

Introgressing Mutants



Introgression Line Library



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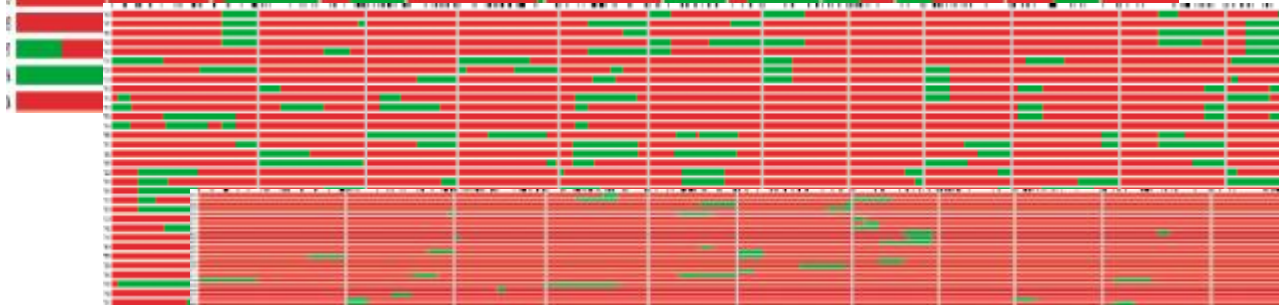
BC1



BC1 Selection



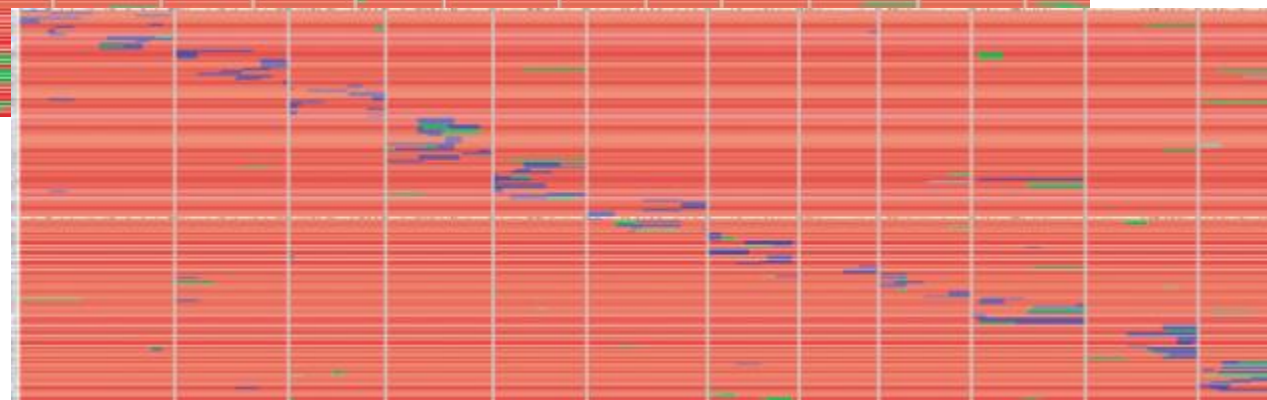
BC2 Selection



BC3 Selection



BC3S1 Selection



Trends in Plant Sci 8: 330-334

Mutant Stocks

Mutant x Bowman



F1 x Bowman



BC1 x Bowman



BC2 x Bowman



BCn x Bowman



Selfing

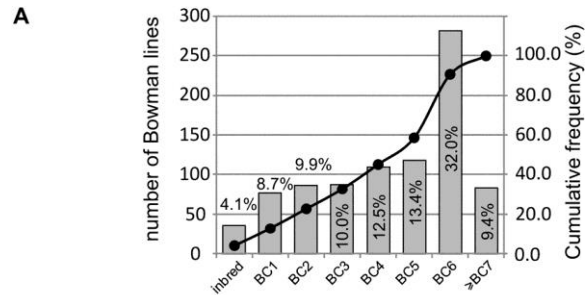
Identify
Mutant



Bowman Mutant Origins



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B

| | Total | inbred | BC1 | BC2 | BC3 | BC4 | BC5 | BC6 | >=BC7 |
|-------------|-------|--------|-----|-----|-----|-----|-----|-----|-------|
| Bonus | 185 | 5 | 10 | 19 | 28 | 27 | 25 | 59 | 12 |
| Foma | 60 | | 6 | 13 | 10 | 9 | 7 | 14 | 1 |
| Betzes | 41 | 1 | 2 | 3 | 2 | 6 | 16 | 10 | 1 |
| Akashinriki | 34 | | | | 3 | 5 | 3 | 15 | 8 |
| Morex | 32 | 6 | 6 | 4 | 5 | 7 | 1 | 2 | 1 |
| Step toe | 31 | 3 | 7 | 5 | 7 | 4 | 2 | 3 | |
| Volla | 22 | | 2 | 2 | 3 | 4 | 4 | 7 | |
| Birgitta | 21 | | 1 | 1 | 2 | 2 | 3 | 9 | 3 |

C

| | Total | inbred | BC1 | BC2 | BC3 | BC4 | BC5 | BC6 | >=BC7 |
|------------------------|-------|--------|-----|-----|-----|-----|-----|-----|-------|
| spontaneous | 298 | 11 | 25 | 31 | 17 | 27 | 52 | 95 | 40 |
| X-ray | 125 | 2 | 6 | 7 | 8 | 20 | 16 | 55 | 11 |
| fast neutron | 109 | 14 | 13 | 12 | 20 | 17 | 8 | 21 | 4 |
| sodium azide | 73 | | 3 | 8 | 11 | 8 | 9 | 25 | 9 |
| ethyl methanesulfonate | 61 | 1 | 4 | 9 | 7 | 10 | 7 | 17 | 6 |
| ethylene imine | 52 | 1 | 6 | 5 | 11 | 6 | 8 | 12 | 3 |
| γ -ray | 39 | 1 | 5 | 4 | 3 | 3 | 4 | 18 | 1 |

D

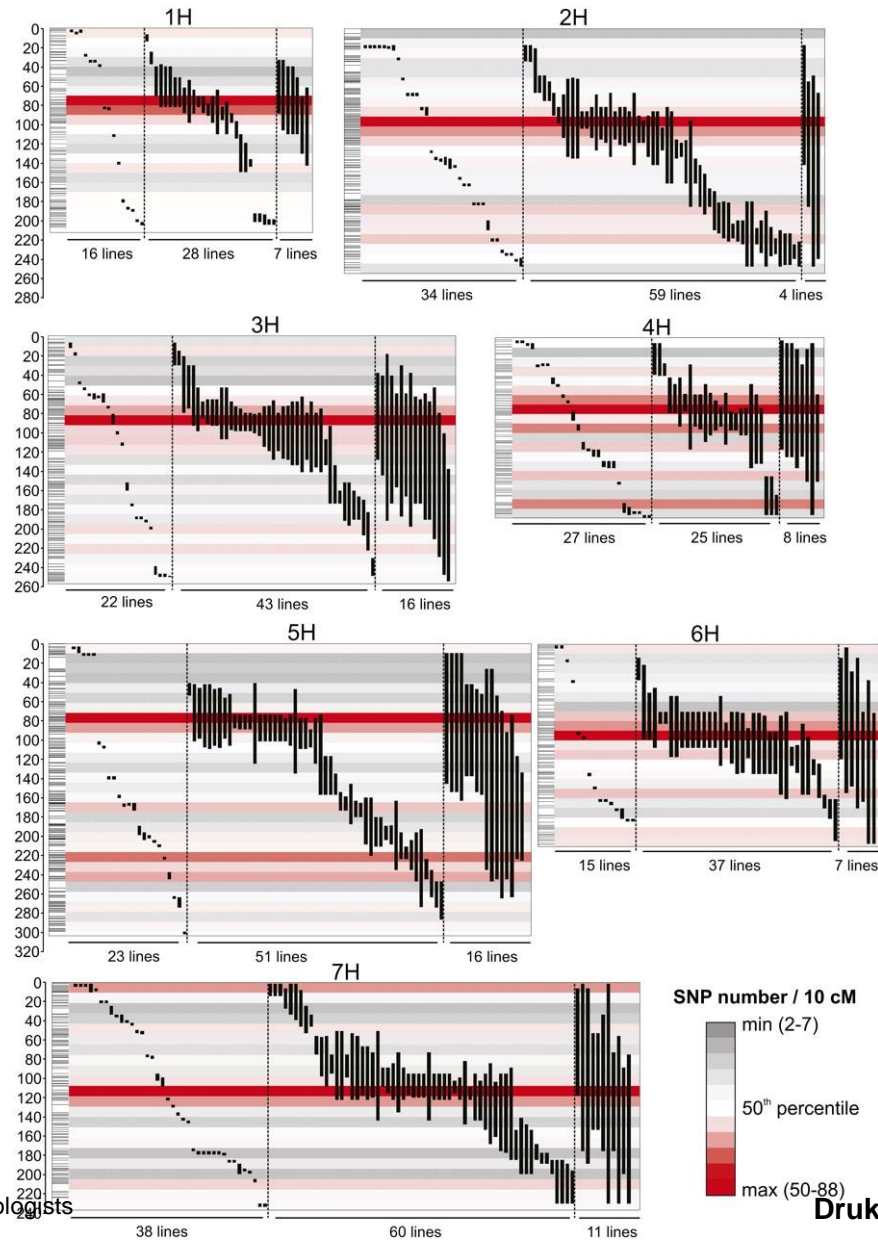
| | Total | inbred | BC1 | BC2 | BC3 | BC4 | BC5 | BC6 | >=BC7 |
|--------------------|-------|--------|-----|-----|-----|-----|-----|-----|-------|
| Male sterile | 105 | | 11 | 20 | 4 | 6 | 21 | 35 | 8 |
| Eceriferum | 92 | | 2 | 8 | 11 | 16 | 7 | 40 | 8 |
| Semidwarf | 57 | | 9 | 7 | 11 | 13 | 8 | 7 | 2 |
| Laxatum | 48 | 2 | 7 | 10 | 10 | 5 | 6 | 8 | |
| Dense spike | 47 | | 2 | 4 | 5 | 9 | 8 | 16 | 3 |
| Chlorina | 43 | 6 | 5 | 2 | 4 | 4 | 3 | 12 | 7 |
| Short awn | 38 | | 1 | 4 | 2 | 5 | 7 | 12 | 7 |
| Brachytic | 31 | | 2 | | 1 | 2 | 6 | 17 | 3 |
| Erectoides | 30 | 1 | | 2 | 2 | 2 | 5 | 13 | 5 |
| Necrotic leaf spot | 29 | 7 | 6 | 1 | 5 | 4 | 3 | 3 | |
| Desynapsis | 24 | | 3 | 2 | 2 | 6 | 10 | | |
| Early maturity | 22 | | 3 | 1 | | 5 | 2 | 7 | 4 |



