**Fundamentals of Genomic Prediction and Data-Driven Crop Breeding
(August 4-8, 2025)**
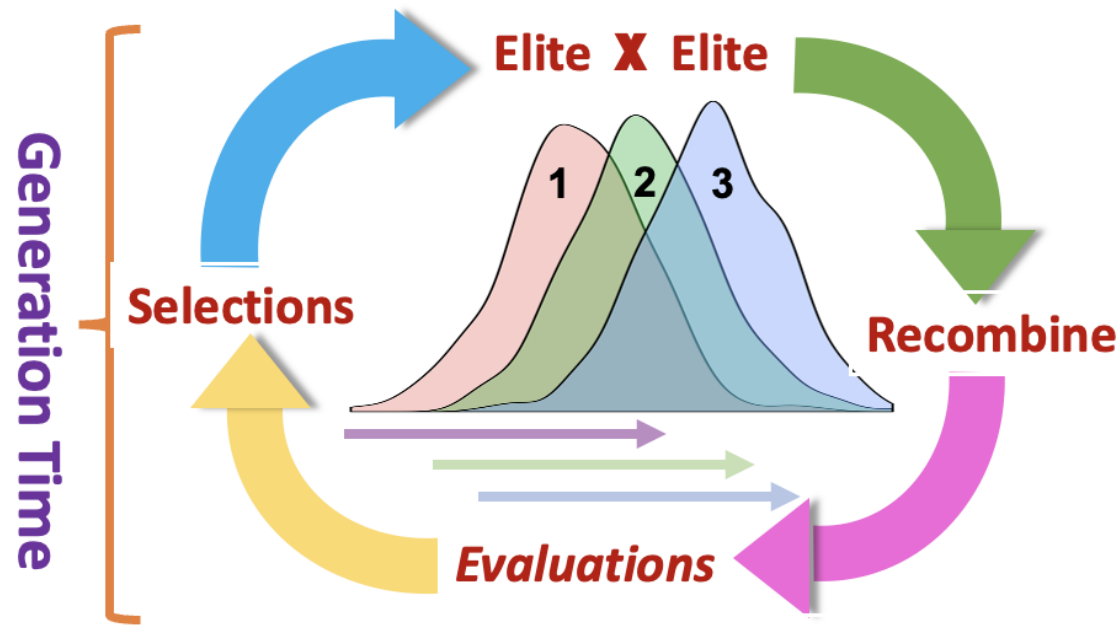
Understanding Usefulness Criterion and Optimal Parental Contributions
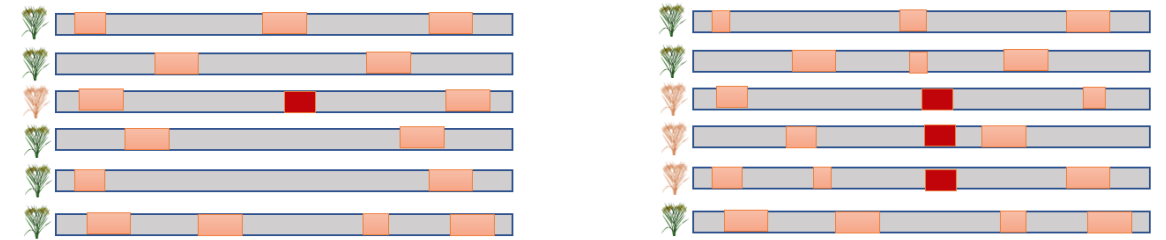
**Module 5
August 8, 2025**

