

Connecting performance under drought with genotype through phenotype Associations in rice

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- Development and implementation of standardized phenotyping and environmental characterization protocols-**Report**
- A large, multilocation data set on the physiological response of a diverse collection of *Oryza* accessions to water deficits at the reproductive stage - **Report**
- Genotype × environment interactions for the traits measured
- Traits of phenotypic plasticity related to performance under drought
- Genes (or genetic regions) and alleles associated with the traits measured
- On this basis, potential markers for marker-assisted selection (MAS) for agronomic performance under water deficit

Countries and ecosystems for managed drought screening

Countries	Centres	Season
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Field phenotyping

Lowland

Philippines	IRRI (1)	DS
India	Ranchi (3)	WS
India	Tamil Nadu (4)	WS
Thailand	Biotec (5)	WS

Upland

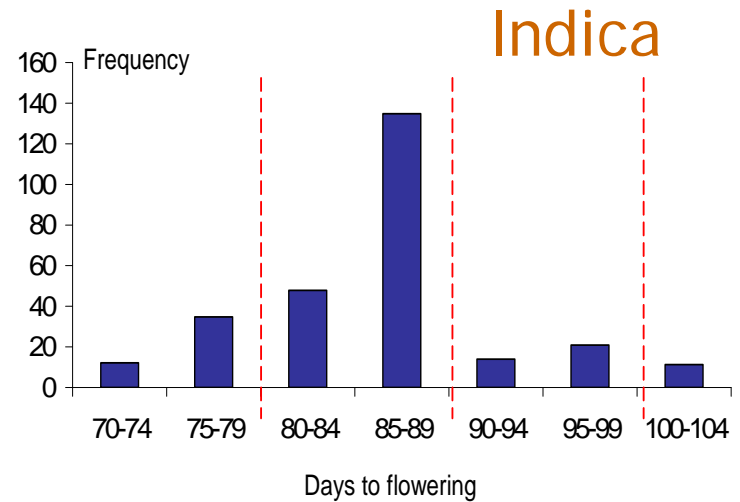
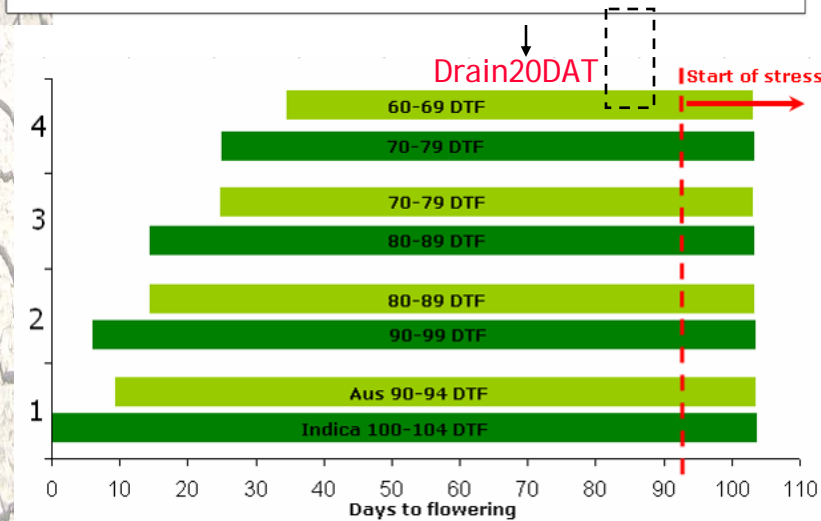
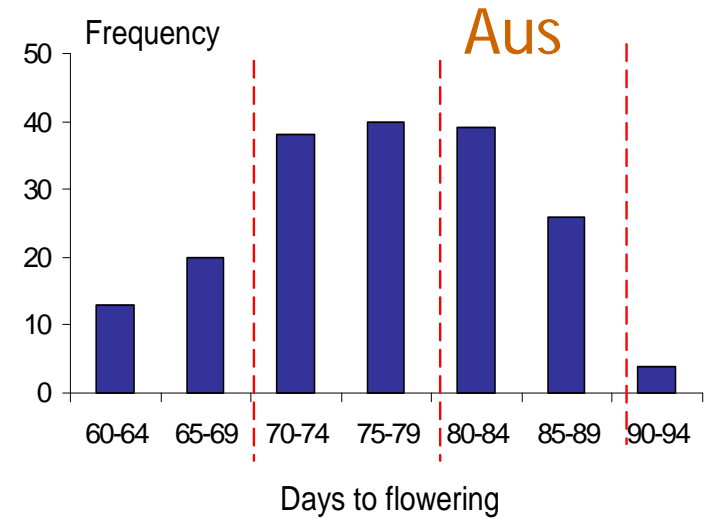
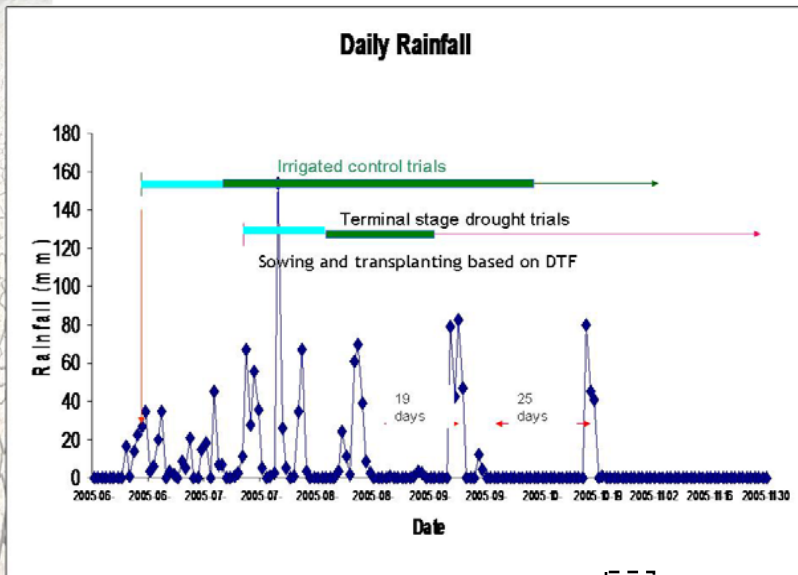
India	Cuttack (2)	DS
Nigeria	WARDA (6)	WS