Mutant Introgression Segments



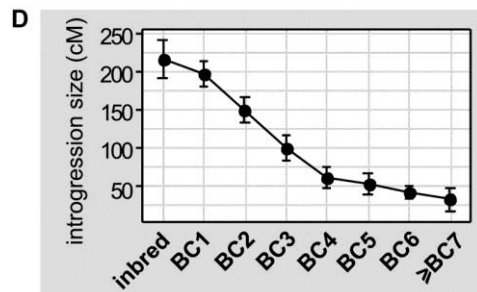
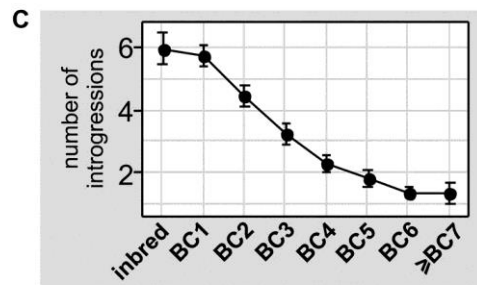
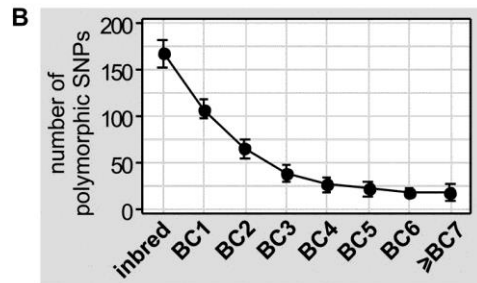
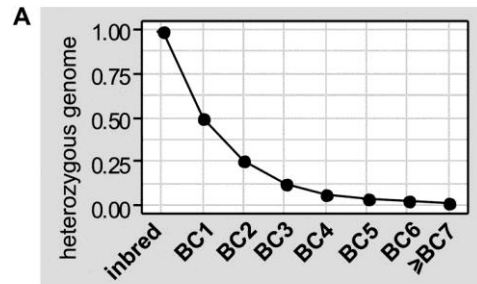
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Backcrossing clean-up



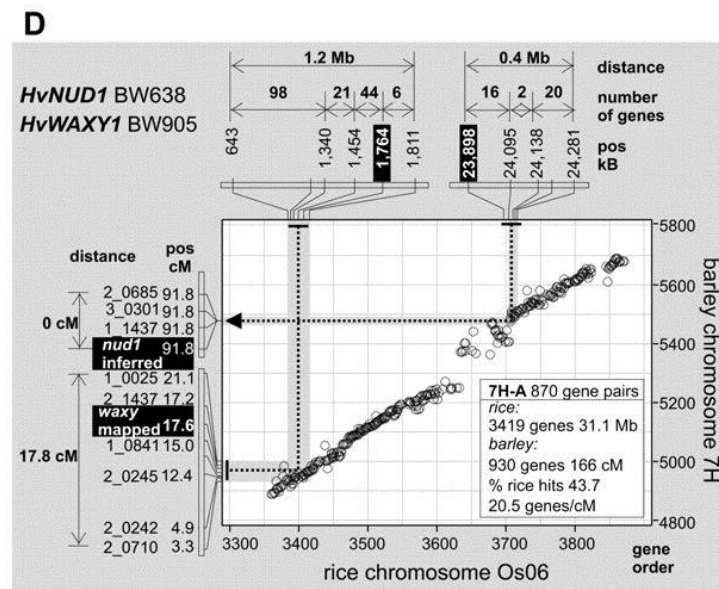
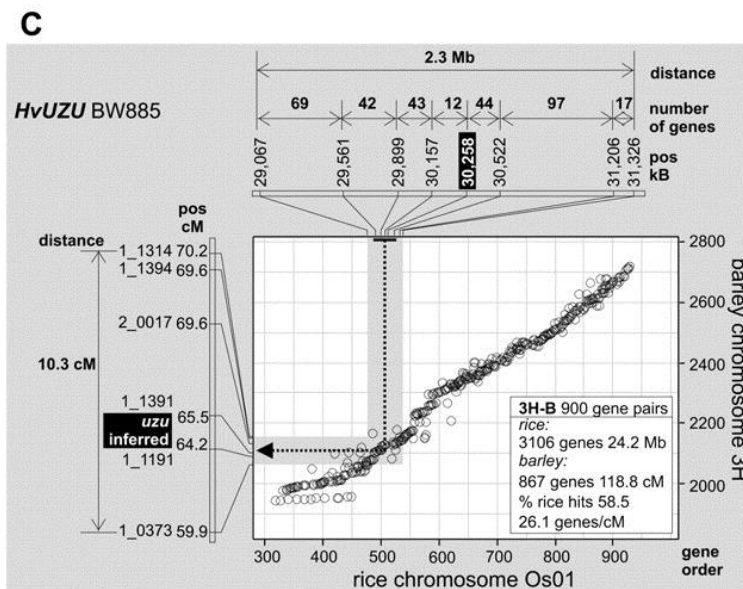
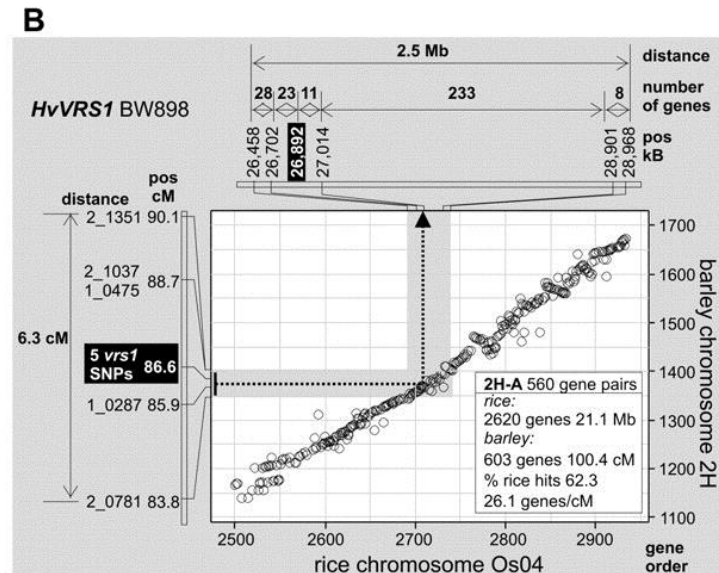
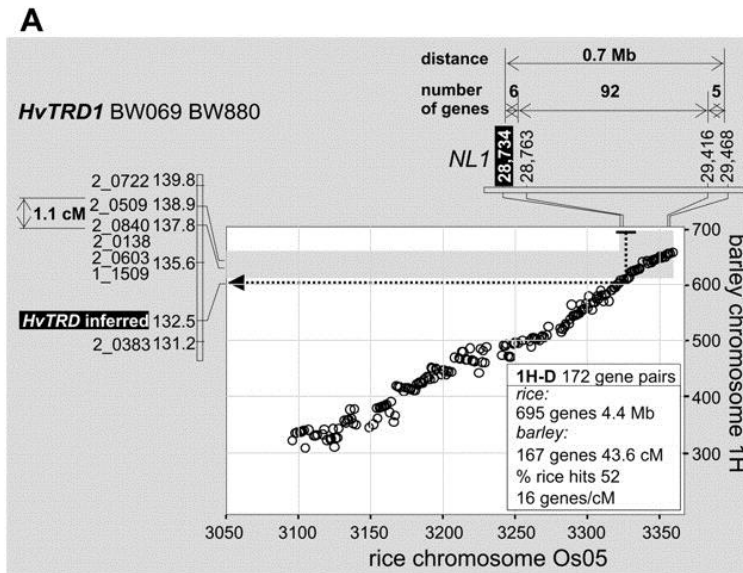
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Identifying causal genes



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Investigating natural variation in barley to identify genes involved in adaptation



Luke Ramsay

Variation within cultivated barley



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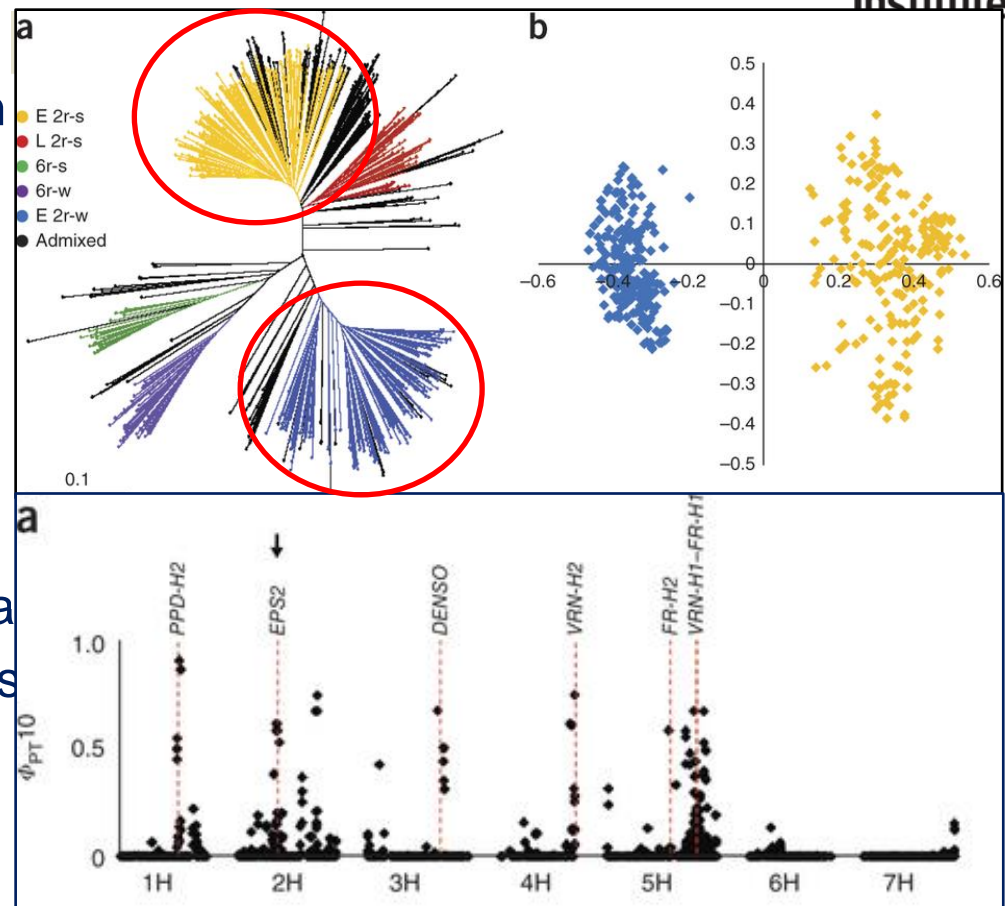
- Genome wide association genetics
- Driven by development of SNP genotyping platform
- Brought different areas of research together
- Gene space sequence - step-change for barley genetics

