Line breeding: Bulk, Pedigree, Backcross

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Types of cultivars

1. Pure-line (uniform, narrow base)
2. Open-pollinated (diverse, broad base)
3. Hybrid (heterosis, high yield)
4. Clonal (vegetative propagation)
5. Apomictic (seed without fertilization)
6. Multilines (isolines for disease resistance)

Genetic structure of cultivars

1. ◈ Homozygous & Homogeneous → Pure lines, very uniform
   ➞ (gen stability + identical plants in a field)

2. ◈ Heterozygous & Homogeneous → F1 hybrids, uniform look
   ➞ (uniform outside, but genetic mix inside)

3. ◈ Heterozygous & Heterogeneous → Synthetics/composites, diverse
   ➞ (diversity, mixed plants, natural variation)

4. ◈ Homozygous & Heterogeneous → Landraces, mixtures of uniform genotypes
   ➞ (blocks of similar but different groups → mosaic of lines)

Common plant breeding notations

F (filial): Progeny of a cross (e.g., F1, F2, F3).
⊗ symbol: Denotes selfing (self-pollination).
S notation: Alternative to F notation (e.g., S0, S1).

Inbred line systems:
System I: Based on current generation (F3, F4, F5).
System II: Shows origin + current generation
(e.g., F2:3, F2:4, F4:5).

Common plant breeding notations

Pedigree Notations in Plant Breeding

- **“/”** → indicates a cross (e.g., A/B).

- **“/2/” or “/3/”** → order of crossing (second, third cross).

- **“*”** → indicates a backcross.

- **Example 1:** Grivna/3/Pobeda/Simonida/2/Igra
→ Three sequential crosses.

- **Example 2:** Igra×3/Grivna
→ Igra backcrossed three times to Grivna.

Mass selection

Mass selection is the **oldest plant breeding method**, formally described by Johannsen (1903)

Main points:

- Improves the population, does not create new genes.
- Selection is based on visible traits. 👀
- Works in one generation per cycle.
- Can be one-time or repeated. 🔁
- Improves the average performance of the population.

Mass selection

Application:

Maintaining cultivar purity – removing off-type plants.

Developing cultivars – from a base population (e.g., after hybridization).

Adapting cultivars to new environments – selecting traits like maturity.

Improving disease resistance – useful for horizontal, durable resistance.

Roguing during breeding programs – eliminating undesirable plants to reduce costs.

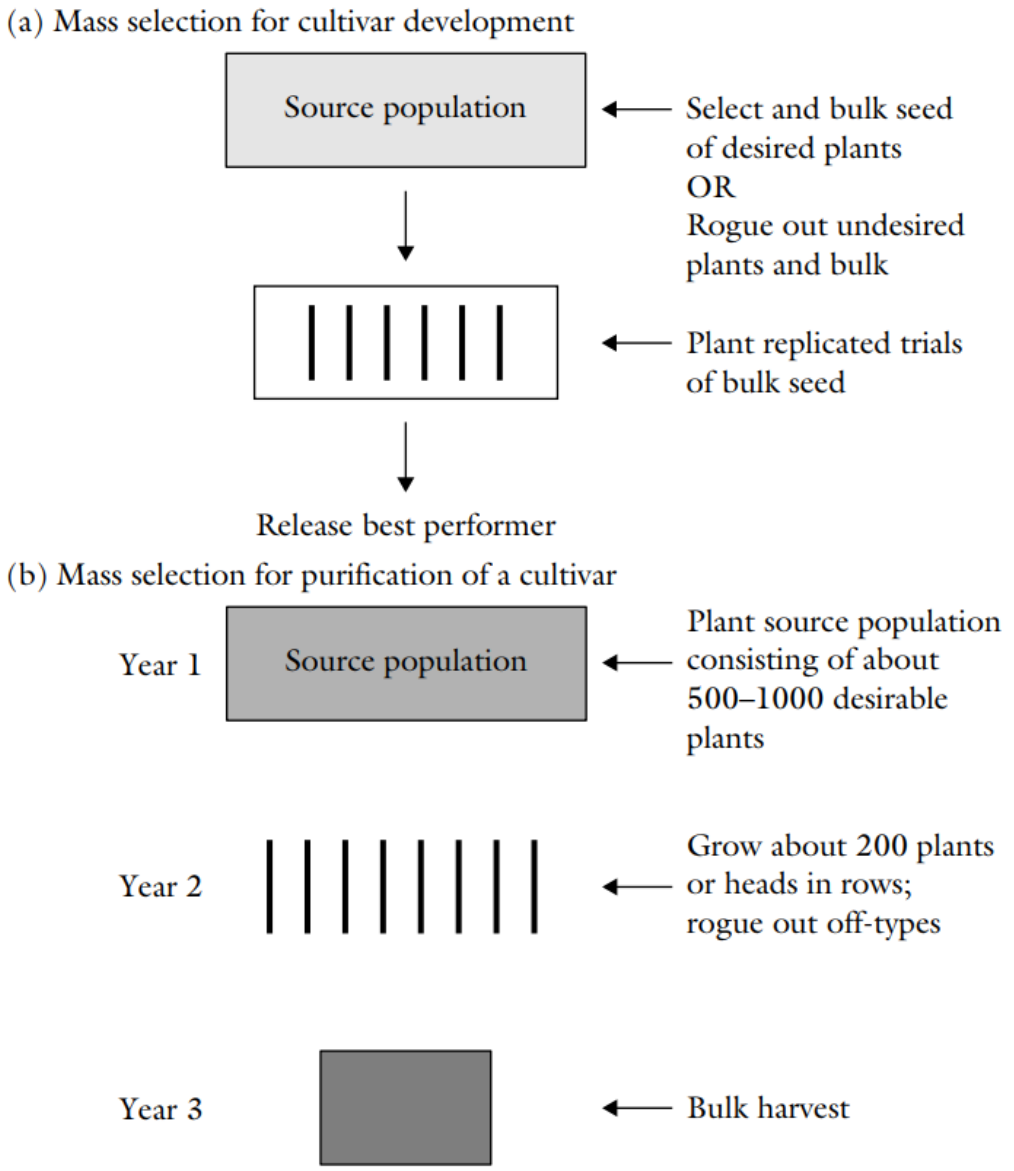
Mass selection

General procedure:
Remove plants with undesirable traits (negative selection).
Select desirable uniform plants (positive selection).
Combine harvested seed into a bulk for the next generation.