Waseem Hussain and Mahender Anumalla
Rice Breeding Innovations Platform
IRRI

Why Re-cycling the Parents

Improving What You Improved is Key

Aim is to Increase the combination of Favorable alleles

Yield is a complex Trait, can be improved by combining all the favorable allele combinations
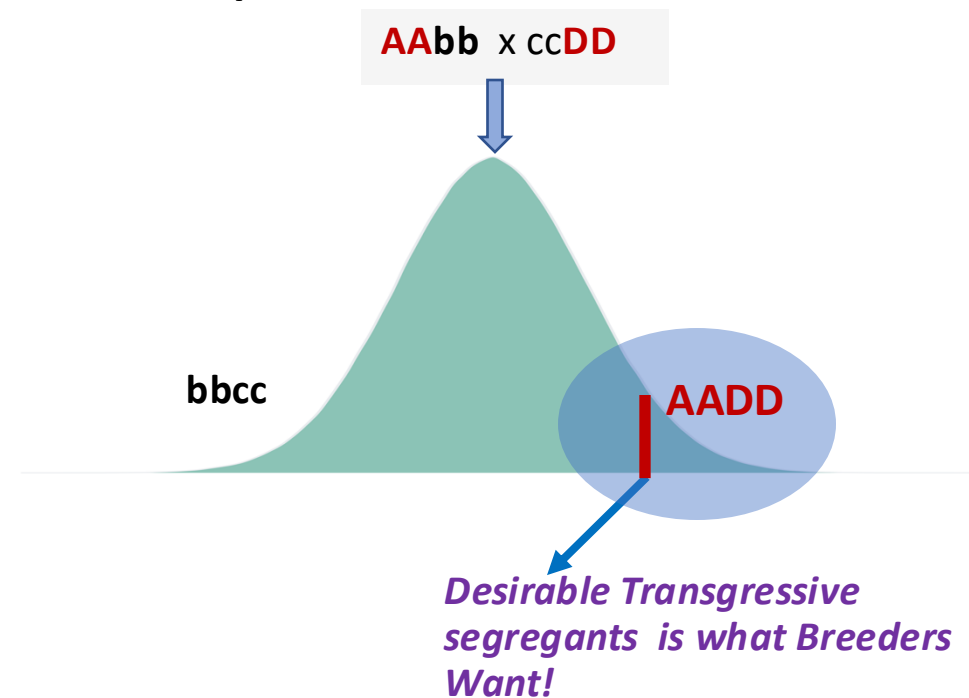
Recurrent selection Breaks linkages and creates variation

Crossing is the Key
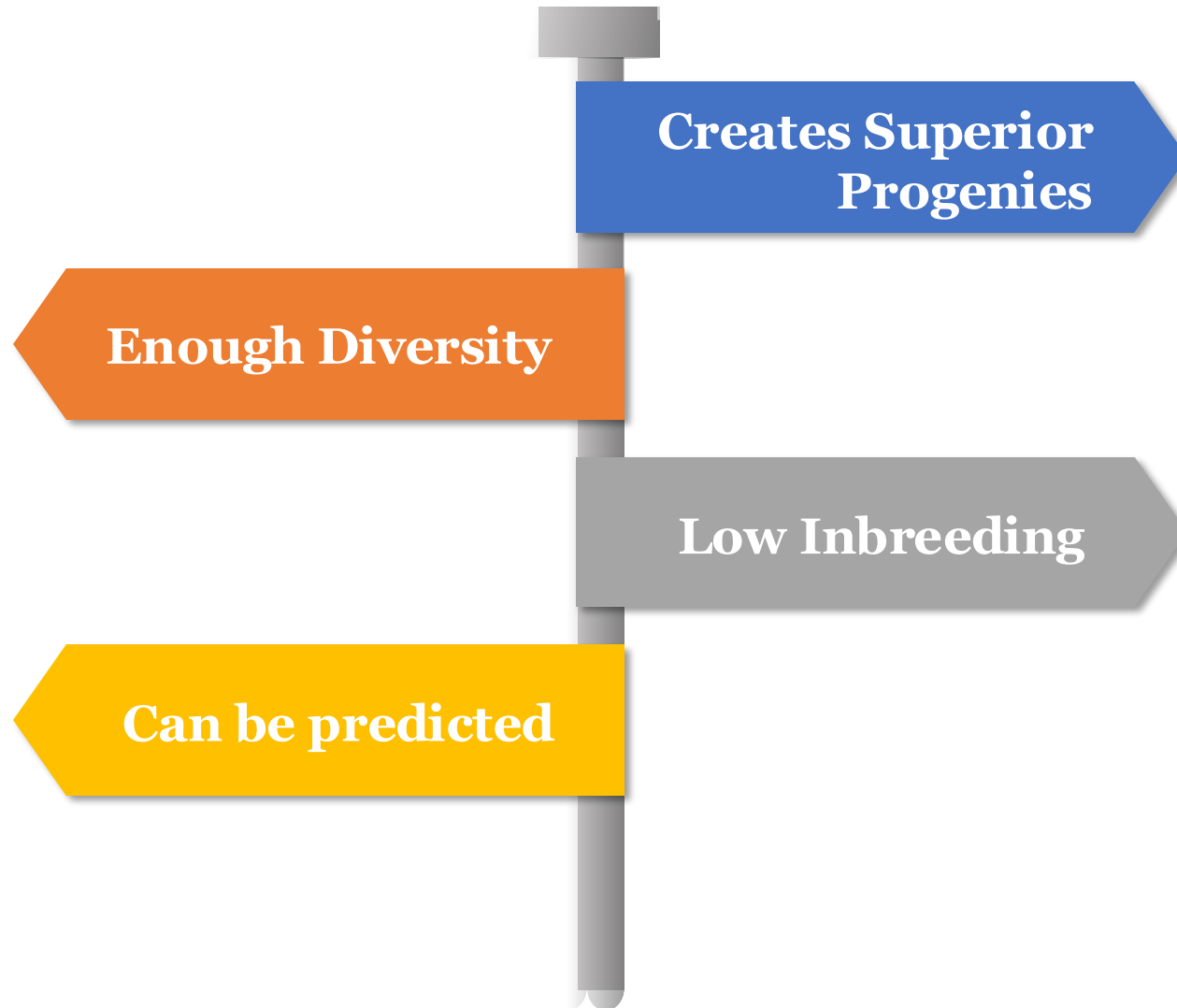## *(Right parents in Right Combinations)*

