Cap Dev Lectures series:

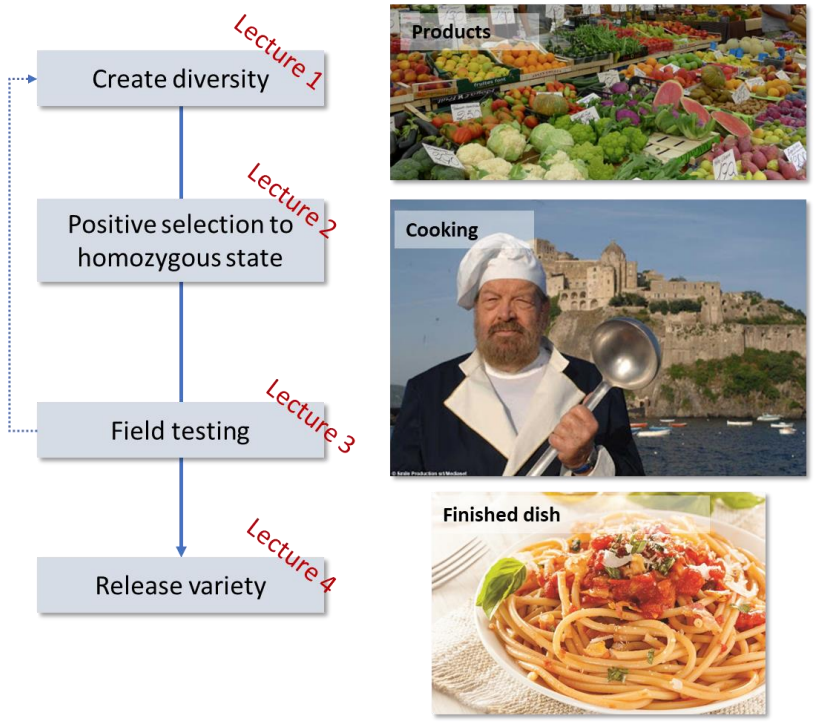
Breeding autogamous cereals - a complete lecture from *Parents to Farms*

Filippo M Bassi
senior durum wheat breeder

@fillobax

Lecture 5 – April 21st 2022

- **Improving parental selection by genomics (L1)**
  - GWAS to combine QTLs
- **Improving inbreeding advancement by genomics (L2)**
  - MAS for untestable traits
  - GS for recycling time
  - Risk of loosing intensity
- **Improving Stage 1-2 yield trials by genomics (L3)**
  - Higher accuracy with genomic GxE models
- **Improving Release and certification by genomics (L4)**
  - Selection for homogeneity by markers
  - PVP by genetic passports
- **Improving Genetic gain by genomics**
  - The equation and how it changes



Parental selection: genomics augmentation

- Parental selection can not be blind
  - How would you use genomic to improve this step?

Parental selection: genomics augmentation

- Select 2 parents for a new top yielding var with resistance to 2 diseases and good quality

Phenotypic data

Trait	P1	P2	P3	P4	New var
Yield	5	5	6	6	>5
Disease 1	R	S	R	S	R
Disease 2	S	R	R	S	R
Quality	Y	Y	N	N	Y

Parental selection: genomics augmentation

- Select 2 parents for a new ***top yielding var with resistance to 2 diseases and good quality***
  - Now you have GWAS data: which one would you combine?

Phenotypic data

Trait	P1	P2	P3	P4
Yield	5	5	6	6
Disease 1	R	S	R	S
Disease 2	S	R	R	S
Quality	Y	Y	N	N