Model-assisted phenotyping

France	CIRAD (7)	
Philippines	IRRI (1)	



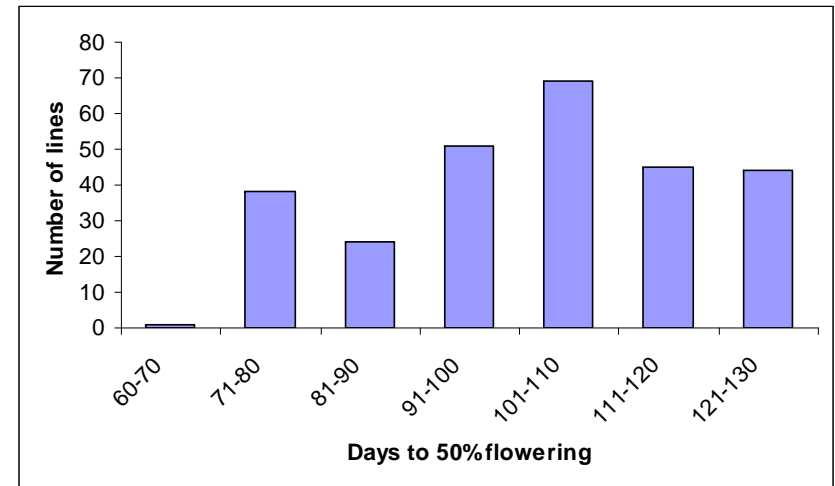
Standardization of phenotyping



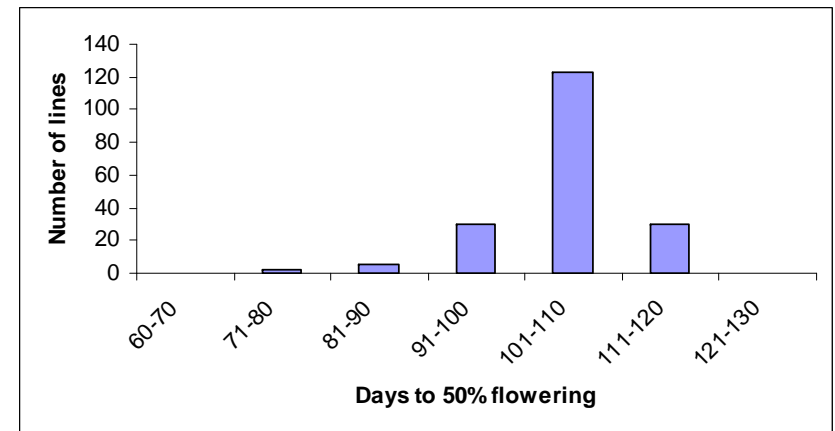
DTF based staggered planting

1.1. Phenological characterization of 1000 accessions under well-watered conditions: IRRI

- Accessions grown under well watered conditions and drought stress at IRRI
- Detailed phenological observations recorded and lines classified into seven groups
- Final grouping will include the phenological observations from different countries



