ICARDA
Science for resilient livelihoods in dry areas

Cap Dev Lectures series:

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

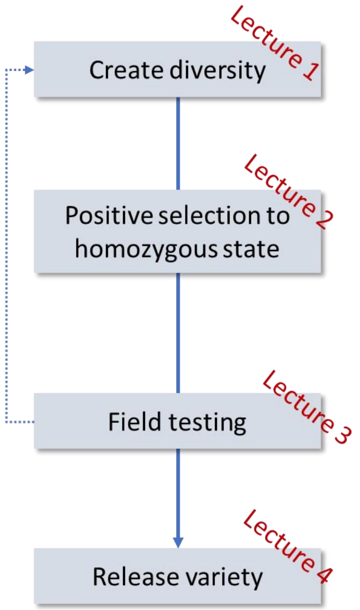
Filippo M Bassi
senior durum wheat breeder

@fillobax

Lecture 2 – April 7th 2022

- **Progression to inbreeding (F1 to F5)**
  - Inbreeding
  - Intensity of selection
  - What traits can be selected for
  - Heterogeneity
  - Selection history
  - Practical examples

- **Breeding schemes**
  - Logistics of a breeding program


Create diversity

Positive selection to homozygous state

Field testing

Release variety

Inbreeding

- At each generation, half of the alleles are fixed in one homozygous state
  - Why is that important?

Generation	Heterozygosity	Inbreeding
F1	100.0%	0.0%
F2	50.0%	50.0%
F3	25.0%	75.0%
F4	12.5%	87.5%
F5	6.3%	93.8%
F6	3.1%	96.9%
F7	1.6%	98.4%

Inbreeding: it also reduces your options

We want allele A-

F1: Aa

Aa	A	a
A	AA	Aa
a	aA	aa

Gen	Frequency			
	AA	Aa	aa	A-
F2	25%	50%	25%	75%
F3	38%	25%	38%	63%
F4	44%	13%	44%	56%
F5	47%	6%	47%	53%
F6	48%	3%	48%	52%

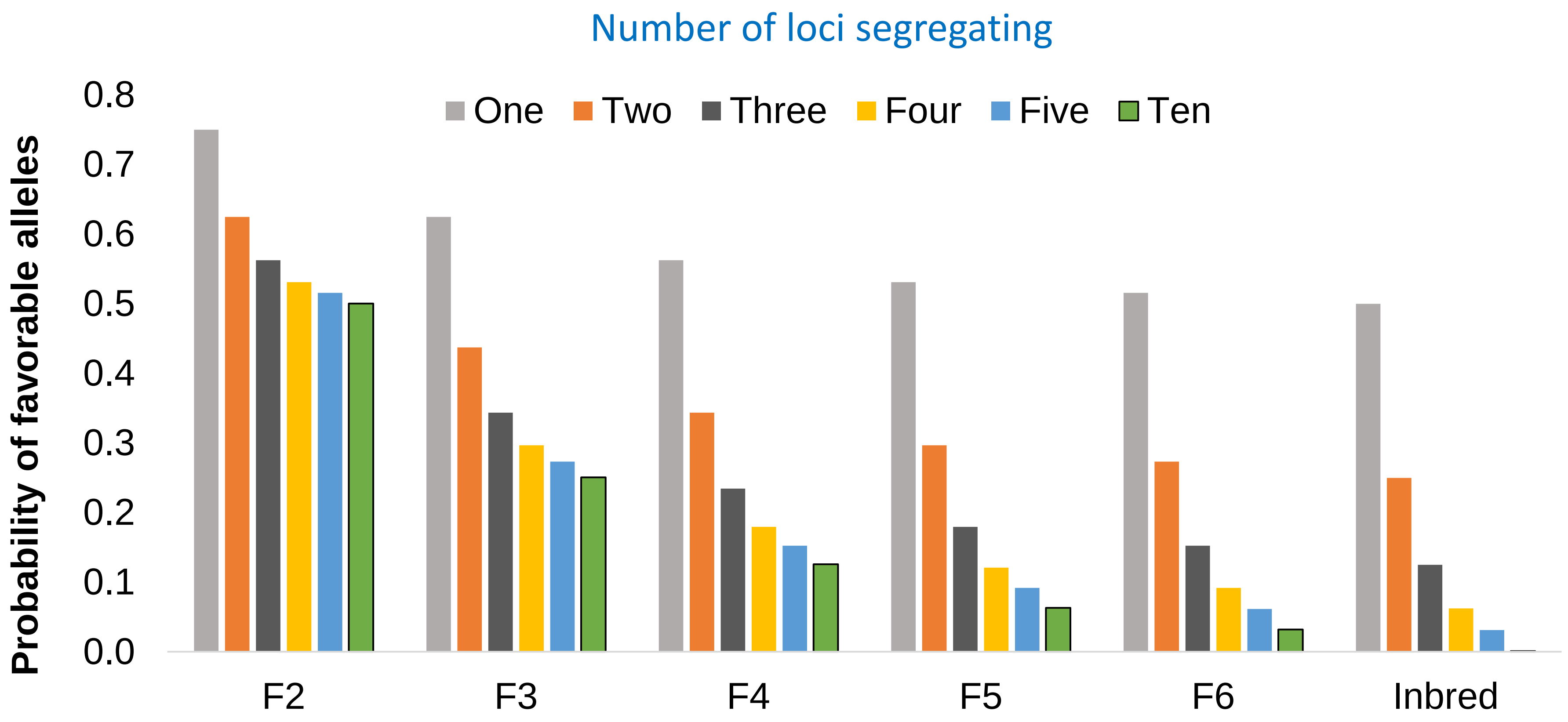
We want allele A- B-

F1: AaBb

AaBb	AB	aB	Ab	ab
AB	AABB	AaBB	AABb	AaBb
aB	aABB	aaBB	aABb	aaBb
Ab	AAbB	AabB	AAbb	Aabb
ab	aAbB	aaBb	aAbb	aabb

	Frequency									
	AABB	aaBB	AAbb	aabb	aAbb	aABB	AABb	aaBb	AaBb	A-B-
F2	6%	6%	6%	6%	13%	13%	13%	13%	25%	56%
F3	14%	14%	14%	14%	9%	9%	9%	9%	6%	39%
F4	20%	20%	20%	20%	5%	5%	5%	5%	0%	31%
F5	22%	22%	22%	22%	3%	3%	3%	3%	0%	28%
F6	24%	24%	24%	24%	1%	1%	1%	1%	0%	26%

