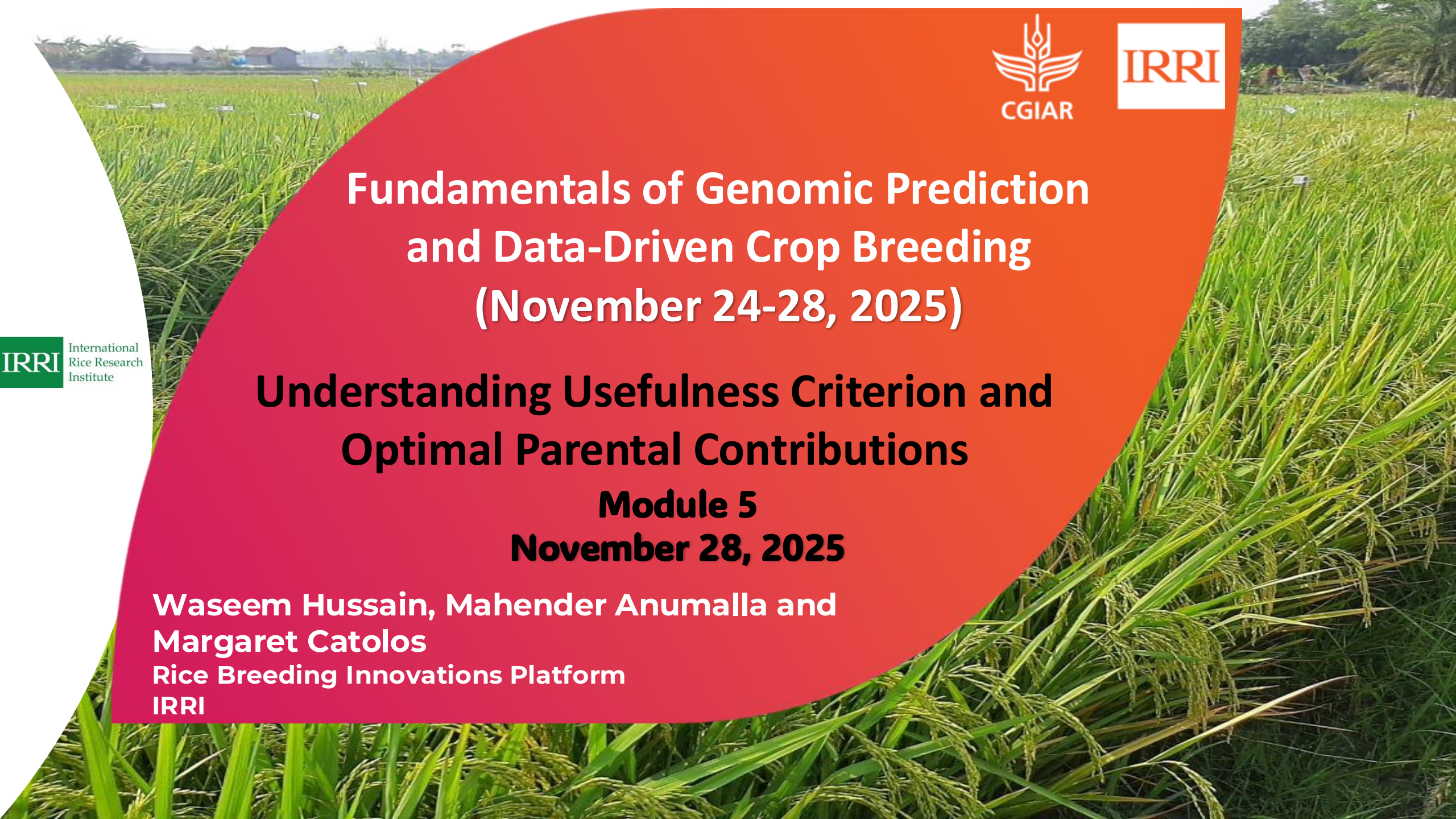


Fundamentals of Genomic Prediction and Data-Driven Crop Breeding (November 24-28, 2025)