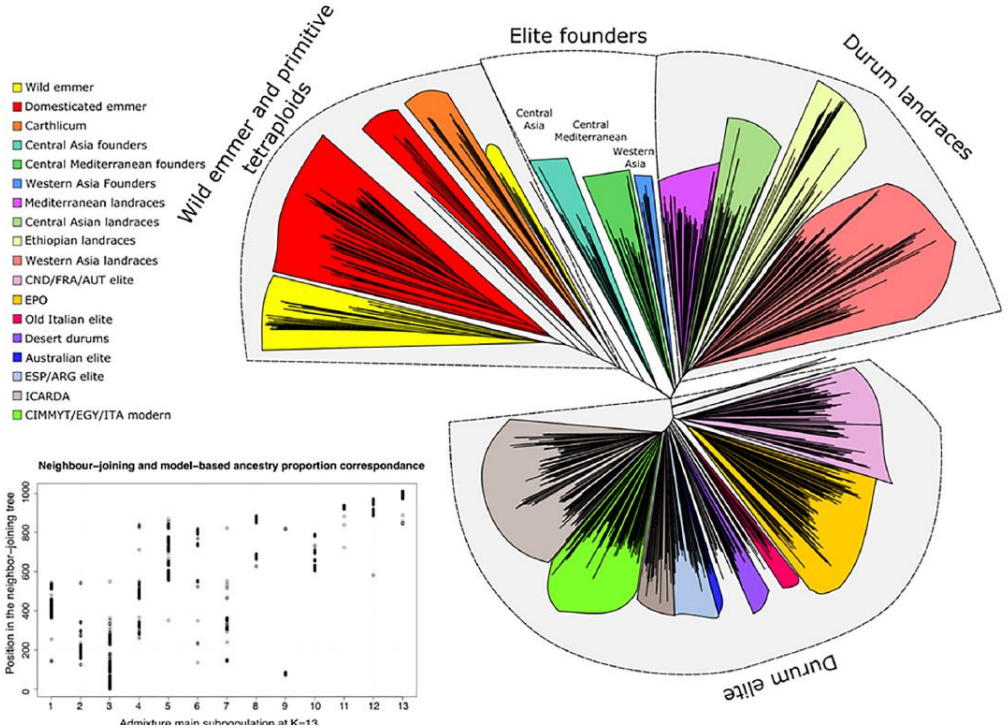
New var
>5
R
R
Y

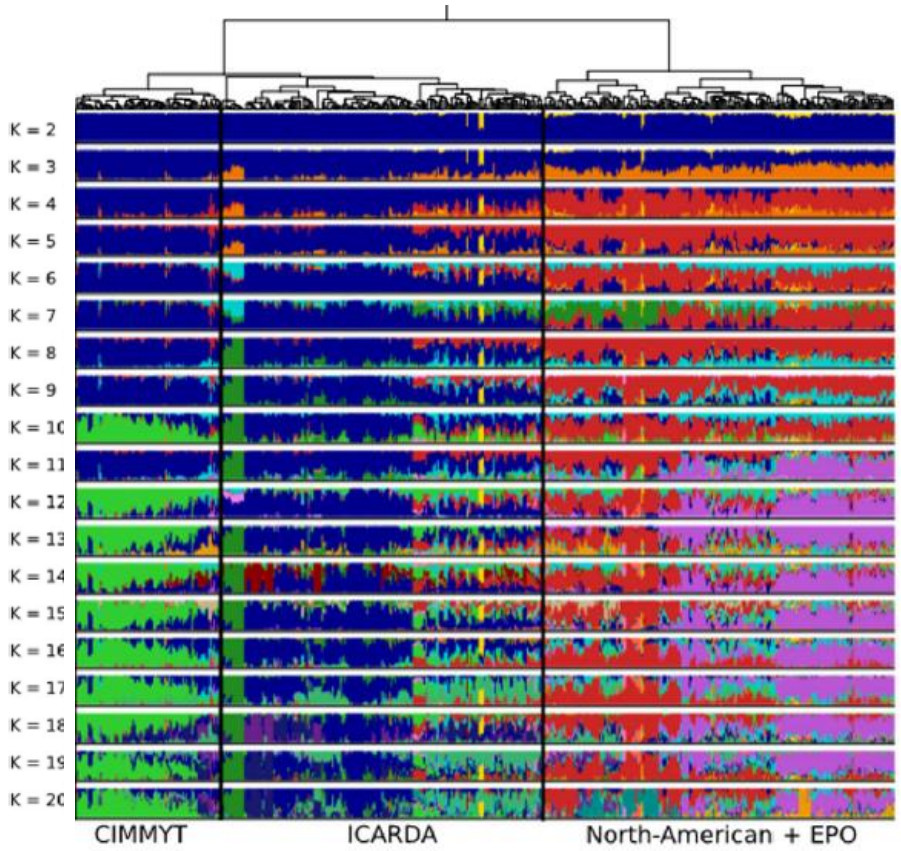
Genomic data

Trait	P1	P2	P3	P4
Yield QTL 1	N	Y	Y	Y
Yield QTL 2	Y	N	Y	Y
Disease 1 QTL 1	Y	N	Y	N
Disease 2 QTL 2	N	Y	Y	N
Quality QTL 1	Y	N	N	N
Quality QTL 2	N	Y	N	N

Parental selection: genomics augmentation

- Parental selection can be improved via GWAS and also based on ***genetic diversity***
- Ideally we also want to know the linkage between traits (neg or pos correlation)
  - PopVar is a R script that can be used for this scope



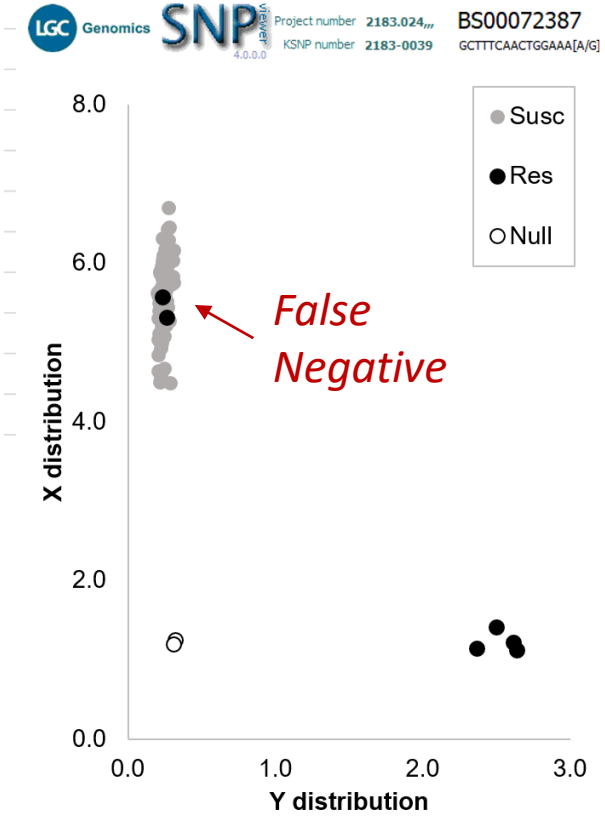


Progress to inbreeding: genomics augmentation

- How do you think molecular markers can improve this step?

Progress to inbreeding: MAS

- Marker Assisted Selection:
  - Traits controlled by 1 or few genes can be selected by MAS
  - That is why is very important to “validate” GWAS discoveries (example of Hessian fly)

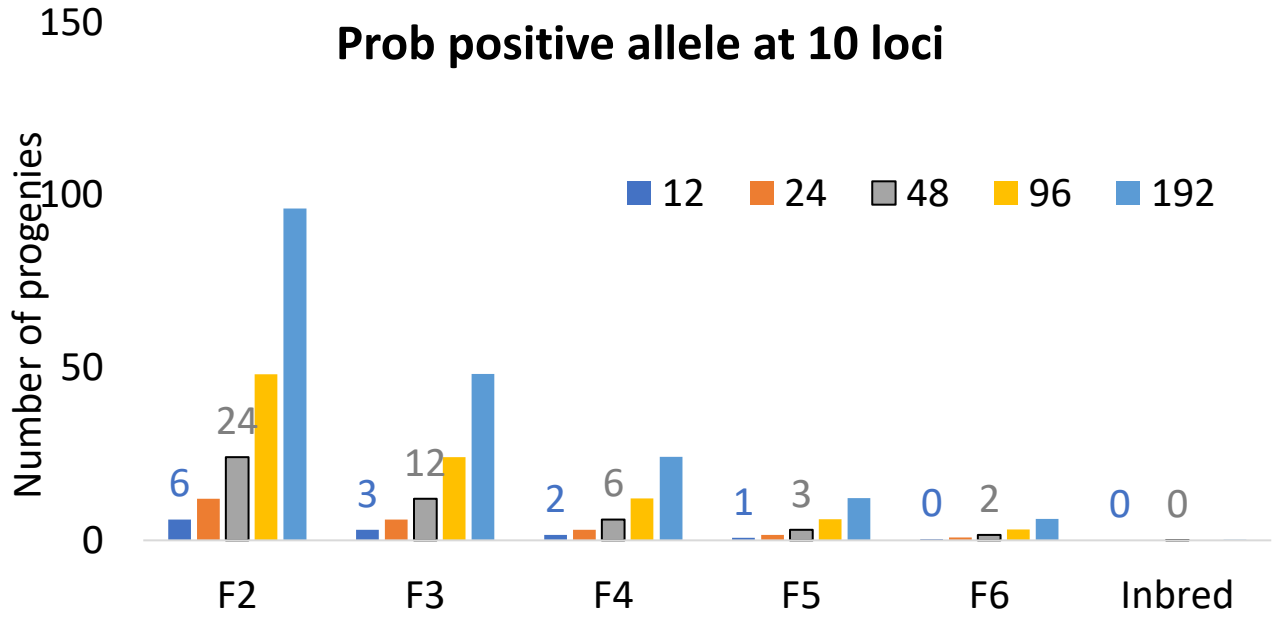


Allele	Type	HF response	N	Ratio
Suscept.	**TN**	**Susceptible**	**610**	**93%**
	FN	*Resistant*	*45*	*7%*
Resistant	FP	Susceptible	0	0%
	TP	**Resistant**	**32**	**100%**