Typical cycle:
Year 1 – sow a heterogeneous population; remove off-type plants.

Year 2 – evaluate the bulk seed in a trial; compare with the original cultivar.

Bulk harvest; repeat cycle if necessary.



Mass selection

Genetic aspects

•Cross-pollination contamination may introduce heterozygotes.
•Dominant heterozygotes often **cannot be distinguished** from homozygotes.
•In **self-pollinated species** – heterozygosity decreases with each generation.
•In **cross-pollinated species** – gene frequencies remain stable unless selection is very strong.

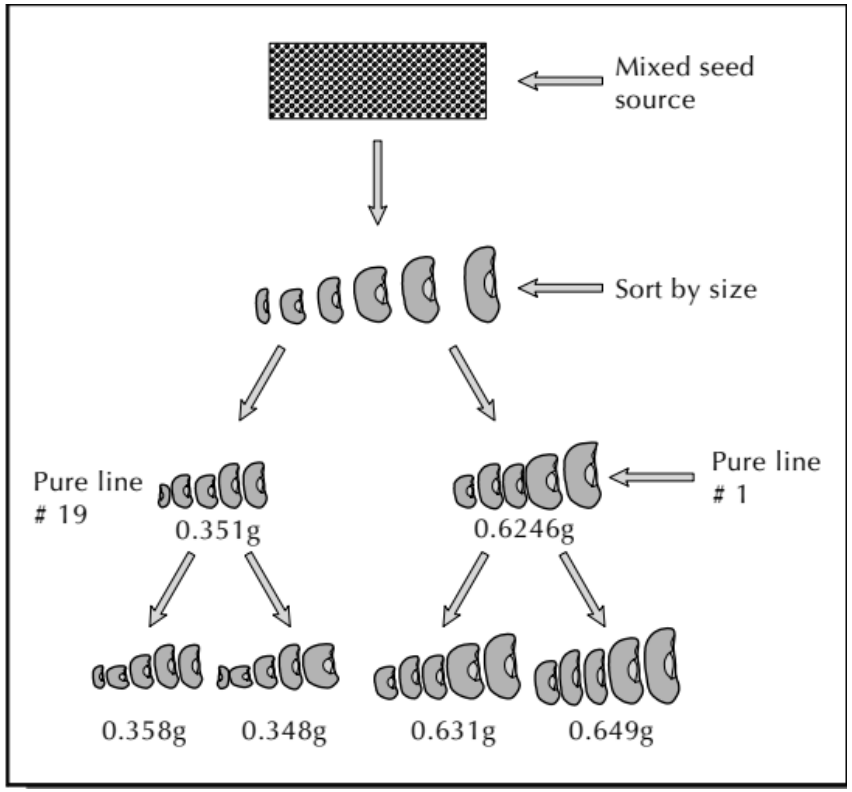
•Mass selection works best when:
- The trait has **high heritability**,
- The environment is **uniform**,
- The pathogen is **evenly distributed** (for disease resistance).

Mass selection

Advantages	Disadvantages
Simple, quick, and inexpensive.	Effective for **high-heritability traits**.
Large populations can be handled easily	Less uniform than pure-line selection
Produces populations that are **phenotypically uniform**.	Requires a uniform environment for accuracy
	Heterozygotes remain undetected → may segregate later

Pure line

- Developed by Wilhelm Johannsen (1903)
- Selection in self-pollinated crops
- Produces genetically uniform “pure lines”
- No variation within a line
  (only environment affects traits)



Pure line

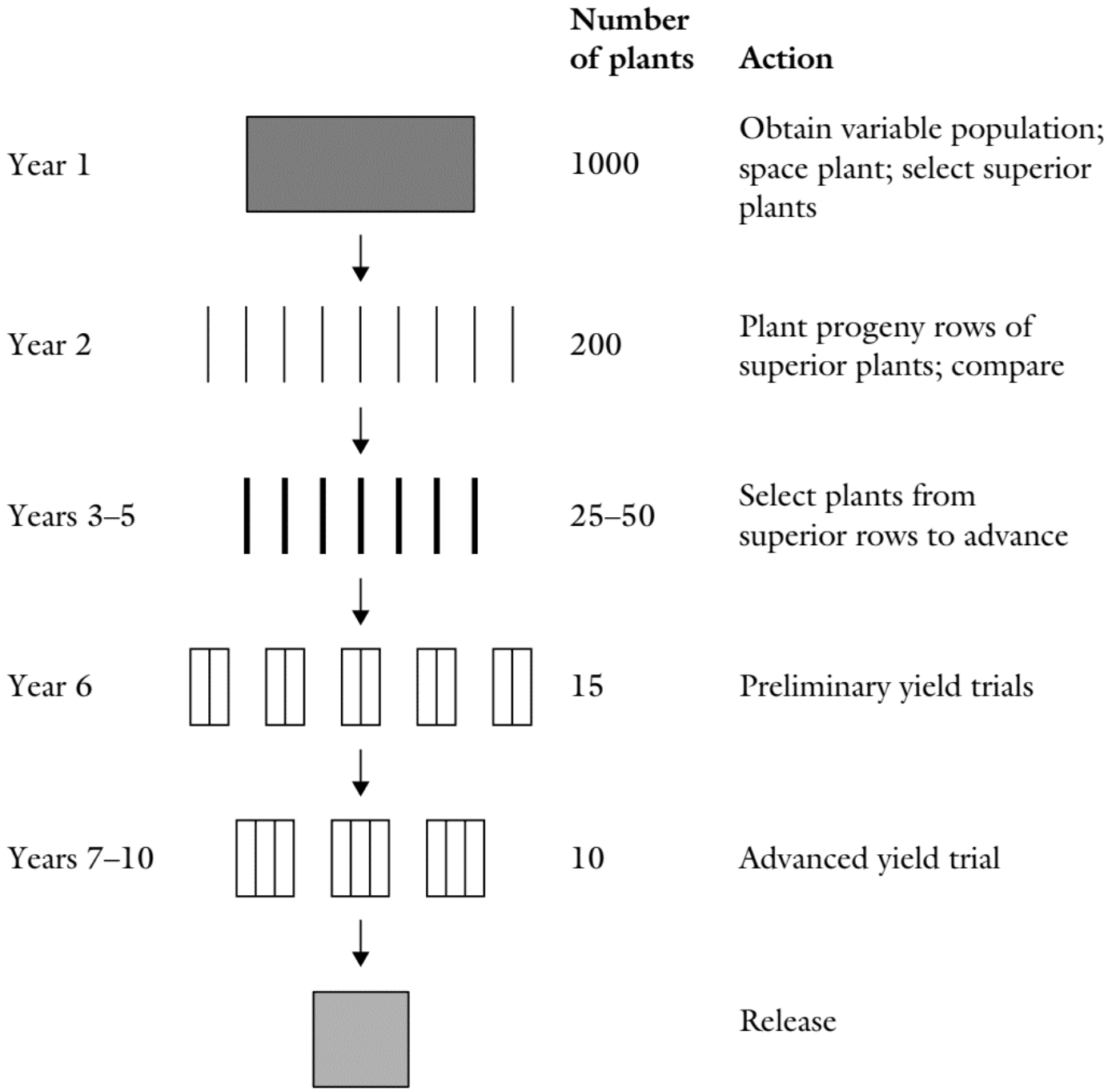
Application:

- Needed for uniformity in farming & industry
- Useful for mechanized harvest
- Consistent quality for food processing
- Important in ornamental crops
- Basis for new cultivars and hybrids

Pure line

Procedure of Pure-line Selection:

- Select individual plants (Year 1)
- Grow progeny rows (Year 2)
- Remove off-types,
  test performance (Years 3–6)
- Multi-location trials (Years 7–10)
- Release the best line



Pure line

Advantages	Disadvantages
Simple and cheap	Narrow genetic base
Very uniform cultivars	Susceptible to diseases
Good for low heritability traits	No new variation created

Pedigree selection

Introduction and Main Points

- Pedigree selection: a widely used method for breeding self-pollinated species
- Main difference from mass or pure-line selection → variability is created by hybridization.
- First described by H.H. Lowe in 1927.
- Method: continuous individual selection after crossing + keeping detailed ancestry records.
- Records allow tracing progeny back to F2 individual plants.

Pedigree selection

Application

- Used for crops where individual plants can be observed, described, and harvested separately.
- **Crops:** peanuts, tobacco, tomato, cereals
- Effective when qualitative traits are targeted for improvement.

Pedigree selection

	Generation		Number of plants	Action
Year 1		$P_1 \times P_2$		Select parents and cross
Year 2	F_1		50–100	Bulk seed; space plant for higher yield
Year 3	F_2		2000–5000	Space plant for easy visual selection
Year 4	F_3		200	Select and plant in spaced rows
Year 5	F_4		100	Identity superior rows; select 3–5 plants to establish family in progeny rows
Years 6–7	$F_5 - F_6$		25–50	Establish family progeny rows; select individual plants to advance each generation
Year 8	F_7		15	Conduct preliminary yield trials; select individual plants to advance
Years 9–11	$F_8 - F_{10}$		5–10	Conduct advanced yield trials with more replications and over locations and years
			1	Cultivar release

Pedigree selection

Genetic Aspects

- Records allow precise tracking of genetic variation.
- Breeder creates variability through choice of parents.
- More effective for breeding **controled by single genes**.
- Product (cultivar): relatively narrow genetic base
- Records help ensure only lines with desired genes are advanced.

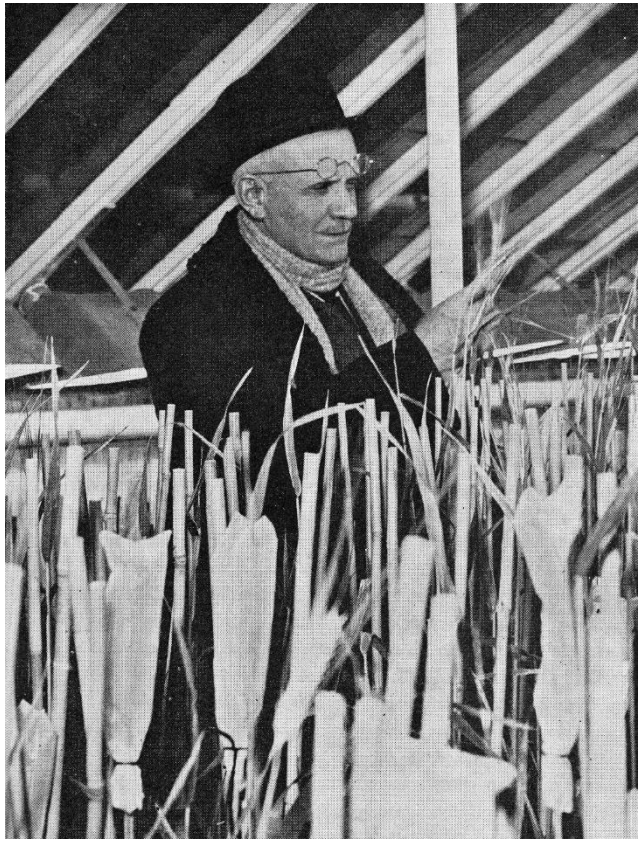
Pedigree selection

Advantages	Disadvantages
Strong record keeping = catalog of genetic info.	Time-consuming, requires 10–12 years.
Selection based on both phenotype and genotype.	Record keeping is slow and resource-intensive.
Produces high genetic purity.	Not suitable for species where plants are hard to isolate.
Allows advancement only of desired lines.	Less effective for quantitative traits or horizontal resistance
	Early generation selection for yield (F2) often not efficient