Inbreeding: it also reduces your options



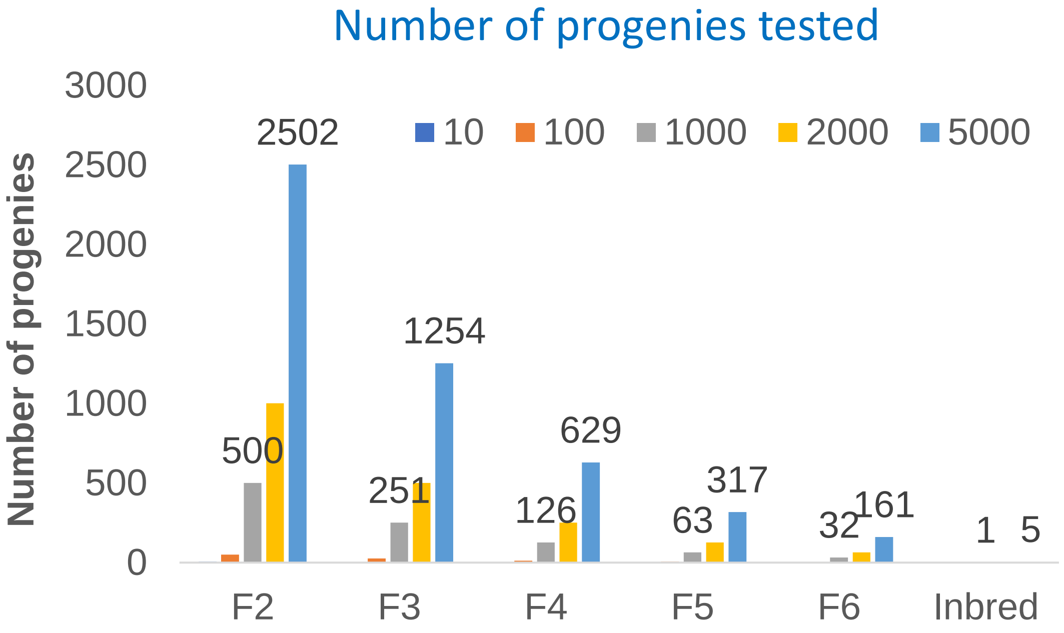
P= Inbreeding x 0.5^n + Heterozygosity

Inbreeding: a friend to be understood

- **When crossing parents that are very genetically different it would be hard to select for all segregating traits (**i.e. pre-breeding**)**
- **Selection in early generation has more chances of finding positive progenies**
- **Population size needs to be large enough to account for the number of segregating loci**

Intensity of selection: forget at your own cost

- Assuming 10 QTLs segregating, only screening >1000 progenies as inbred can be found 1
- The little row is not sufficient to find positive progenies
- This is called “***intensity of selection***”



Accuracy of selection: forget at your own cost

- Also, not all traits can be selected for in early generations:
  - Highly heritable traits can be effectively selected in single plants
  - Low heritability traits need entire plots

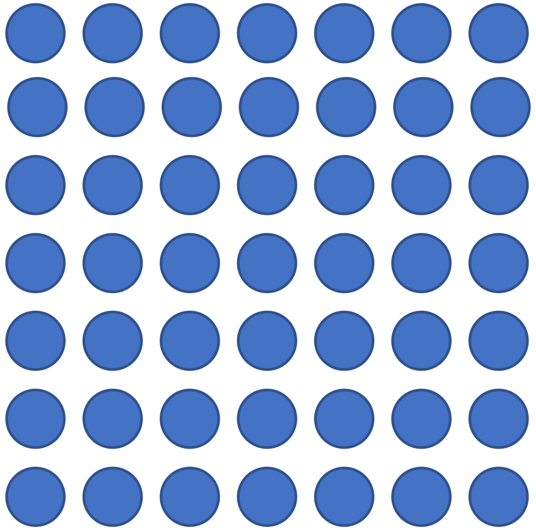
This is a combination of "***accuracy of selection"*** and "***heritability***" of the trait

  - *What traits can be selected for in F2>F4?*

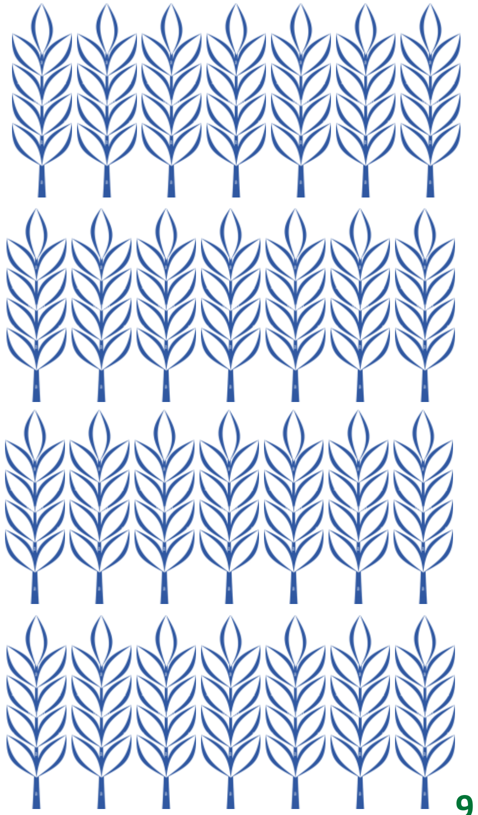
Heterogeneity and inbreeding

Starting from a
100% inbred spike

We get 100% inbred
identical grains



That will produce
100% inbred and
identical spikes

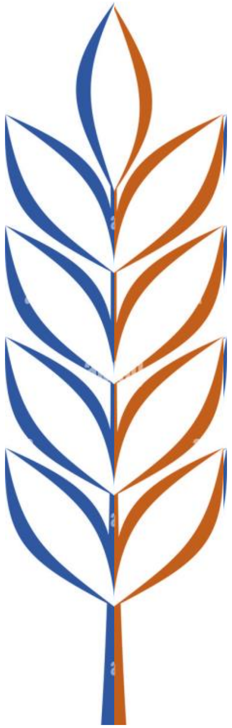


Heterogeneity and inbreeding

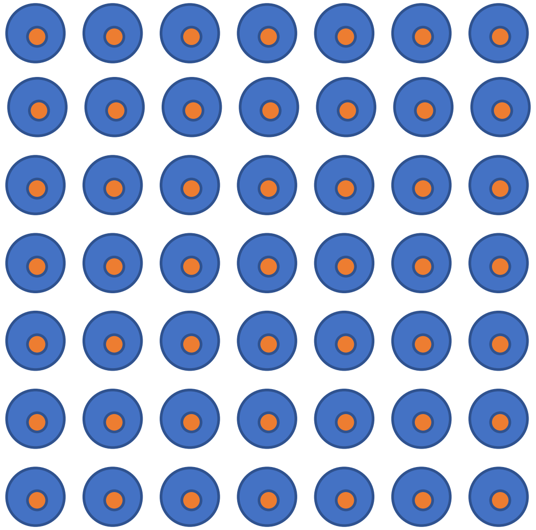
- An inbred line produces 100% identical seeds
- What about a non inbred line?