Understanding Usefulness Criterion and Optimal Parental Contributions

Module 5

November 28, 2025

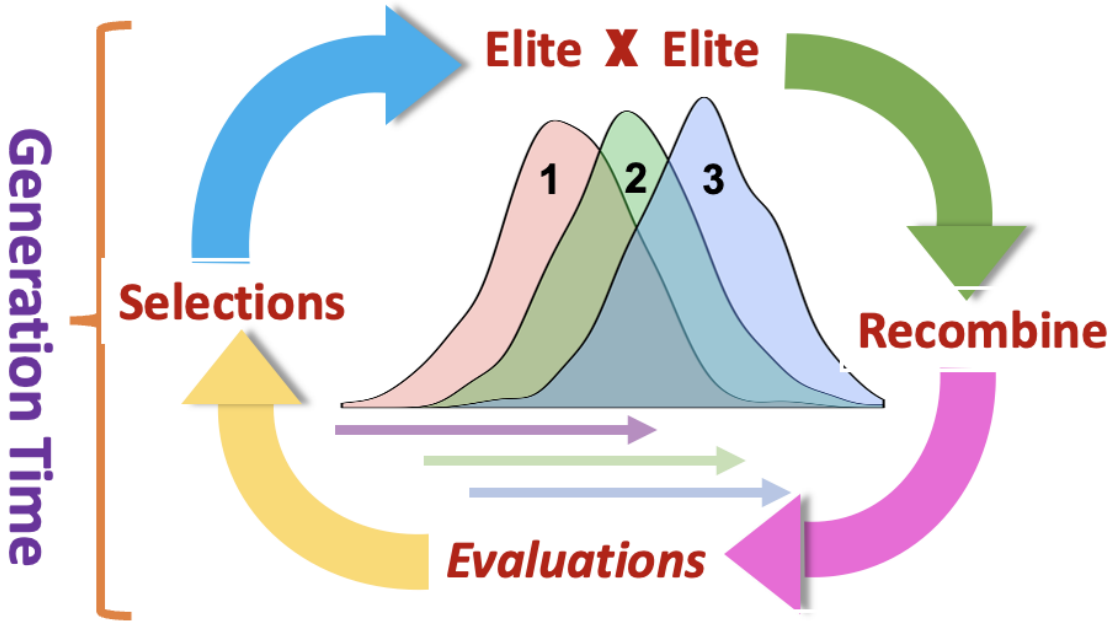
Waseem Hussain, Mahender Anumalla and Margaret Catolos

Rice Breeding Innovations Platform

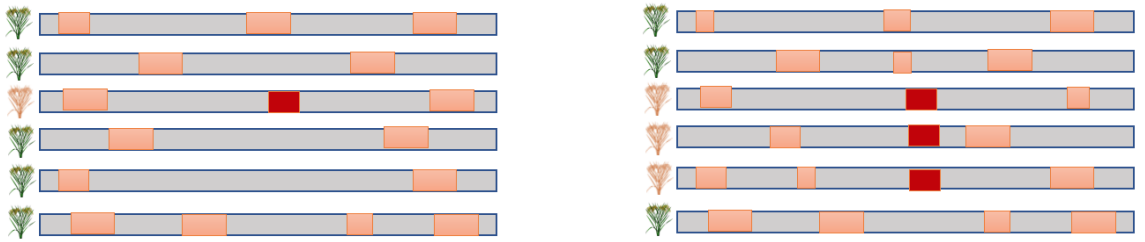
IRRI

Why Re-cycling the Parents

Improving What You Improved is Key



Recurrent selection Breaks linkages and creates variation



Aim is to Increase the combination of Favorable alleles

Yield is a complex Trait, can be improved by combining all the favorable allele combinations

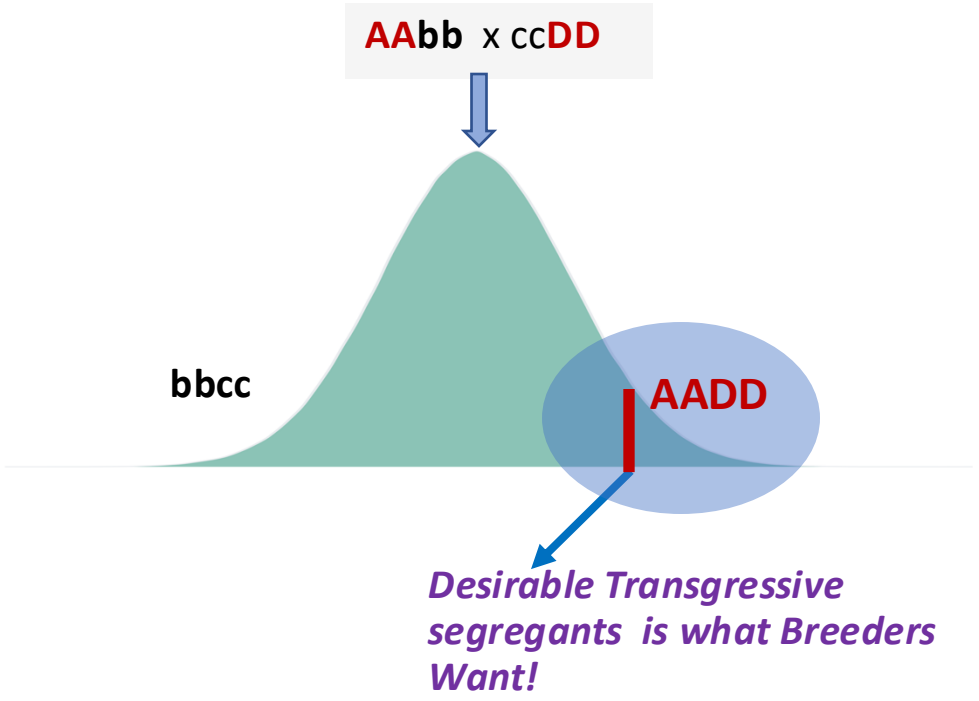
Crossing is the Key

(Right parents in Right Combinations)