Delineation of winter : spring division

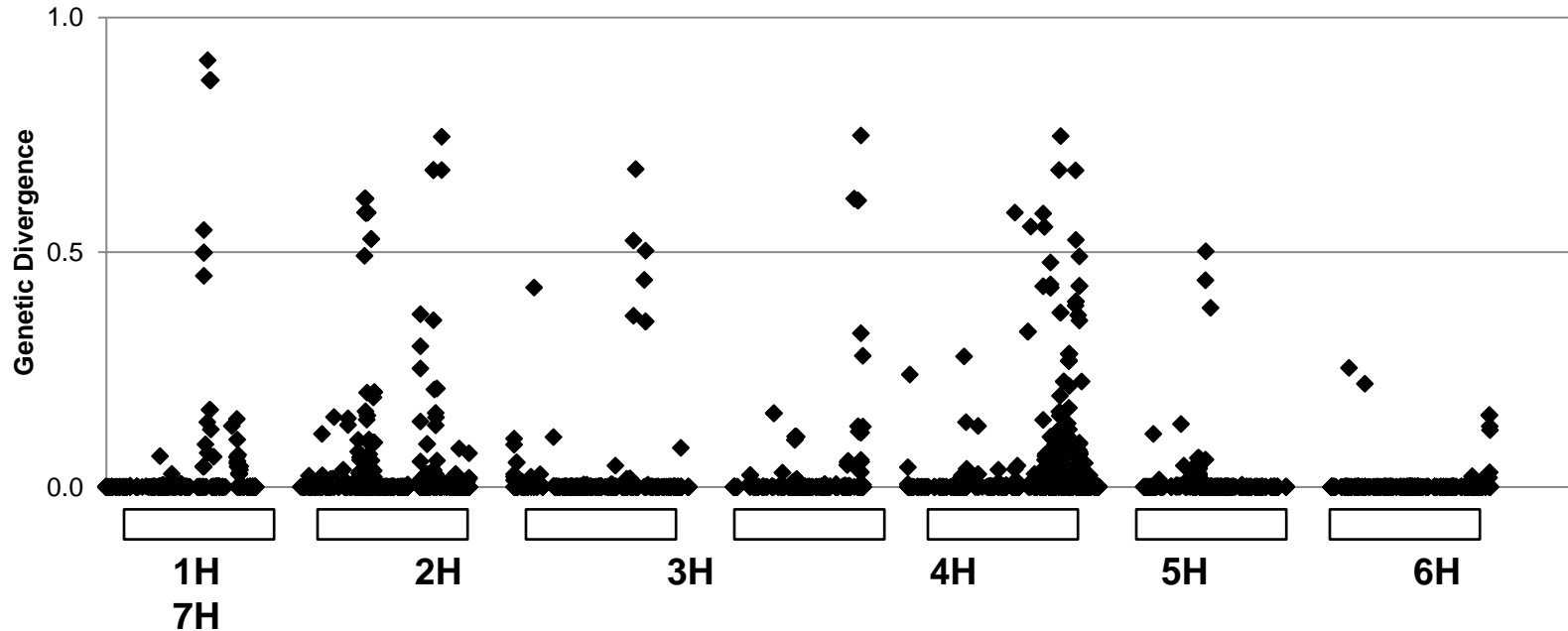


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- SNP discovery with RNA-Seq
- 9K iSelect genotyping platform
 - Community uptake
- Detailed SNP genotyping cultivated barley germplasm
- Winter: Spring division
- 9K iSelect - genetic linkage map
- Comparison – genomic regions associated with difference



Genomic regions associated with Spring/Winter divergence



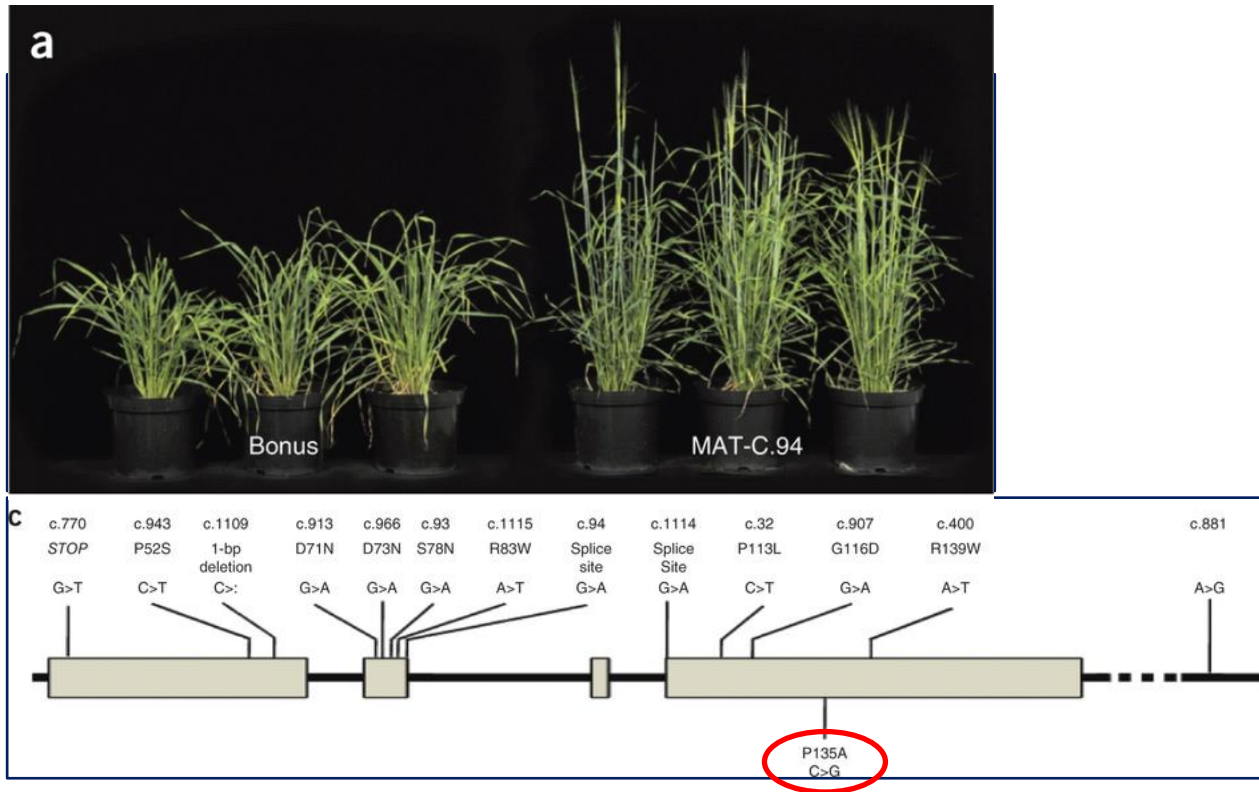
F_{ST} is a measure of genetic differentiation.

Peaks represent where one allele is present in the winter population and another allele is present in the spring population

Candidate gene discovery & verification

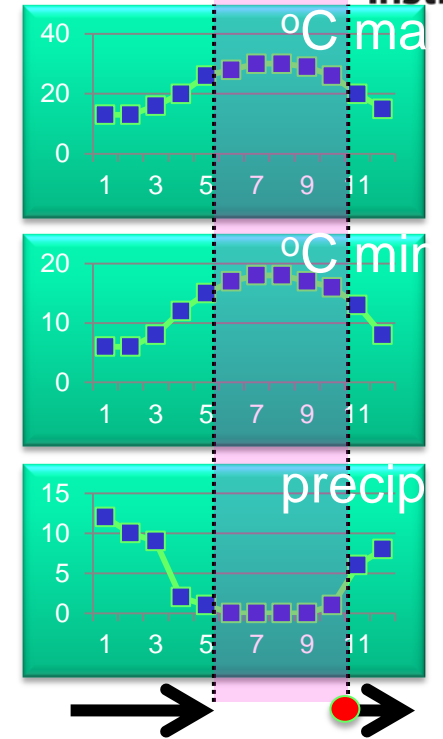
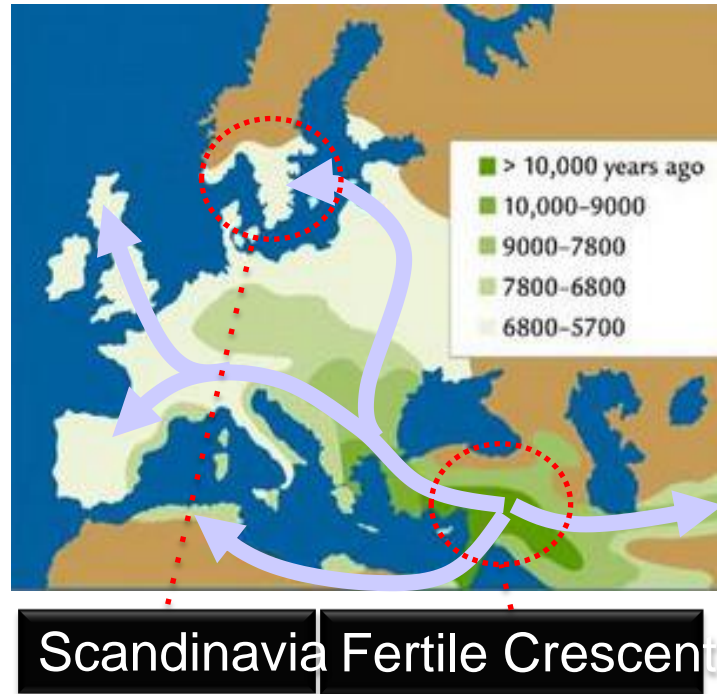
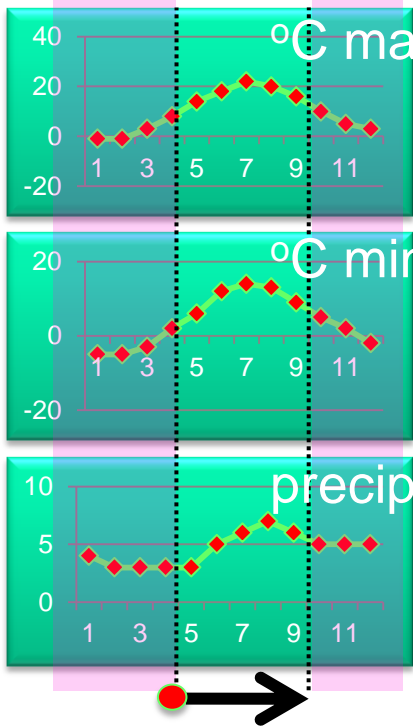


