

# ómica

A stylized graphic on the right side of the page. It features a white DNA double helix structure that curves upwards and to the right. The top of the helix is filled with a pattern of white binary code (0s and 1s) on a dark green background. The helix is composed of white lines and dots, creating a sense of depth and movement.

El futuro  
es de todos

Gobierno  
de Colombia



# Técnicas y Métodos para la Fenotipificación de Cultivos Agrícolas

Fenotipificación en cultivos de arroz



Maria Camila Rebolledo  
PhD Crop Ecophysiology;  
Scientist at CIAT and CIRAD.

Modelado y Control de Drones autónomos para monitoreo agrícola



Julian Colorado  
PhD in Robotics – UAV Control  
Profesor Javeriana Bogotá

Herramientas HW/SW para fenotipificación



Iván Mondragón  
PhD in Robotics – UAV Vision  
Profesor Javeriana Bogotá

Fusión sensorial de imágenes aéreas para fenotipado



Hernan Benitez  
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# Fenómica y mejoramiento de cultivos

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Fenómica



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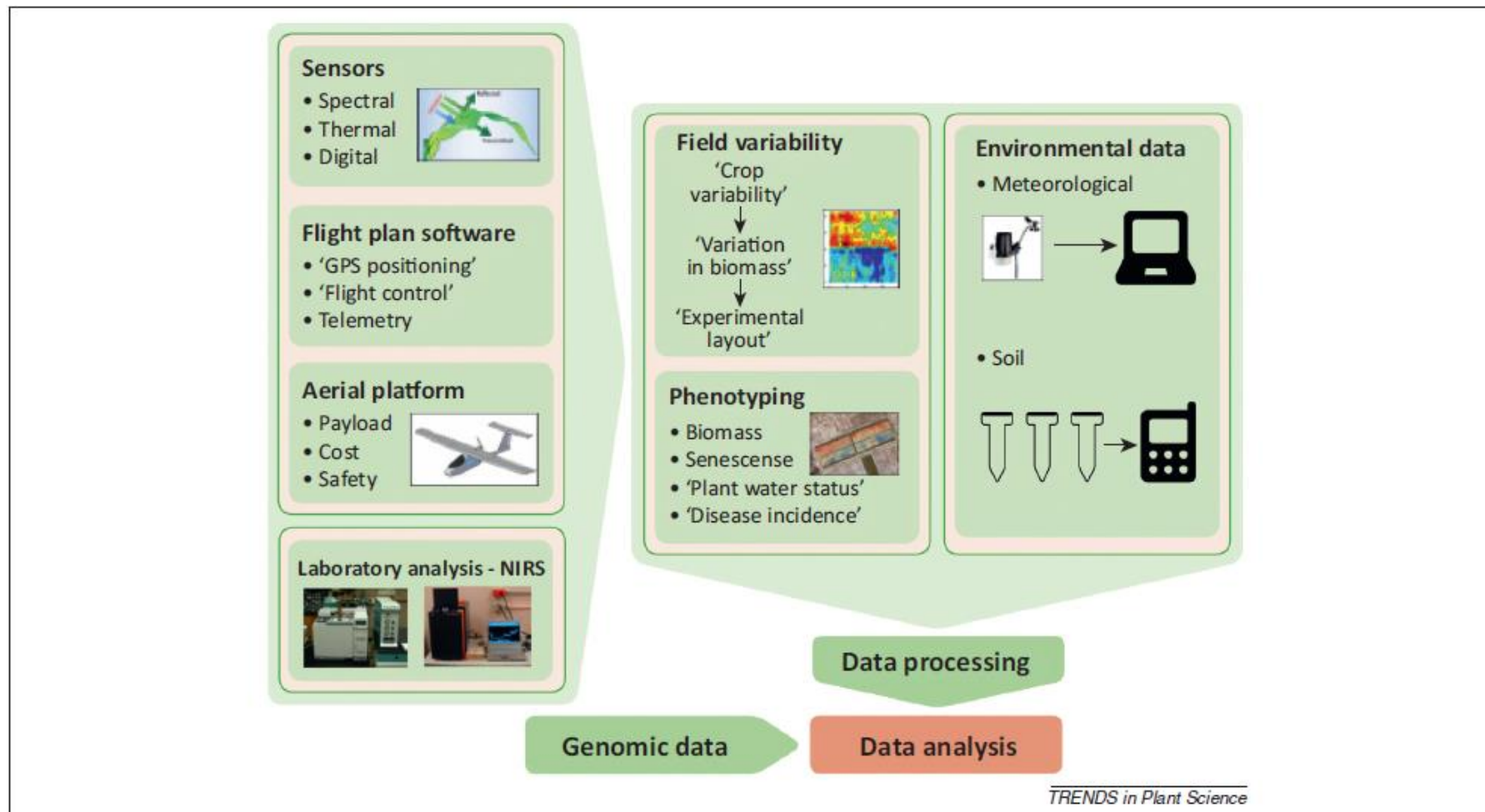
## WHY?