Crossing is one of the main decisions of a breeding program

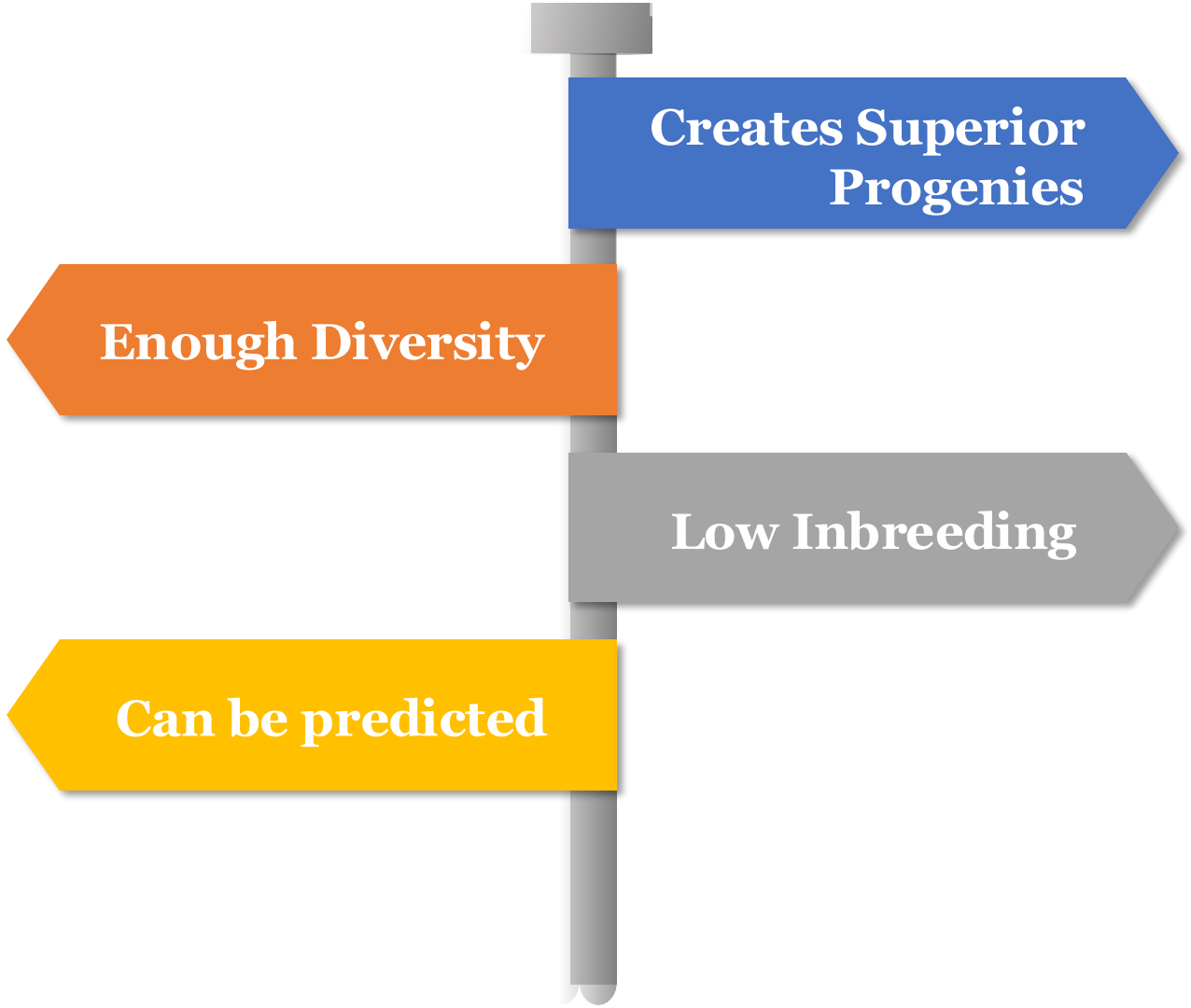
- **Crossing is main driving engine to make Response to Selection effective.**
- **Response to selection is driven by the additive effect genes/substitution effects that give rise to transgressive segregants.**
- **Transgressive segregants results in extreme Phenotypes that Breeders select.**

