

# ASPIR:

Advanced Sequencing & Phenotyping for Improved Rice

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Rice  
Science  
for a Better  
World 

# Global Rice Science Partnership



Research  
Program on  
Rice  
Global Rice  
Science  
Partnership

**IRRI**



**(GRiSP)**  
AfricaRice



**Product lines for theme 1: *Harnessing genetic diversity to chart new productivity, quality, and health horizons***

**1.1. *Ex situ* conservation and dissemination of rice germplasm**

**1.2. Characterizing genetic diversity and creating novel gene pools**

**1.2.1 SNP Consortium for high density genotypes**  
*(H Leung)*

**1.2.2 Global phenotyping network for key traits**  
*(M Dingkuhn)*

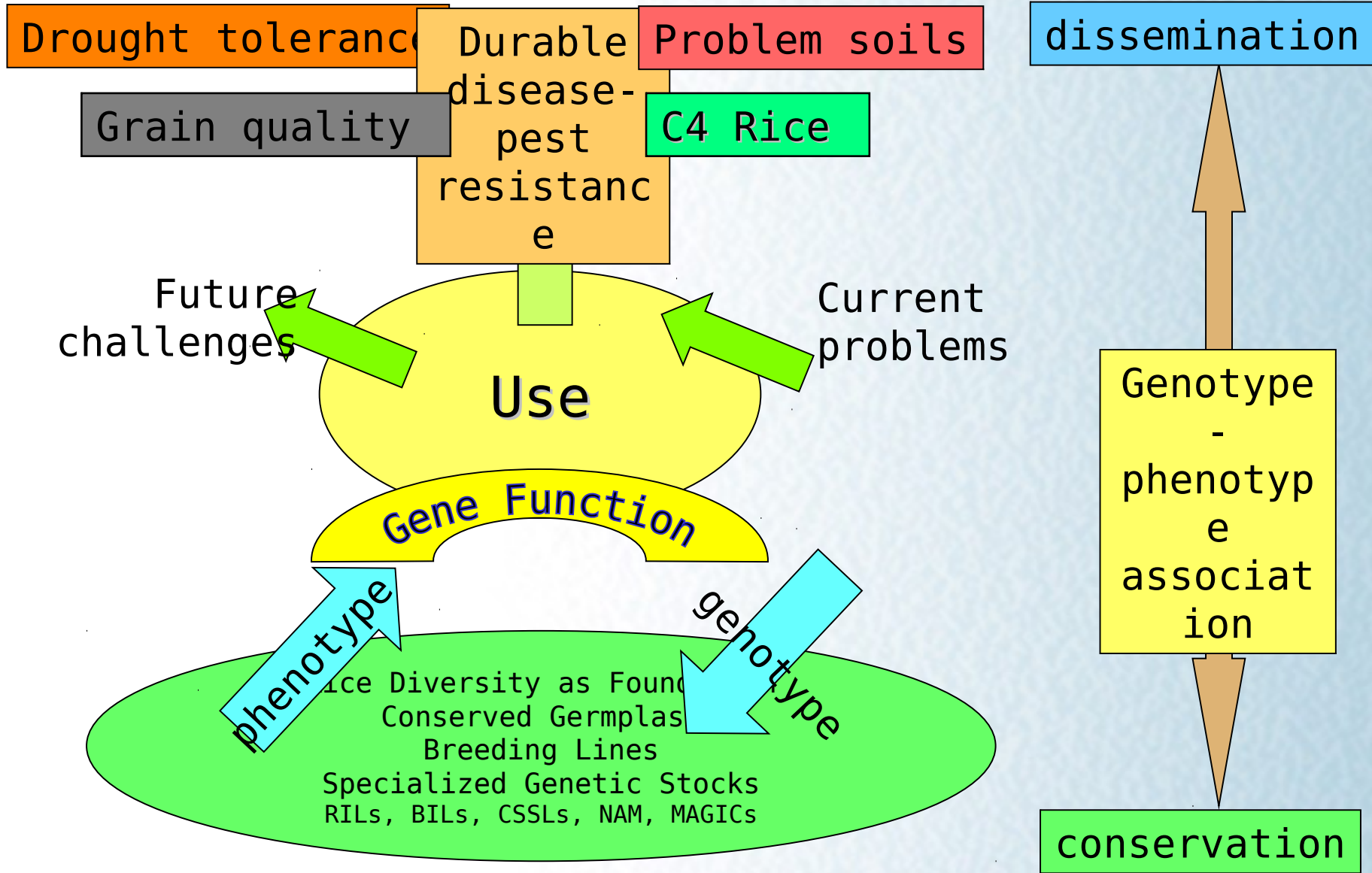
**1.2.3 Whole genome sequencing of genebank stocks**  
*(K McNally)*

