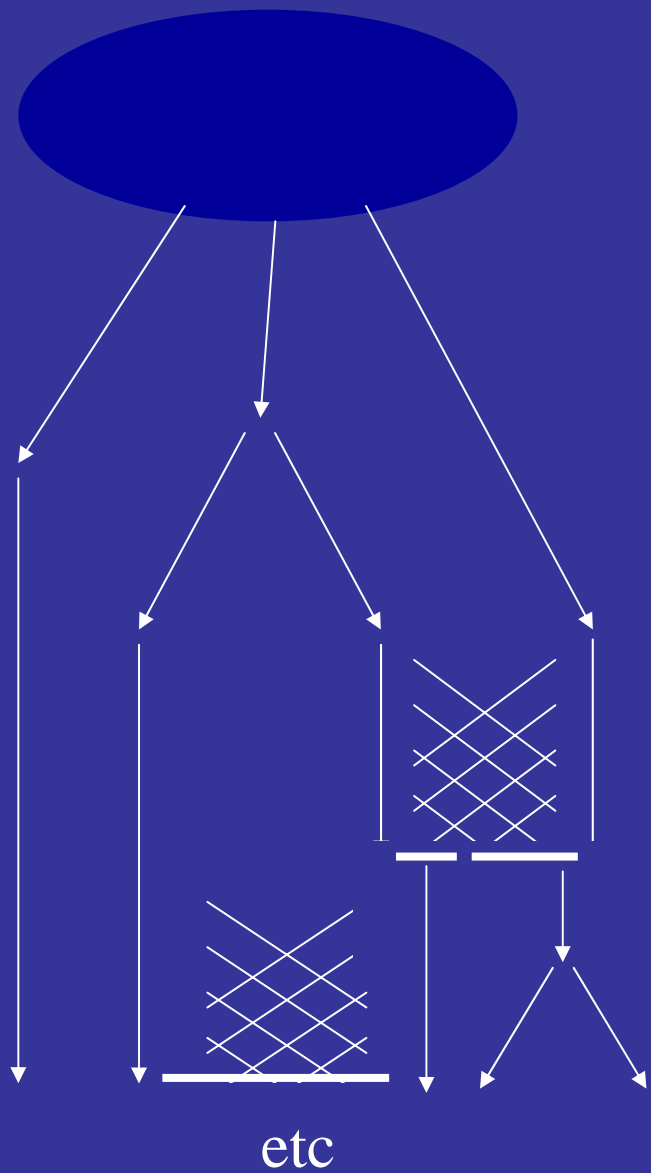


Linkage disequilibrium (LD), association studies and population structure

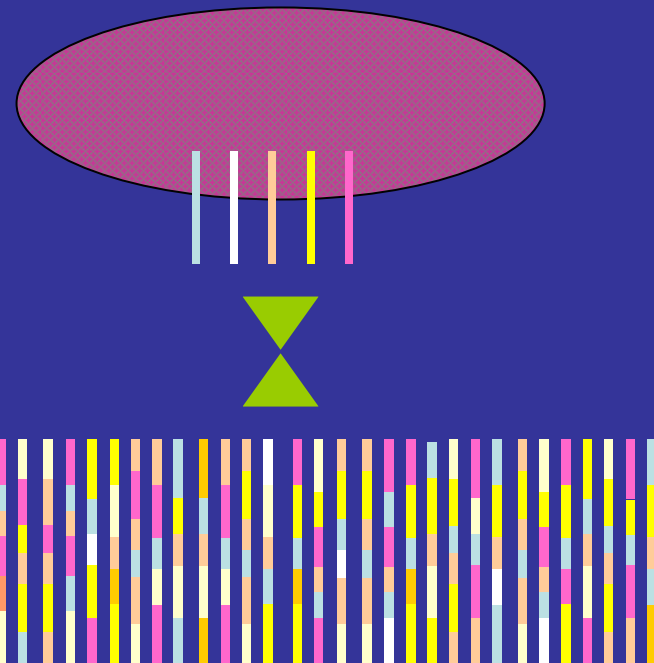
Maize	outbreeder	0.4-7 kb
Barley	inbreeder	10-20 cM
D Wheat	inbreeder	10-20 cM
Sorghum	inbreeder	2-4 cM
		10 kb
Rice	inbreeder	100 kb
Sugarcane	outbreeder	10-20 cM