Transgressive Segregation is caused by Dispersion of favorable alleles

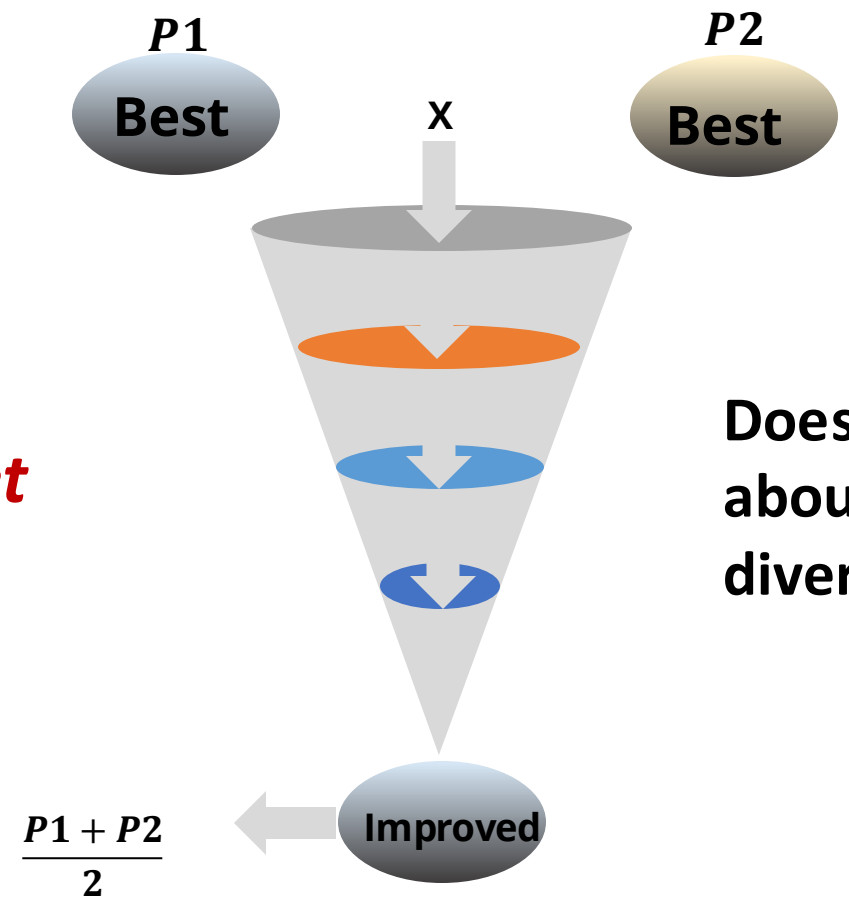


Mackay et al. 2002: https://doi.org/10.1111/pbi.13481

What is an Ideal Cross in Crop Breeding