**1.2.4 Specialized populations for genetic studies** *(G Gregorio)*

*RILs, NAM, MAGICs*

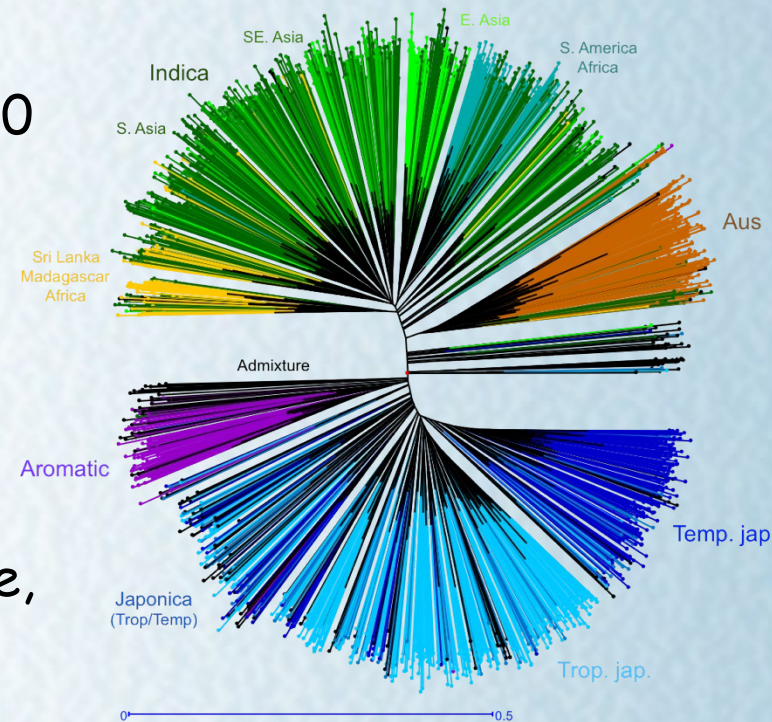
**GWAS**

# Public Genetic Diversity Research Platform



# Rice SNP Consortium for enabling genome-wide association studies (GRiSP 1.2.1)

- Developed high-density genotyping Affy arrays with 700K SNPs (from 1M)
- Includes newly discovered SNPs from a SNP discovery pool of >27M SNPs from 150 genomes and other projects
- **Genotype 2000 rice genetic stocks spanning range of diversity**
  - **Almost complete**
- <http://www.ricesnp.org>
- Partners include Cornell, USDA, AfricaRice, Cirad, Bayer CropSciences, Syngenta AP, CIAT and many others
- **Precise phenotyping of traits in target environments for an integrated Rice Diversity Platform**