Crossing is one of the main decisions of a breeding program

o **Crossing is main driving engine to make Response to Selection effective.**

o **Response to selection is driven by the additive effect genes/substitution effects that give rise to transgressive segregants.**

o **Transgressive segregants results in extreme Phenotypes that Breeders select.**

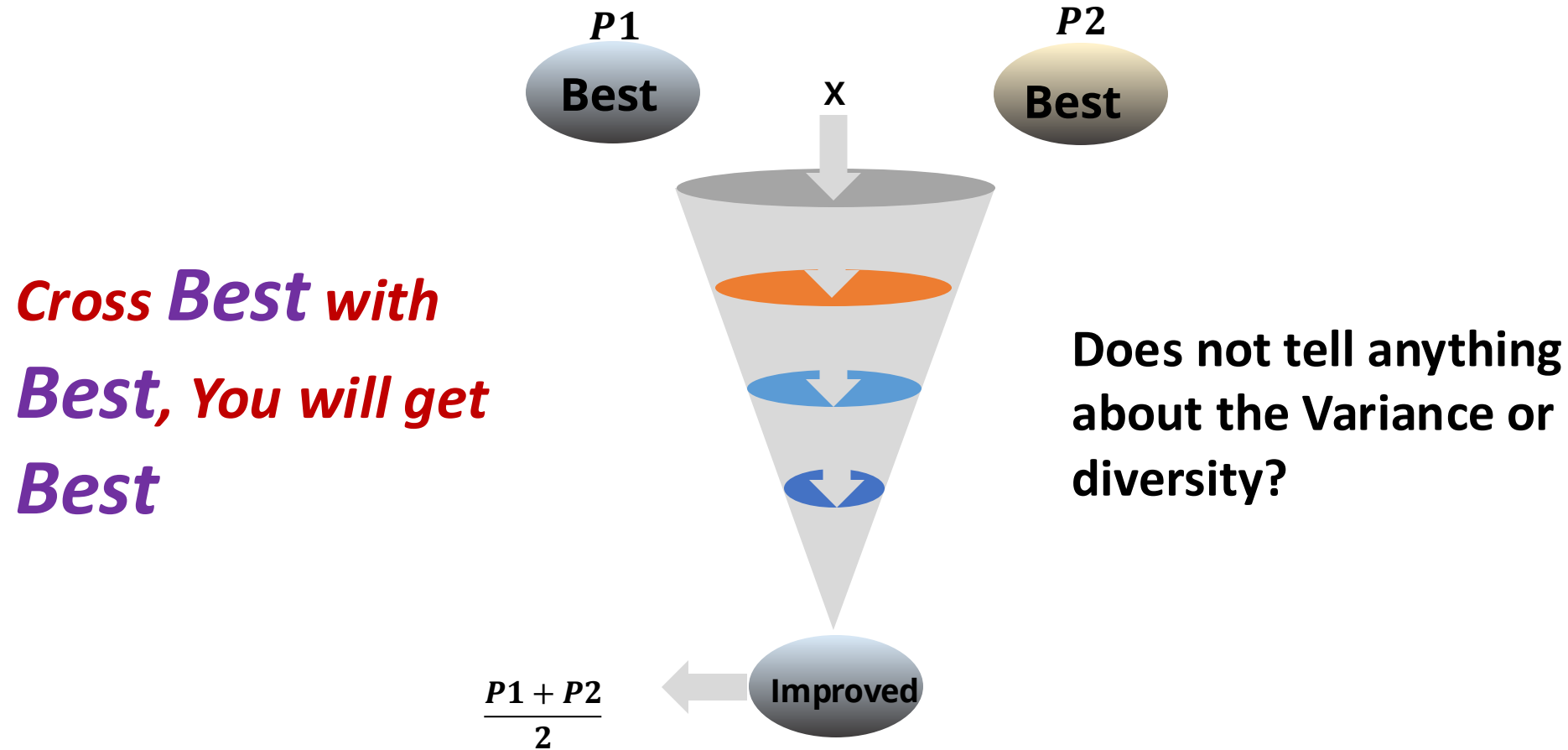**Transgressive Segregation is caused by Dispersion of favorable alleles**

AAbb x cc**DD**

bbcc

AADD

Desirable Transgressive segregants is what Breeders Want!

What is an Ideal Cross in Crop Breeding

Creates Superior Progenies

Enough Diversity

Low Inbreeding

Can be predicted

What is that Ideal Cross

$P1$

Best

X

$P2$

Best

*Cross **Best** with*

***Best**, You will get*

Best

Does not tell anything about the Variance or diversity?

$$\frac{P1 + P2}{2}$$

Improved

Crossing an Elite with Non-Elite?

P1

None Elite

X

P2

Elite line

$$\frac{P1 + P2}{2}$$

Improved

Diversifies but at cost of mean performance

Contaminates whole elite gene pool

Pushes mean breeding value back

(A)

Key:
- Population: Elite x Resource
- Population: Elite x Elite

Frequency of progenies

Best progenies

σ^2

σ^2

μ μ

Grain yield performance

(B)

Usefulness of a cross (Mg ha^{-1})