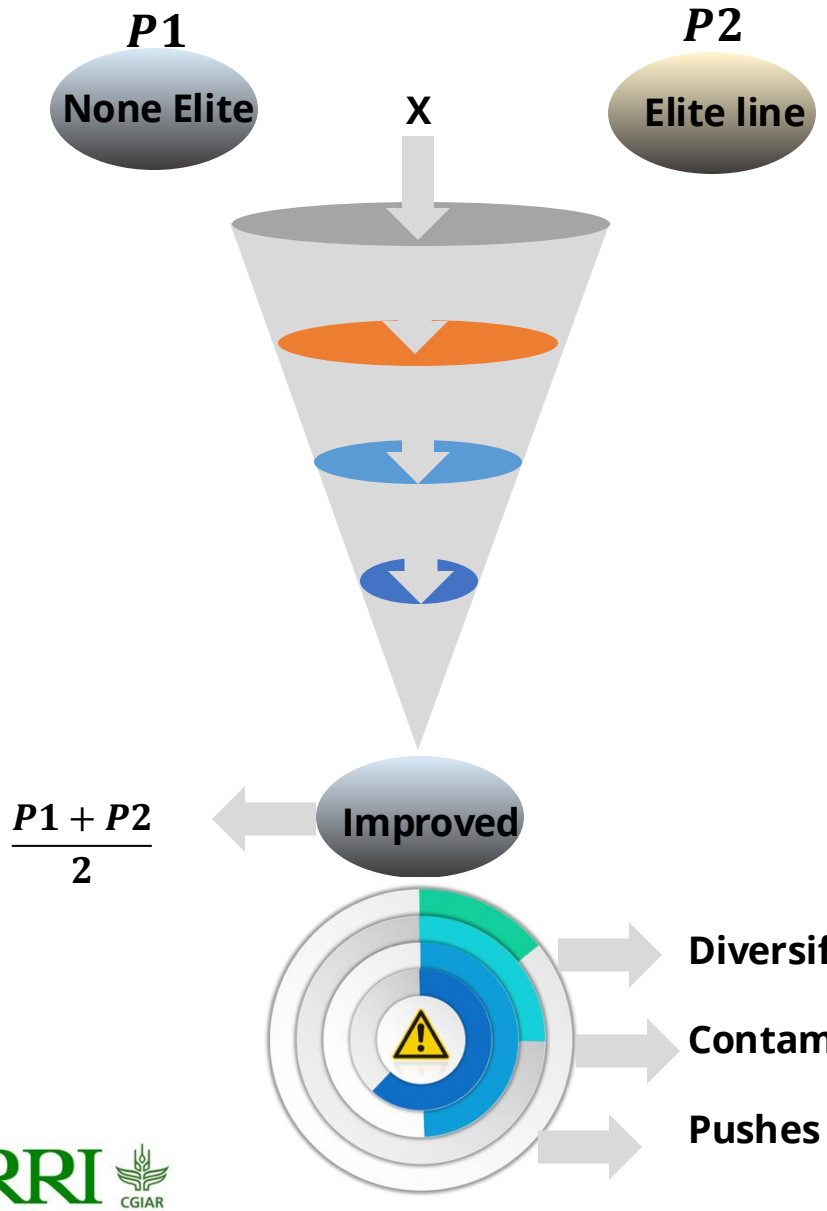
What is that Ideal Cross

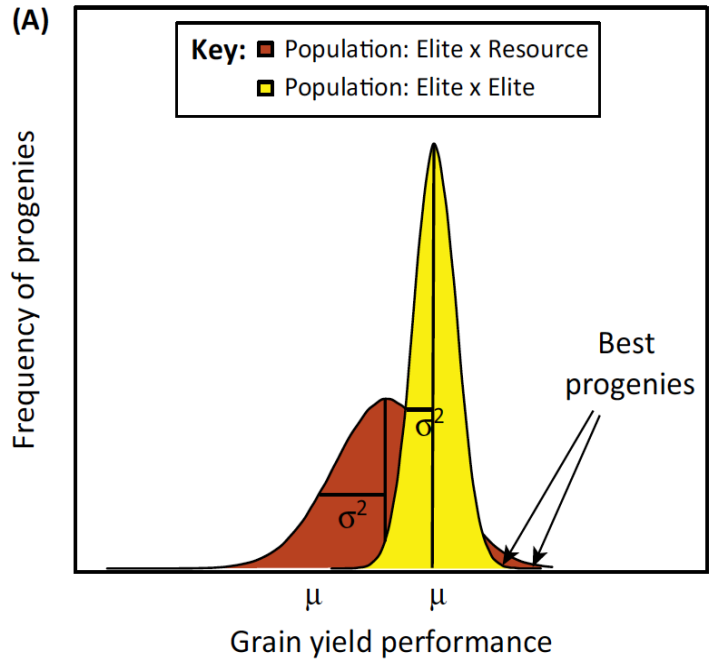


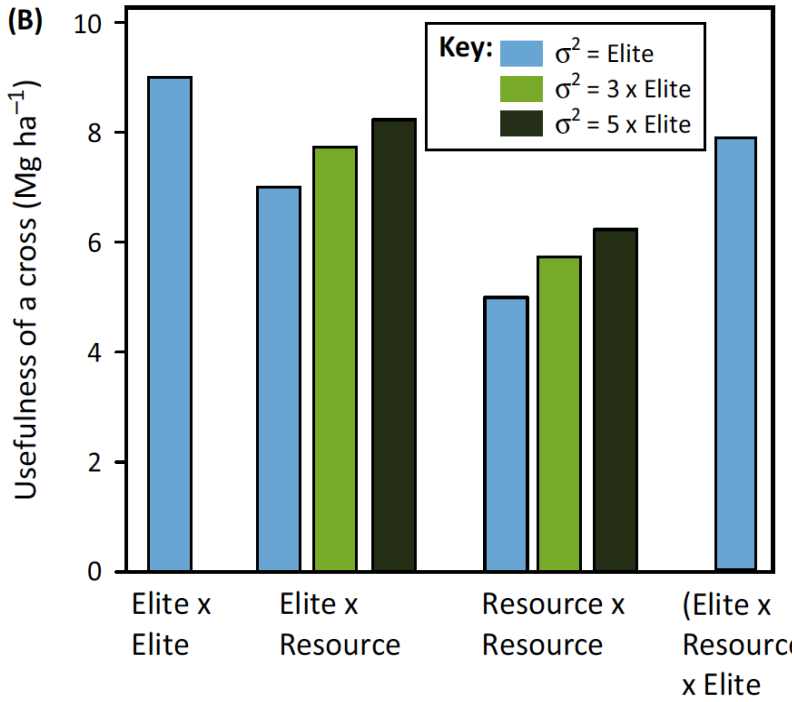
Cross Best with Best, You will get Best

Does not tell anything about the Variance or diversity?