### Increase breeding efficiency (Time, cost, accuracy)

Genetic gain is influenced by six factors:

- genetic diversity that can be accessed
- precision with which a trait can be measured
- selection intensity applied
- Relevance of the trait for in the target environment/ the user
- time and costs

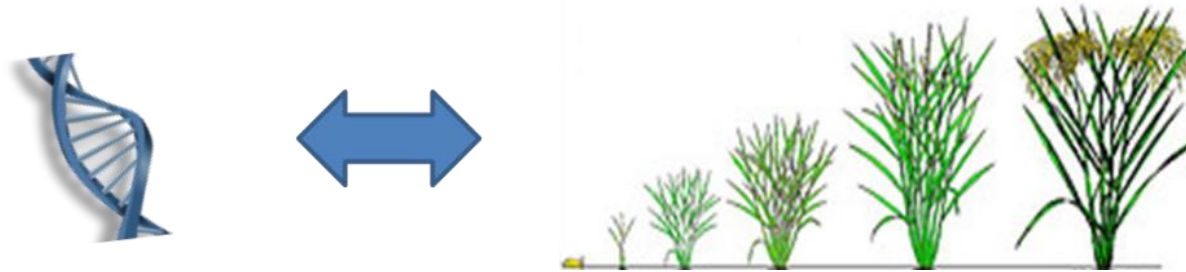
## HTP phenotyping during the breeding process



**Figure 3.** Summary of the different components of the breeding process where high-throughput phenotyping is involved. These include evaluation of key traits at the right moment, assessment of spatial variability, environmental characterization, and further integration of all the information.

## What breeders do with HTP data?

Association phenotype– genotype.