reviewed by Gupta et al, 2005

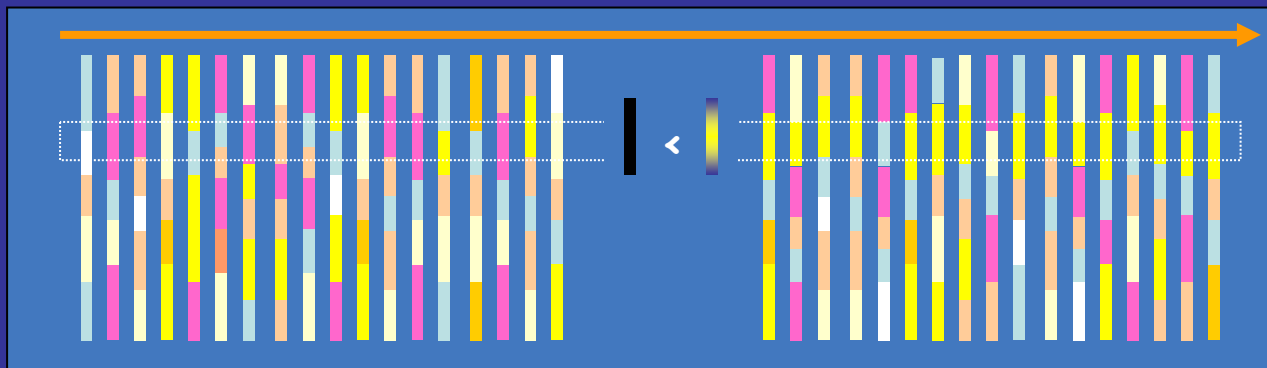
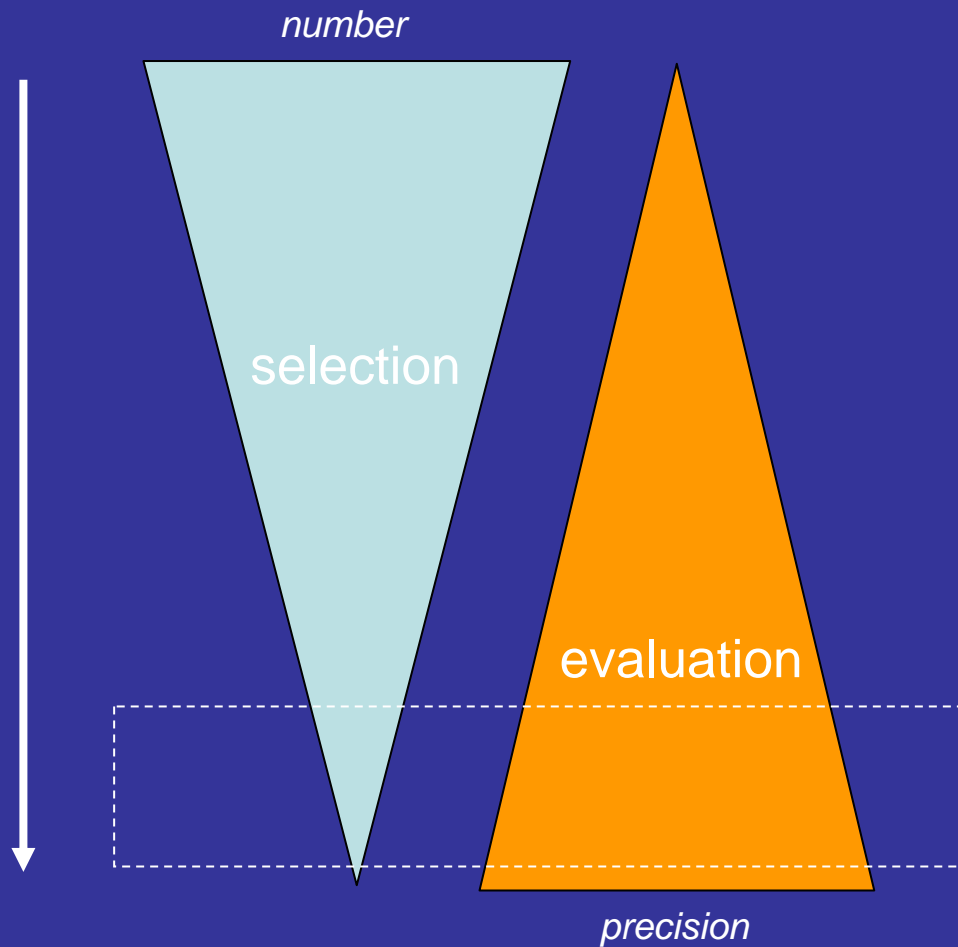
LD assessment