Indica lines under non-stress



AUS lines under non-stress

1.1. Phenological characterization of 1000 accessions under well-watered conditions: India, WARDA, Thailand

- Decision to grow only relevant genotypes at different sites
- 215 accessions sent to WARDA, CIRAD (Japonica)
- 711 accessions sent to Thailand (Aus and Indica)
- 711 accessions sent to CRRI, Cuttack, India (Aus and Indica)
- 711 accessions sent to TNAU, Cuttack, India (Aus and Indica)
- Phenological characterization in progress in Thailand
- Phenological characterization completed at TNAU, India and is in progress at CRRI, Cuttack, India
- Phenological characterization in progress in WARDA



Phenological characterization: India

Phenological traits for indica and Aus lines

Traits	Situation	Mean	Min	Max
DTF	Control	91	61	110
	Stress	86	71	117
PHT	Control	74	63	87
	Stress	64	43	81
Pan Len	Control	21	17	24
	Stress	20	13	25
Biomass kg/plot	Control	2.25	1.73	3.46
	Stress	1.43	0.57	1.99
GYKGP kg/ha	Control	2873	1811	3566
	Stress	609	28	1189
HI	Control	0.38	0.26	0.66
	Stress	0.14	0.01	0.37

699 accessions grown under control and reproductive stage drought stress and characterized for phenological traits

Lines classified into seven groups

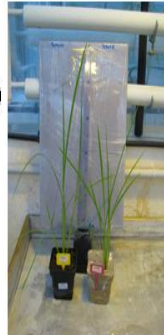


TNAU, Coimbatore, India

CIRAD – AIVA unit: Phenotyping of japonica rice response to vegetative drought

2009 Experiment:

- dry-down design (CIRAD greenhouse, Montpellier France)
- **203 genotypes** and 3 reps (temporal)
- one liter pots (no genotypic rooting differences)



2 treatments
 - irrigated
 -Stressed (drought at leaf-6 stage)
 (Dry down)

Stress monitored gravimetrically (balance): **FTSW 1=>0.2**
 (Fraction of Transpirable Soil Water)

Traits measurements and analyses

Along dry-down (FTSW 1, 0.8,0.6,0.4,0.2)

- Plant daily transpiration (manually weighted)
- Tiller number, leaf number, IH, last formed leaf size, phyllochron
- Plant leaf rolling and senescence indices

At end stress (FTSW0.2)

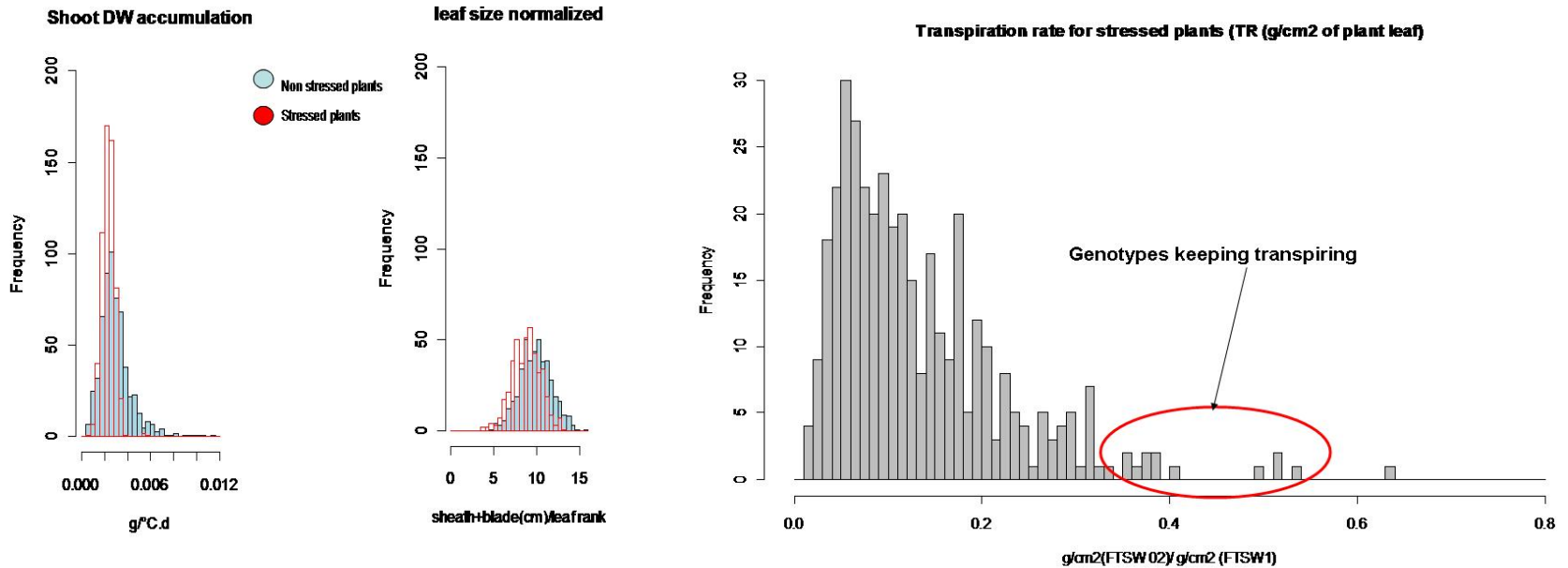
- Shoot DW
- [Sugar] in source (expanded) & sink (expanding) leaves: hexoses, sucrose, starch