**Objective:** Identify markers (SNPs) and genomic regions that can be associated with a quantitative trait.

### **Perspectives:**

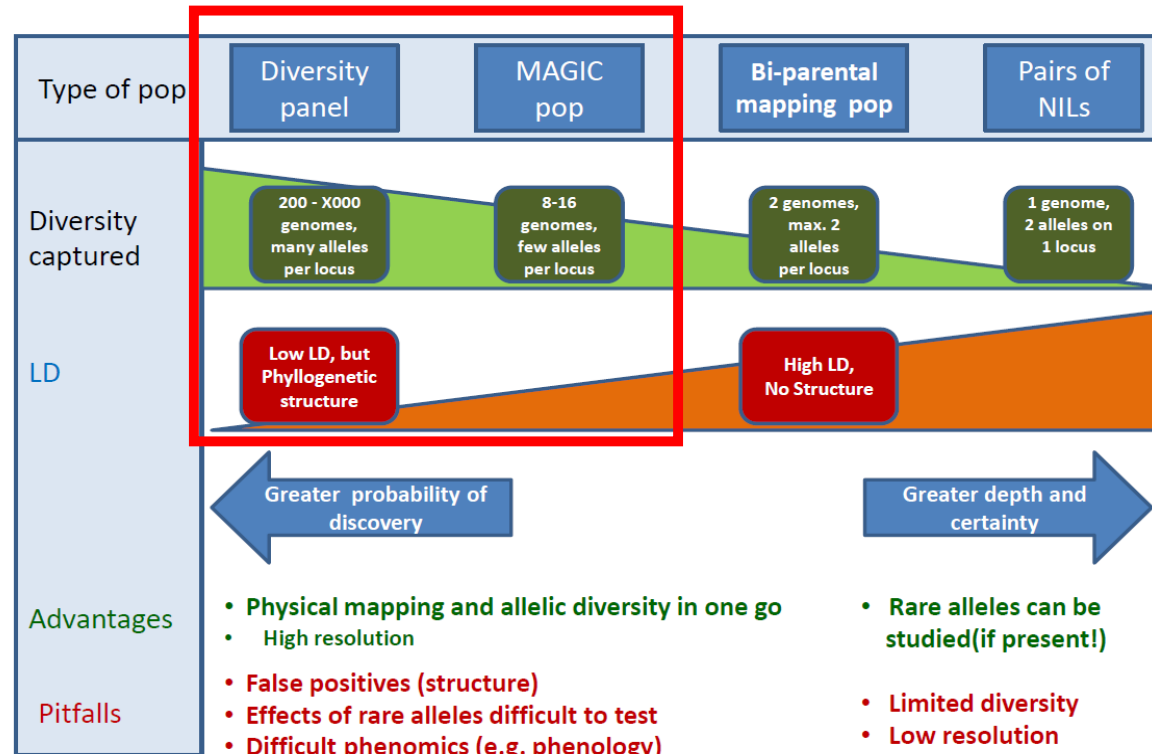
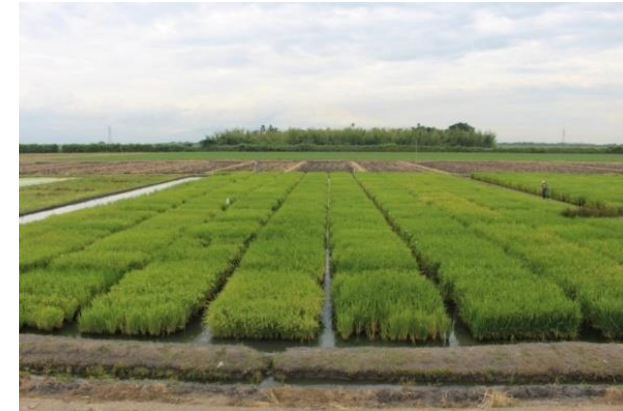
Marker assisted selection (MAS) and development of NILs to accelerate breeding.