Domestication



Breeding



Case of a breeding programme

Association studies

genotyping

LD analysis

phenotyping

Irrigation system



Capacities

Support from modeling

Courtesy of B Sine et al, Ceraas, Senegal

PI	Year	Project
Warburton	2004 comm	Genotyping of composite germplasm set, Tier 1, maize
Warburton	2004 comm	Genotyping of composite germplasm set, Tier 1, wheat
McNally	2004 comm	Genotyping of composite germplasm set, Tier 1, rice
Billot	2004 comm	Genotyping of composite germplasm set, Tier 1, sorghum
Zhang	2004 comm	Genotyping of composite germplasm set, Tier 1, barley
Blair	2004 comm	Genotyping of composite germplasm set, Tier 1, common bean
Ferguson	2004 comm	Genotyping of composite germplasm set, Tier 1, cowpea
Upadhyaya	2004 comm	Genotyping of composite germplasm set, Tier 1, chickpea
Fregene	2004 comm	Genotyping of composite germplasm set, Tier 1, cassava
Ghislain	2004 comm	Genotyping of composite germplasm set, Tier 1, potato
Roux	2004 comm	Genotyping of composite germplasm set, Tier 1, Musa
Baum	2005 Comm	Completing genotyping of composite germplasm set of barley
Warburton	2005 Comm	Completing genotyping of composite germplasm set of wheat
Hash	2005 Comm	Completing genotyping of composite germplasm set of sorghum
Upadhyaya	2005 Comm	Completing genotyping of composite germplasm set of chickpea
Upadhyaya	2005 Comm	Molecular characterization of tier 2 (orphan) crops -- Finger Millet
Upadhyaya	2005 Comm	Molecular characterization of tier 2 (orphan) crops -- Pigeon Pea
Ghislain	2005 Comm	Molecular characterization of tier 2 (orphan) crops -- Sweet Potato
Furman	2005 Comm	Molecular characterization of tier 2 (orphan) crops – Lentil
Upadhyaya	2005 Comm	Molecular characterization of tier 2 (orphan) crops – Groundnut
Lebrun	2005 Comm	Molecular characterization of tier 2 (orphan) crops – Coconut
Mahalakshmi	2005 Comm	Molecular characterization of tier 2 (orphan) crops -- Yam
Glaszmann	2005 Comm	Assessing DArTs as a genome-wide scanning technology
McNally	2005 Comm	Assessing Ecotilling as a methodology for targeted genotyping and SNP discovery
Perrier	2005 Comm	Development of decision support systems for sampling germplasm (SP4)
de Vicente	2005 Comm	Association analysis in the course of varietal improvement
Duraes	2005 Comm	Supporting emergence or reference drought tolerance phenotyping centers
de Raissac	2005 Comm	Whole-plant modeling (with SP3)
Alvez	2005 Comp	Identifying the physiological and genetic traits that make cassava one of the most drought tolerant crops (with SP3)
McCouch	2005 Comp	Measuring linkage disequilibrium across three genomic regions in rice
Lorieux	2005 Comp	Exploring Natural Genetic Variation: Developing Genomic Resources and Introgression Lines for Four AA Genome Rice Relatives
Ribaut	2005 Comp	Development of informative DNA markers through association mapping in maize to improve drought tolerance in cereals (with SP2)
Warburton	2005 Comp	Characterization of genetic diversity of maize populations: Documenting global maize migration from the center of origin
Baum	2005 Comp	Allele Mining Based on Non-Coding Regulatory SNPs in barley germplasm

CHENNAI WORKSHOP

The program (appendix) was organised in sessions representing the structure of SP1:

Review of results on tier 1 crops; eleven presentations

Selected experiences (from outside the GCP)