Key:
- σ^2 = Elite
- σ^2 = 3 x Elite
- σ^2 = 5 x Elite
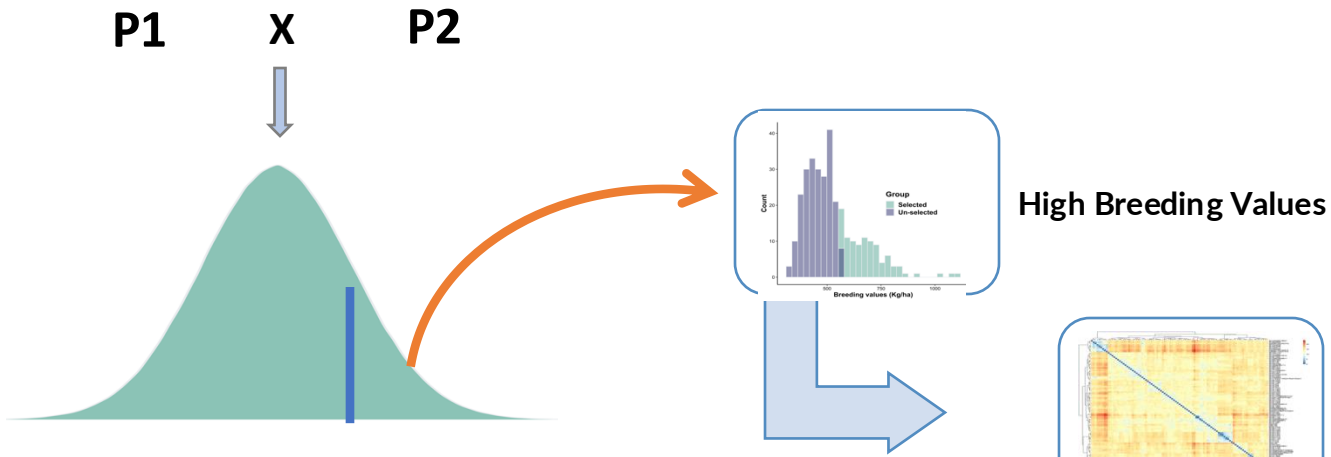
Elite x Elite   Elite x Resource   Resource x Resource   (Elite x Resource) x Elite

The increased genetic variance due to using genetic resources can barely counterbalance the lower mean
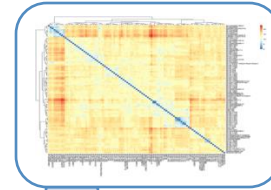
IRRI
CGIAR

Longin et al, 2017; https://doi.org/10.1016/j.tplants.2014.06.012

Right Parents and Right Crosses

Five Step Process to Select and Cross

P1   X   P2

High Breeding Values

Diversity (Relationship matrix)
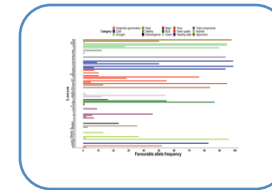
Major locus criterion

Transgressive Segregants

One Rice Breeding Framework

- 30 crosses/pipeline
- n(n-1) or n(n-1)/2,
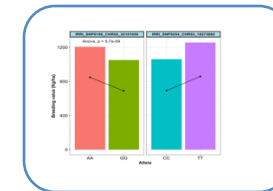- For example, 61 Parents =3,599 crosses
- Excluding 3,569 cross combinations!

Do We Know Which Cross is Best

Usefulness Criterion

$$U = \mu + \sigma_P^2$$

Designing Crossing Block is Random!!!!

Designation	IR16T1538	IR16F1251	IR 126952-28-55-9-9-4-2-7	IR 126957-B-48-5-1-3	IRRI 185	IR13V163	IR16T1662
IR16T1538							
IR16F1251							
IR 126952-28-55-9-9-4-2-7	X				X		
IR 126957-B-48-5-1-3							
IRRI 185			X				
IR13V163							
IR16T1662							
IR 91648-B-117-B-1-1							
IR19L1046							X
IR15L1737			X				
IR18T1025							
IR 117755-B-80-1-AJY 1-2							
GSR IR 1-5-D20-D3-Y2			X	X			
IR16M2035							
IR16F1037							
IR 117764-B-24-1-2							
IR15F1912					X		X
IR16F1147							
IR15F1709							
IR15F1729						X	
IR16T1159					X		
IR13L499							
IR14V1034							