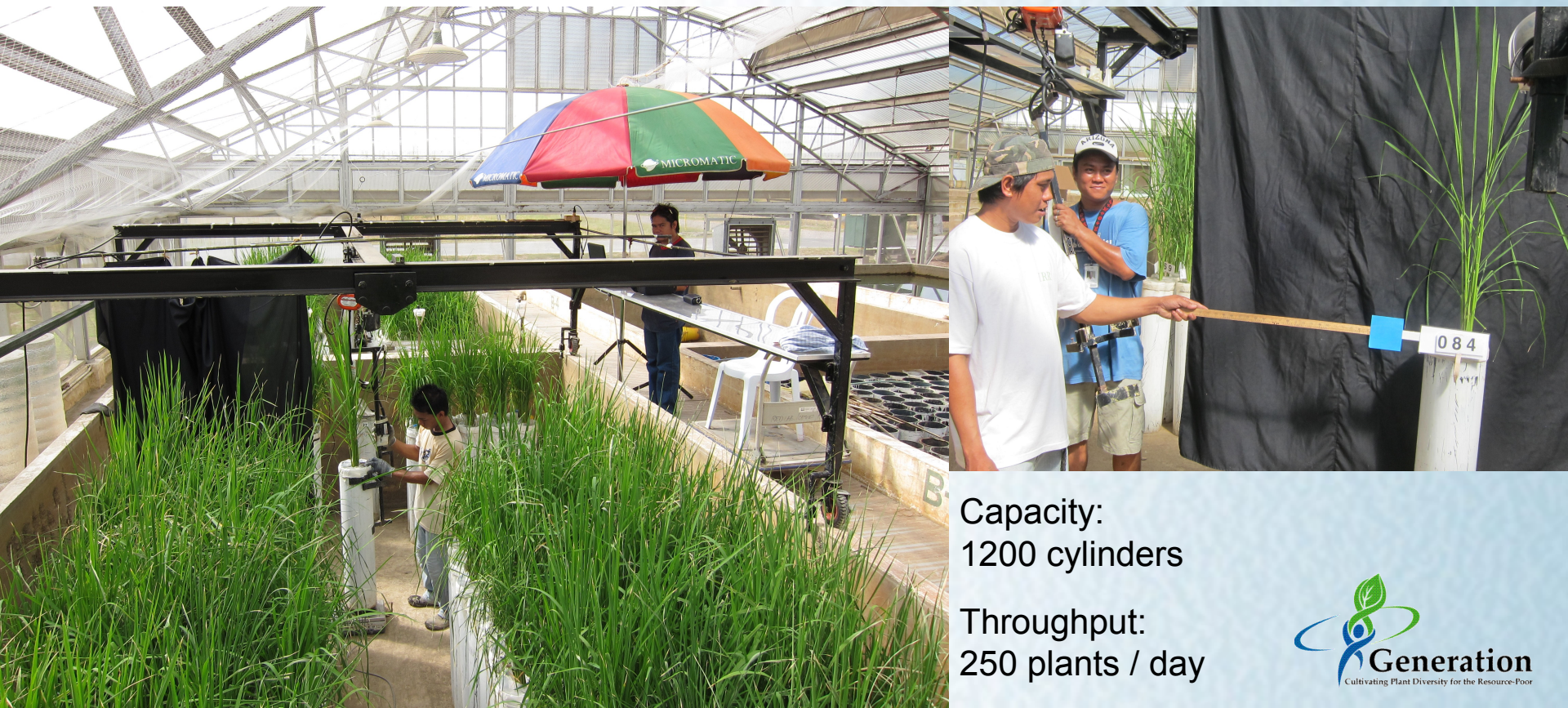


2k lines x 700k SNPs

# Phenotyping for GWAS with panels from 2K set

- *GCP roots/drought Aus panel (250 entries) for vegetative stage drought stress and roots (IRRI) and roots (Adam Price, Aberdeen)*