Bulk population breeding

Introduction

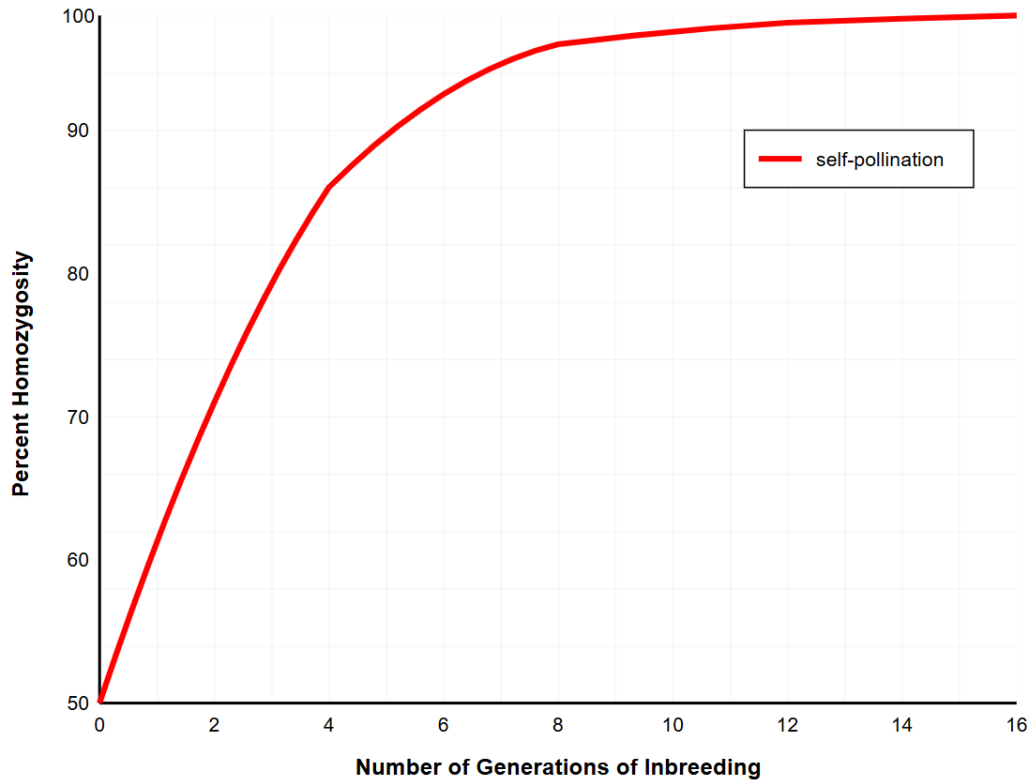
- Developed by Nilsson-Ehle, expanded by Harlan in barley
- Natural selection acts in early generations
- Artificial selection delayed until later generations
- Uses large segregating populations
- Applied mostly in self-pollinated crops



Bulk population breeding

Main Points

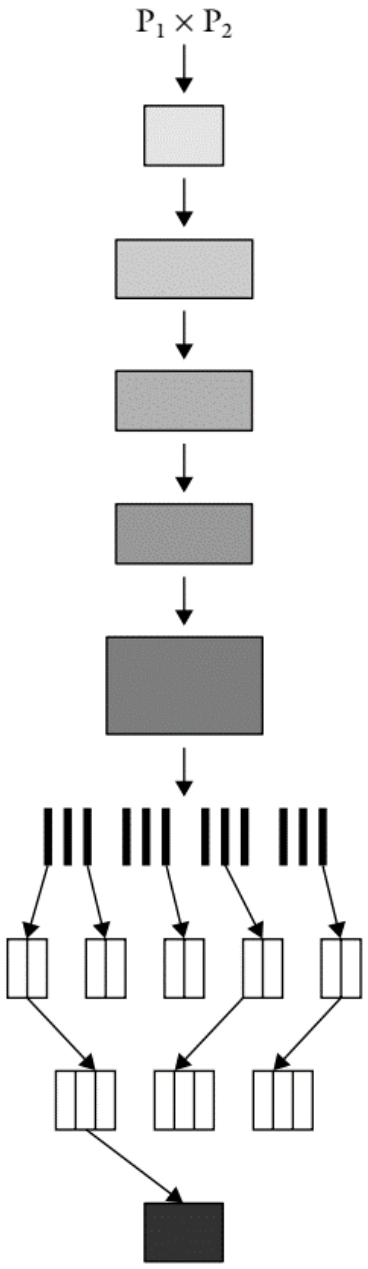
- Natural selection removes weak genotypes
- Artificial selection delayed until ~F5 or later
- Homozygosity increases with each selfed generation
- By F6 ≈ 98.9% homozygosity
- Fewer resources needed in early generations



Bulk population breeding

Procedure of Bulk Method

- Cross parents → grow F1, bulk harvest
- Plant 2000–3000 F2 plants → bulk harvest
- Repeat bulk planting until F4
- Space-plant F5 → select 10% best plants
- F7 → preliminary yield trials
- F8–F10 → advanced yield trials



	Generation	Number of plants	Action
Year 1			
Year 2	F_1	50–100	Bulk and space plant F_1
Year 3	F_2	2000–3000	Bulk and plant at commercial seeding rate
Year 4	F_3	2000–3000	Bulk and plant at commercial seeding rate
Year 5	F_4	2000–3000	Bulk and plant at commercial seeding rate
Year 6	F_5	3000–5000	Space plant; select superior plants
Year 7	F_6	300–500	Select and establish family rows from plants or heads
Year 8	F_7	30–50	Conduct preliminary yield trials
Years 9–11	$F_8 - F_{10}$	10	Conduct advanced yield trials
		1	Cultivar release

Bulk population breeding

Advantages	Disadvantages
Simple, low cost in early generations	Superior but weak genotypes may be lost
Natural selection helps adaptation	Lengthy process (cannot use off-season nurseries easily)
Handles large populations	Genetic drift and uneven representation
Selection when plants are nearly homozygous	Not suited for widely spaced crops

Single seed descent

Introduction

Developed to **speed up inbreeding** before selection

First concept: Goulden (1941) → F6 in 2 years

Formal description: Brim (1966), called "modified pedigree"