IRRI CGIAR

Right Parents and Right Crosses

Approach to Cross

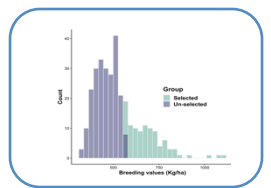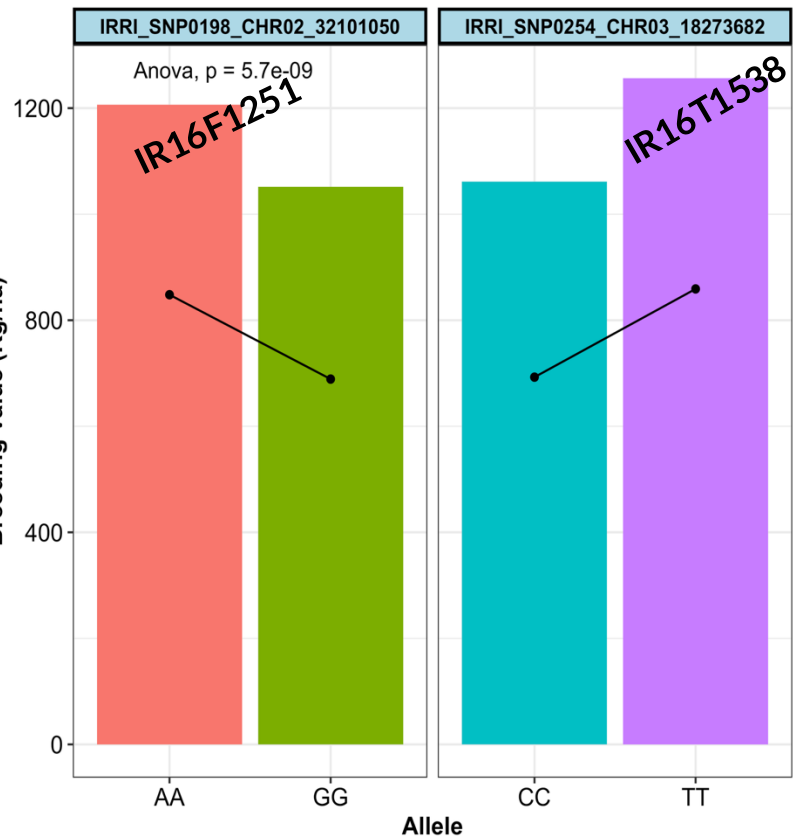Can We have the lines with different favorable QTLs for Grain Yield Breeding Values

Designing Crossing Block is Random!!!!

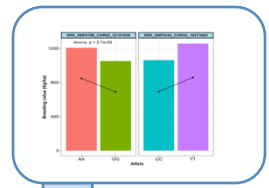| Designation	IR16T1538	IR16F1251	IR 126952-28-55-9-9-4-2-7	IR 126957-B-48-5-1-3	IRRI 185	IR13V163	IR16T1662
IR16T1538							
IR16F1251							
IR 126952-28-55-9-9-4-2-7	X				X		
IR 126957-B-48-5-1-3							
IRRI 185			X				
IR13V163							
IR16T1662							
IR 91648-B-117-B-1-1							
IR19L1046							X
IR15L1737			X				
IR18T1025							
IR 117755-B-80-1-AJY 1-2							
GSR IR 1-5-D20-D3-Y2			X	X			
IR16M2035							
IR16F1037							
IR 117764-B-24-1-2							
IR15F1912					X		X
IR16F1147							
IR15F1709							
IR15F1729						X	
IR16T1159					X		
IR13L499							
IR14V1034							