Heterogeneity and inbreeding

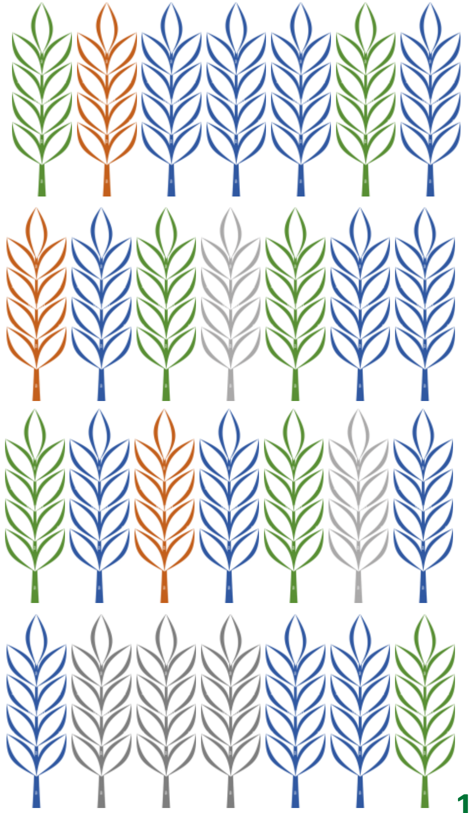
Starting from a 50%
inbred spike (F2)



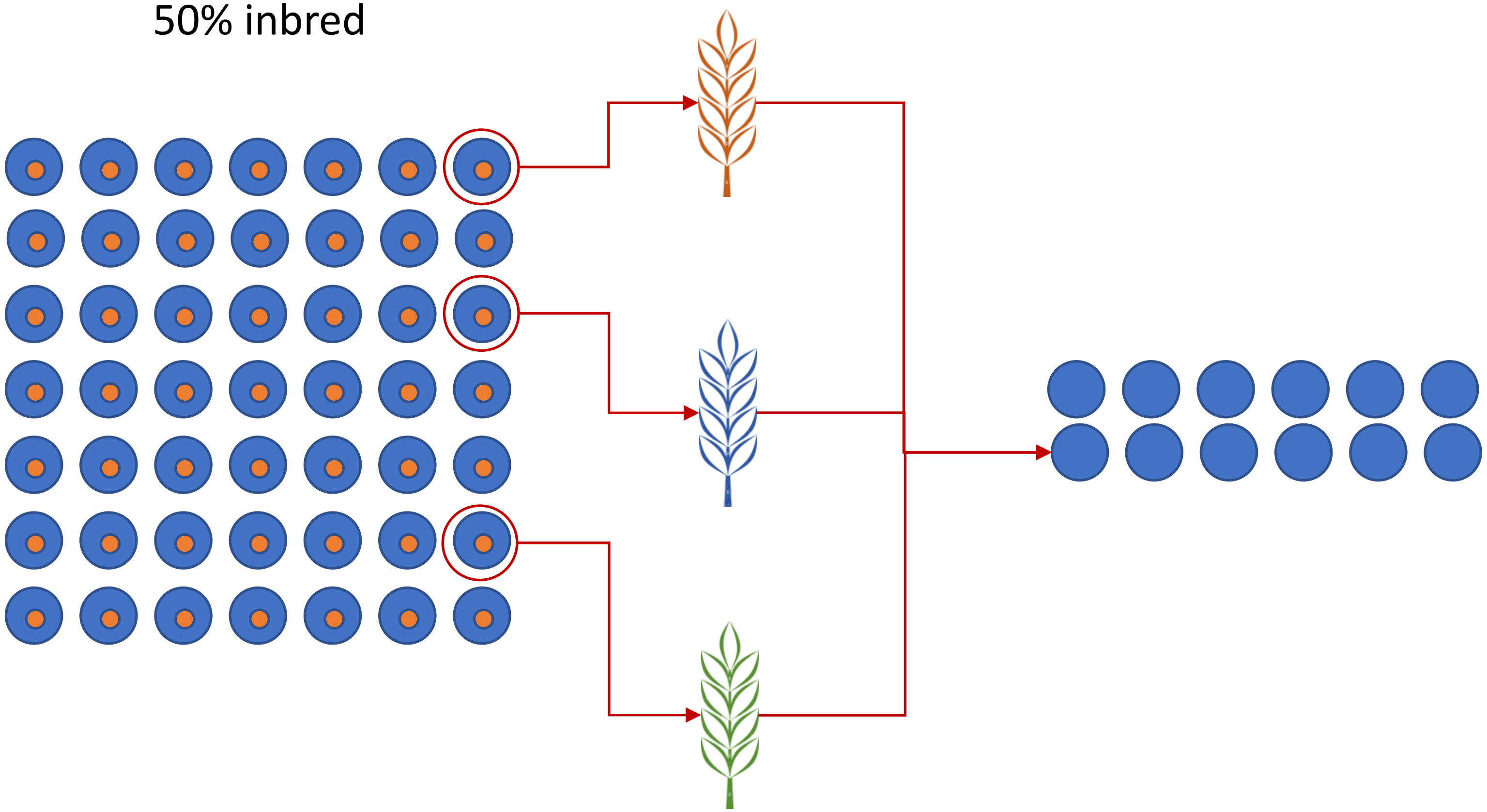
We get 75% inbred
grains, which differ
for 50% of their DNA