Crossing an Elite with Non-Elite?







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

Diversifies but at cost of mean performance

Contaminates whole elite gene pool

Pushes mean breeding value back

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

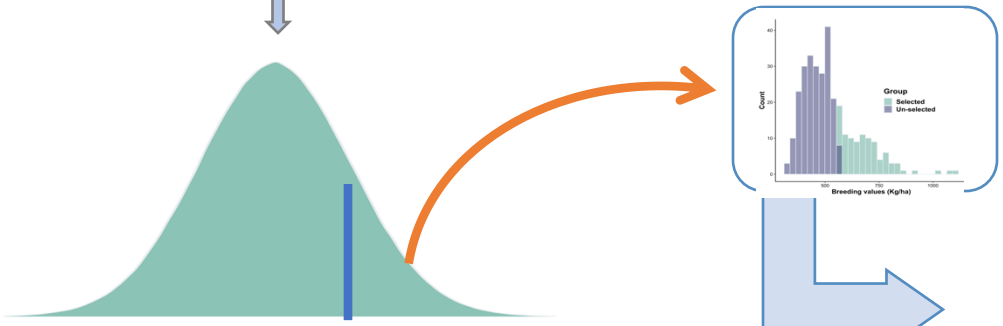
Right Parents and Right Crosses

Designing Crossing Block is Random!!!!

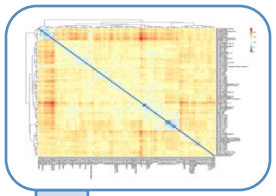
Designation	IR16T1538	IR16F1251	IR 126952-28-55-9-9-4-2-7	IR 126957-B-48-5-1-3	IRRI 185	IR13V163	IR16T1662
IR16T1538							
IR16F1251							
IR 126952-28-55-9-9-4-2-7	X				X		
IR 126957-B-48-5-1-3							
IRRI 185			X				
IR13V163							
IR16T1662							
IR 91648-B-117-B-1-1							
IR19L1046							X
IR15L1737			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							

Five Step Process to Select and Cross

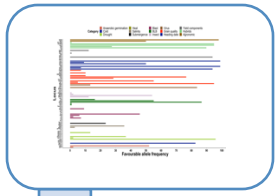
P1 X P2



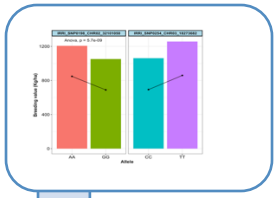
High Breeding Values



Diversity (Relationship matrix)



Major locus criterion



Transgressive Segregants

Usefulness Criterion

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

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

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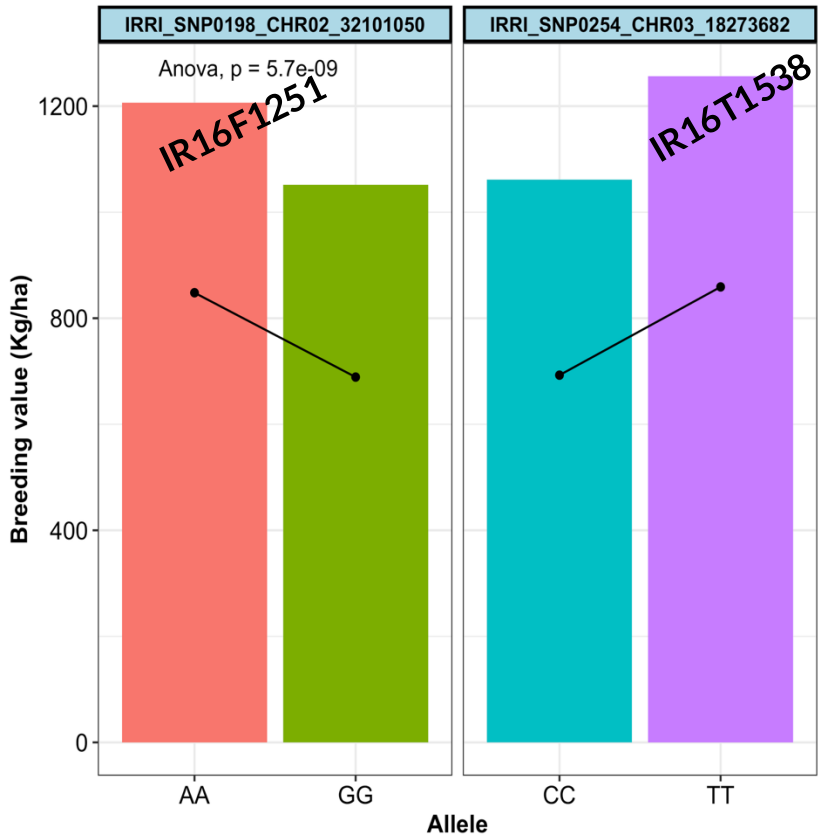
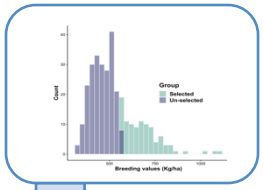
Right Parents and Right Crosses