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- 9K iSelect - genetic linkage map – synteny
- Candidate gene; barley homologue of *Centroradialis*
- Barley mutant collection - derived NILs genotyped
- Early heading Praematurum-c (*mat-c*) allelic series

Adaption to new environments - *HvCEN*



- Fixation of haplotype III in European Spring barley
- Post domestication selection of existing allelic form – shift in flowering time



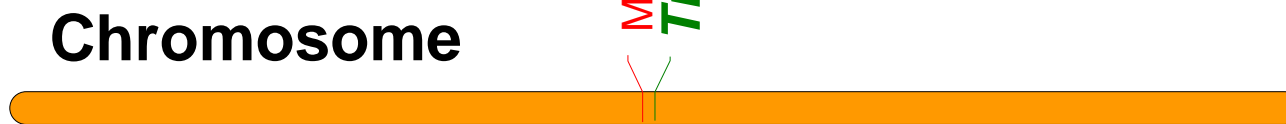
Markers in backcrosses

- Backcross Inbred Lines (BILs) for mapping
- Backcross conversions
 - Marker assisted breeding in Australia
 - Fixation of target genes e.g. TILLING
- Advanced Backcross QTL
 - Examples in many crops now
- Single Recombinant Chromosome Substitution Libraries (RCSLs)
 - Work on barley in UK and USA

Flanking Markers – Major Gene

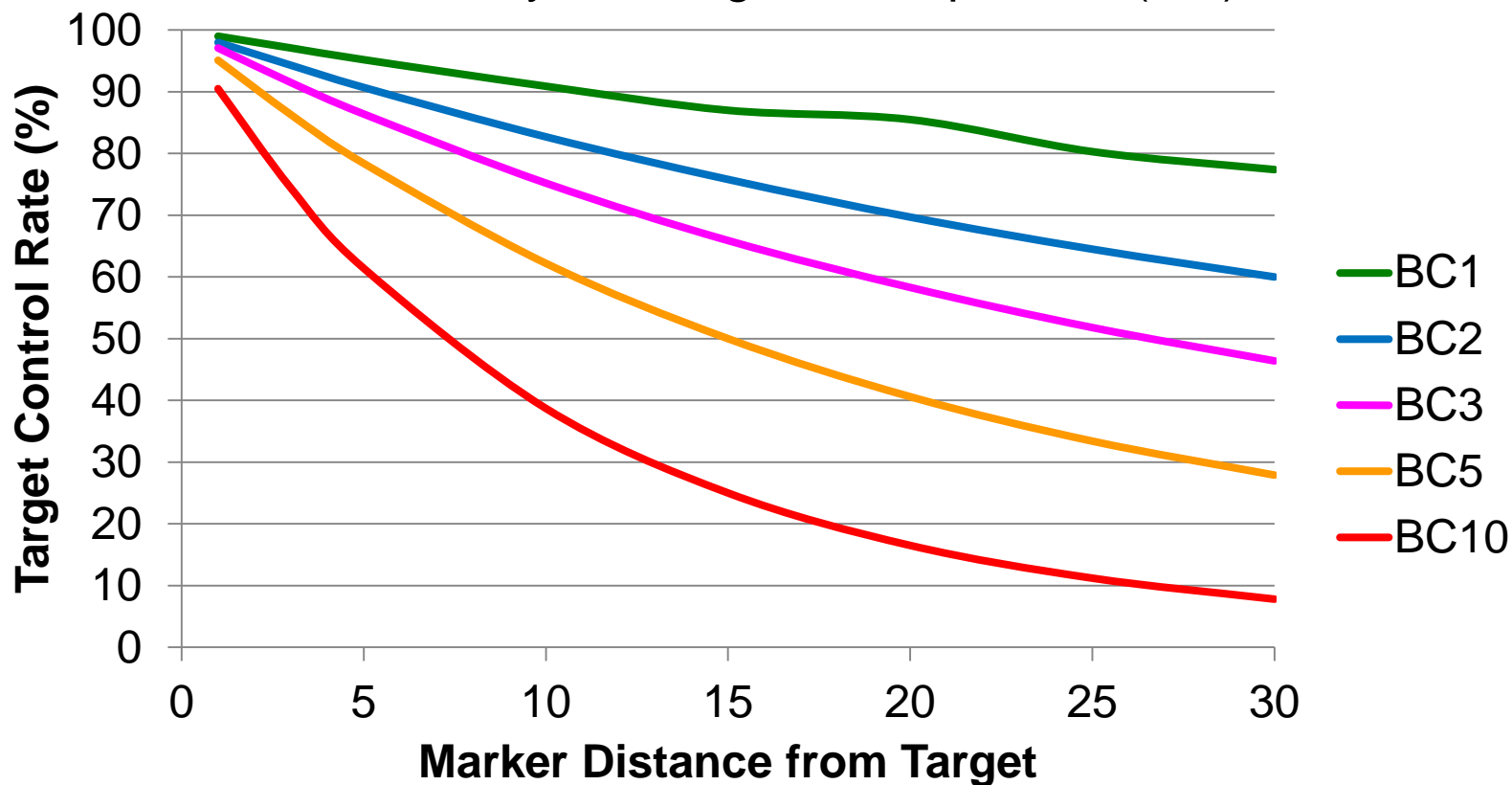


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Marker
Trait
98
100

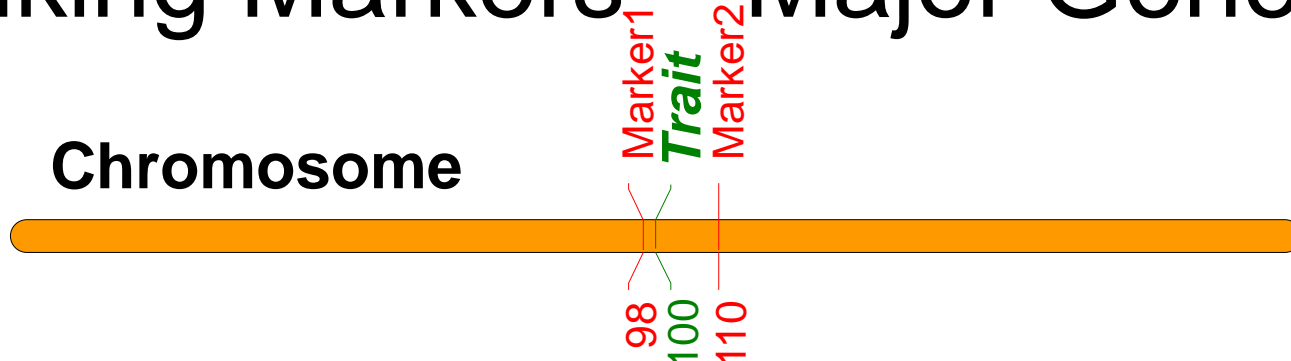
TCR = Probability that target is still present $(1-\theta)^n$