## What kind of panel?

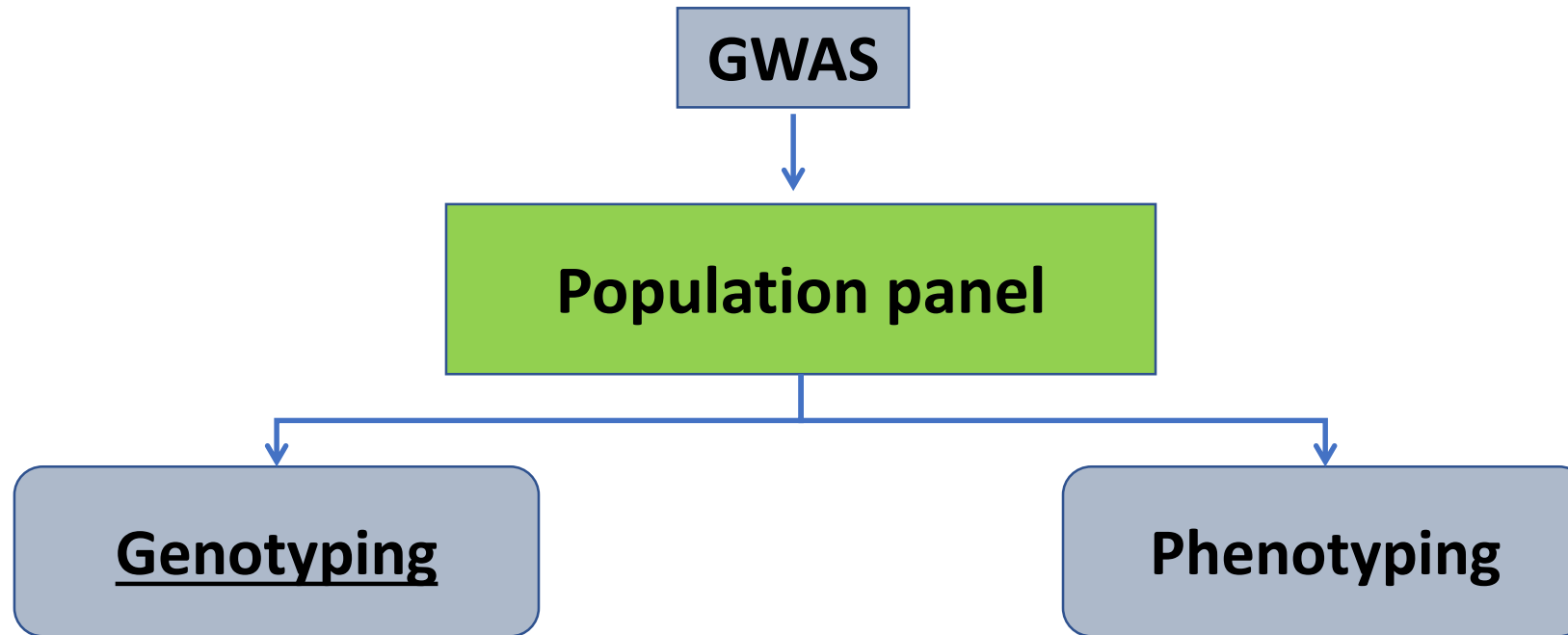
DIVERSITY PANEL



BREEDING PANEL

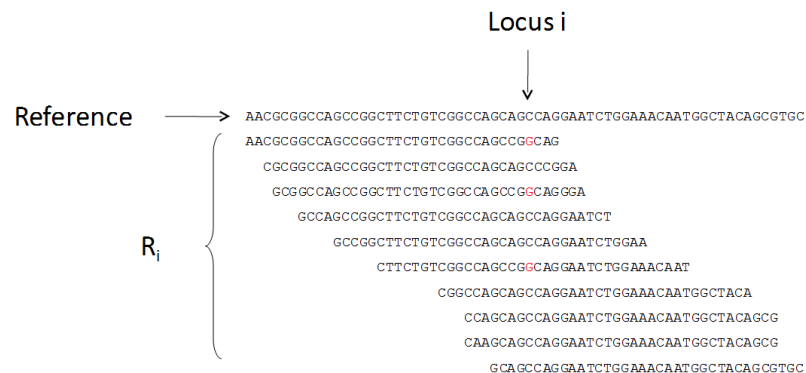


# Fenómica y mejoramiento de cultivos



- Extraction and sequencing of DNA.
- Thousand of SNPs to provide high genome coverage.

- Complex traits:  
More than 40 only at CIAT.