## Greenhouse lysimeter facility



Capacity:  
1200 cylinders

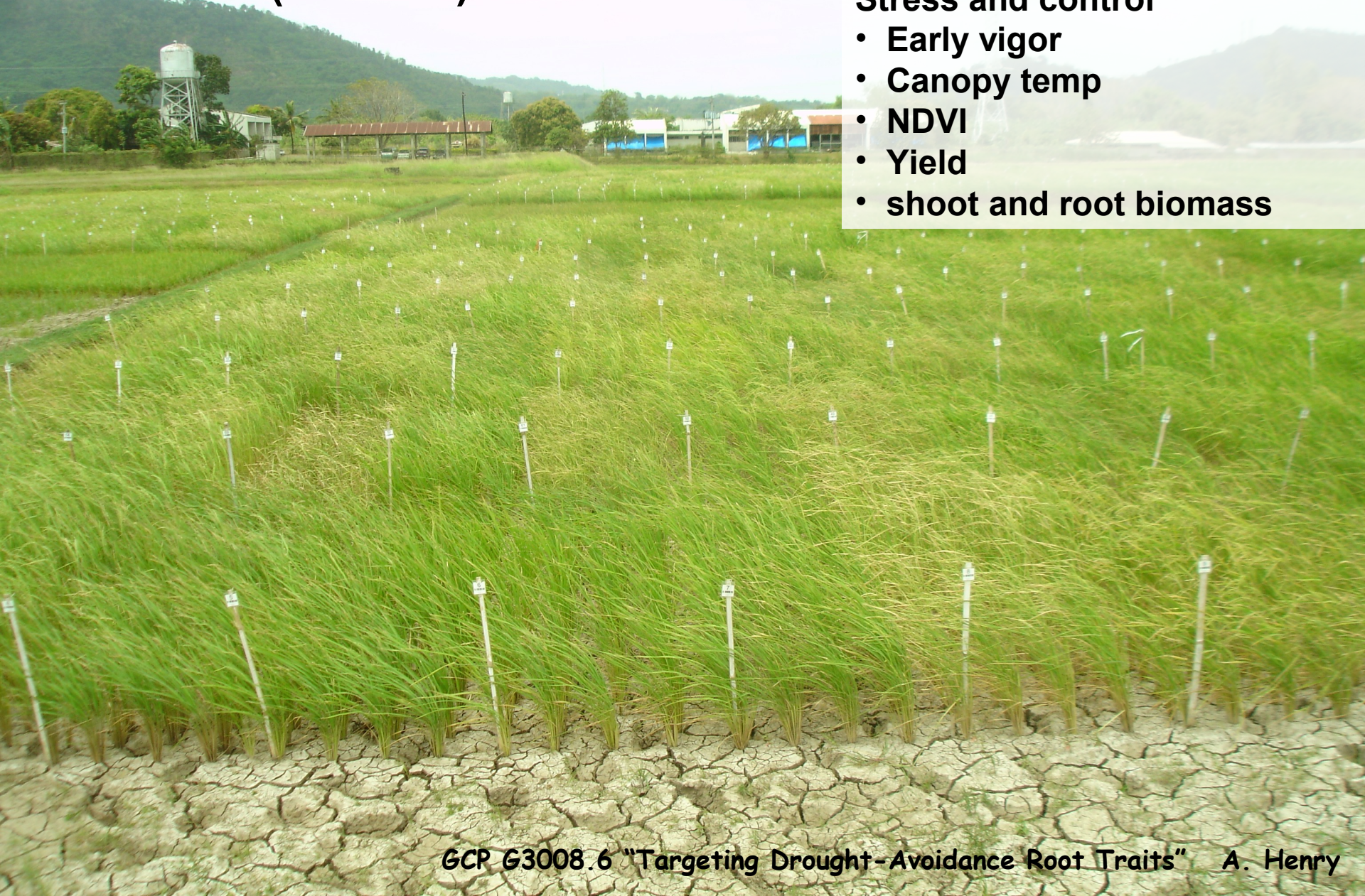
Throughput:  
250 plants / day

# Phenotyping of association panels for GWAS (PL 1.2.2)

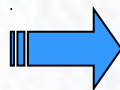
Aus lines 2010DS and 2011DS  
220+ lines

Stress and control

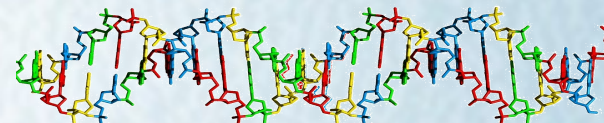
- Early vigor
- Canopy temp
- NDVI
- Yield
- shoot and root biomass