That will produce
75% inbred and 50%
different spikes



Heterogeneity and inbreeding



F2 population from
A / B
50% inbred

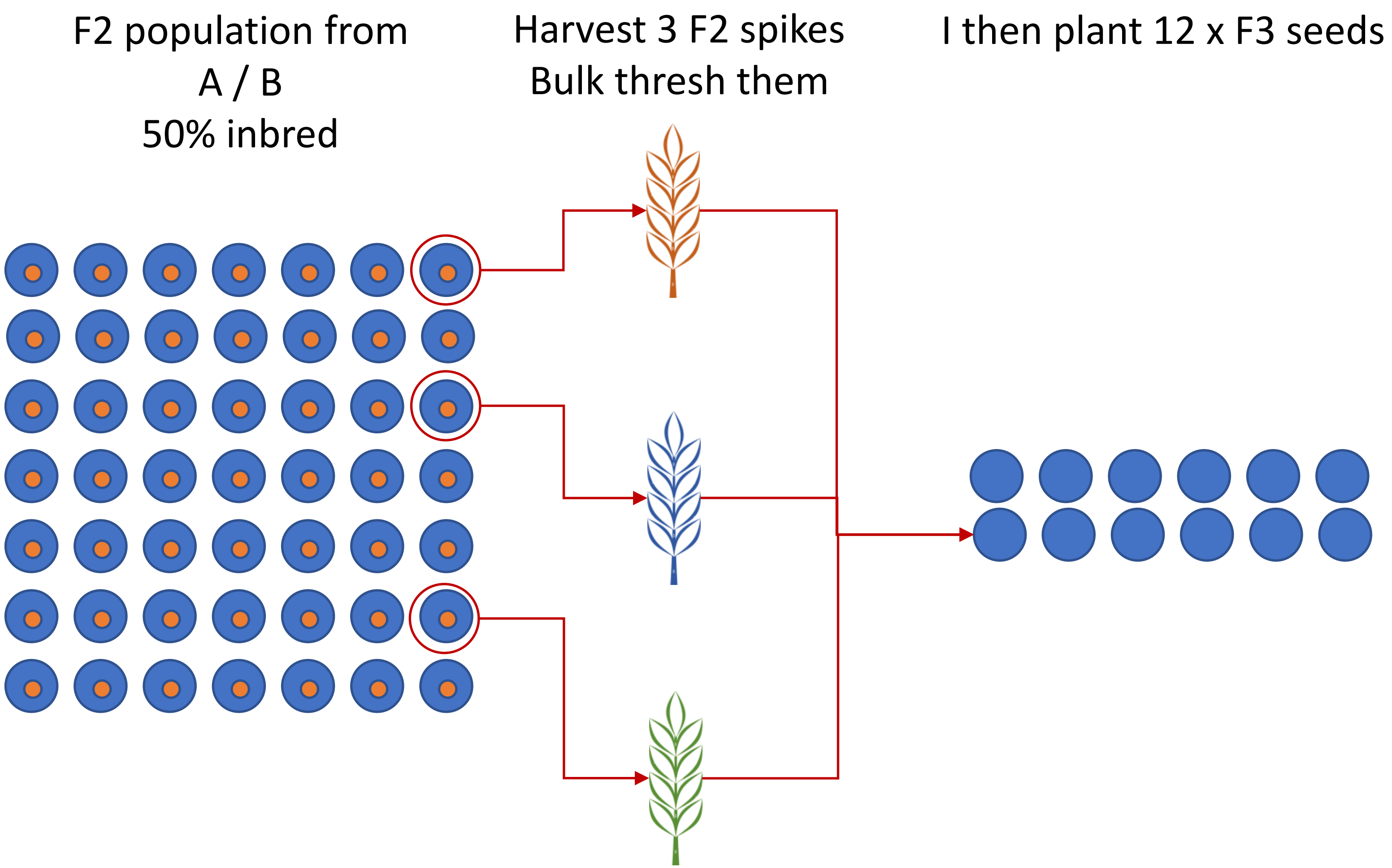
Harvest 3 F2 spikes
Bulk thresh them

I then plant 12 x F3 seeds

What would be the
inbreeding of each?

????

Heterogeneity and inbreeding



F2 population from
A / B
50% inbred

Harvest 3 F2 spikes
Bulk thresh them

I then plant 12 x F3 seeds

What would be the inbreeding of each?

F3: 75% inbred

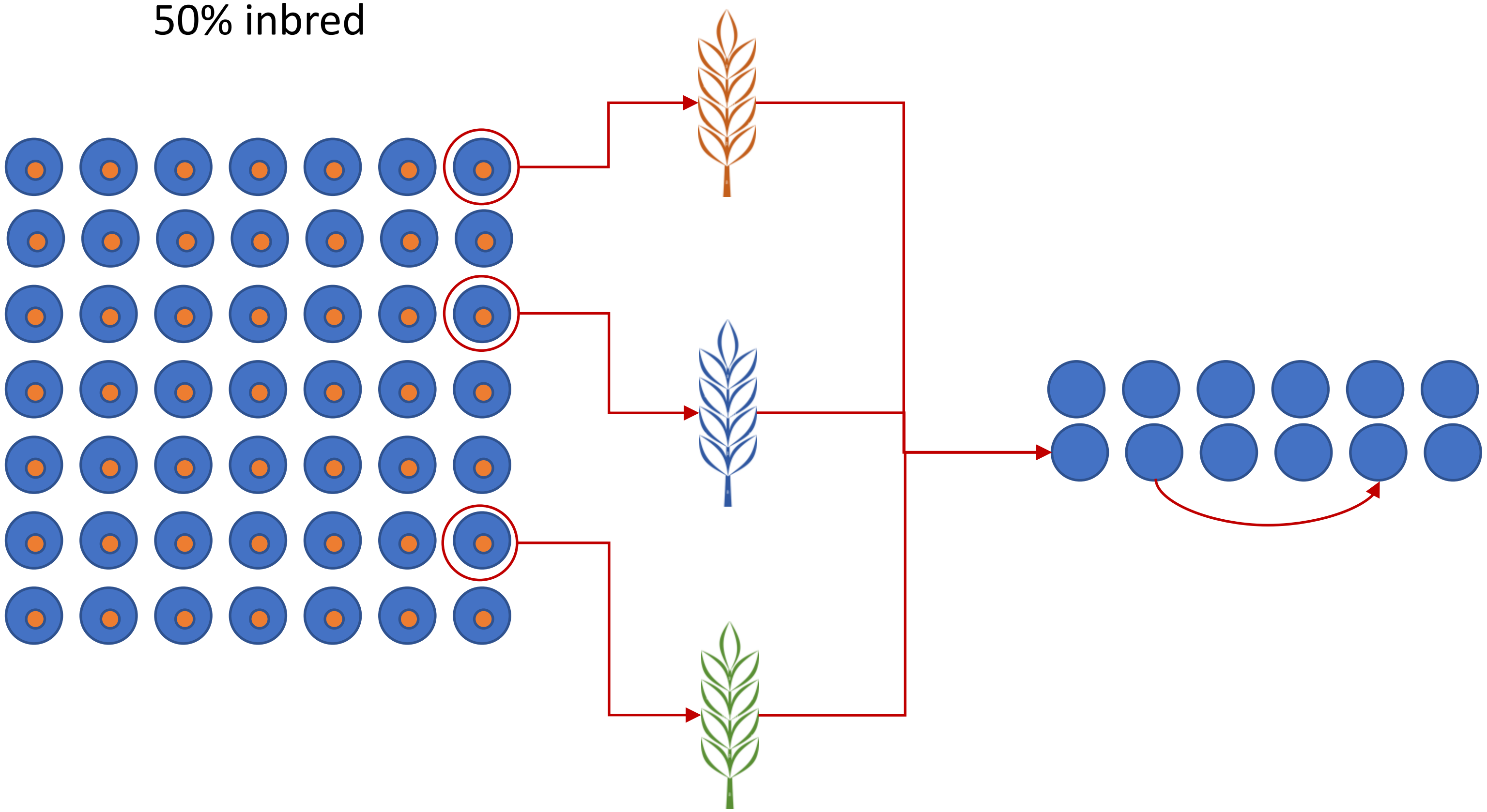
Heterogeneity and inbreeding

F2 population from
A / B
50% inbred

Harvest 3 F2 spikes
Bulk thresh them

I then plant 12 x F3 seeds

What would be the
similarity between each?