Bassi et al. 2019 Doi: 10.1007/s11032-019-0927-1

Progress to inbreeding: MAS

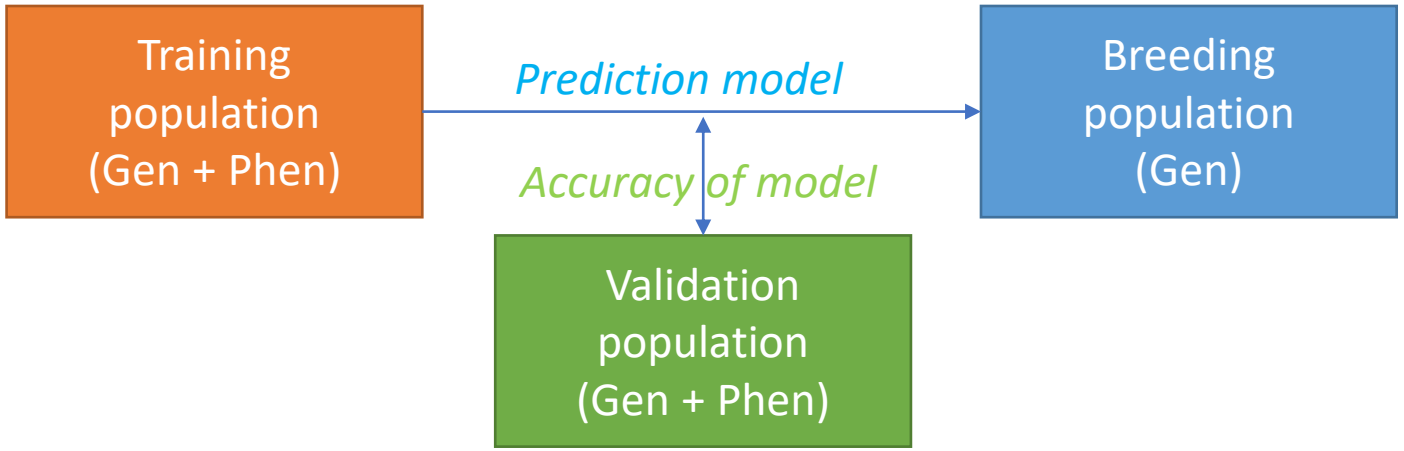
- Marker Assisted Selection:
  - Keep in mind the issue of *intensity vs inbreeding*
    - Screening 12 progenies in F4 is ok, while at F6 it would fail
      - Why not testing **192 then?**



Progress to inbreeding: GS

- Genomic models are used to predict the performances of untested material
  - It can improve **recycling time**
  - It can improve **accuracy**
  - It certainly cost **intensity**: KASP with 96-192 markers: 5 USD per sample

  100 populations x 48 progenies + 200 parents as TP = ***25K USD per year***

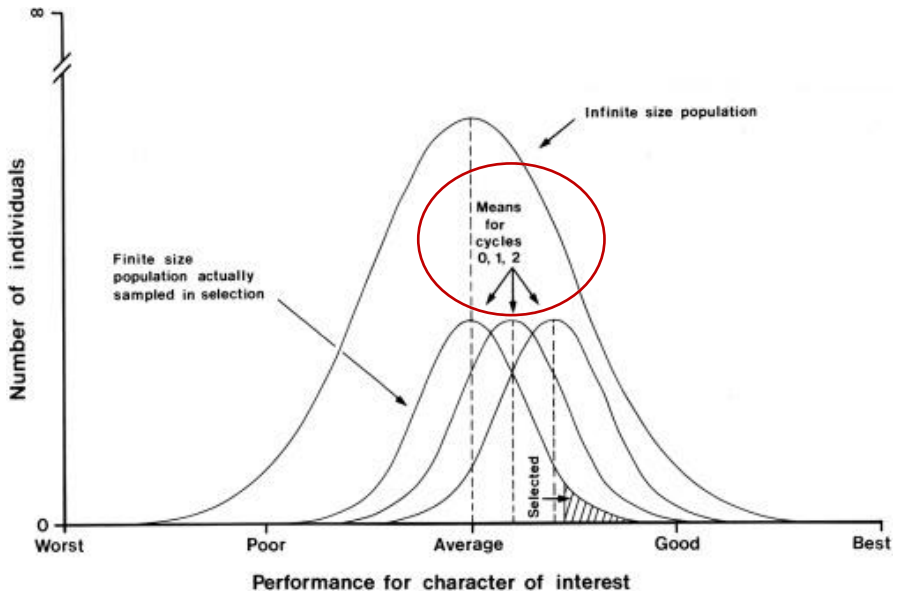


Zaim, et al. 2021*. Combining QTL analysis and genomic predictions for four durum wheat populations under drought conditions.* *Frontiers.*

GS Approach: keeping intensity is difficult

- Using 48 progenies it is possible to select up to **10 loci** per selection cycle in F2 to F4
  - A ***recurrent mating scheme*** allows to select 10 loci each cycle, hence **30 in 3** cycles

P= (Inbreeding x 0.5^n) + Heterozygosity



Cycle 0

P1 x P2 segr 30 loci

..

F4 select for 10 loci

..

Stage 2 (10 loci)

Full-sibs mating

Cycle 1

F4 x F4 segr 20 loci

..

F4 select for 10 loci

..

Stage 2 (20 loci)

Full-sibs mating

Cycle 2

F4 x F4 segr 10 loci

..

F4 select for 10 loci

..

Stage 2 (30 loci)

Training population: Relatedness is *accuracy*

A training population can only model those alleles for which it is segregating

"Far-related" training populations can not predict the allelic interactions of the breeding pop

- Training pop in **full-sib** relationship with breeding pop is ideal to ensure high accuracy

GY	DRO	IG	YG	SW
DRO	0.47	-0.08	-0.11	0.07
IG	-0.09	0.41	0.00	0.08
YG	-0.07	-0.02	0.35	-0.08
SW	0.06	0.29	-0.13	0.37

Full sibs

Pedigree

IC : Icamor/Gidara2

DRO : Jennah Khetifa/Cham1//T.dicoccoides600545/2*Omrabi5

SW : SW Algia//Gidara1/Cham1

YG : Omrabi3/Omsnima1//Gidara2

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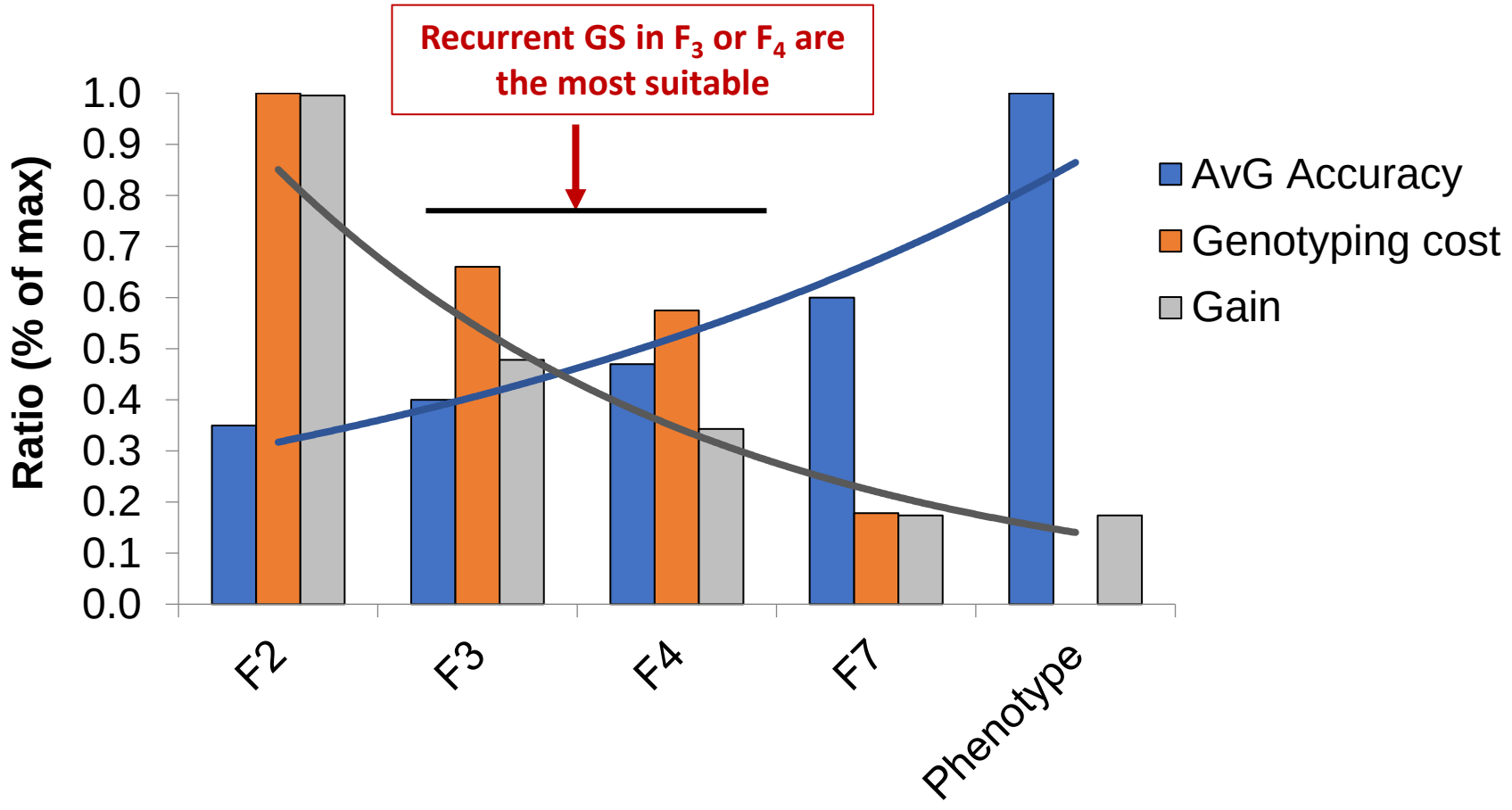
Breeding GS schemes: cost vs genetic gain