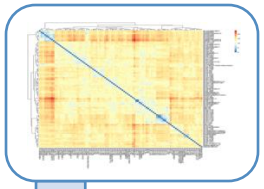
Approach to Cross

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

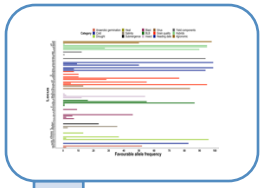




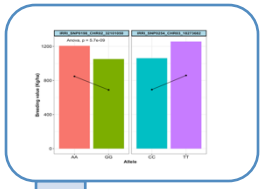
Selecting High breeding value lir based on Yield



Relationship among lines based on GRM



Selection based on Mendelian traits/major locus



Dispersed QTLs based on Grain Yield BV.

Usefulness Criterion

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

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							
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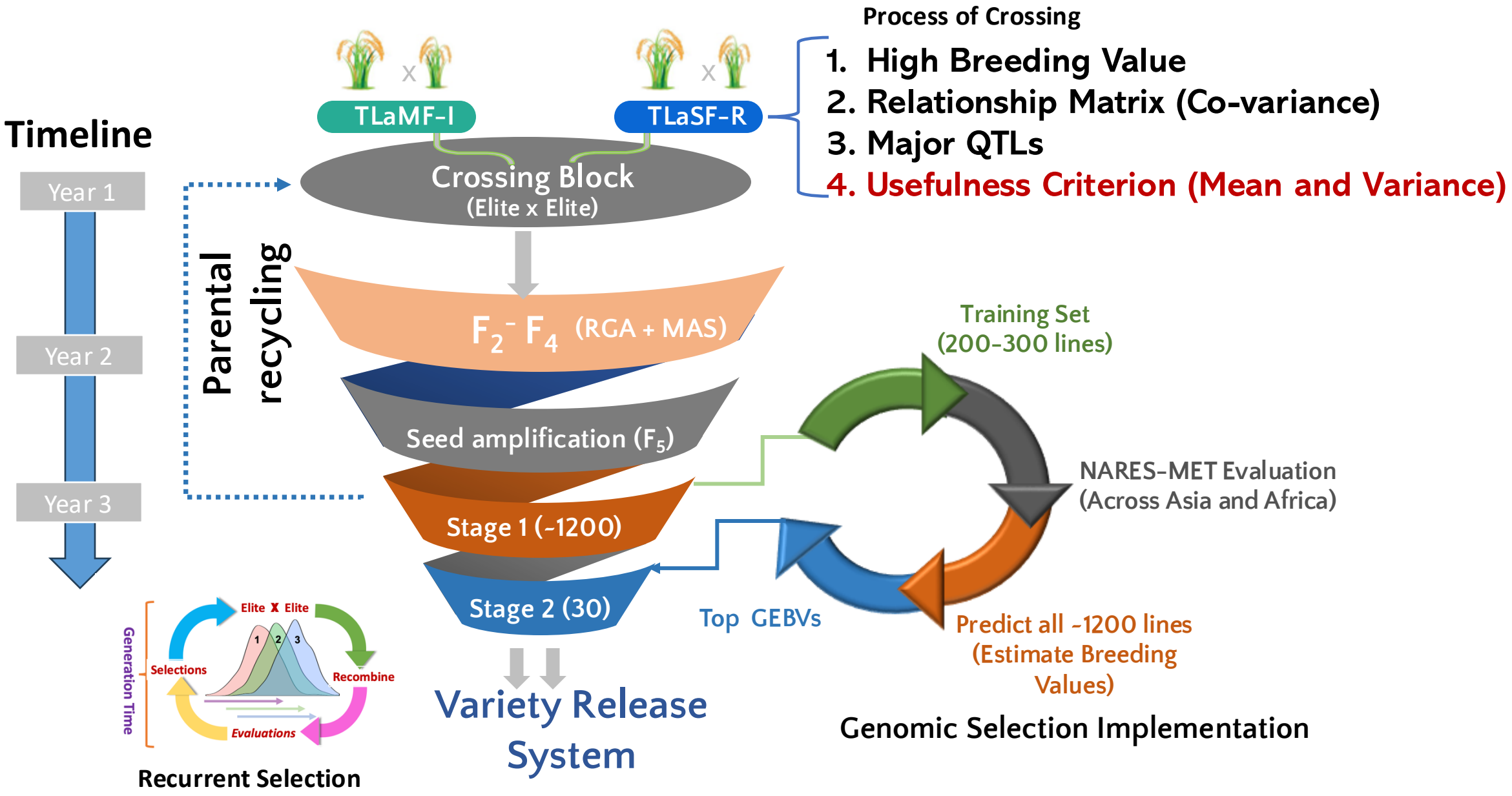
IR 117764-B-24-1-2							
IR15F1912					X		X
IR16F1147							
IR15F1709							
IR15F1729						X	
IR16T1159					X		
IR13L499							
IR14V1034							