- Wheat at Inra

- Barley at IPK

- Maize at Cornell University

Review of other ongoing SP1 projects

- Phenotyping platform and modeling

- Genotyping methodologies; DArTs and EcoTILLing

- LD assessments

- Further genotyping in maize

- Association studies in maize

Use of molecular data for association studies

- Subsampling prior to phenotyping

- Controlling population structure

Research activities of the guests from NARS; twelve presentations

Population structure, phenotypic information and association studies in long-generation crops

- Coconut in Vanuatu

- Yam in Vanuatu

- Potato at CIP

- Cassava at CIAT

- Musa at CARBAP

SP1 perspectives

- The viewpoint of germplasm curators

- The viewpoint of GCP observers

- The viewpoint of NARS representatives

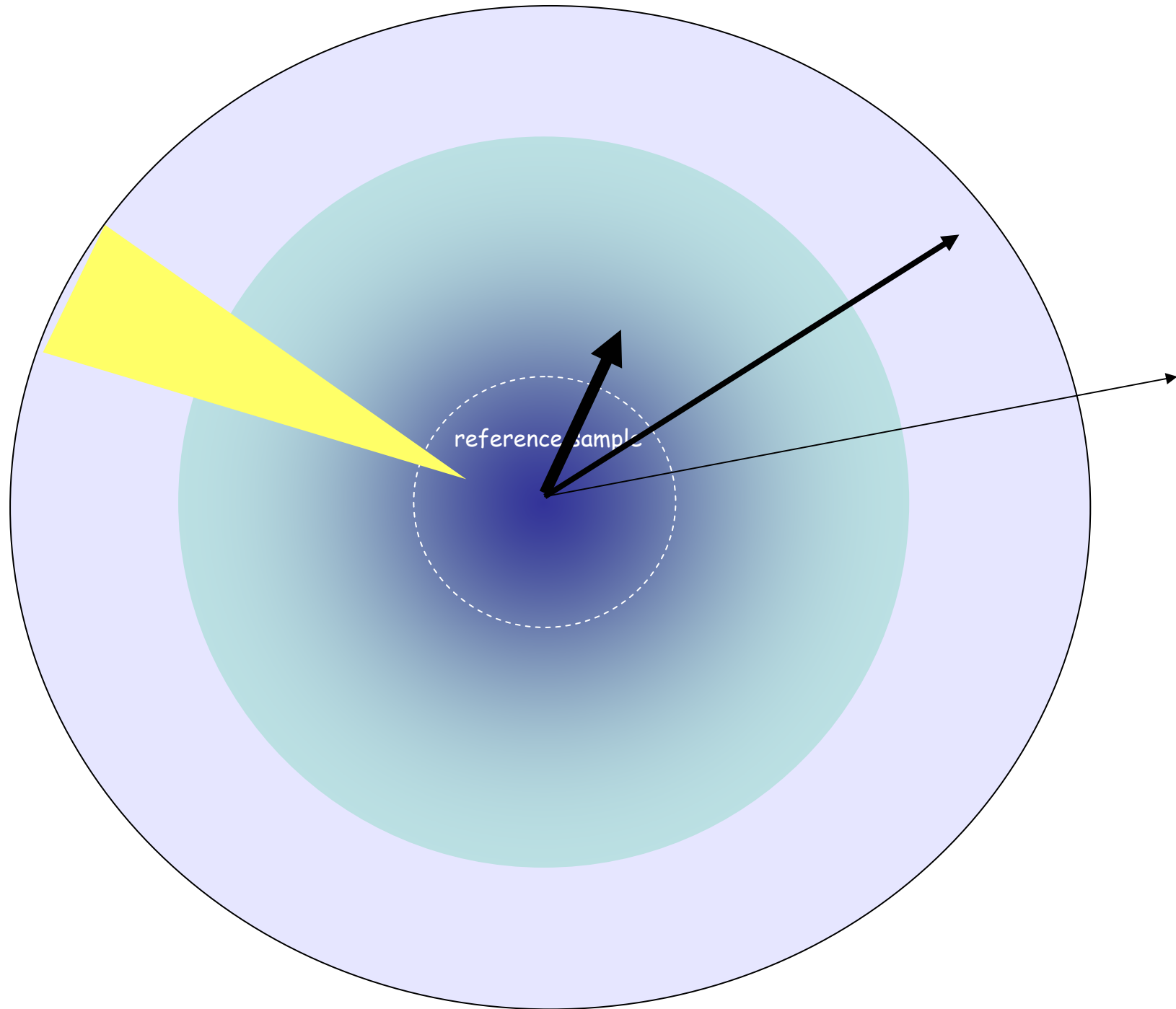
General discussion on SP1 and SP5 perspectives