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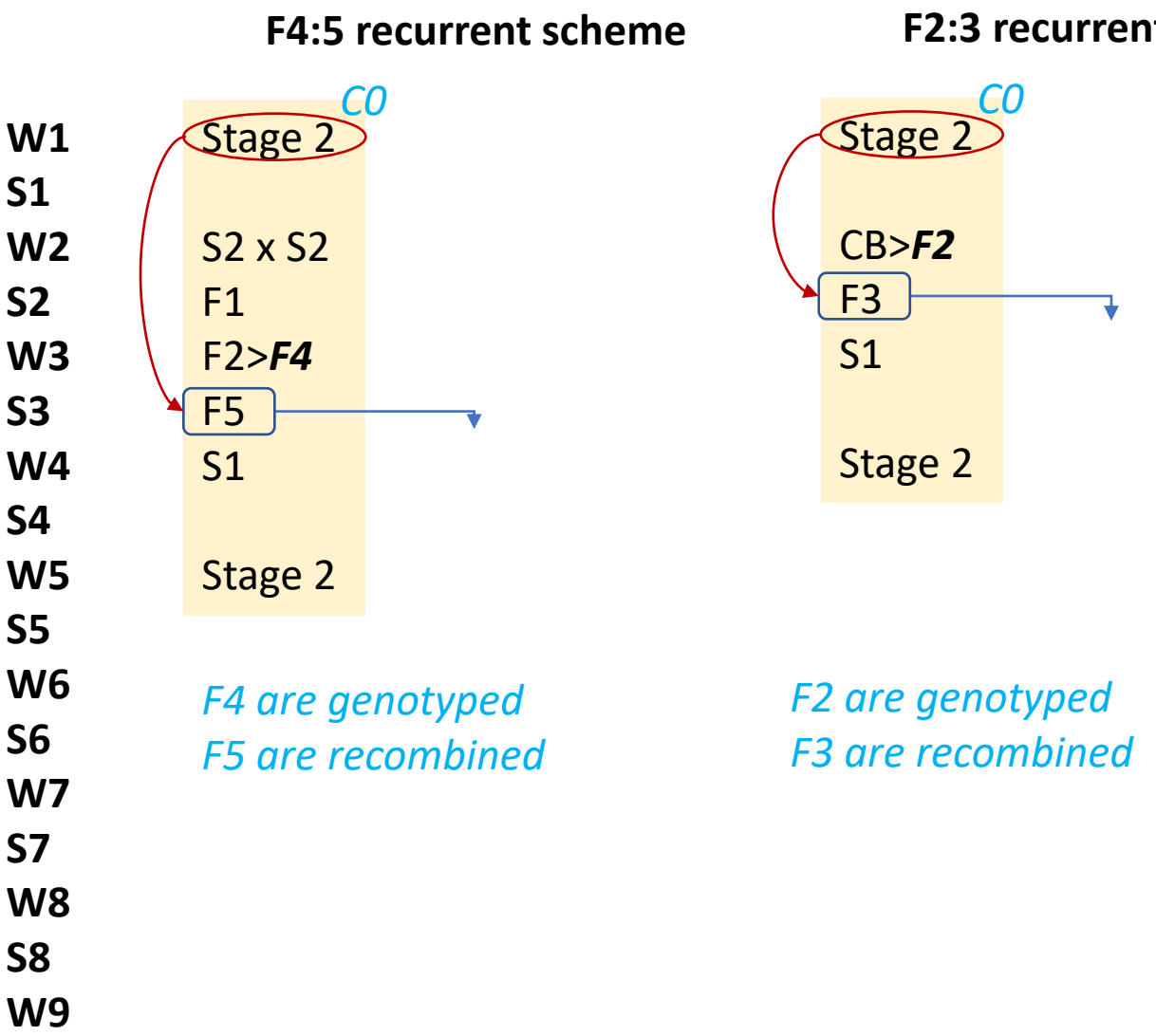
Designing a GS scheme: cost vs accuracy vs speed