- Experimental Design:  
2 years  
3 repetition (RCBD)  
900 plots  
300 varieties



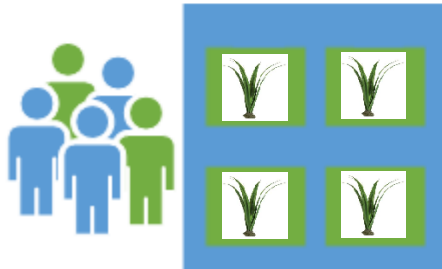
# Association using TASSEL

Genotypic input



GWAS Model:  
GLM,MLM1(2)

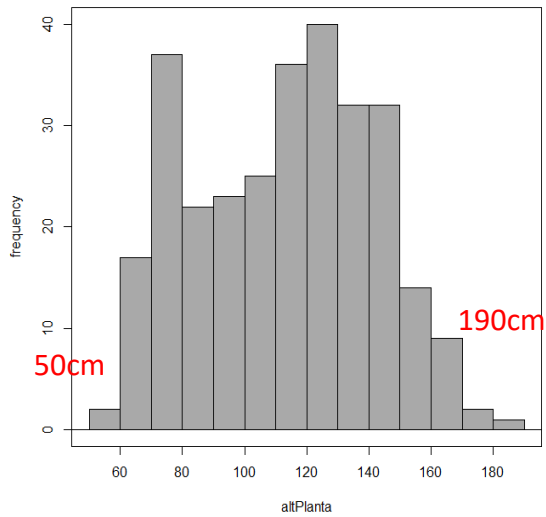
Phenotypic input



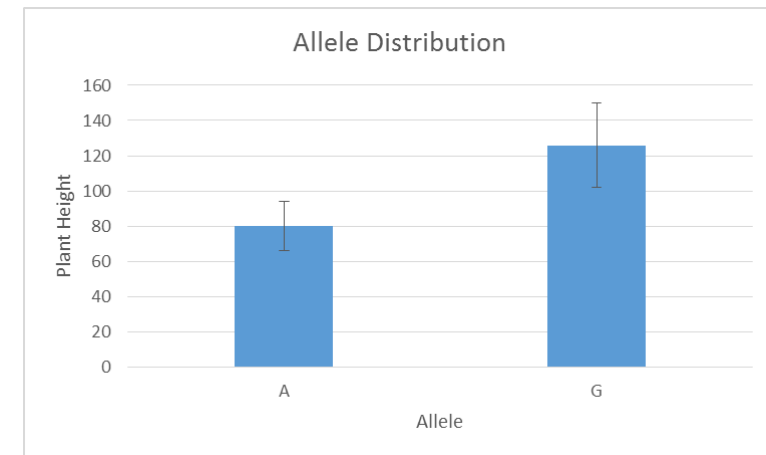
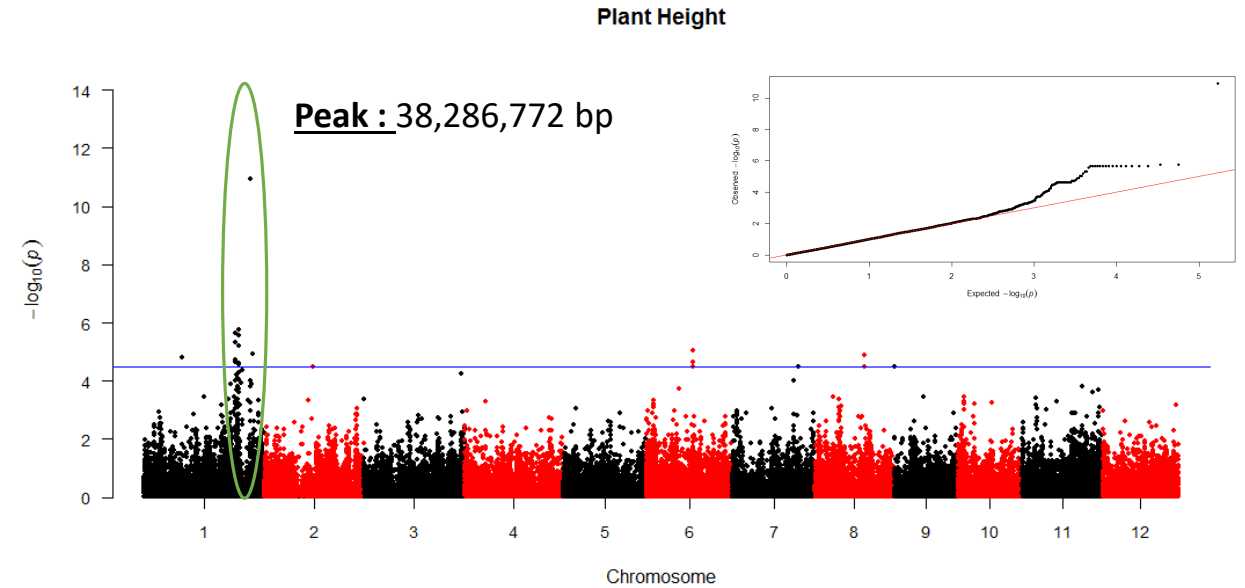
Stats