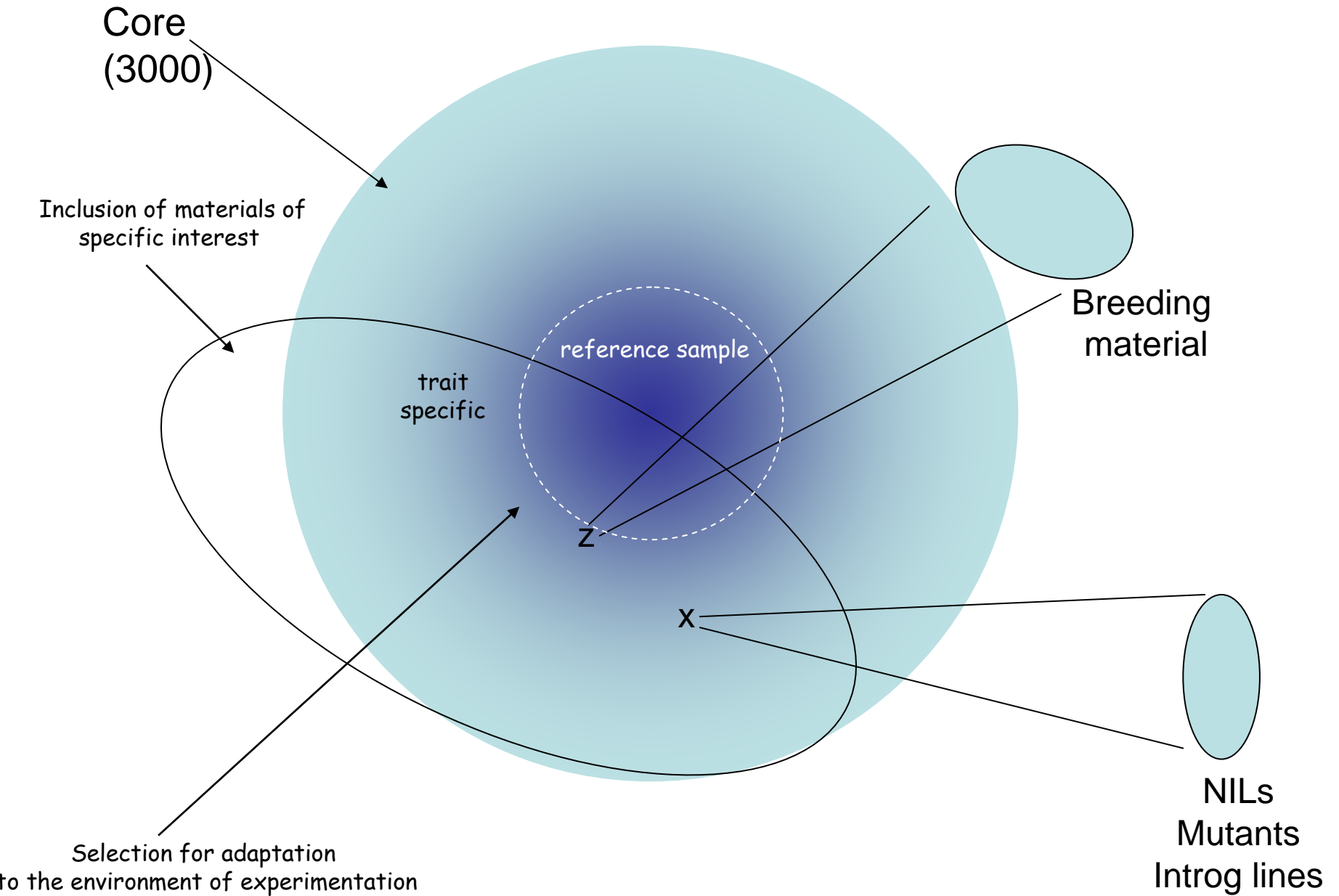
Table 1. Molecular characterization of core samples in GCP crops