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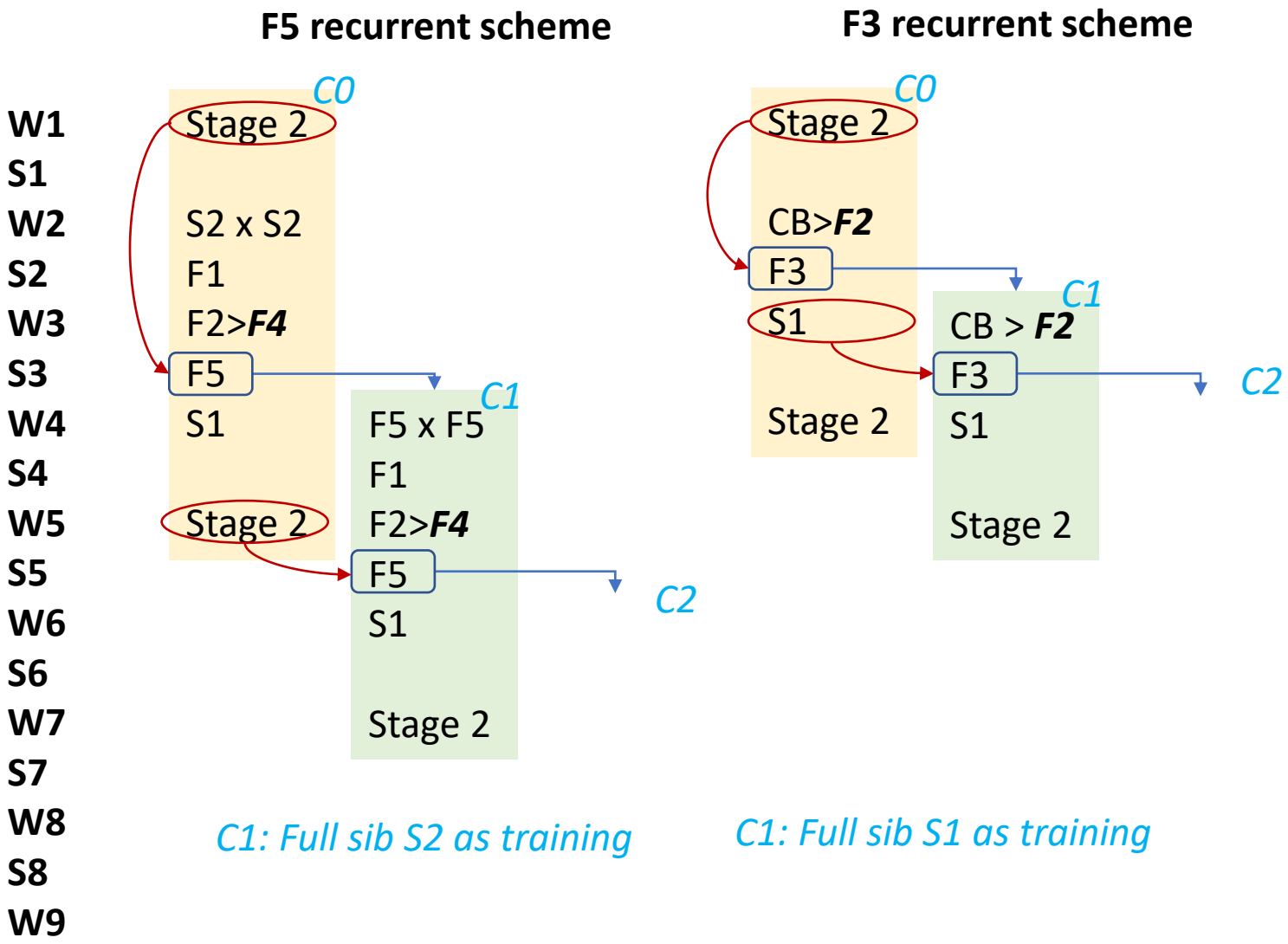

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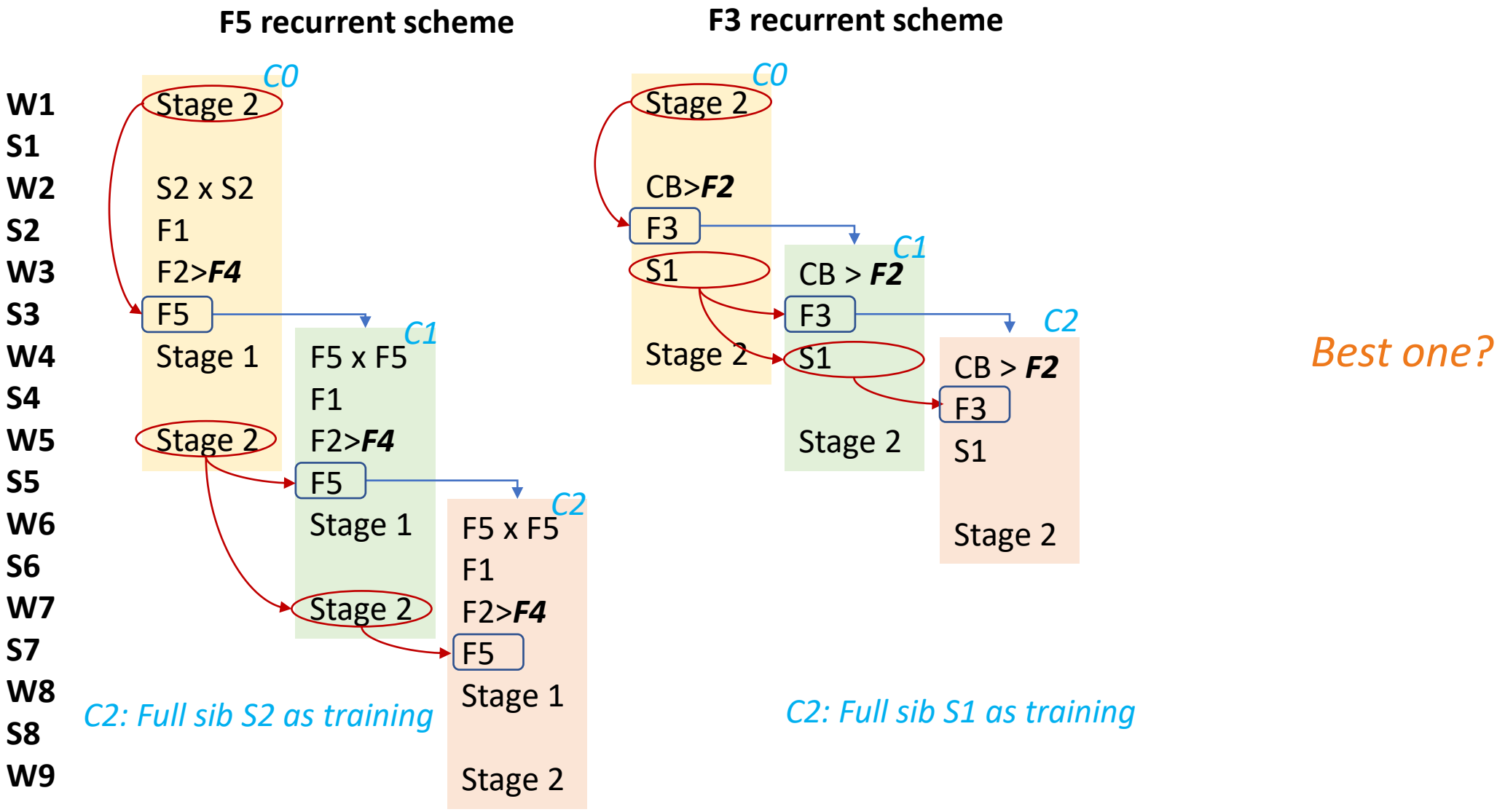