Widely used in soybean and small grains

Single seed descent

Main points

Rapid inbreeding without early selection

One seed per plant advanced → F2 to F5

Focus: reach homozygosity fast

Selection begins at F5/F6

Single seed descent

Steps

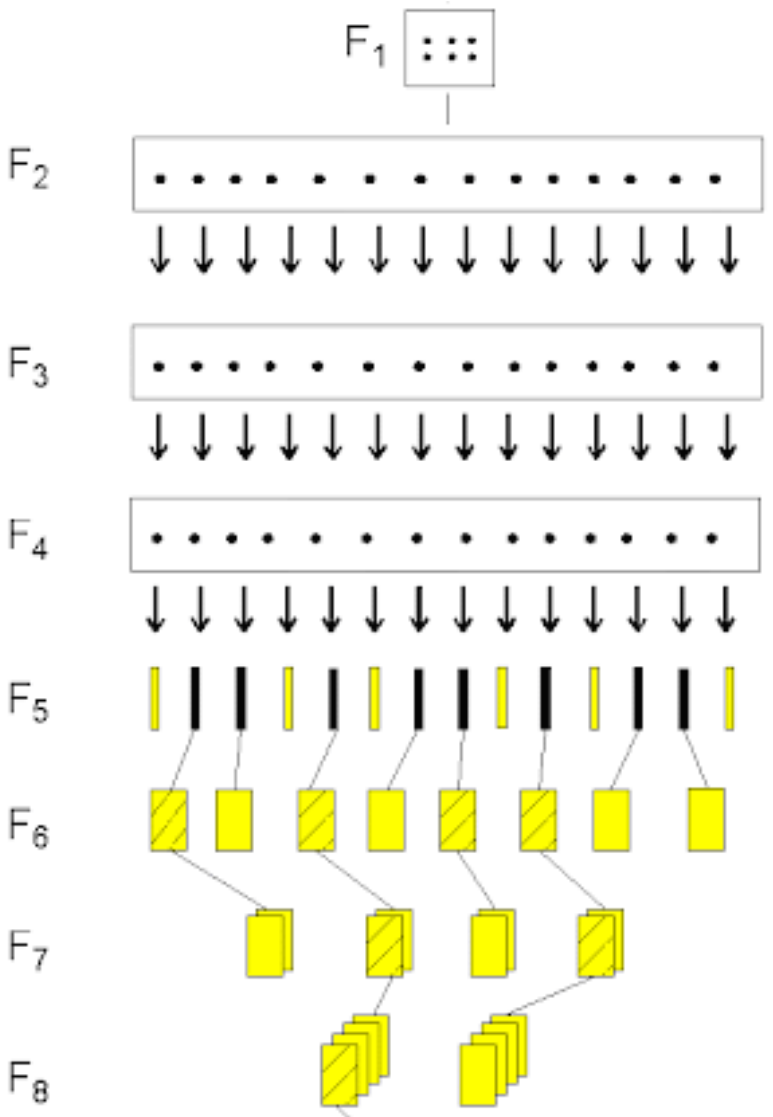
Year 1: Cross parents → F1

Year 2: Grow 50–100 F1 plants

Year 3: Grow 2000–3000 F2, harvest 1 seed per plant

Year 4–6: Continue single seed advance to F5

Year 7+: Select best families, yield trials, cultivar releases



Single seed descent

Genetic points

- Each line descends from a unique F2 plant
- Heterozygosity decreases fast → by F6 mostly homozygous
- No natural selection (only random survival)
- Risk: genetic drift, loss of alleles

Single seed descent

Advantages	Disadvantages
Fast and simple, 2–3 generations per year	No natural selection benefit
Small space needed (greenhouse possible)	Possible loss of good genes (drift)
Shortens breeding program	Risk if seed fails to germinate
Maintains broad diversity	Selection delayed until late generations

Modified Single seed descent

Main points

Early low-intensity selection

Selection of best plants → F2 to F5

Focus: more combinations, smaller material

Selection begins at F5/F6

Modified Single seed descent

Steps

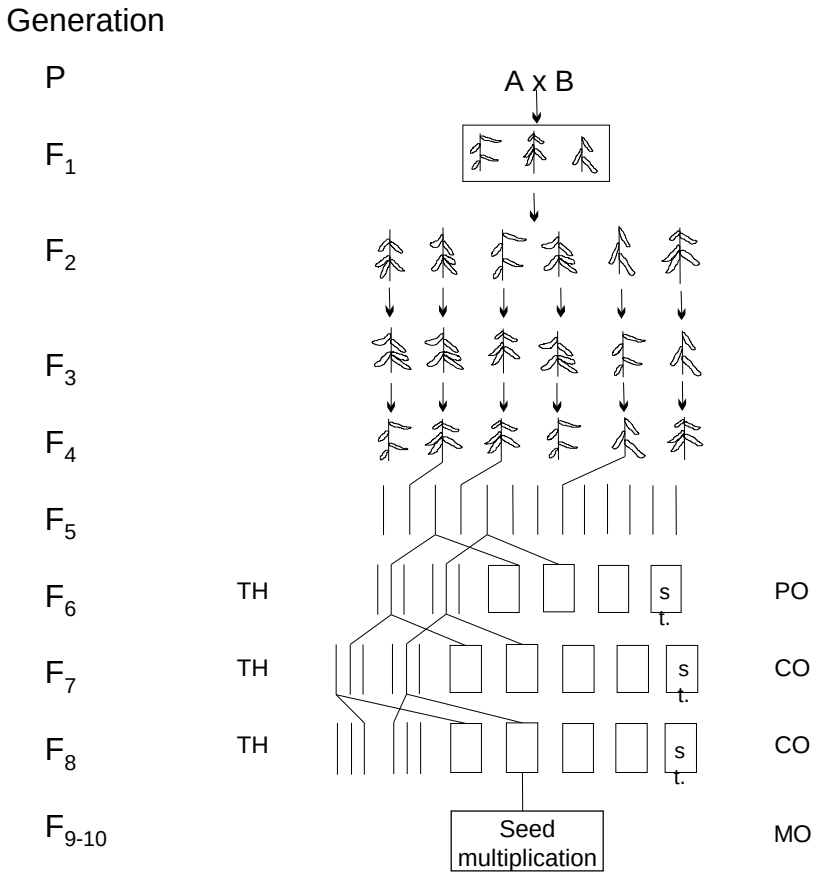
Year 1: Cross parents → F1

Year 2: Grow 50–100 F1 plants

Year 3: Grow 2000–3000 F2, harvest 50-100 best plants

Year 4–6: Continue advance to F5

Year 7+: Select best lines, yield trials, cultivar releases



Modified Single seed descent

Advantages	Disadvantages
Higher selection intensity	One generation per year only
Reduced risk of good genes loss	
Maintains broad diversity	
No winter nurseries expenses	

Backcross breeding

Introduction

- Replace undesirable gene → with desirable one.
- Keep all good traits of recurrent parent.
- Donor parent gives missing gene.
- Repeated crossing → “modified inbreeding”.
- Used to improve adapted cultivars without losing qualities.