Effects

# GWAS validation for Plant Height Semi-dwarf1 (SD1)



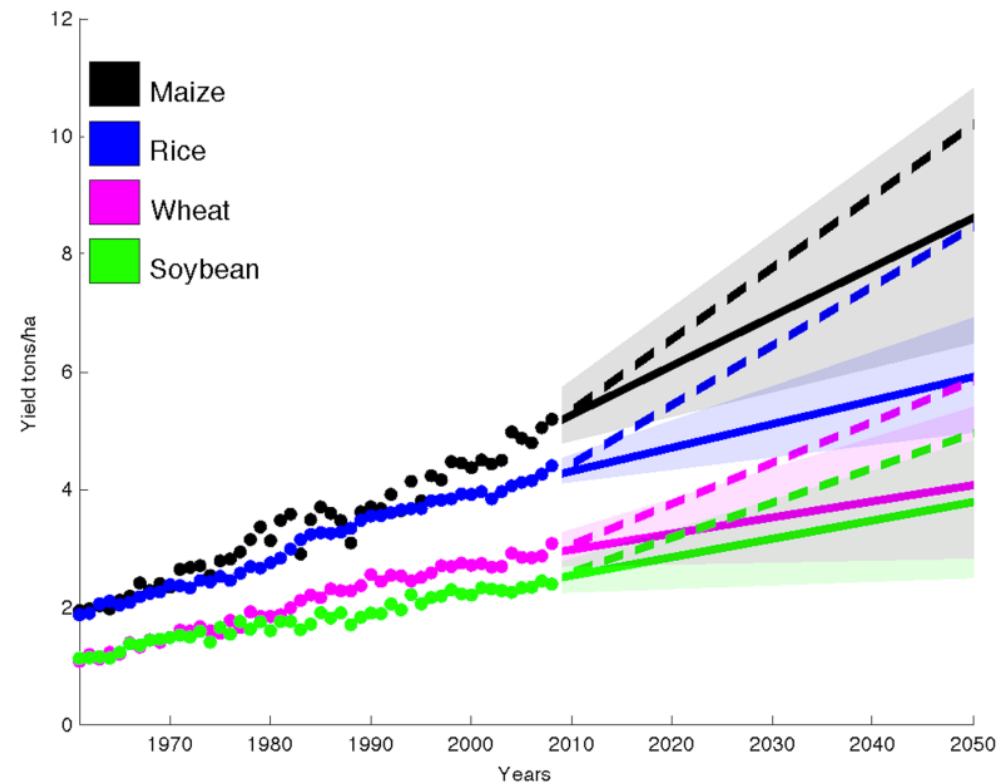
**Gene SD1 : 38,382,382bp - 38,385,504bp**



# Rice in LAC : Ecophysiology and linkage with breeding



**Diversity of environments**  
 -Irrigated areas:  
**Temperate and tropical**  
 -Rainfed areas:  
**Favorable, savannas and traditional upland**