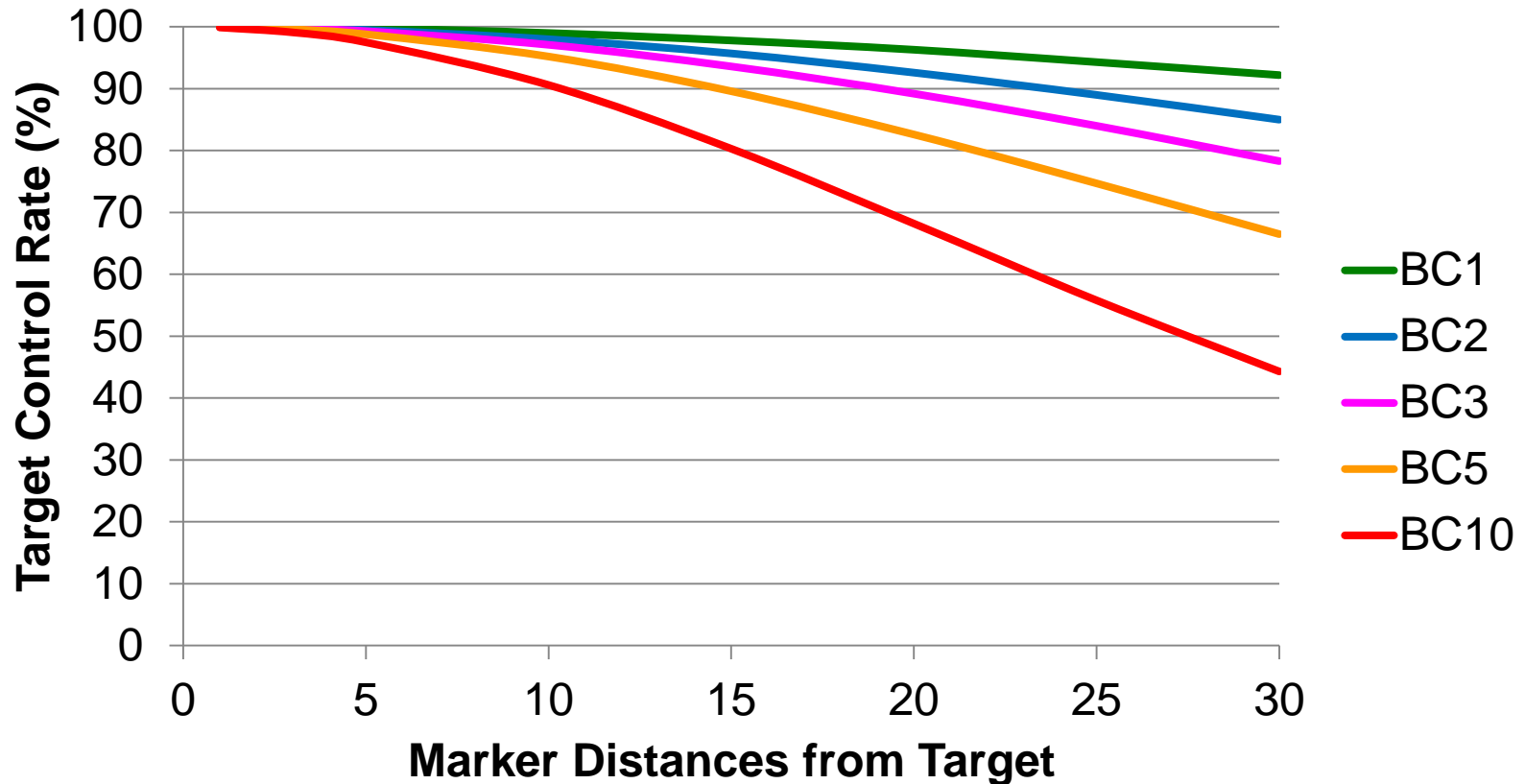
Flanking Markers – Major Gene



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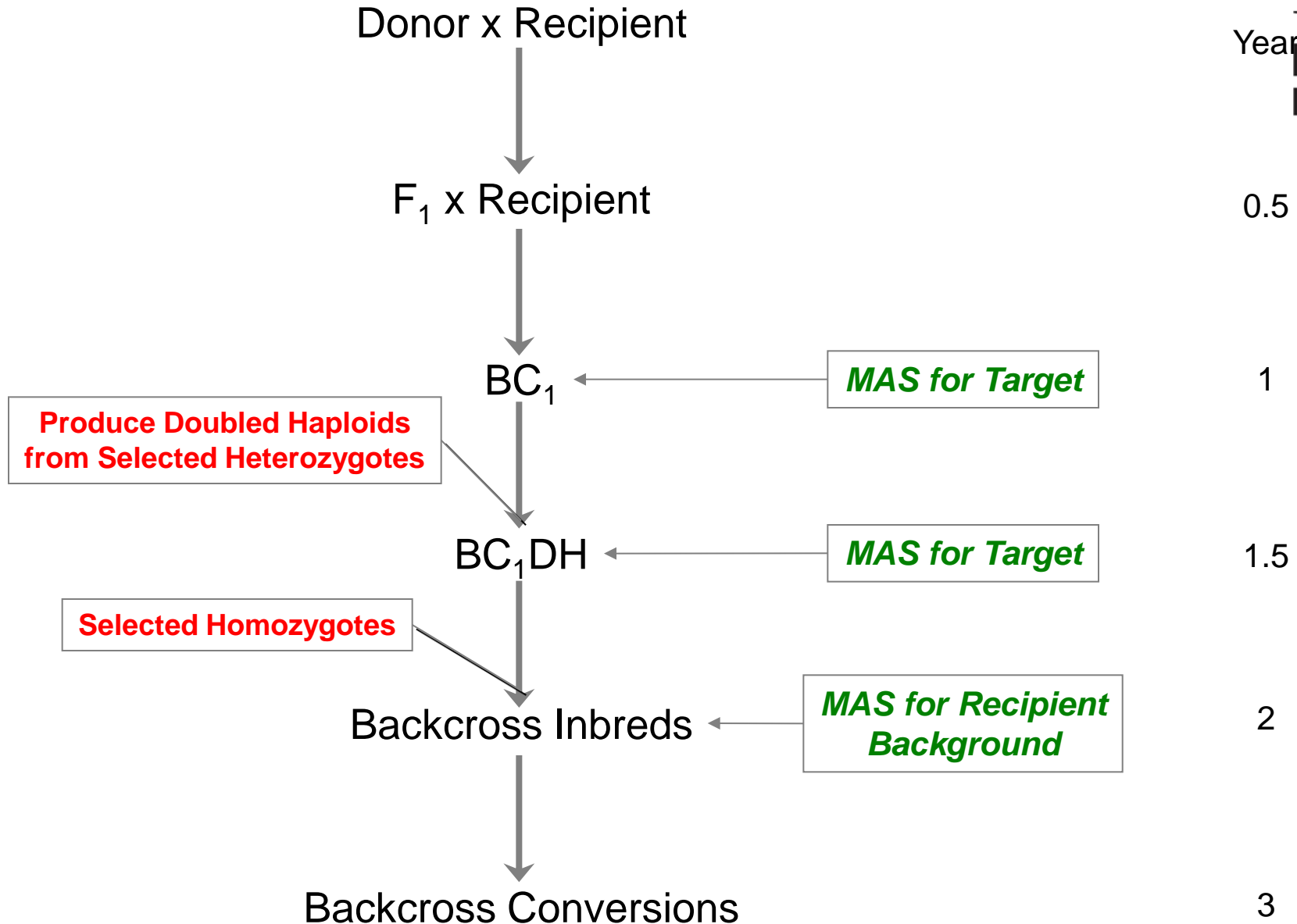
TCR = Probability that target is still present $[(1-\theta_1)(1-\theta_2)/(1-\theta)]^n$



DH & Markers in backcrosses



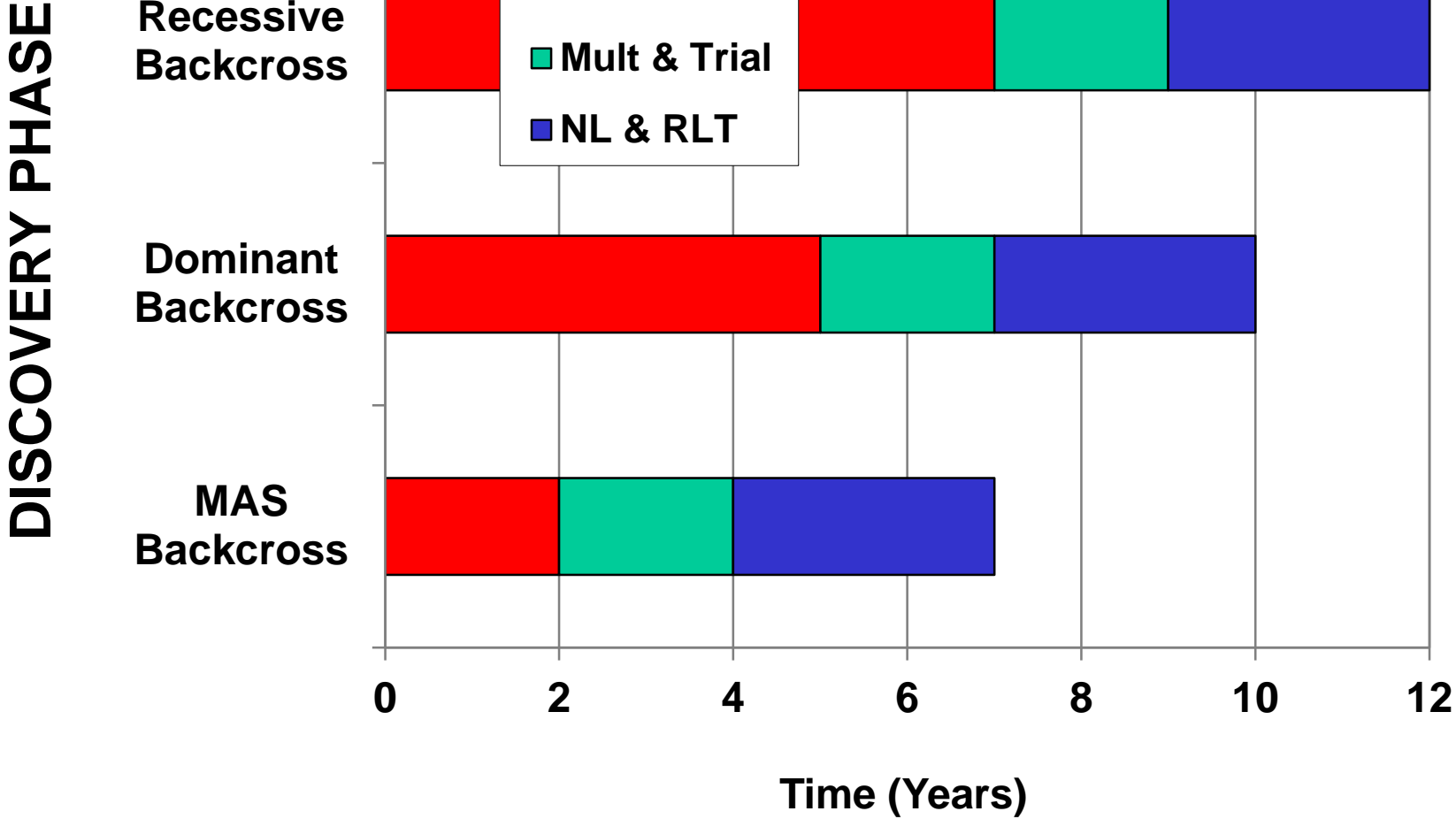
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Benefits of MAS in Backcross Conversions