Backcross breeding

Dominant gene transfer

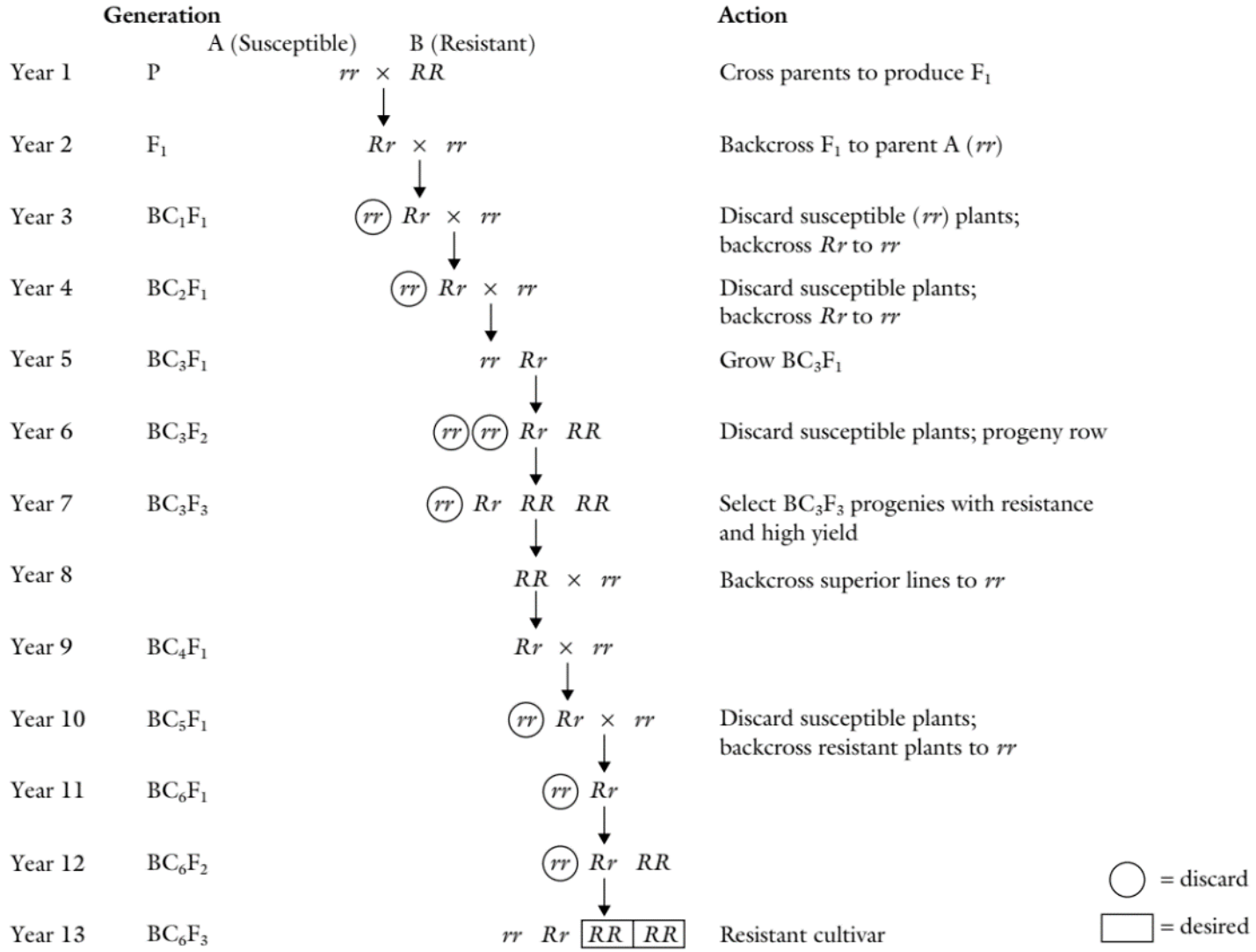
Start: Donor (RR) × Recurrent (rr) → F1.

Repeated backcross with recurrent parent (BC1–BC5).

Selection after each cycle → keep heterozygotes, discard recessives.

Screening for target trait

Yield testing before cultivar release.