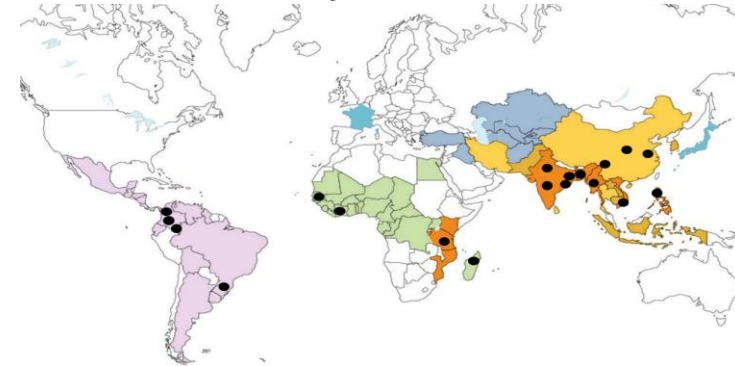


Ray DK, Mueller ND, West PC, Foley JA (2013) Yield Trends Are Insufficient to Double Global Crop Production by 2050. PLoS ONE 8(6): e66428. doi:10.1371/journal.pone.0066428

## Rice Ecophysiology and linkage with breeding



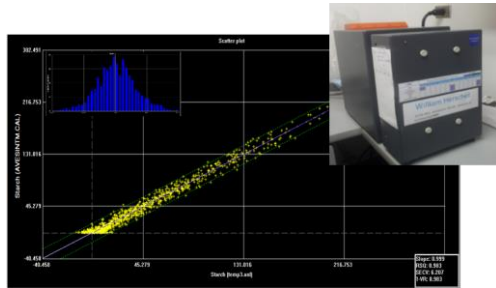
## Rice Global Array (IRRI-AfricaRice-CIRAD-CIAT-IRD)



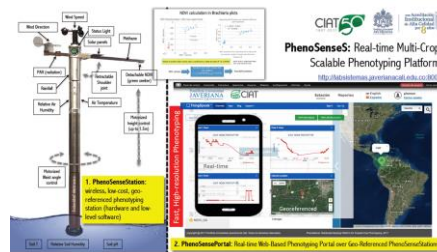
## Development / Adaptation of HTP phenotypic tools and QTL-Gene discovery



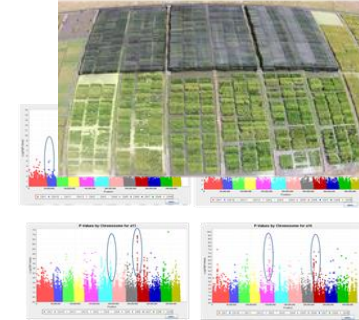
Aerial Biomass (Colciencias-Colombia – Universidad Javeriana Bogotá)



Non structural Carbohydrates : Increase Carbon translocation to grains (CIAT)



Environmental sensing (CIAT- Universidad Javeriana Cali)



Low radiation tolerance (Colombia Cientifica-OMICAS)



High Night temperature tolerance (Colombia Cientifica OMICAS)

## Current approach at AgBio for breeding

Issues	Environment sensing	Aerial crop sensing	Belowground crop sensing	Controlled conditions crop sensing
<b>Tools</b>	<ul style="list-style-type: none"> <li>• Small and portable meteorological stations</li> <li>• GASMET for GHG</li> </ul>	<ul style="list-style-type: none"> <li>• UAVs</li> <li>• Plant sensing (multispeq)</li> <li>• Small cameras with automatic capture</li> </ul>	<ul style="list-style-type: none"> <li>• GPR</li> <li>• Soil sampling</li> </ul>	<ul style="list-style-type: none"> <li>• Growth chambers with controlled env.conditions, hydroponics</li> <li>• Image analysis "medium-throughput"</li> <li>• Chemical analysis using NIRS</li> </ul>
<b>What are we sensing?</b>	<ul style="list-style-type: none"> <li>• Actual climatic-soil conditions</li> </ul>	<ul style="list-style-type: none"> <li>• Biomass, grain yield , NUE and WUE</li> <li>• Photosynthetic efficiency</li> </ul>	<ul style="list-style-type: none"> <li>• Root biomass</li> </ul>	<ul style="list-style-type: none"> <li>• Root morphology, grain filling, carbohydrates (starch sucrose) remobilisation, grain /forage quality, plant architecture</li> <li>• Aluminium and Phosphorus tolerance, Tolerance to high temperature, Drought Tolerance, Tolerance to low light.</li> <li>• Biotic stress tolerance (bacteria/virus)</li> </ul>
	<ul style="list-style-type: none"> <li>• Greenhouse gas emissions (soil+plants+animals)</li> </ul>		<ul style="list-style-type: none"> <li>• Soil carbon stocks</li> </ul>	