Modeling (estimate parameter value for each genotype)

- 1) **one-curve model**: transpiration rate response to FTSW (threshold)
- 2) **Ecomeristem model**: parameters controlling plant morphogenesis response to Env (radiation, water, temperature), e.g.:
 - Tillering response to C assimilate availability
 - Leaf potential dimensioning
 - Potential phyllochron
 - Leaf transpiration, expansion and appearance rate response to FTSW
 - Assimilation rate response to FTSW

Phenotyping Japonica Cultivars: CIRAD

First results : Traits distribution
(203 genotypes, 3 repetitions, 2 treatments)



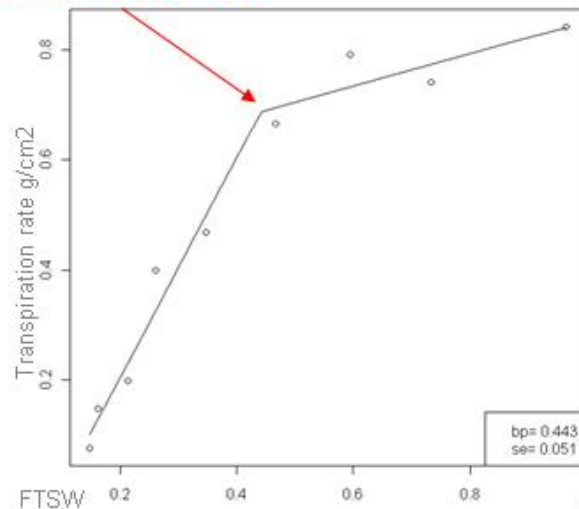
Large variations among genotypes for shoot DW accumulation, leaf size and transpiration ratio

Transpiration rate responses to FTSW

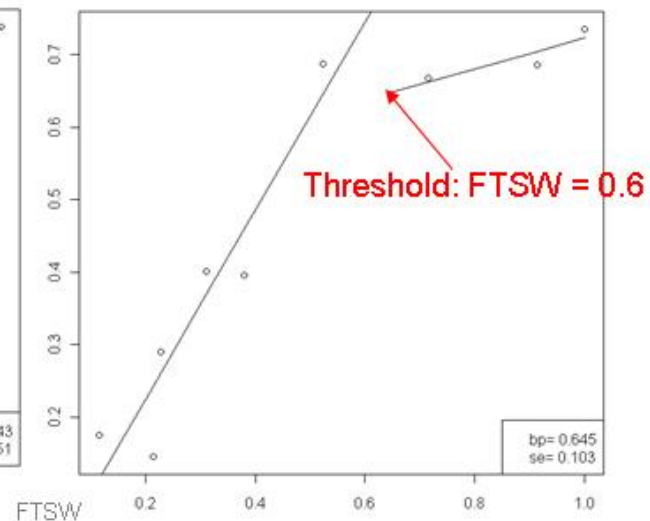
Bilinear regression with breakpoint (bp) for 4 genotypes and 2 repetitions