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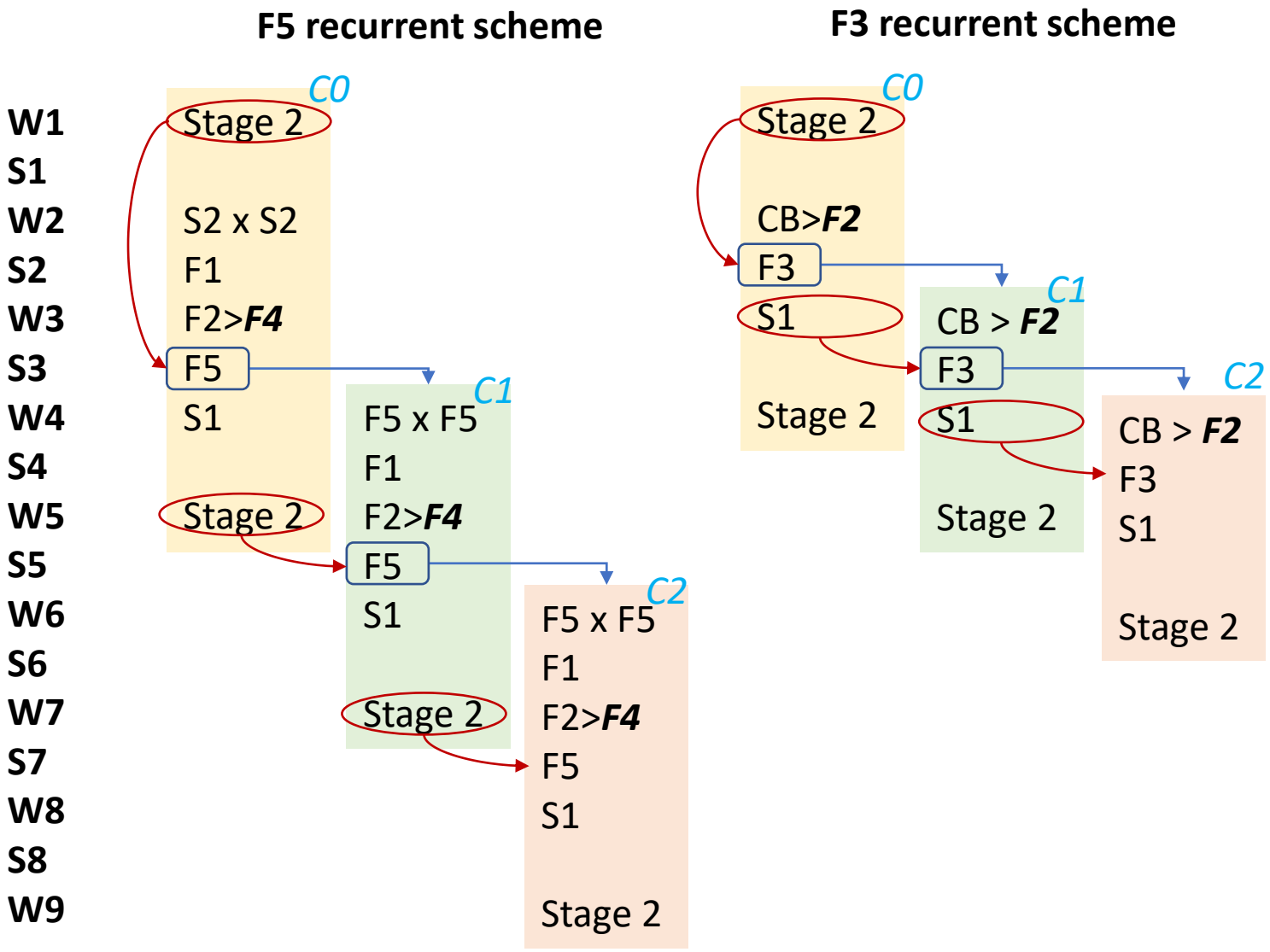

	Shuttle	F5	F3
Accuracy	0.5	0.5	0.2
Intensity	1.5	1	1
Heritability	-	-	-
Time	5	3	2
GG (U)	6x	7x	4x
P. positive	2%	3%	6%

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Stage 1 and 2 yield trials: Genomic augmentation

- What elements could be improved?

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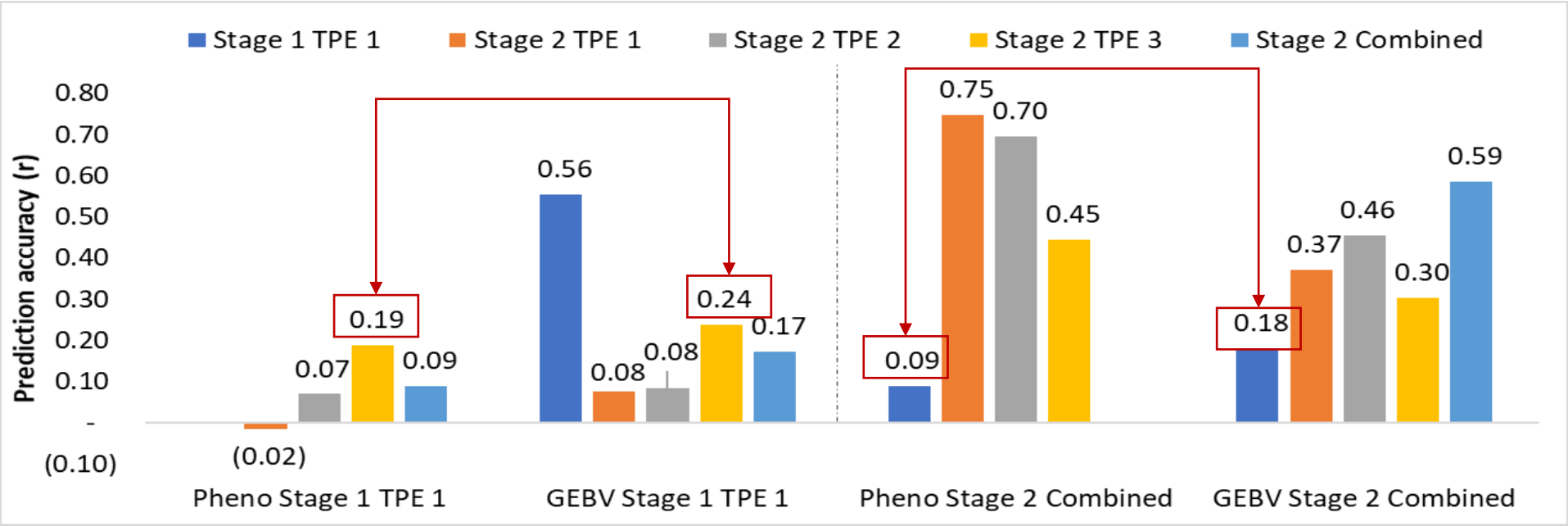
- What elements could be improved?
  - *Assessment of complex traits with high accuracy: index*
  - *GxE at Stage 1*



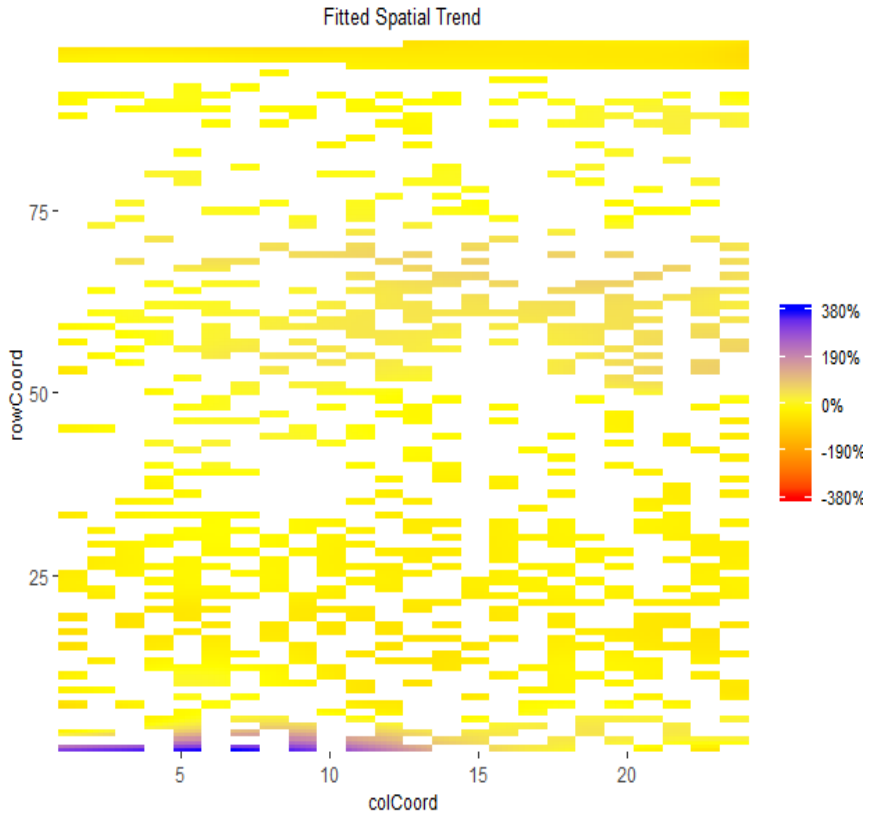
Phenotypic predictions of one site (TPE) to another are very poor: GEBV are better at controlling GxE