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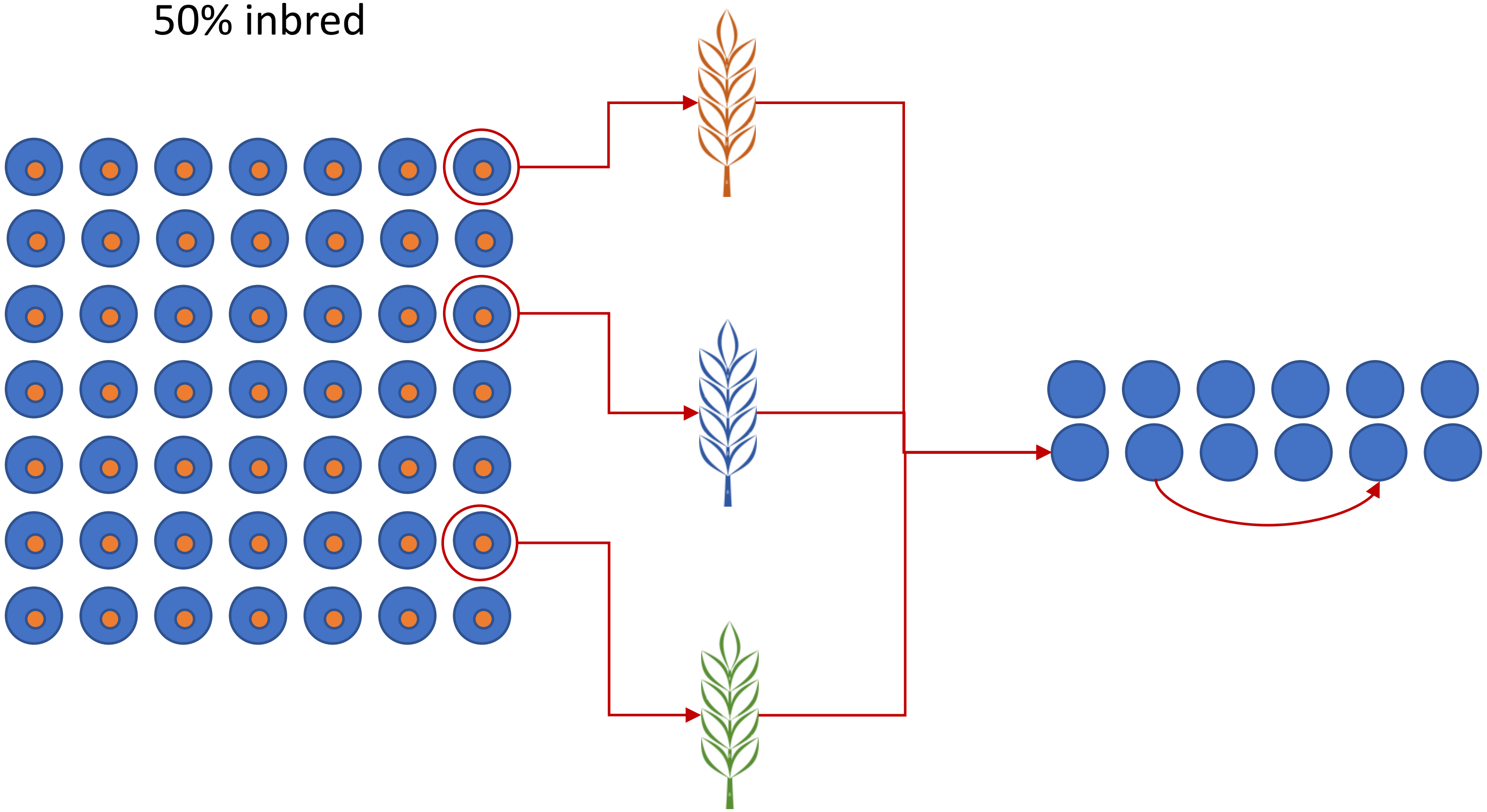
Heterogeneity and inbreeding



F2 population from
A / B
50% inbred

Harvest 3 F2 spikes
Bulk thresh them

I then plant 12 x F3 seeds

What would be the
similarity between each?

Homogeneity: 50%

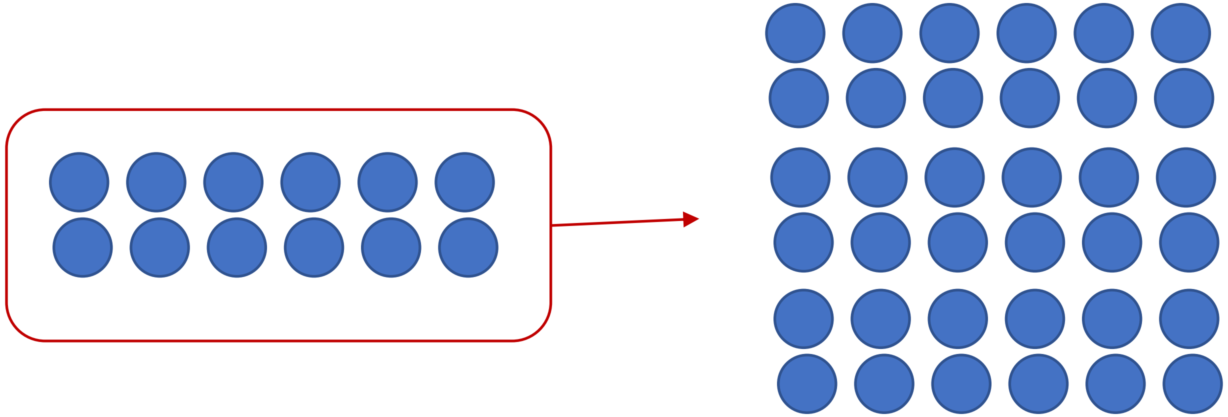
Heterogeneity and inbreeding

I then plant 12 x F3 seeds

Bulk harvest

I then plant 36 x F4 seeds

If I bulk harvest them, what will be the inbreeding of the resulting individuals?