Method underway to be automatised for 203 genotypes

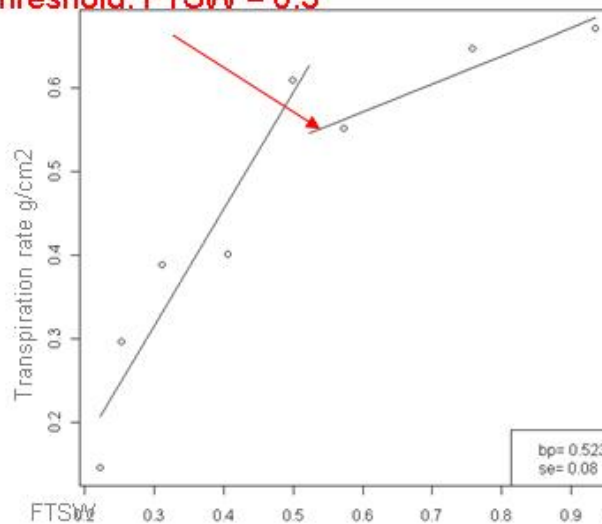
Threshold: FTSW = 0.4 **Génotype 43**



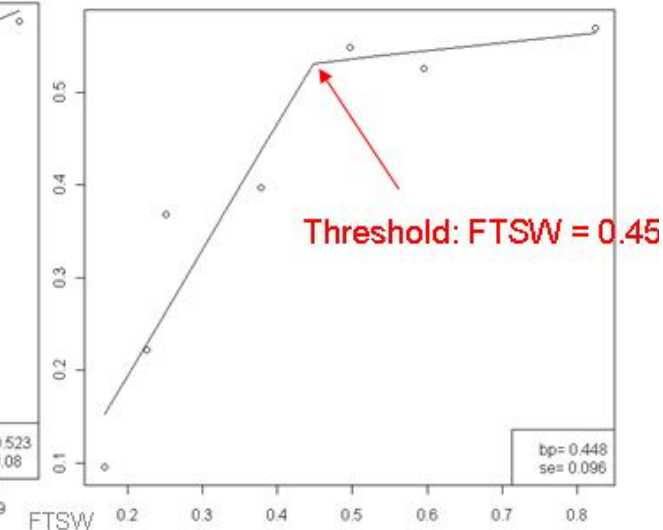
Génotype 60



Threshold: FTSW = 0.5 **Génotype 172**



Génotype 175

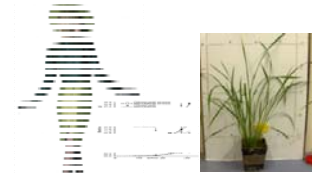
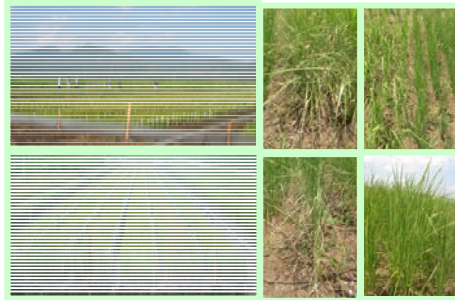


Linkage with other projects



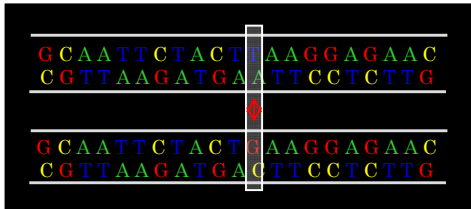
1000 diverse Oryza accessions

Phenotyping drought response across 6 environments

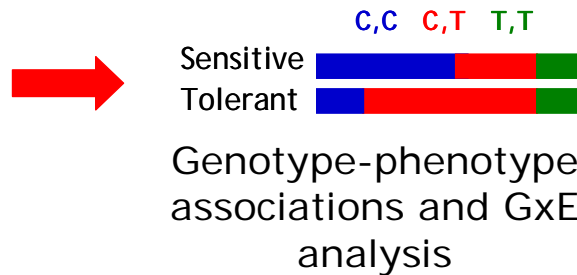


calibrated	MGR	Ict	SLAp	Phyllochron	
IR64	Average	1.19	0.98	38.18	37.12
	SE	0.024	0.017	10.497	0.303