Crop	Lead institution and partners	year start – end	Core sample genotyping target N acc. x N loci	Genotyping % mid-2005
Rice	IRRI-CAAS-CIAT-WARDA-Agropolis	2004-2005	3000 x 50	50
Maize	CIMMYT-CAAS-IITA-Agropolis	2004-2005	1775 x 50	40
Wheat	CIMMYT-CAAS-ICARDA-Agropolis	2004 - 2006	(2600 + 400) x 50	60
Sorghum	ICRISAT-Agropolis-CAAS	2004 - 2006	(700 + 2300) x 50	30
Barley	ICARDA-CAAS	2004 - 2006	(500 + 2500) x 50	30
Common bean	CIAT-EMBRAPA	2004-2005	3000 x 50	60
Cowpea	IITA	2004-2005	2000 x 50	-
Chickpea	ICRISAT-ICARDA	2004 - 2006	286 + 2714	50
Cassava	CIAT-EMBRAPA-IITA	2004-2005	3000 x 36 + DArTs	60
Potato	CIP	2004-2005	1000 x 50	80
Musa	IPGRI-IITA-Agropolis	2004-2005	960 x 50	20
Finger millet	ICRISAT	2005-2006	1000 x to be det'd	
Groundnut	ICRISAT-EMBRAPA	2005-2006	1000 x 20	
Pigeon pea	ICRISAT	2005-2006	1000 x 20	
Lentil	ICARDA	2005-2006	1000 x 30	
Yam	IITA	2005-2006	350 x 20	
Coconut	Agropolis	2005-2006	1000 x 22	
Sweet potato	CIP	2005-2006	500 x 50	
Pearl millet	ICRISAT	2006	to be determined	

- Take your time for developing good markers
- (receive and) follow recommendations (after interactive process)
- Hetero(zygo-genei)ty...

- Objective: Mining
 - Accessing; including in focus
 - Locating; in the genome
 - Validating
 - Ranking; haplotypes
 - Elucidating; functional modification
- Trait: Assessability? Heritability?
- Population: LD?
- Approach: Screening? (LD)mapping? Association?





Selection of materials for phenotyping experiments

- SSR genotyping more? When?
- SNPs in rice
- Across-crops (ortho-)allelic diversity
- Open access to users' initiative (SP1/SP3/SP5)
- Phenotyping (materials?)

Time	Output-based	Project	Speaker
8:00-8:30	Plan for the day, Report of the Chennai workshop		Jean Christophe Glaszmann, SP1
8:30-8:40	structure of genetic resources for each crop accurately described (including tools) a set of reference germplasm, data and methods available for designing comparative studies with the view to identifying associations for each crop (including LD assessment for priority crops) <i>(*: dvpt HTP genotyping techniques)</i>	Groundnut core collection/genotyping #03f	Hari Uppadyaya, ICRISAT
8:40-8:50		Lentil core collection/genotyping #03e	Bonnie Furman, ICARDA
8:50-9:00		Pigeon pea core collection/genotyping #03b	Hari Uppadyaya, ICRISAT
9:00-9:10		Coconut genotyping; LD assessment #03g	Jean Christophe Glaszmann, Agropolis
9:10-9:20		Sweet potato core collection/genotyping #03c	Marc Ghislain, CIP
9:20-9:45		Cassava genotyping; traditional and breeding materials #02j and #08	Martin Fregene, CIAT
9:45-10:10		Maize genotyping; migrations out of America #02a and comp#14	Susanne Dreisigacker, CIMMYT
10:10-10:30*		DArT markers #04	Andrzej Kilian, DArT PL
10:30-10:50			Coffee break
	continued <i>(*: dvpt HTP genotyping techniques)</i>		
10:50-11:25		Potato genotyping; wild/traditional and breeding materials #02j and #08	Merideth Bonierable and Marc Ghislain, CIP
11:25-11:55*		Rice genotyping; #02c, #35 and #05 high throughput SNP development; EcoTILLing	Ken McNally, IRRI
12:00-12:30		SP4 presentation, X Perrier	
12:30-13:30		Lunch	
13:30-14:30	a set of phenotyping facilities accessible for GCP germplasm samples a crop and whole plant modeling framework to support assessment of tolerance to drought	Plenary session with other subprograms	
14:30-14:50		Phenotyping network at Embrapa	Frederico Duraes, EMBRAPA
14:50-15:15		General discussion on genotyping, phenotyping and global SP1 perspectives	
15:15		Coffee break	
15:45-17:00	Begin parallel sessions (see page 5 of agenda)		