Selecting High breeding value lines based on Yield
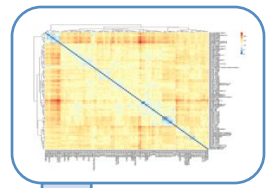
Relationship among lines based on GRM
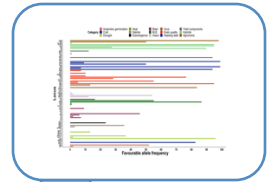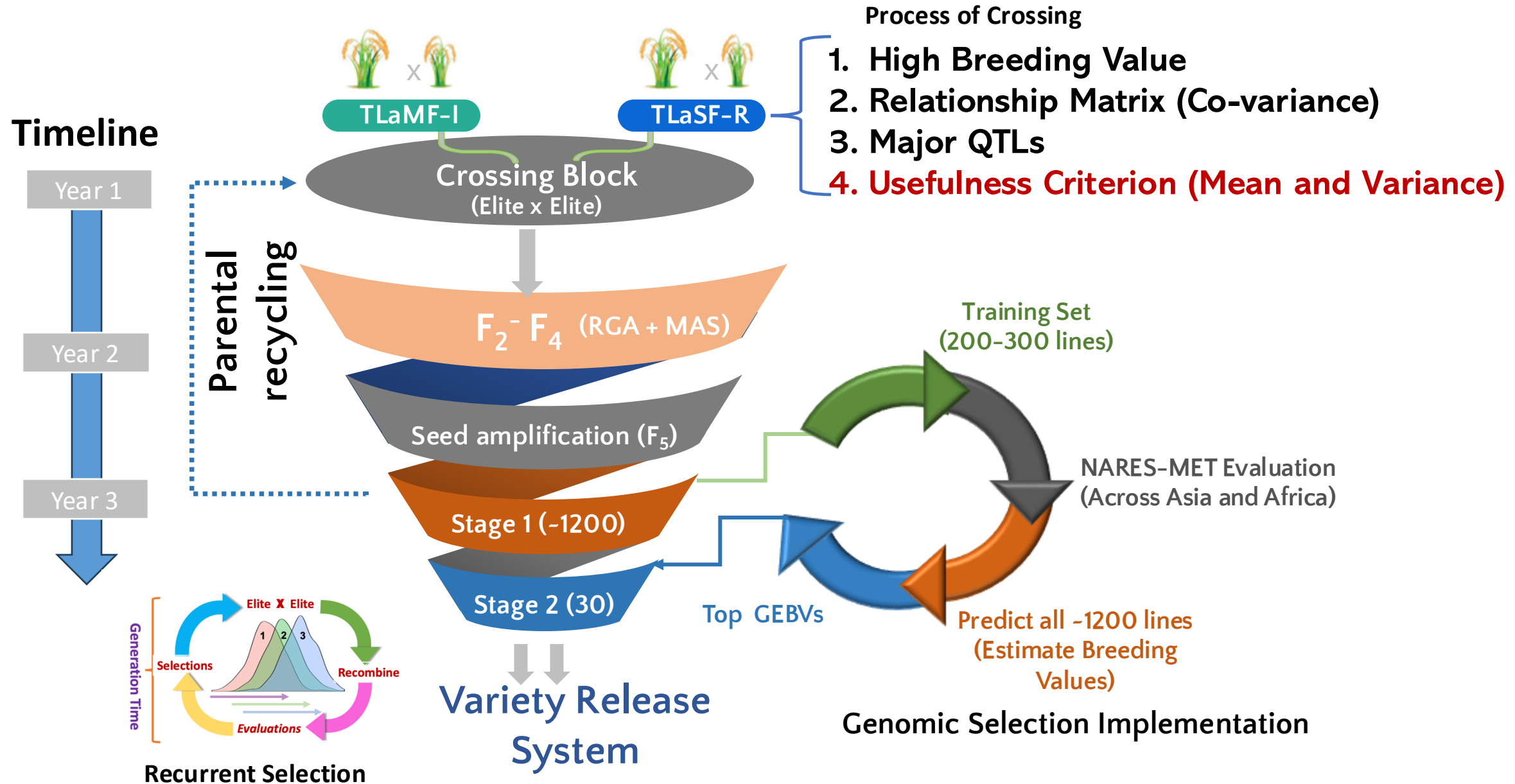
Selection based on Mendelian traits/major locus

Dispersed QTLs based on Grain Yield BV.

Usefulness Criterion

IRRI_SNP0198_CHR02_32101050

Anova, p = 5.7e-09

IR16F1251

IRRI_SNP0254_CHR03_18273682

IR16T1538

Breeding value (Kg/ha)

1200
800
400
0

AA   GG   CC   TT

Allele

$$U = \mu + \sigma_P^2$$

Genomic Selection in IRRI's Global Rice Breeding

Usefulness Criterion

➢ *Schnell and Utz (1975)*, the "**Usefulness**" is expected cross mean plus the expected selection gain

➢ $U = \mu + \sigma^2 P$

➢ Predict the mean and genetic variance of a cross

➢ *High GEBV*
➢ *High contribution and expected genetic gain*