# ASPIR -- Sequencing the Genebank



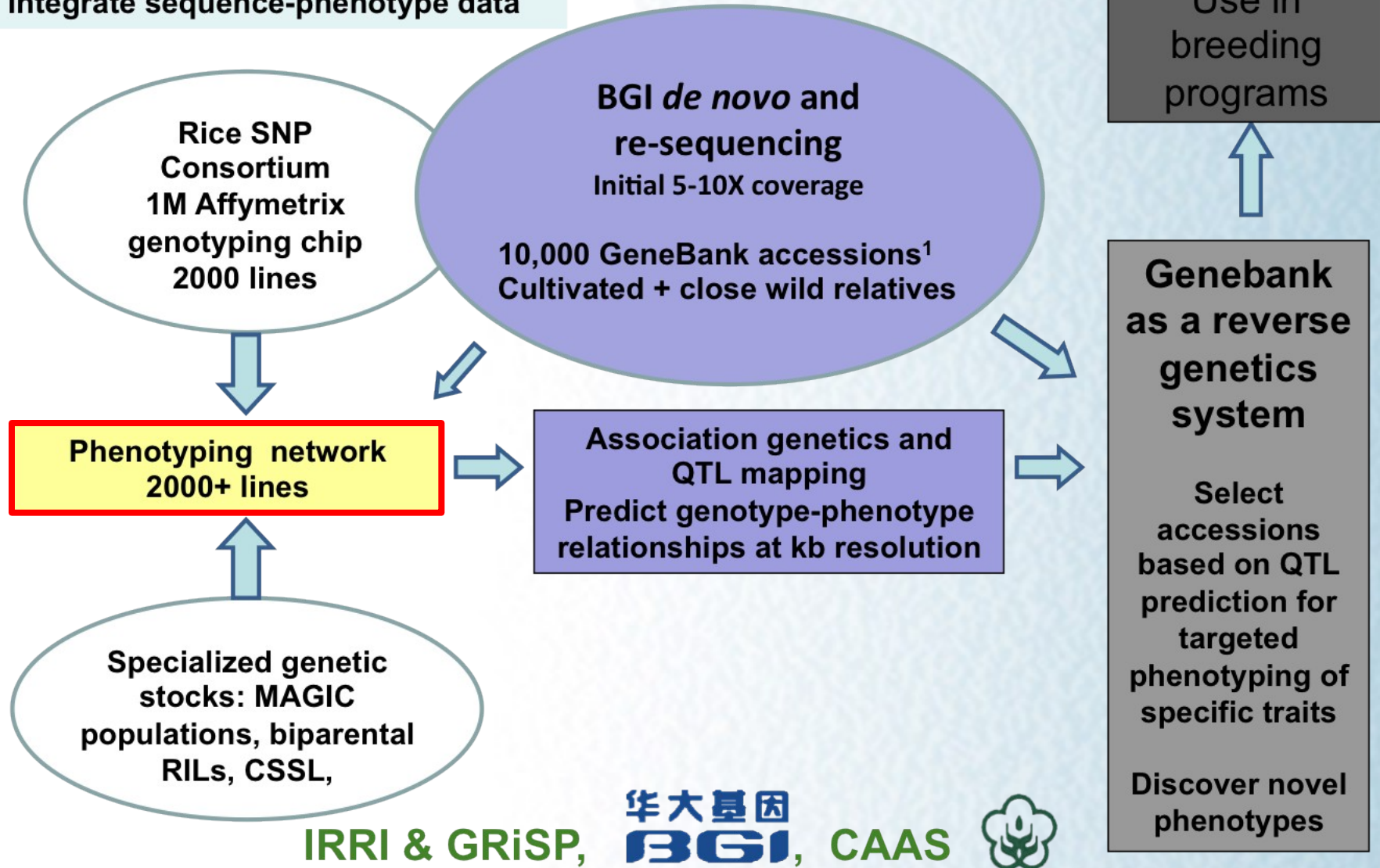
3 to 10%  
sampling,  
then NGS @  
 $\geq 10X$  depth



Apply low-cost  
sequencing  
by next generation  
technology

- Working with BGI-Shenzhen and CAAS to sequence 3,000 to 10,000 genomes
- 3,095 samples from IRRI and 620 from CAAS for 1<sup>st</sup> phase
- Final sequencing data ( $>10X$  depth) on 3,042 samples obtained
  - 17 Tbases trimmed reads,  $>14X$  depth average, 2.5 G SNPs
  - 1<sup>st</sup> announcement at 10<sup>th</sup> ISRFG (Chiang Mai, Nov 26-29)

**Bioinformatics and database to  
Integrate sequence-phenotype data**



<sup>1</sup> Including publicly accessible germplasm from IRRI, CIRAD, AfricaRice, CIAT and regional collections