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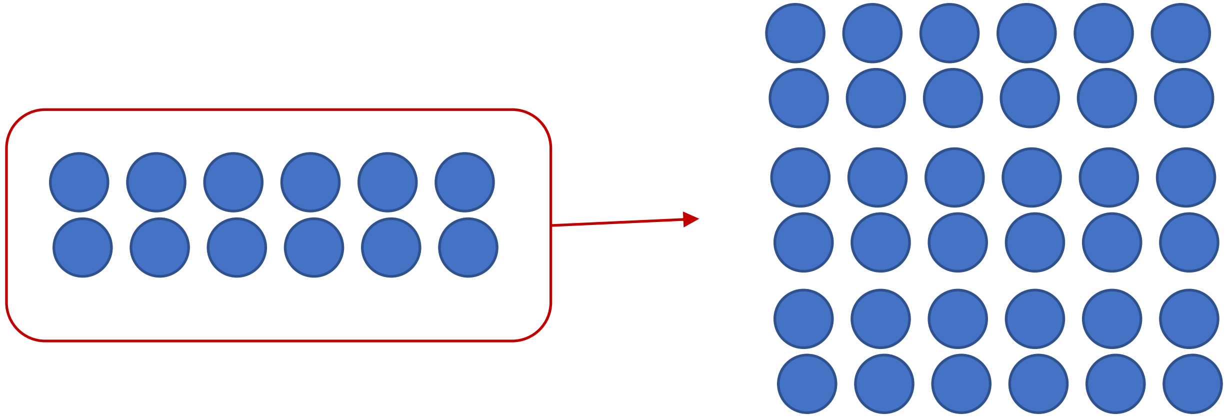
Heterogeneity and inbreeding

I then plant 12 x F3 seeds

Bulk harvest

I then plant 36 x F4 seeds



If I bulk harvest them, what will be the inbreeding of the resulting individuals?

F4: 87.5%

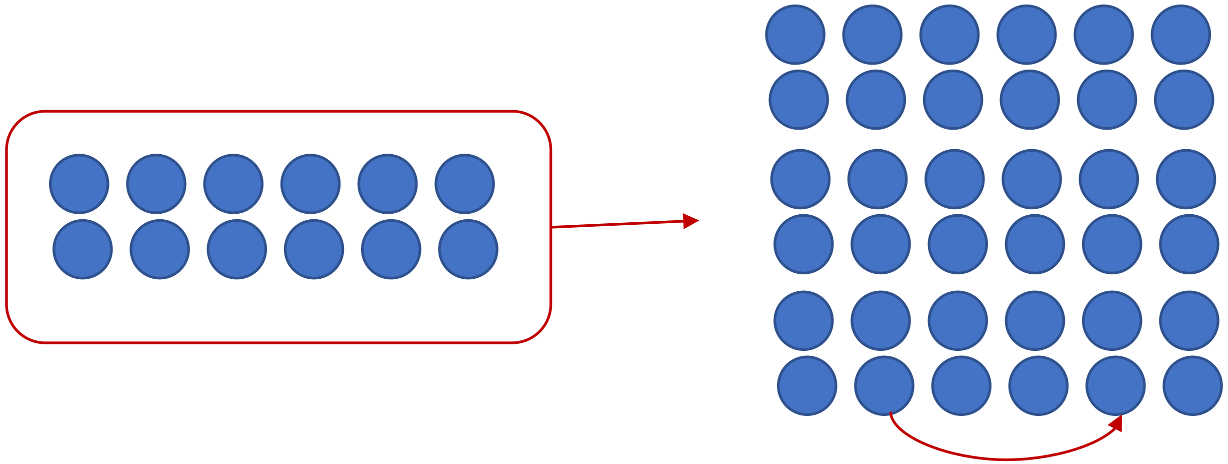
Heterogeneity and inbreeding

I then plant 12 x F3 seeds

I then plant 36 x F4 seeds

What would be the
difference among them?

Bulk harvest



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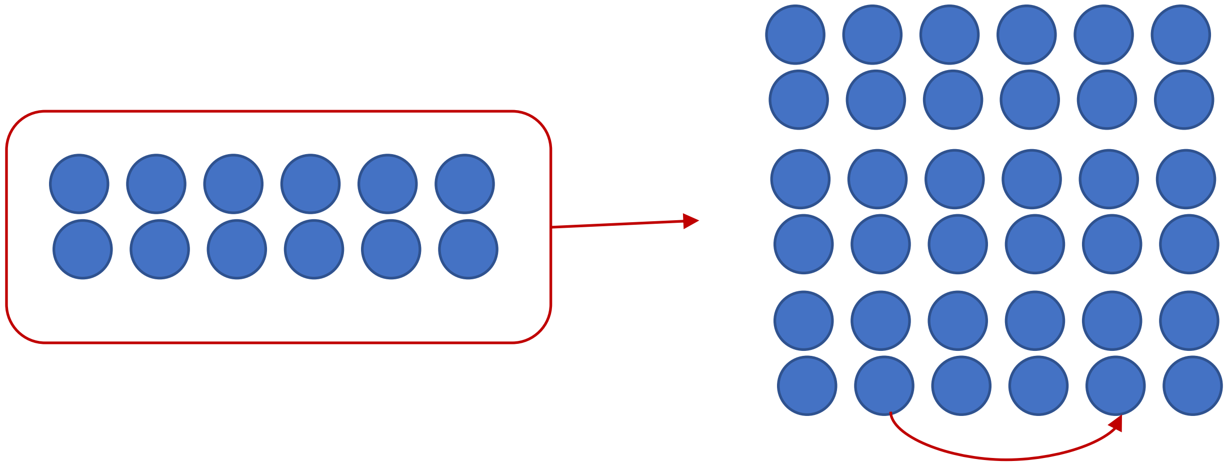
Heterogeneity and inbreeding

I then plant 12 x F3 seeds

I then plant 36 x F4 seeds

What would be the difference among them?

Bulk harvest



Still 50% of original bulking

To bulk or not to bulk

- Proceeding by pedigree (single plant/spike or pod) advances homogeneity together with inbreeding
- Proceeding by bulking (2 or more plants/spikes) advances inbreeding but block homogeneity

		Homogeneity								
Gen	**Inbr.**	**Pedigree**	**Bulk F1**	**Bulk F2**	**Bulk F3**	**Bulk F4**	**Bulk F5**	**Bulk F6**	**Bulk F7**	**Bulk F8**
F1	0.000	0.000	0.000							
F2	0.500	0.500	0.000	0.500						
F3	0.750	0.750	0.000	0.500	0.750					
F4	0.875	0.875	0.000	0.500	0.750	0.875				
F5	0.938	0.938	0.000	0.500	0.750	0.875	0.938			
F6	0.969	0.969	0.000	0.500	0.750	0.875	0.938	0.969		
F7	0.984	0.984	0.000	0.500	0.750	0.875	0.938	0.969	0.984	
F8	0.992	0.992	0.000	0.500	0.750	0.875	0.938	0.969	0.984	0.992
F9	0.996	0.996	0.000	0.500	0.750	0.875	0.938	0.969	0.984	0.992
F10	0.998	0.998	0.000	0.500	0.750	0.875	0.938	0.969	0.984	0.992
F11	0.999	0.999	0.000	0.500	0.750	0.875	0.938	0.969	0.984	0.992
F12	1.000	1.000	0.000	0.500	0.750	0.875	0.938	0.969	0.984	0.992

So why breeders bulk?