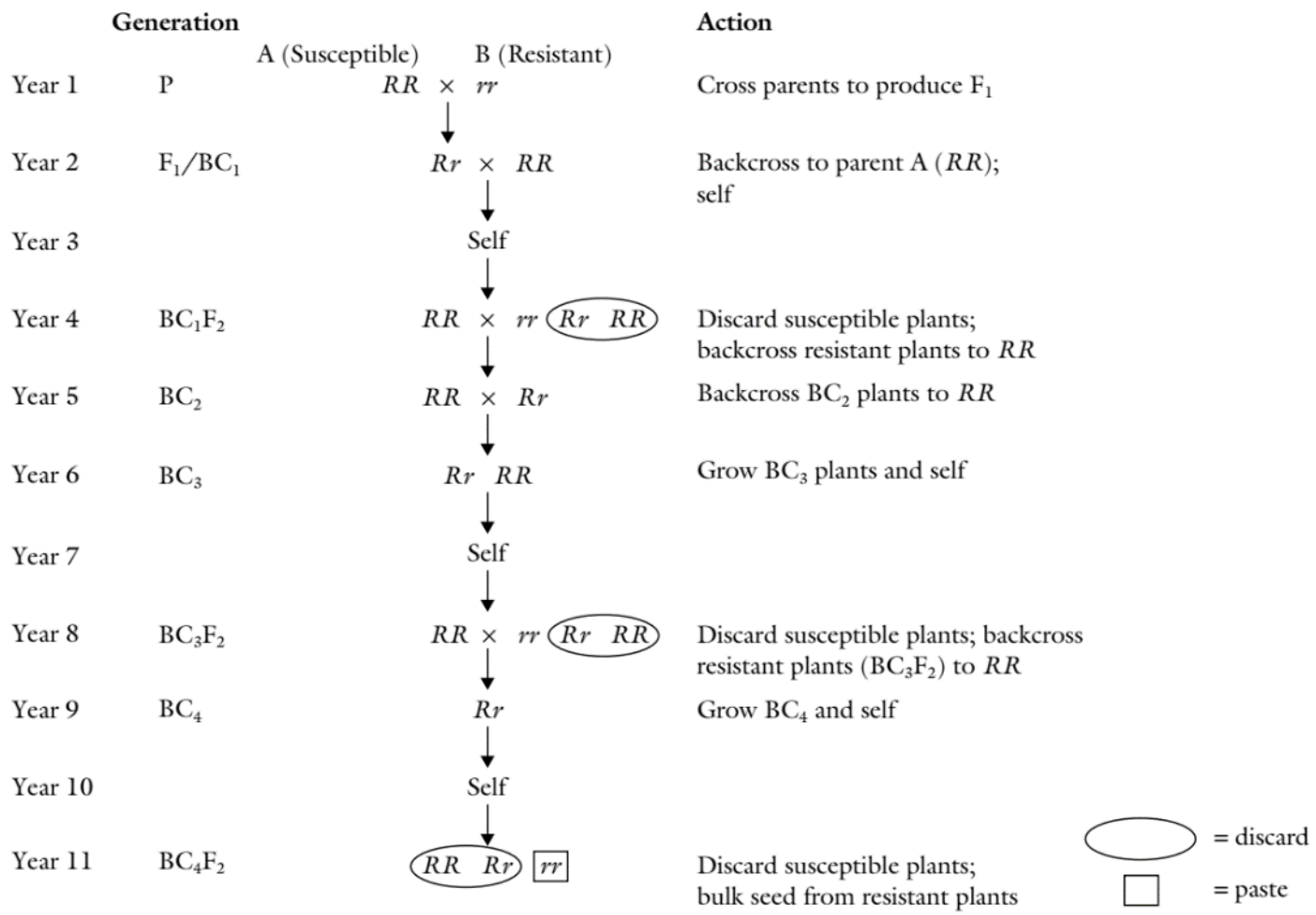
Backcross breeding

Transferring a Recessive Gene

Core Challenge:
Recessive genes aren't visible after a cross.

Solution
Each cross must be followed by selfing and screening.

Timeline:
15-16 years to develop a new variety.



Backcross breeding

Genetic points

Progeny Similarity:
After 4 backcrosses, the new cultivar is ~94% identical to the recurrent parent.

The Challenge of "Linkage Drag":
Undesirable genes can get transferred with the desired one.

Number of Genes Matters:
More genes = more plants needed for selection.

Recessive vs. Dominant:
Recessive genes require an extra step (selfing) to be identified.

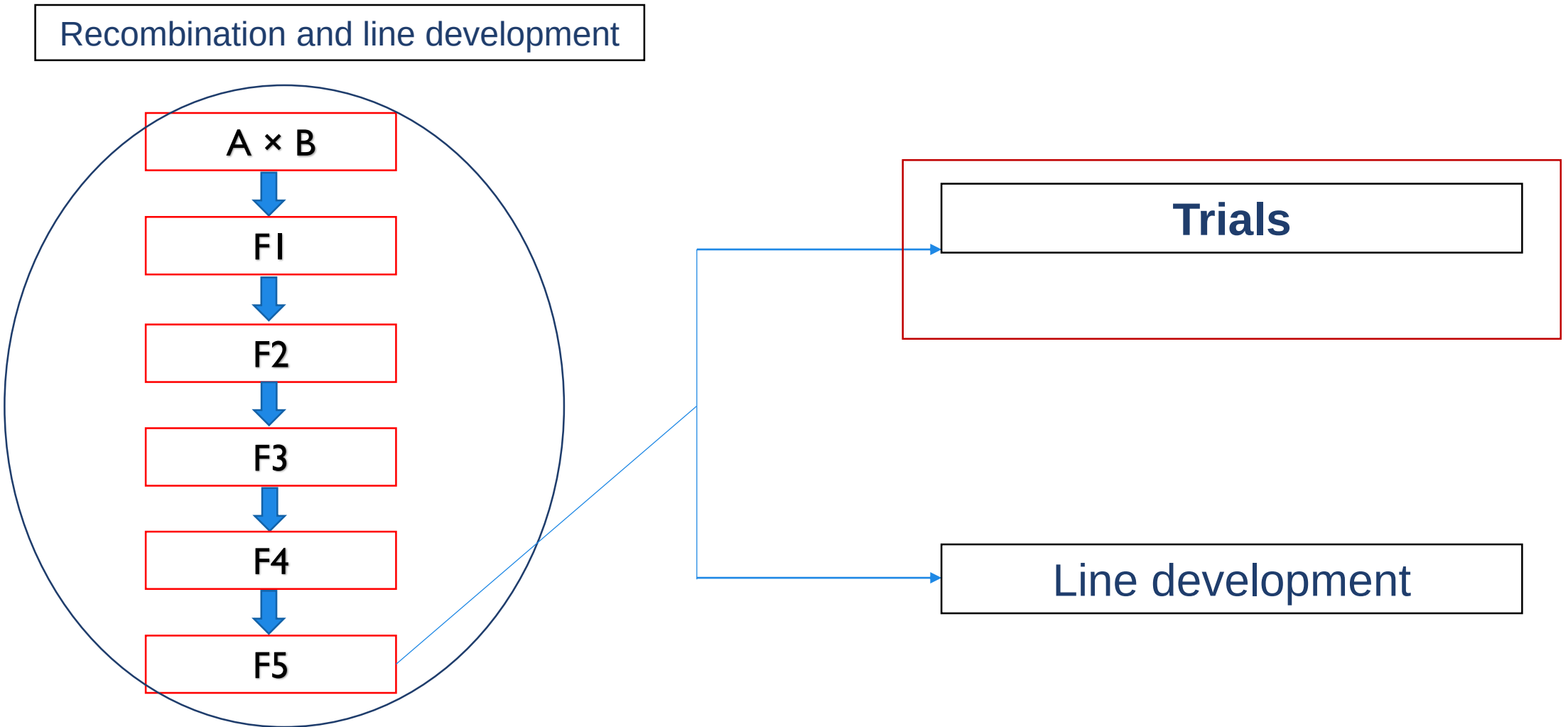
Backcross breeding

Advantages	Disadvantages
Saves time on field testing	Not ideal for complex traits (low heritability)
Predictable and repeatable results	Risk of "linkage drag" (unwanted genes)
Preserves existing good traits	Slower for recessive genes