Genomic Selection in IRRI's Global Rice Breeding



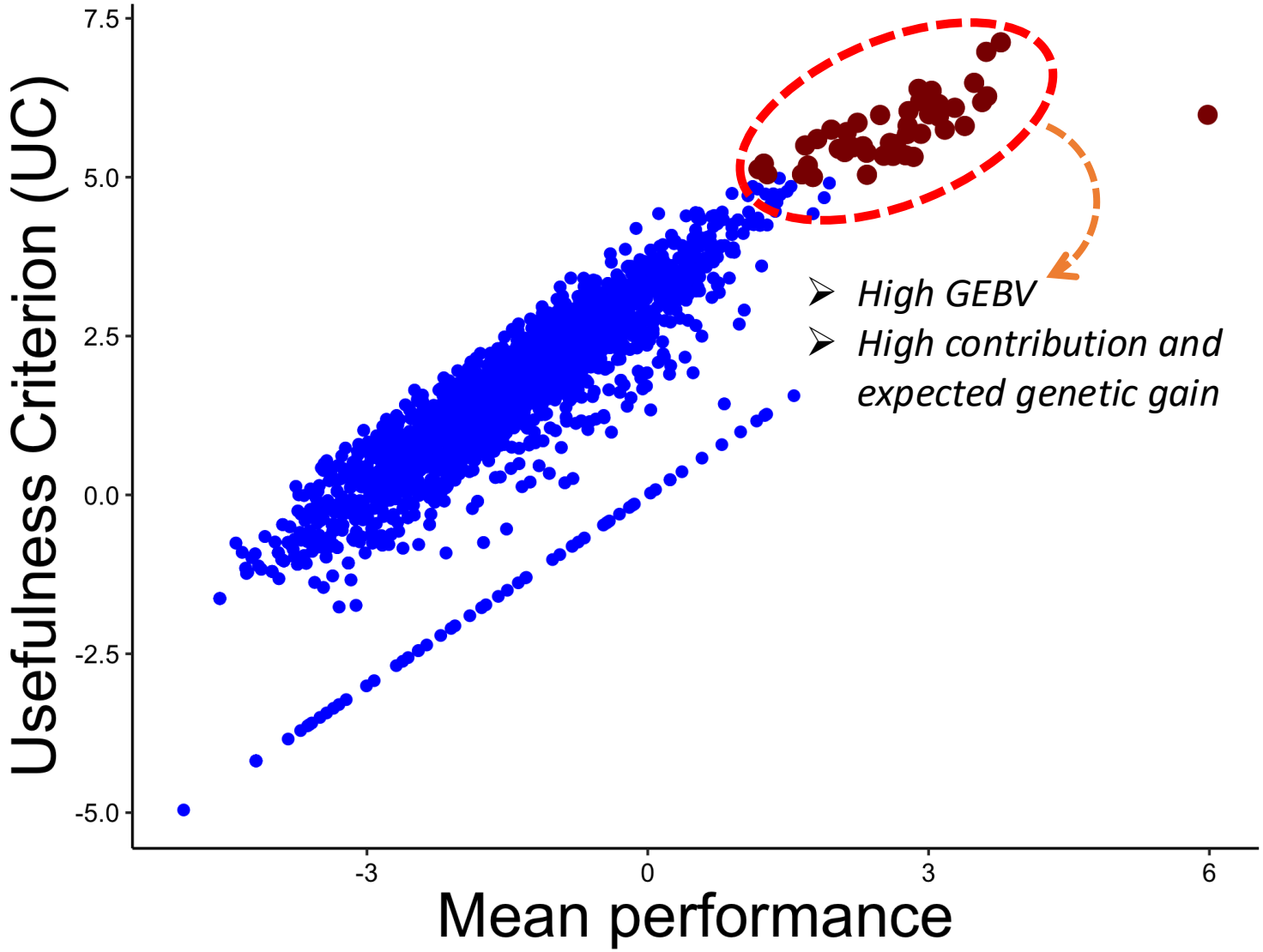
Usefulness Criterion

- *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

Example of Salinity Crosses



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