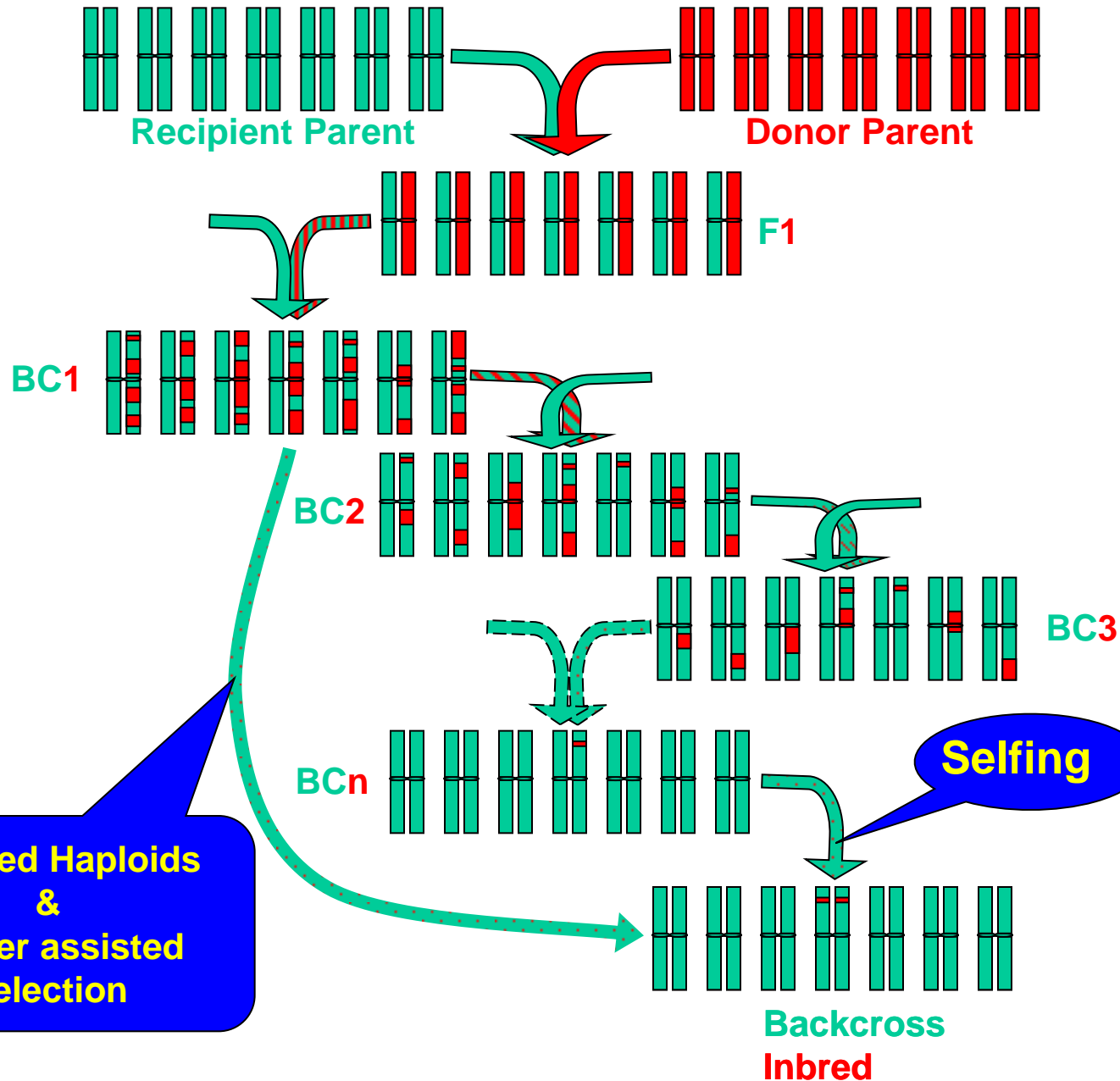
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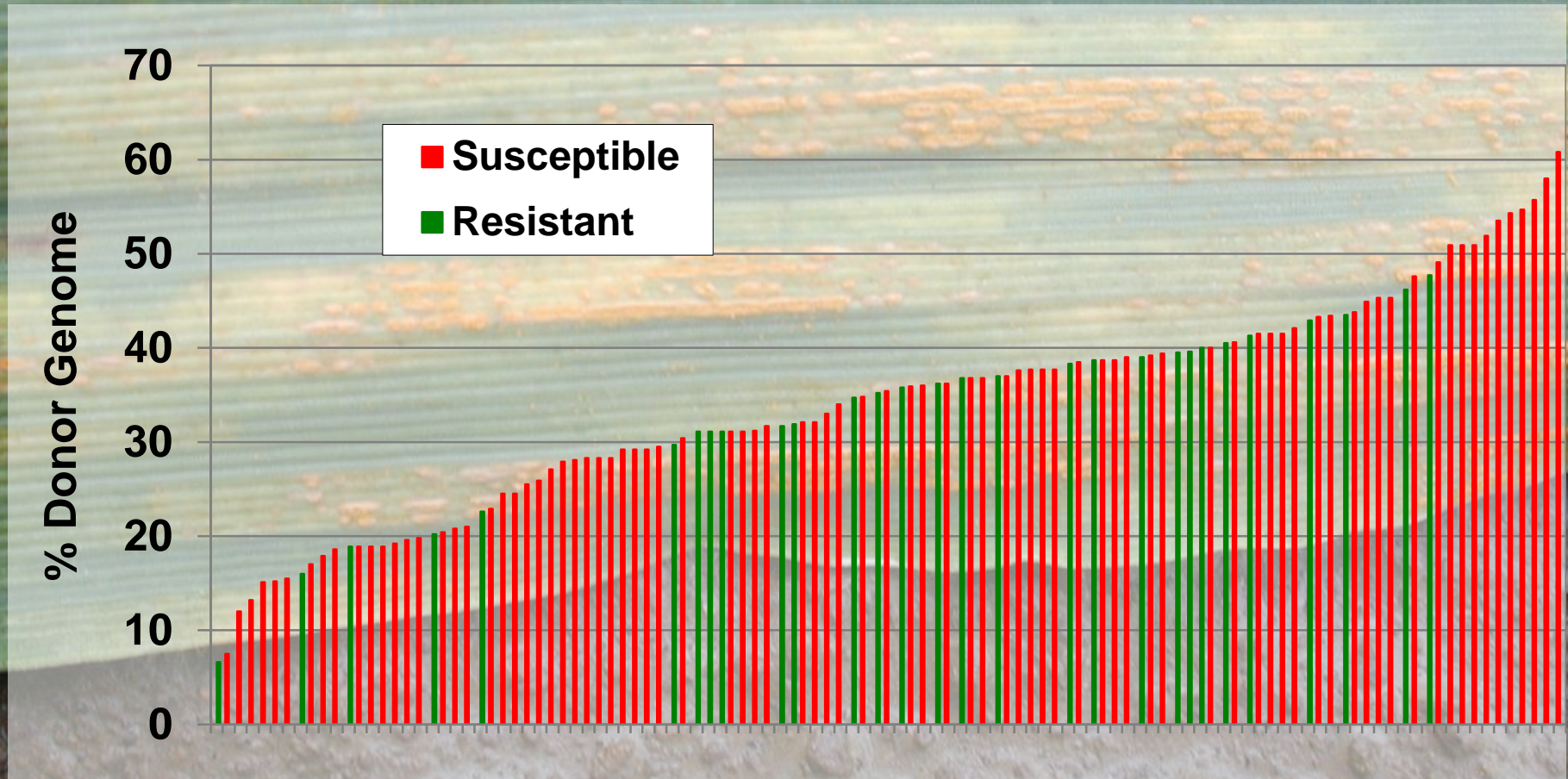
Backcross Conversions



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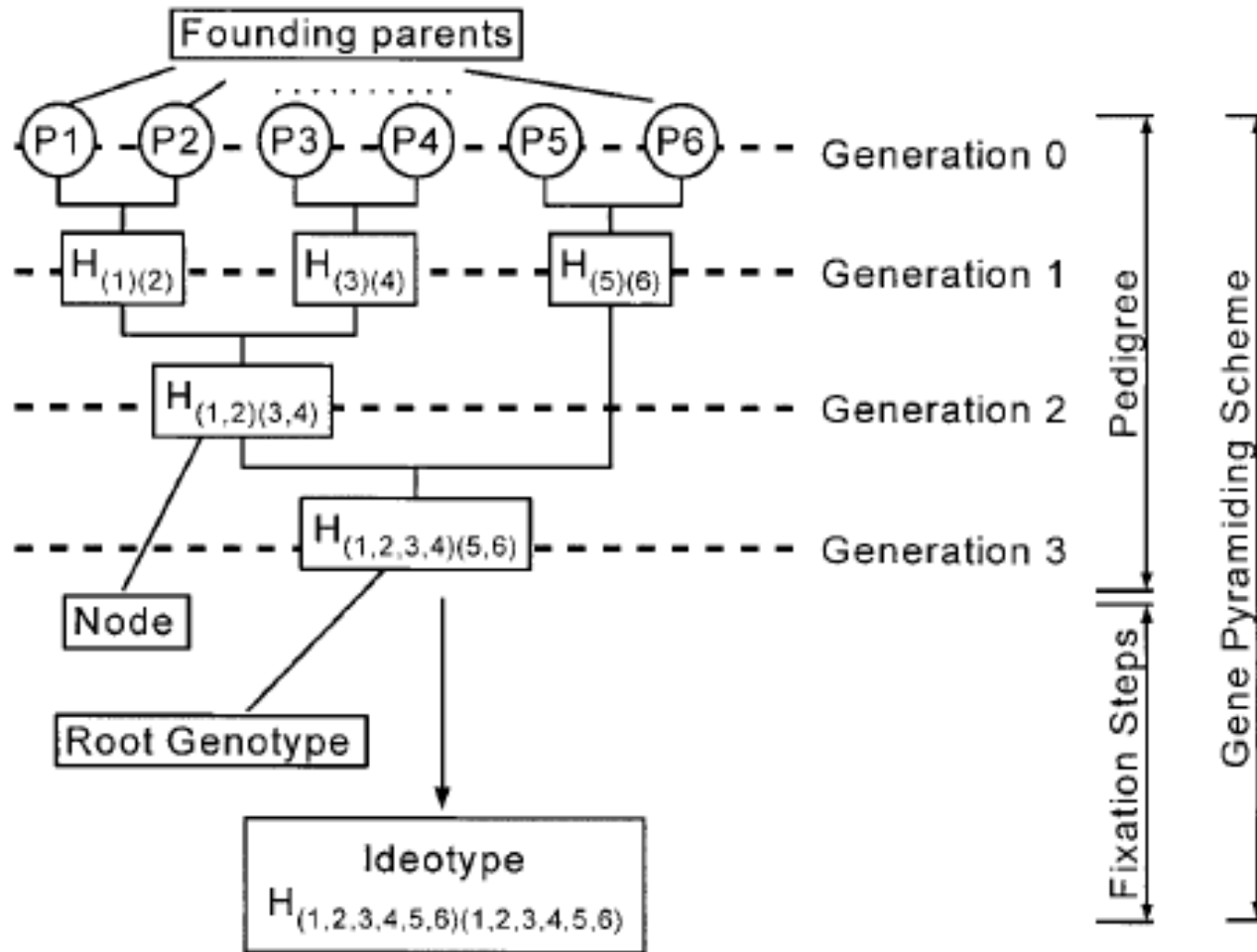
Percentage Donor Genome in Stripe Rust Resistance Introgression (AFLPs)