A Stage 1 training pop has limited ability to predict real performances

Stage 1 sparse testing: Genomic augmentation

- Stage 1 is composed of thousands of lines
  - *Increasing intensity results in genetic gain*
  - *But it comes at extra **cost***
    - *What if we could plant few and predict many?*

Ratio (%)	Stage 1	Stage 2	STD differential	Genetic gain
10.0%	2 400	240	1.750	1.00
5.0%	2 400	120	2.063	1.18
1.0%	2 400	24	2.665	1.52
0.5%	2 400	12	2.892	1.65
0.1%	2 400	2-3	3.253	1.86



Stage 1 sparse testing: Genomic augmentation

- Stage 1 is composed of thousands of lines
  - *Increasing intensity results in genetic gain*
  - *But it comes at extra cost*
    - *What if we could plant few and predict many?*

- If **genotyping cost is less than plot cost**, it is a good approach
  - *Otherwise, only gain will be accuracy, not intensity*
  - *Keep in mind the need to produce seeds for Stage 2*

Ratio (%)	Stage 1	Stage 2	STD differential	Genetic gain
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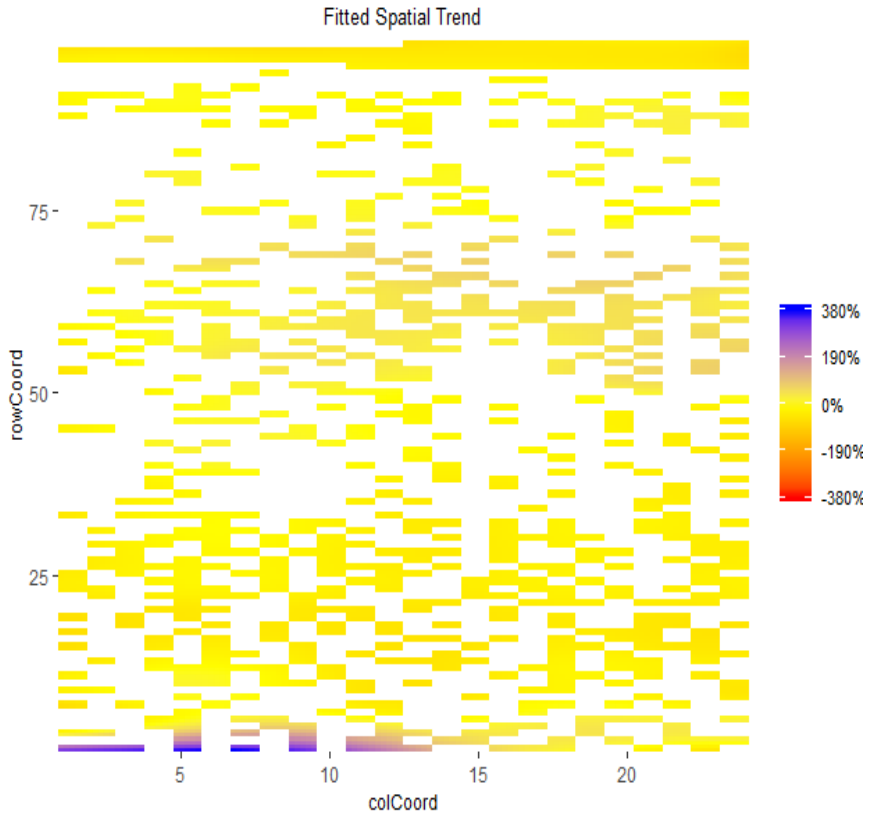
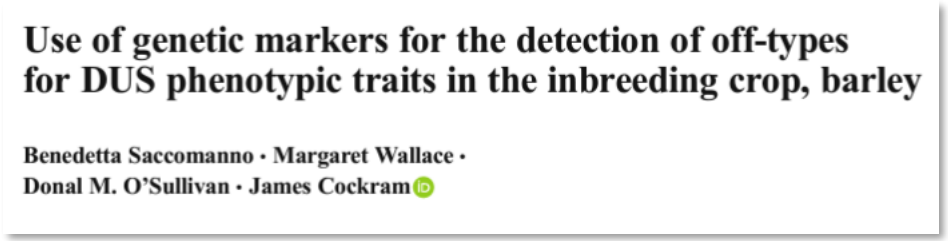


Release and certification: Genomic augmentation

- What elements could be improved?

Release and certification: Genomic augmentation

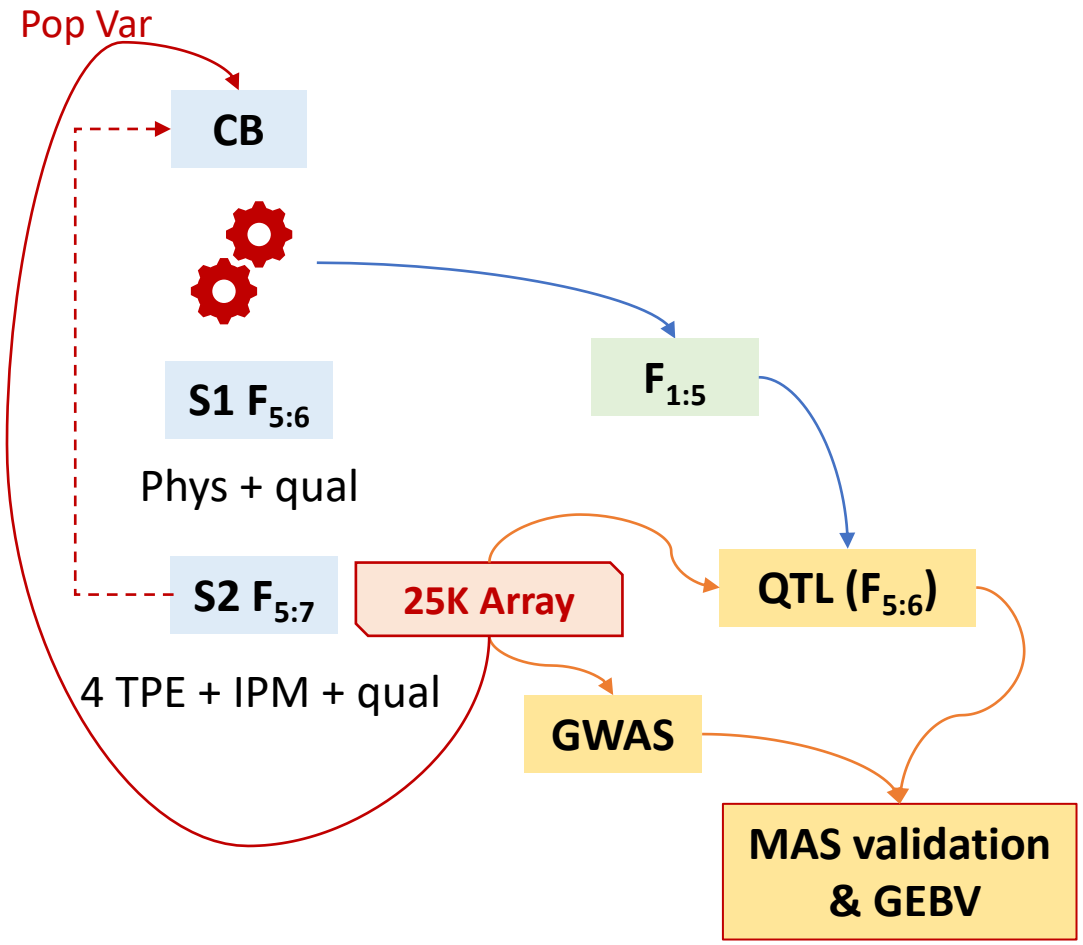
- What elements could be improved?
  - ***Homogeneity***
    - Use markers to accelerate homogeneity
    - Use markers for DUS testing
  - ***Intellectual property protection***
    - Use genetic passports to investigate use of germplasm