Model-assisted phenotyping using EcoMeristem



Genotyping using high density SNP chips (~6 million features)*



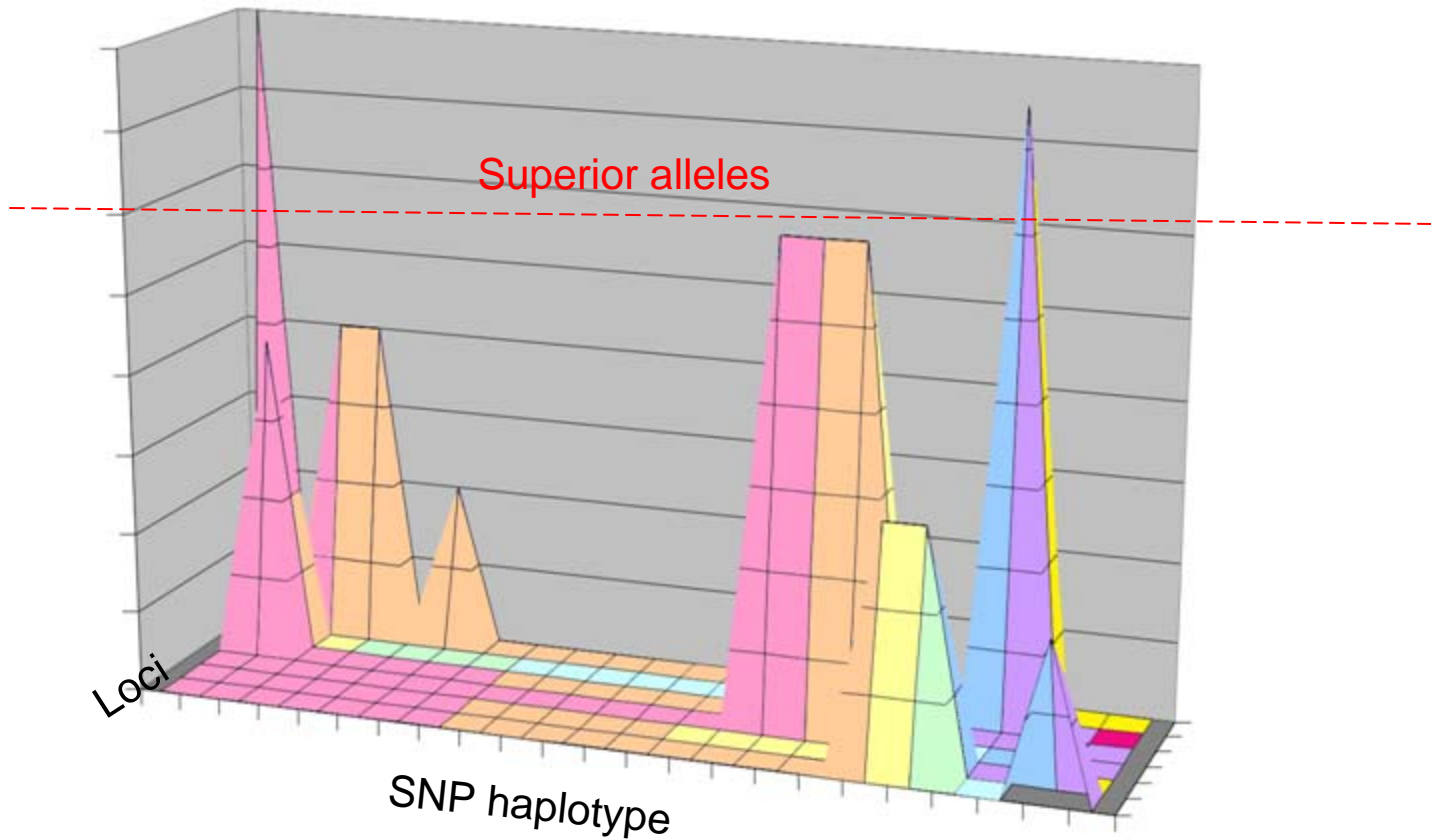
Promising alleles and accessions for drought breeding programs

Schematic overview of project

*to be undertaken by IRFGC

- Seed of 1000 accessions being multiplied at IRRI by SSD, available to partners before next WS season
- Detailed screening of lines at IRRI in DS2010, in India and Thailand in WS2010
- Applying transpiration response curve model to 203 genotypes and Eco-meristem to 20 (method 'tuning') & then 203 genotypes, finalize sugar analyses at CIRAD
- Extrapolating and validating genotype behavior in the field at IRRI in DS2010
- Association studies by 2011

Power of association genetics platform



2010-2011: deep genotyping will allow SNPs to be identified every 4 kb in 2000 accessions

Potential strongly dependant on phenotyping