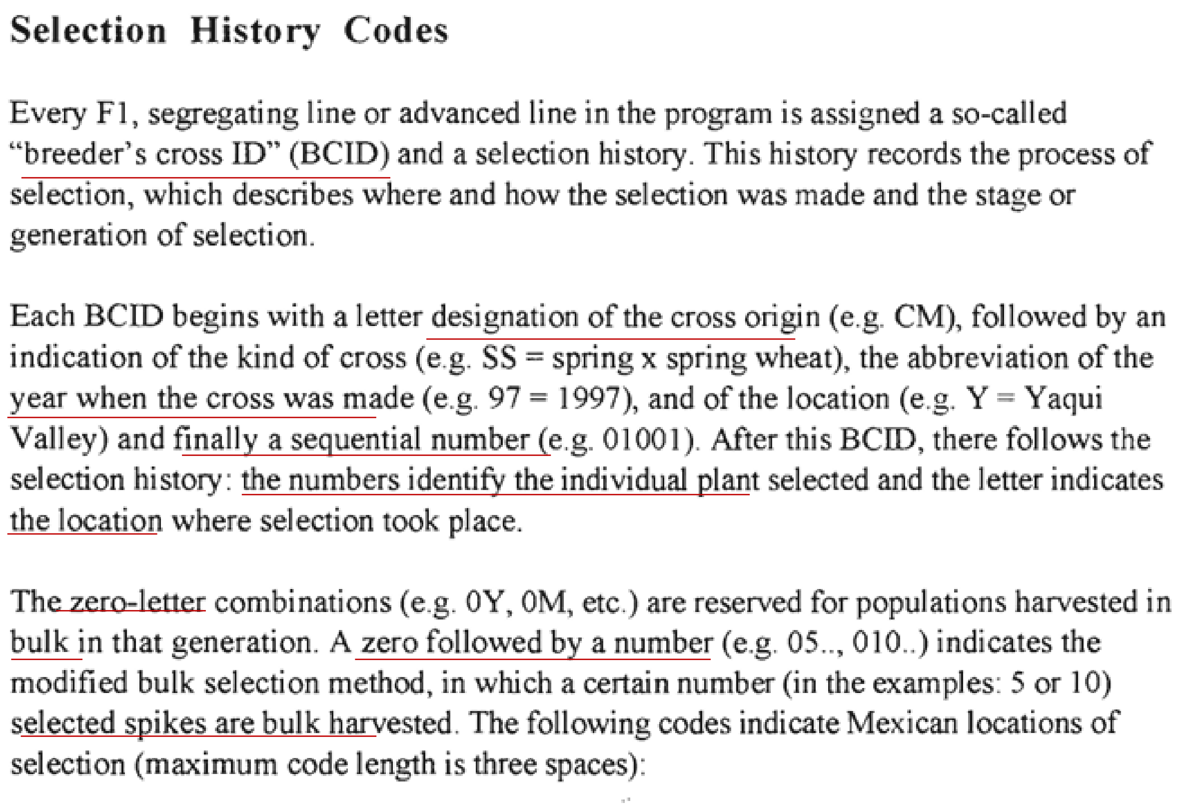
To bulk or not to bulk

- Breeders declare the difference between the two method of advancement:
- **“derived” marked as “:”**

- F4 > 87.5% inbred (homozygous) and 87.5% homogeneous
- F2:4 > 87.5% inbred (homozygous) but only 50% homogeneous as it is derived by bulking F2

Keeping track of changes: selection history

- For this reason, breeders keep track of the bulking vs pedigree using selection history

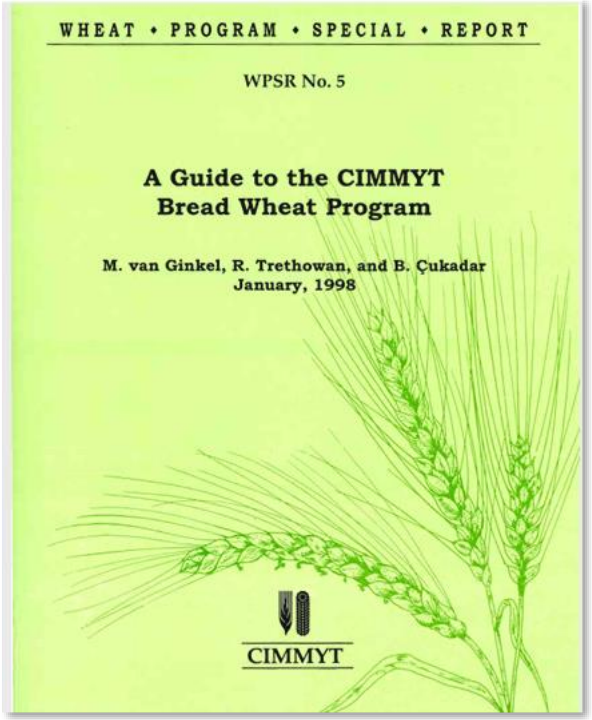


Selection History Codes

Every F1, segregating line or advanced line in the program is assigned a so-called "breeder's cross ID" (BCID) and a selection history. This history records the process of selection, which describes where and how the selection was made and the stage or generation of selection.

Each BCID begins with a letter designation of the cross origin (e.g. CM), followed by an indication of the kind of cross (e.g. SS = spring x spring wheat), the abbreviation of the year when the cross was made (e.g. 97 = 1997), and of the location (e.g. Y = Yaqui Valley) and finally a sequential number (e.g. 01001). After this BCID, there follows the selection history: the numbers identify the individual plant selected and the letter indicates the location where selection took place.

The zero-letter combinations (e.g. 0Y, 0M, etc.) are reserved for populations harvested in bulk in that generation. A zero followed by a number (e.g. 05.., 010..) indicates the modified bulk selection method, in which a certain number (in the examples: 5 or 10) selected spikes are bulk harvested. The following codes indicate Mexican locations of selection (maximum code length is three spaces):



WHEAT • PROGRAM • SPECIAL • REPORT

WPSR No. 5

A Guide to the CIMMYT
Bread Wheat Program

M. van Ginkel, R. Trethowan, and B. Çukadar
January, 1998

CIMMYT

Keeping track of changes: selection history

Cross code:

- _ _ _ 2-3 letters institution ID: *IC*
- _ _ _ 1-3 letters crop code: *D*
- _ _ at ICARDA we keep track of top crosses: (F2) or (F1)
- _ _ 2 digits year: 22
- Dash “-”
- _ _ _ _ 2-4 digits serial number: 0001

ICD(F2)22-0001

- Dash “-”

For each generation add a choice between:

  - 0 for bulk
  - 020 for bulk of 20 spikes (or 030, 040, ..)
  - A number (i.e. 1) indicating the plant harvested by pedigree

- And a 1-3 digit for location

Keeping track of changes: selection history

ICD(F2)22-0001-0SAN-030MCH-0SAN-5MCH-0SAN-0MCH

- A F2 top cross made at ICARDA in 2022 for durum wheat combination 0001 (it matches pedigree)
- The F1 were bulk harvest (all plants) in Summer Annoceur
- For F2 30 spikes were selected in Marchouch and bulk harvested
- The F3 were bulk harvest (all plants) in Summer Annoceur
- The F4 pedigree selection was made and plant number 1 was advanced
- The F5 was bulk harvested in Summer Annoceur
- The F6 was tested in yield trial in Marchouch and bulk harvested

- What would be the inbreeding of the F6?
- What would be the homogeneity of the F6?
  - Is it a true F6 or is it “derived”?