Modified bulk at the Institute of Field and Vegetable Crops

A × B	~ 100 crosses per team / 2 spike per cross
F1	~ 100 pop / 50 plants select: 100 spikes / population and bulk
F2	~ 80 pop / 2000-3000 plants select: 200 spikes and bulk
F3	~ 60 pop / 3000 plants select: 100 spikes / population
F4	~ 60 pop / 100 spike rows select: 100 spikes / population
F5	~ 60 pop / 100 spike rows 2 m long / 5000 rows select: 600 lines with 100 spikes / line

Modified pedigree bulk at the Institute of Field and Vegetable Crops



Modified pedigree bulk at the Institute of Field and Vegetable Crops

Levels of Testing

Phase I: Preliminary trials without replications

Phase II: Trials with replications

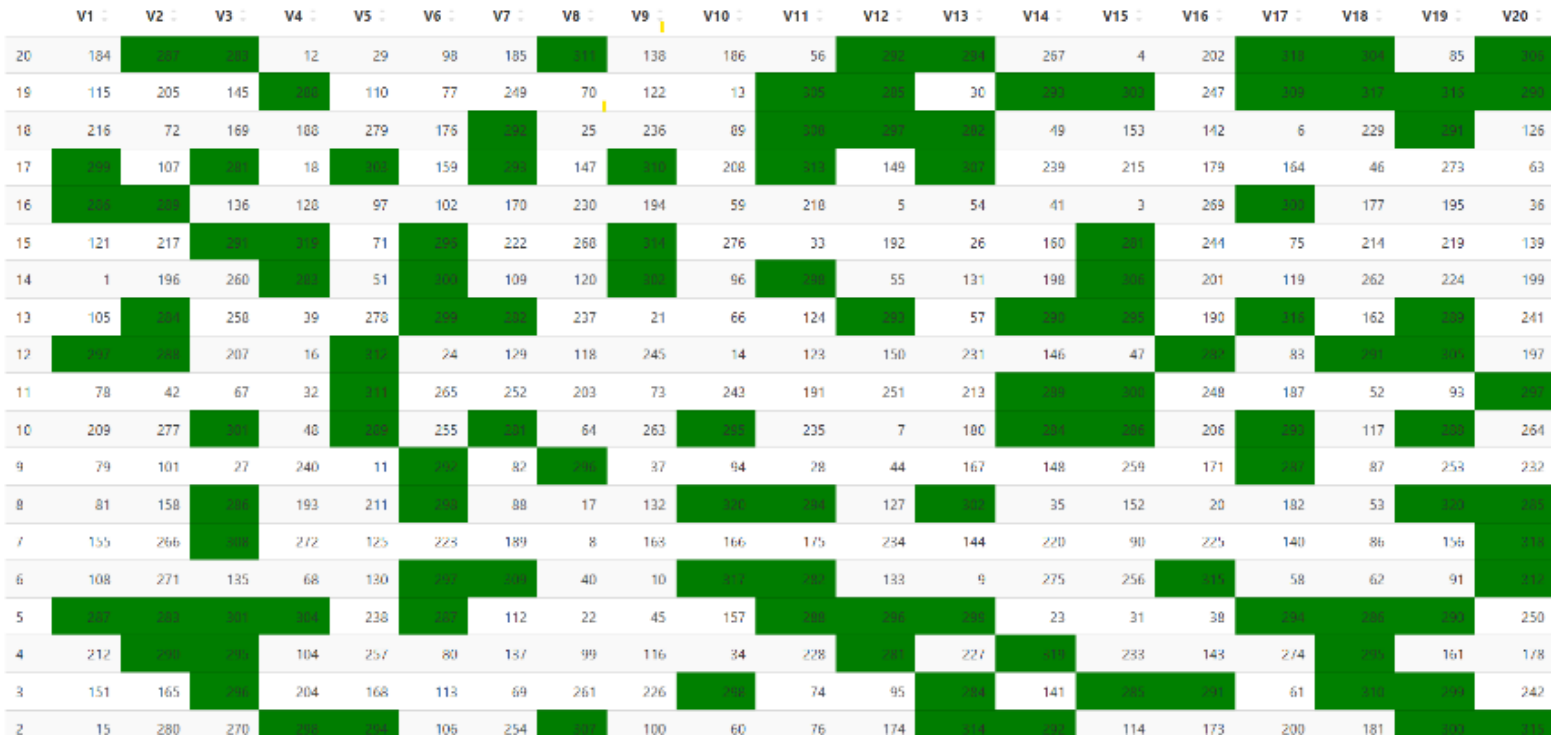
Phase III: Multi-location trials (4 sites)

Phase IV: Advanced multi-location trials (4 sites)

Modified pedigree bulk at the Institute of Field and Vegetable Crops

Phase I – Preliminary Trials (P-rep design)

- 400 lines (with or without replications)
- 40 released varieties
- Location: Rimski Šančevi



Modified pedigree bulk at the Institute of Field and Vegetable Crops

- Randdomized Block Design
- 20 genotypes + 4 standards
- 120 genotypes
- Three replications
- Rimski Šančevi

Modified pedigree bulk at the Institute of Field and Vegetable Crops

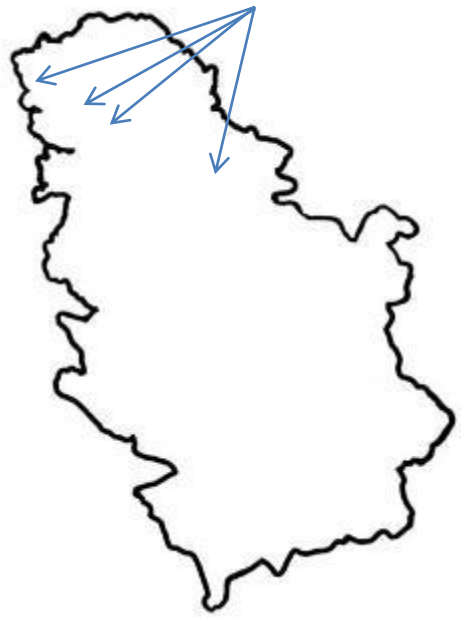
III. Multi-location Trials (4 locations)

- Rimski šančevi, Pančevo, Sombor, Srbobran
- Srbobran 30 genotypes + standards

IV. Multi-location Trials (4 locations)

- Rimski šančevi, Pančevo, Sombor, Srbobran
- 10 genotypes + standards

Multilocation trials



Thank you for your attention!

Any questions?