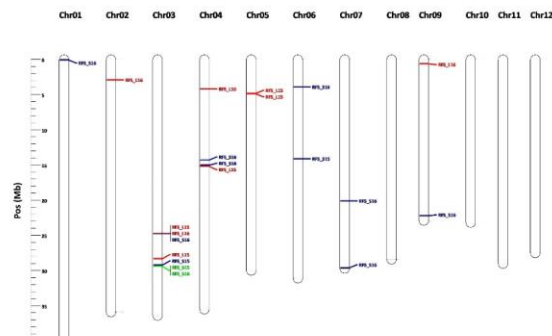
## Trait identification in diversity panels (300 lines, 4 environments)

$$\text{Source:Sink} = \frac{\text{Last ligulated leaf area (source)}}{\text{Panicle weight (sink)}}$$

Plants with lower source:sink ratio showed higher tolerance to low radiation during grain filling



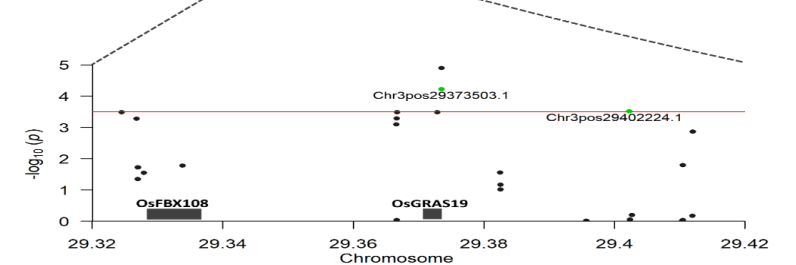
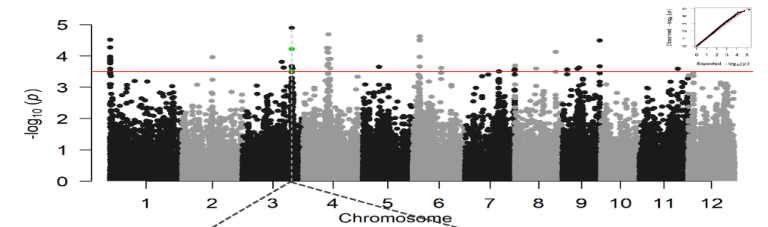
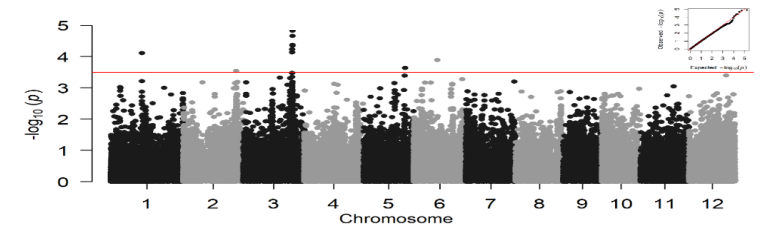
## Genotype : phenotype association study (GWAS) for Source:sink



21 QTLs identified

## OsGRAS19: candidate gene for light use efficiency

- Within a Source:Sink QTL we found OsGRAS19
- GRAS genes are transcription factors unique in plants, playing an important role in plant growth; development; and phytochrome A regulation.
- Its role for low radiation tolerance will be validated in rice or in *A.Thaliana* (AtGRAS-19)



## Agradecimientos







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## Aliados



## Apoyan



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