Basic Pyramiding Steps



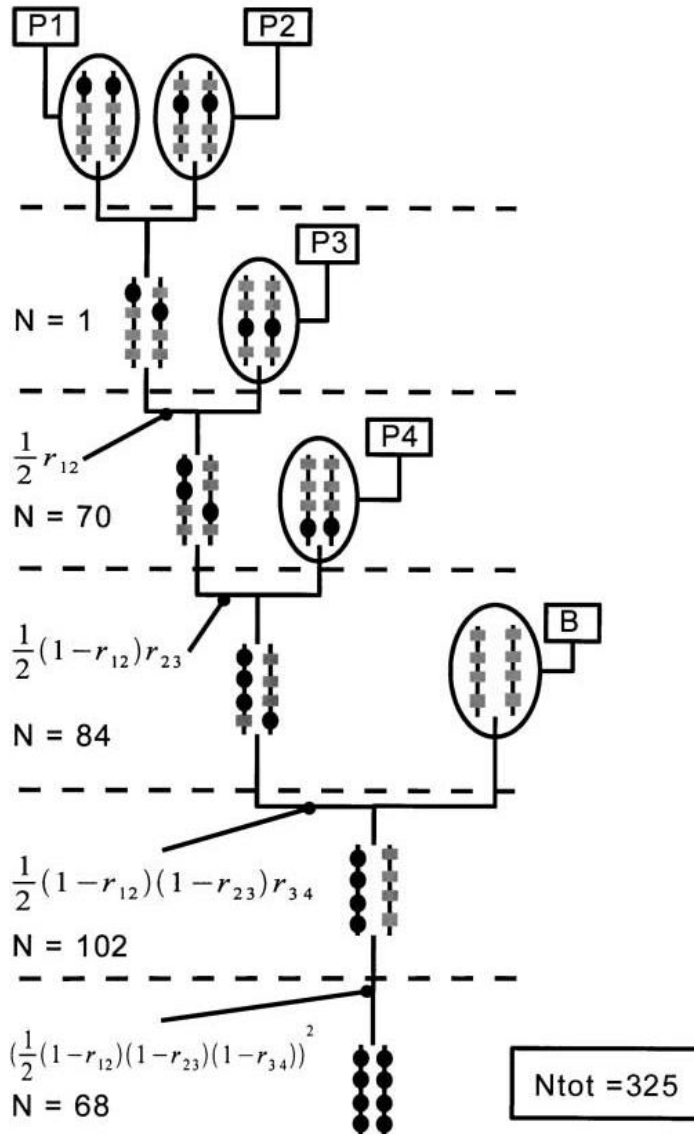
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Pyramiding Incrementally

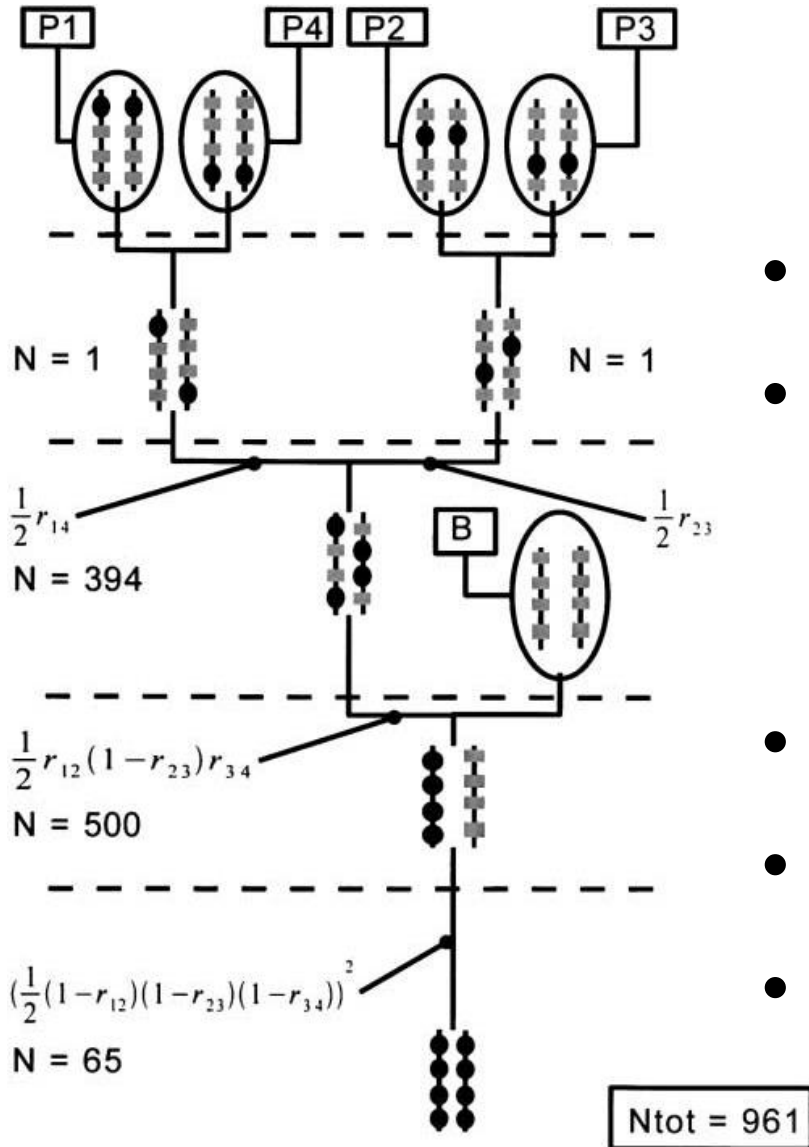


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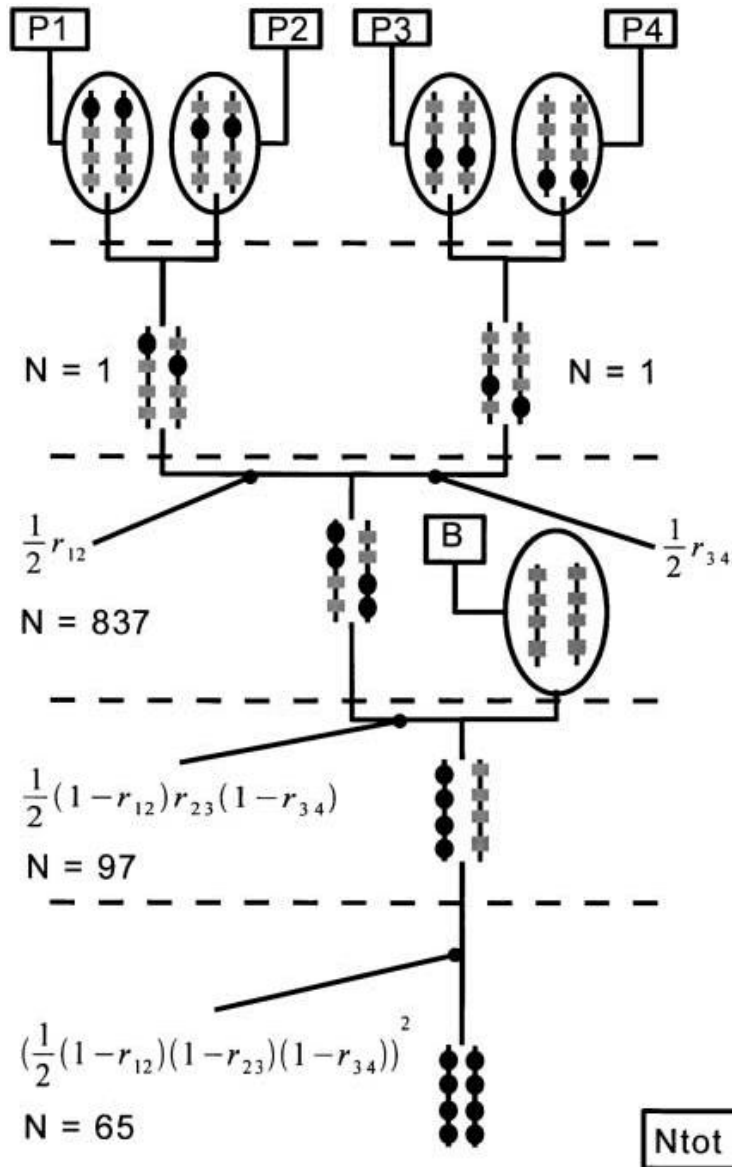
- r_{ij} = recombination between *gene_i* & *gene_j*
- 99% probability
- 3 Pedigree steps
- 2 Fixation steps
- 5 generations total