Use of genetic markers for the detection of off-types for DUS phenotypic traits in the inbreeding crop, barley

Benedetta Saccomanno · Margaret Wallace · Donal M. O'Sullivan · James Cockram

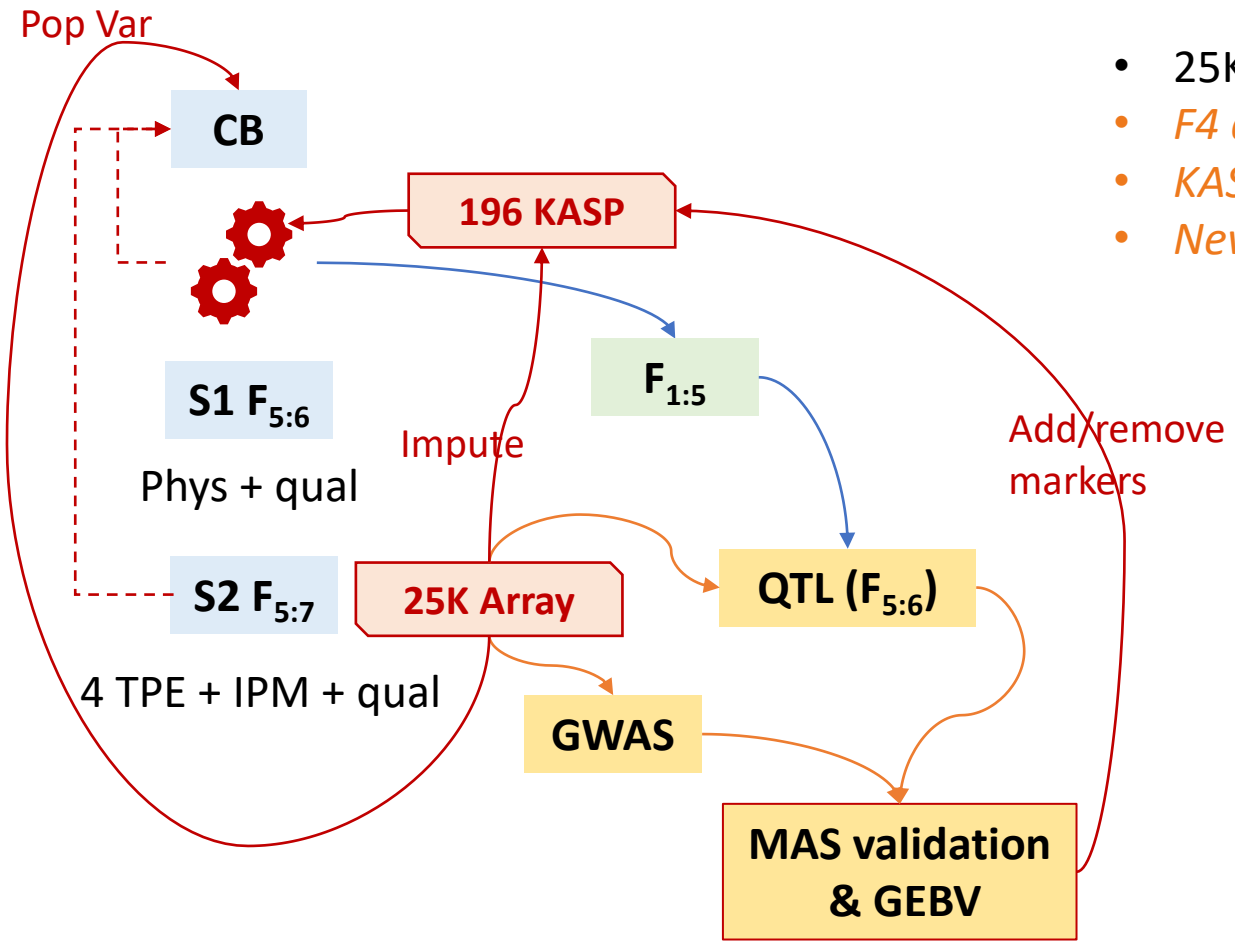
Var name	Origin	**Karim**	**Duilio**	**Meridiano**
		Jori69/Anhinga/Flamingo	Cap.lli//Anhinga/Flamingo	Sim.to/WB881/Duilio/F21
Karim	CIMMYT		**0.92**	0.62
Dulio	Italy	**0.92**		0.62
Nassira	Morocco	0.64	**0.66**	0.42
Don Pedro	Spain	0.63	**0.64**	0.42
Wollaroi	Australia	0.61	**0.63**	0.41
Meridiano	Italy	0.60	**0.62**	
Flaminio	Italy	0.57	0.56	**0.58**

Connecting the dots: molecular breeding



- 25K array is used to genotype Stage 2 and MP

Connecting the dots: molecular breeding



- 25K array is used to genotype Stage 2 and MP
- *F4 are genotyped with 196 KASP*
- *KASP match 25K array probes*
- *New KASP are added/removed*

How can genomic augmentations help us?

$$\text{Genetic gain} = \frac{\text{Accuracy} \times \text{Heritability} \times \text{Selection intensity}}{\text{Recycling time}}$$

Accuracy: reduce experimental error
Heritability: markers are not affected by GxE
Intensity: predict more entries without testing them
Time: predict early and then recombine

Conclusion lecture 5

- The genetic gain equation drives all breeding decisions
- Markers help selecting parents via GWAS and genetic diversity
- MAS/GS assure GG in F2>F5, but need to find balance: **relatedness vs time vs accuracy vs costs**
- GS in Stage 1 can increase accuracy (GxE), helps deploy **index**, and can increase intensity
- Markers can simplify the progress to homogeneity
- Genetic passports are good records to protect IP

- Genotyping is a **cost** and should be treated as such
- Molecular breeding has its own **logistics** to be considered:
  - Few seeds in plants grown in the GH
  - Crossing 1 plant is hard, 10 plants is better
  - Time gap between genotyping and modeling has to be accounted for