# Converting Rice to C4 Metabolism

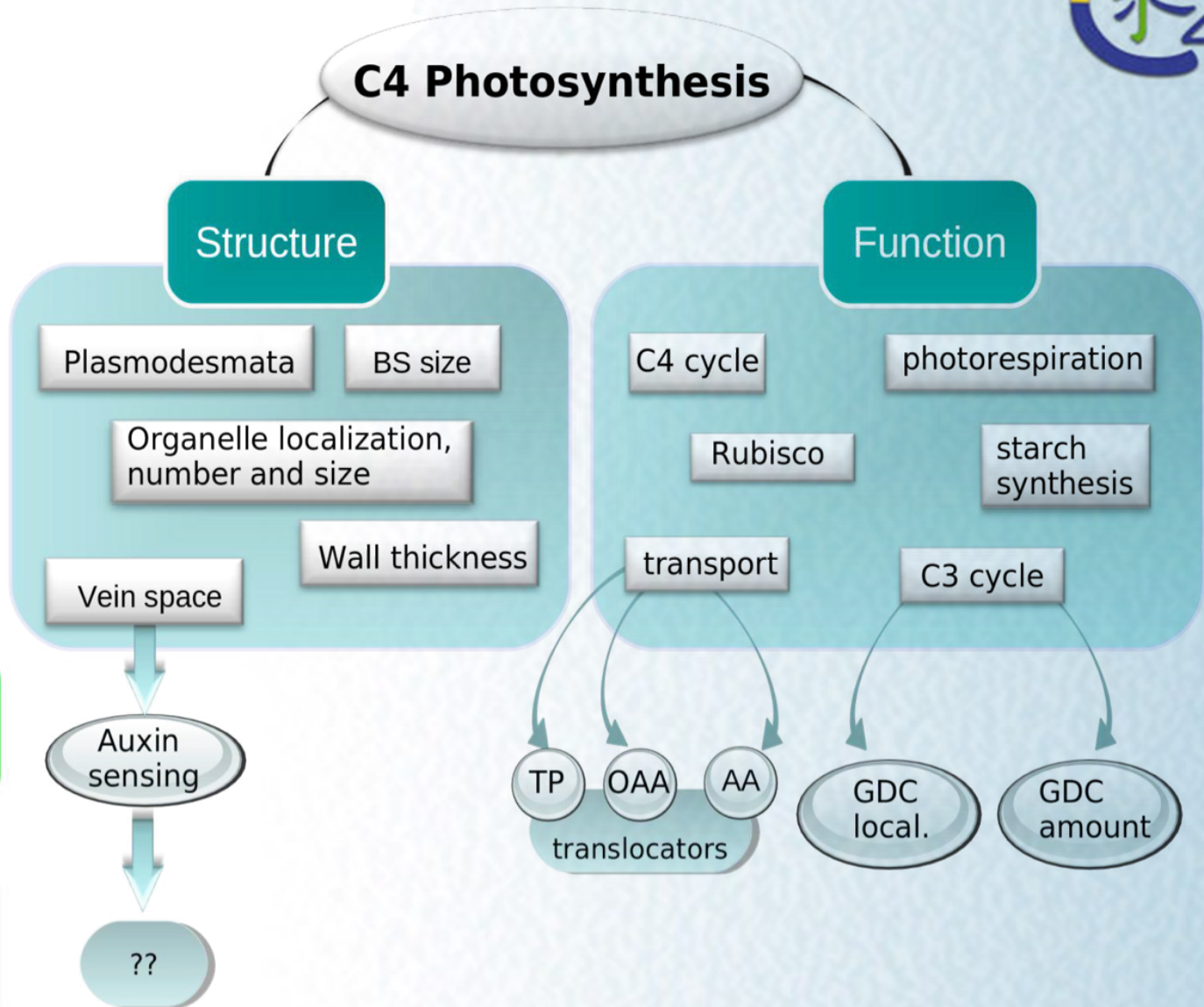


Goal

Trait

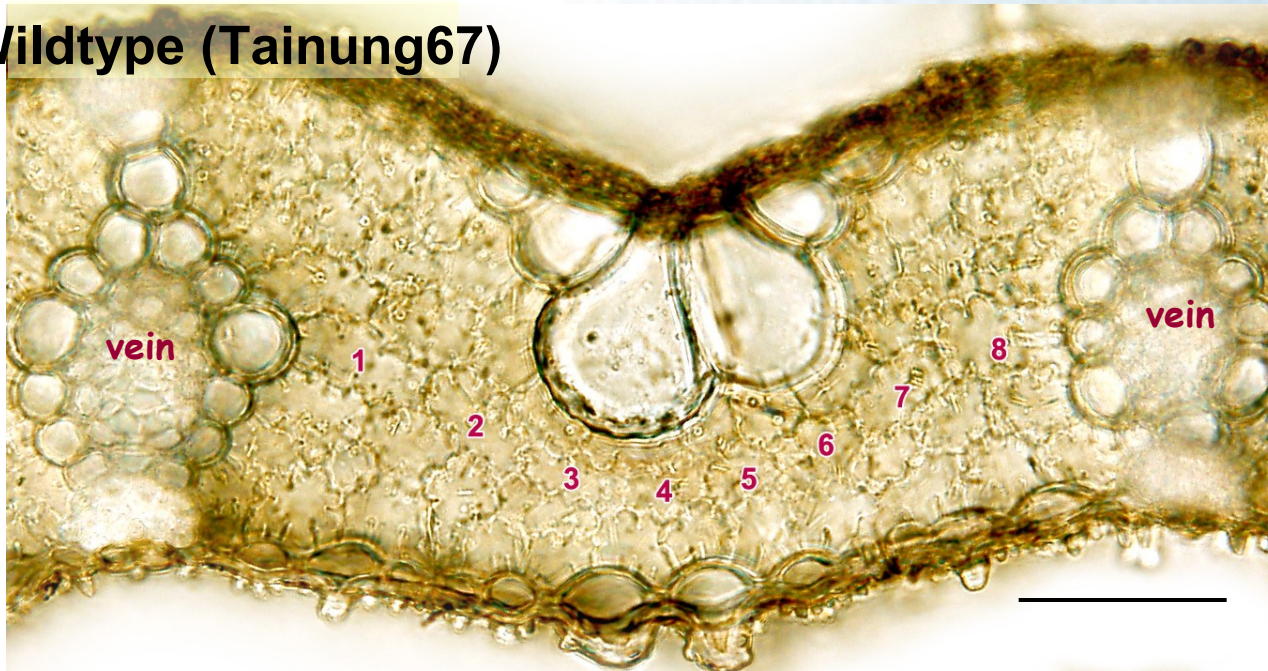
Mechanism

Genetic modifications

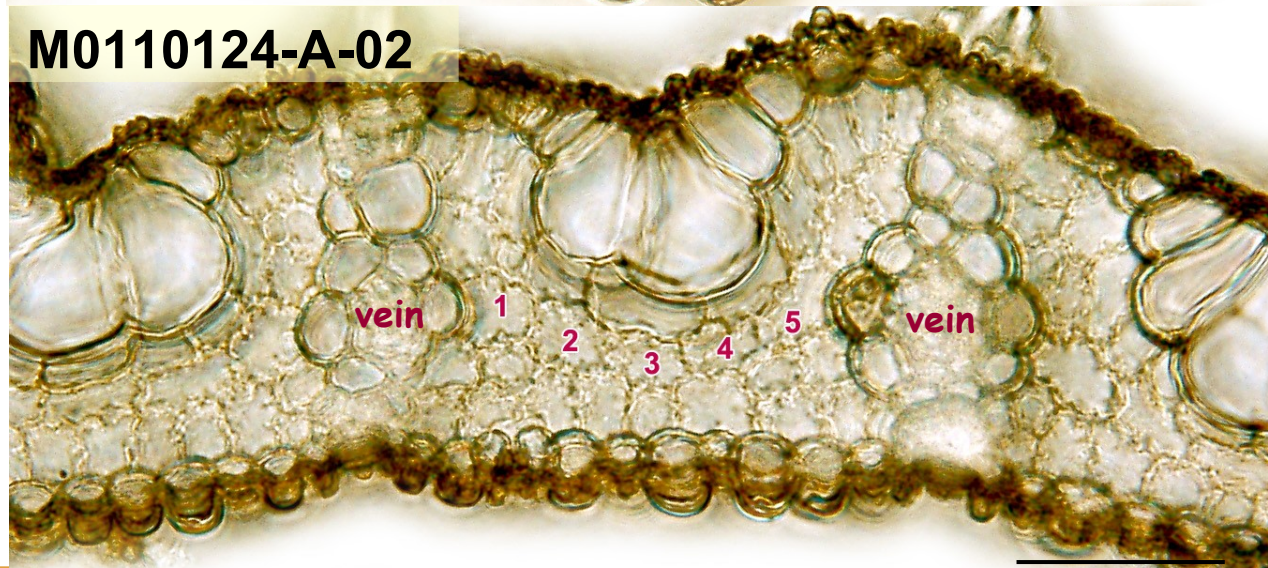


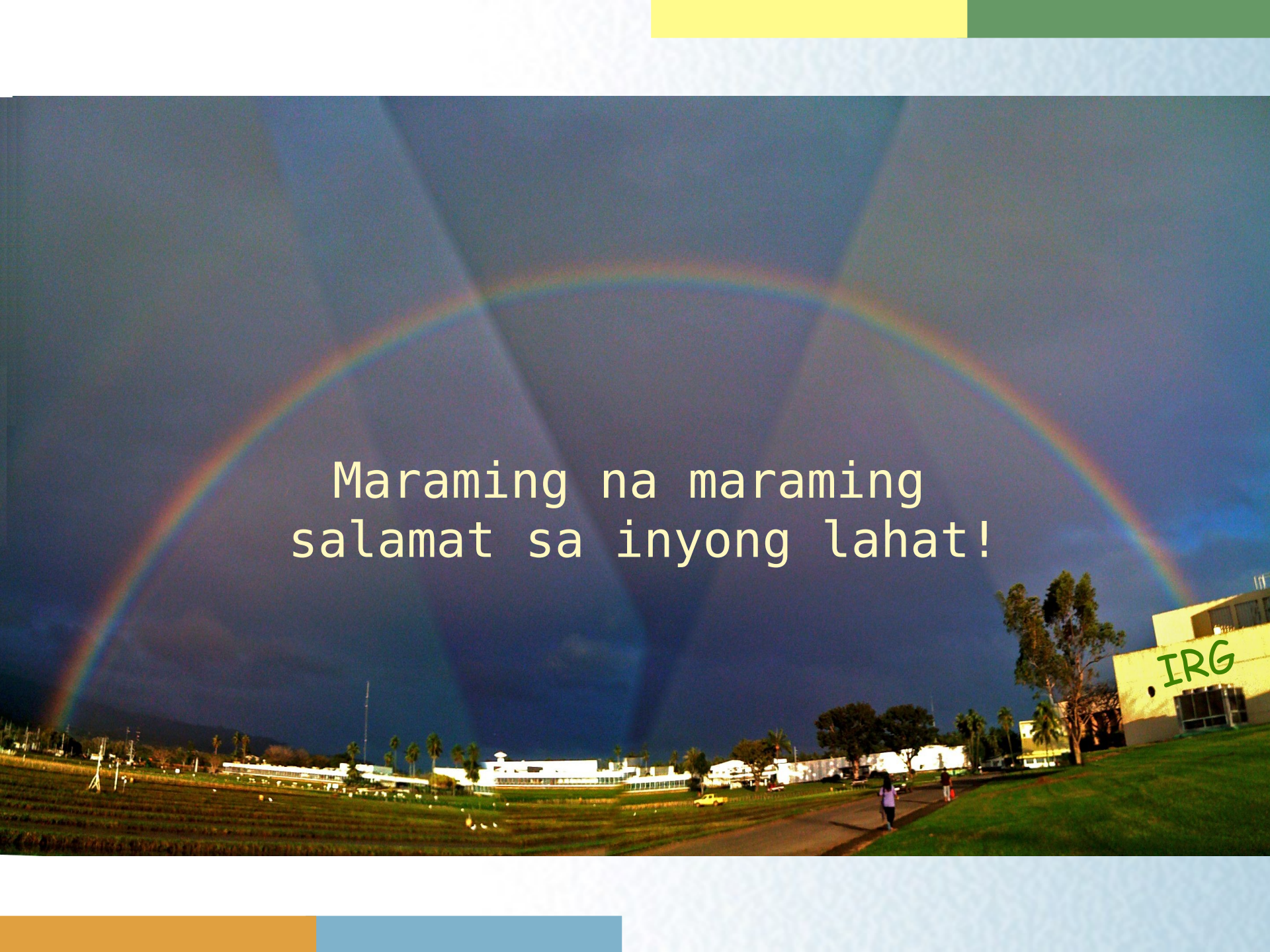
# Transverse leaf section of Rice wild type (Tainung67) and line M0110124 showing the number of mesophyll cells between veins

## Wildtype (Tainung67)



## M0110124-A-02



A vibrant rainbow arches across a dark, stormy sky over a campus. In the foreground, a paved path leads towards a large, modern building with the letters 'IRG' in green on its facade. The building is illuminated, and several people are visible walking on the path. The scene is set against a backdrop of palm trees and other campus buildings under a dramatic, dark sky. The overall mood is one of hope and gratitude.

Maraming na maraming  
salamat sa inyong lahat!