Keeping track of changes: selection history

ICD15-024-0SAN-015MCH-0SAN-1TR-0STR-2TR-0STR-0AREC

ICD15-024-0SAN-015MCH-0SAN-2TR-0STR-1TR-0STR

ICD16(F2)-180-0STR-020TR-0STR-3TR-0STR-0MCH-0MCH

ICD16(F2)-235-0STR-020TR-0STR-1MCH-0SAN-0MCH-0MCH

Keeping track of changes: selection history

ICD15-024-0SAN-015MCH-0SAN-1TR-0STR-2TR-0STR-0AREC

ICD15-024-0SAN-015MCH-0SAN-2TR-0STR-1TR-0STR

ICD16(F2)-180-0STR-020TR-0STR-3TR-0STR-0MCH-0MCH

ICD16(F2)-235-0STR-020TR-0STR-1MCH-0SAN-0MCH-0MCH

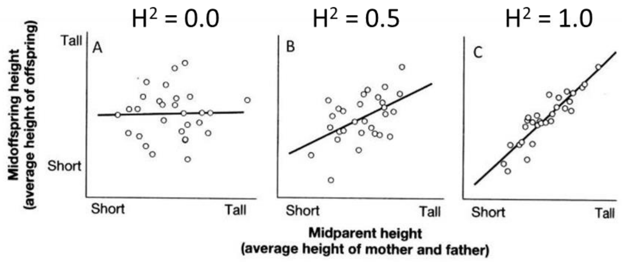
The selection history explains also the breeding method

The breeder equation

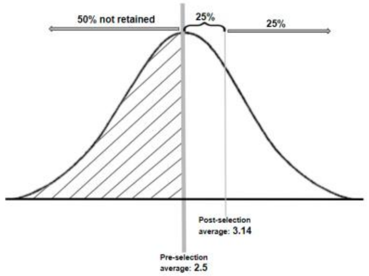
Good accuracy and good precision

Bad accuracy but good precision

Accuracy: how close to the actual value



Heritability: how likely to move a trait from parents



Selection intensity: what proportion of the progenies is advanced each cycle

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

Recycling time in years: how many years between crossing and re-crossing

Advancing to inbreeding: breeding schemes

- **Recycle as fast as possible, but being accurate**
- **Be strategic in selecting highly accurate/heritable traits in early generations (inbreeding)**
- **Keep high intensity (large populations)**
  - What issues are associated with this?

- **Why do we need to arrive to F4-F6 before doing a yield trial?**

Advancing to inbreeding: breeding schemes

	Pedigree method	Bulk method
W1	P1 x P2	P1 x P2
S1		
W2	F_1	F_1
S2		
W3	F_2	$F_{1:2}$
S3		
W4	F_3	$F_{1:3}$
S5		
W5	F_4	$F_{1:4}$
S6		
W6	F_5	F_5
S7		
W7	Stage 1 (F_6)	Stage 1 (F_6)

Advancing to inbreeding: breeding schemes

	Pedigree method	Bulk method	Mixed
W1	P1 x P2	P1 x P2	P1 x P2
S1			
W2	F_1	F_1	F_1
S2			
W3	F_2	$F_{1:2}$	$F_{1:2}$
S3			
W4	F_3	$F_{1:3}$	F_3
S5			
W5	F_4	$F_{1:4}$	$F_{3:4}$
S6			
W6	F_5	F_5	F_5
S7			
W7	Stage 1 (F_6)	Stage 1 (F_6)	Stage 1 (F_6)

Advancing to inbreeding: breeding schemes

	Pedigree method	Bulk method	Mixed	Sel. bulk pedigree
W1	P1 x P2	P1 x P2	P1 x P2	P1 x P2
S1				F_1
W2	F_1	F_1	F_1	$F_{1:2}$
S2				$F_{1:3}$
W3	F_2	$F_{1:2}$	$F_{1:2}$	$F_{1:4}$
S3				F_5
W4	F_3	$F_{1:3}$	F_3	Stage 1 ($F_{5:6}$)
S5				
W5	F_4	$F_{1:4}$	$F_{3:4}$	
S6				
W6	F_5	F_5	F_5	
S7				
W7	Stage 1 (F_6)	Stage 1 (F_6)	Stage 1 (F_6)	

Advancing to inbreeding: breeding schemes

	Pedigree method	Bulk method	Mixed	Sel. bulk pedigree	SSD
W1	P1 x P2	P1 x P2	P1 x P2	P1 x P2	P1 x P2
S1				F_1	F_1
W2	F_1	F_1	F_1	$F_{1:2}$	F_2 & F_3
S2				$F_{1:3}$	F_4
W3	F_2	$F_{1:2}$	$F_{1:2}$	$F_{1:4}$	Stage 1 ($F_{4:5}$)
S3				F_5	
W4	F_3	$F_{1:3}$	F_3	Stage 1 ($F_{5:6}$)	
S5					
W5	F_4	$F_{1:4}$	$F_{3:4}$		
S6					
W6	F_5	F_5	F_5		
S7					
W7	Stage 1 (F_6)	Stage 1 (F_6)	Stage 1 (F_6)		

Advancing to inbreeding: breeding schemes

	Pedigree	Bulk	Mixed	Sel bulk	SSD
Accuracy	High	Low	Med	Low	Low
Intensity	Low	High	Med	High	Low
Heritability	Med	High	High	High	Med
Recycling time	Slow	Slow	Slow	Fast	Very fast
Genetic gain	Low	Medium	Medium	High	High
Cost	High	Low	Medium	Medium	Low

Conclusion lecture 2

- The genetic gain equation drives all breeding decisions
- Inbreeding and heterogeneity need to be recorded and used
- Using tools to increase accuracy for selection of highly heritable traits in F2>4 drives up genetic gain
- Keeping high intensity is fundamental to achieve results
- All schemes are valid, you need to find the one fitting for you