Pyramiding Concurrently - Distant



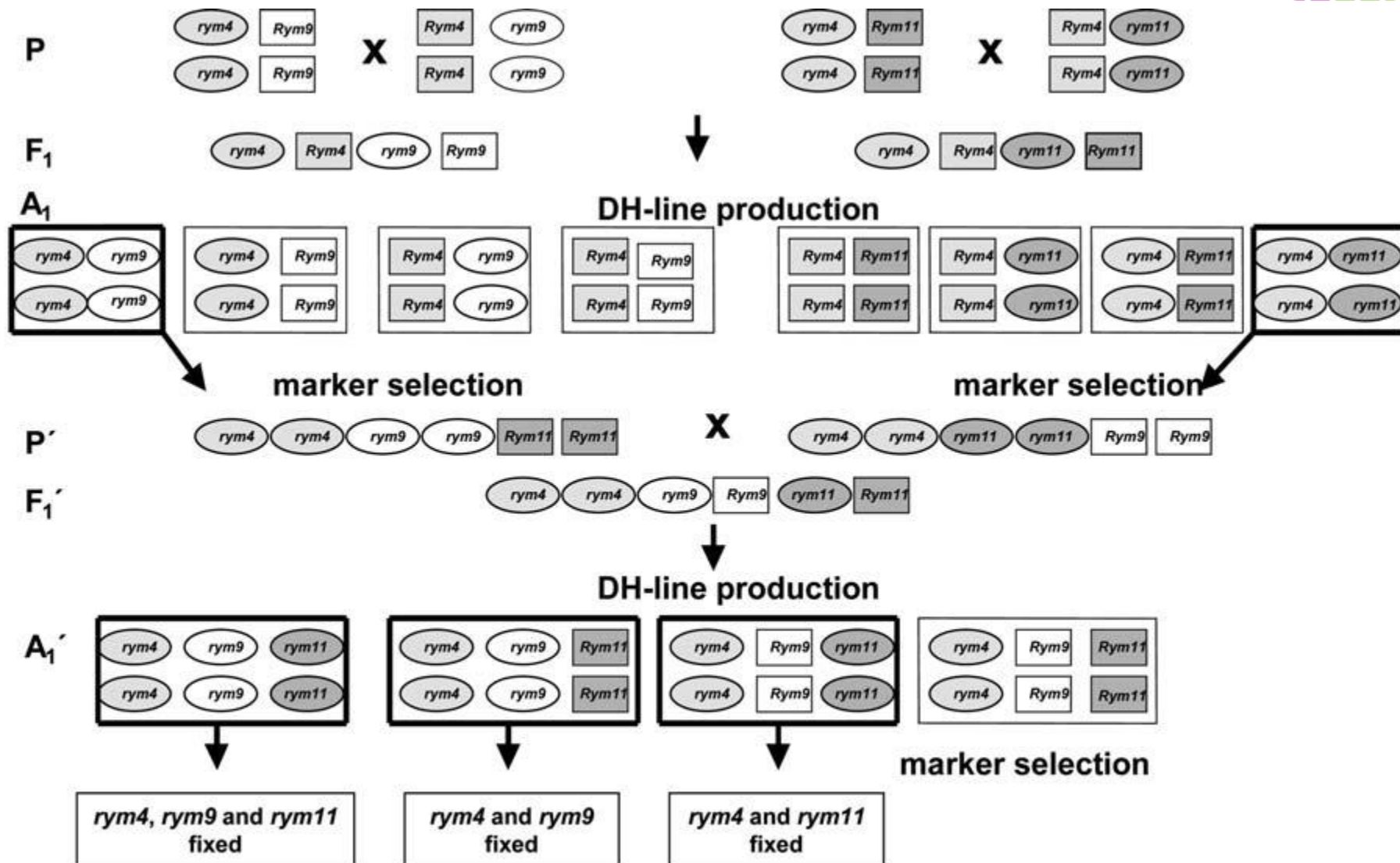
- Parameters same
- Make 1 cross between distant founders
- 2 Pedigree steps
- 2 Fixation steps
- 4 generations total

Pyramiding Concurrently - Close



- Parameters same
- Make each cross between close founders
- 2 Pedigree steps
- 2 Fixation steps
- 4 generations total

Pyramiding virus resistance - 1

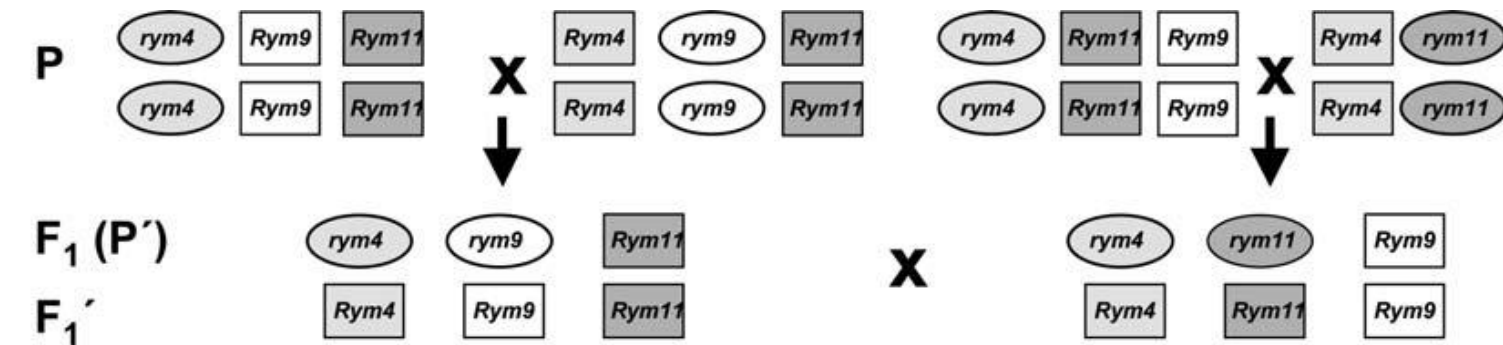


rym = resistance encoding allele; *Rym* = susceptibility encoding allele

Pyramiding virus resistances - 2



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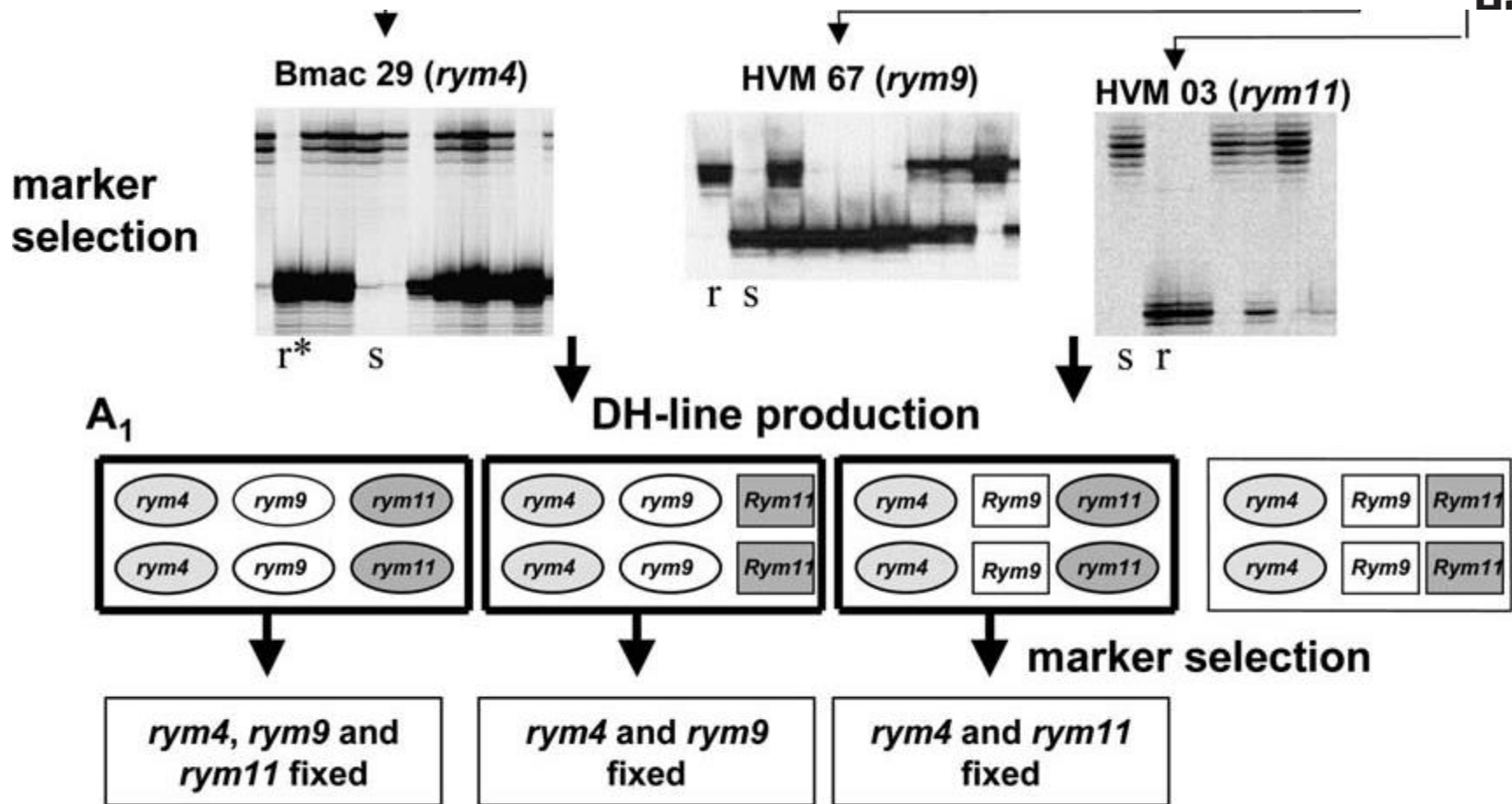


| | | | | |
|------------------------|--|--|--|--|
| ♀ \ ♂ | | | | |
| | (rym4) Rym9 Rym11 | Rym4 (rym9) Rym11 | Rym4 Rym9 Rym11 | (rym4) (rym9) Rym11 |
| (rym4) Rym11 Rym9 | (rym4) Rym9 Rym11 (rym4) Rym9 Rym11 | Rym4 (rym9) Rym11 (rym4) Rym9 Rym11 | Rym4 Rym9 Rym11 (rym4) Rym9 Rym11 | (rym4) (rym9) Rym11 (rym4) Rym9 Rym11 |
| Rym4 (rym11) Rym9 | (rym4) Rym9 Rym11 Rym4 Rym9 (rym11) | Rym4 (rym9) Rym11 Rym4 Rym9 (rym11) | Rym4 Rym9 Rym11 Rym4 Rym9 (rym11) | (rym4) (rym9) Rym11 Rym4 Rym9 (rym11) |
| Rym4 Rym11 Rym9 | (rym4) Rym9 Rym11 Rym4 Rym9 Rym11 | Rym4 (rym9) Rym11 Rym4 Rym9 Rym11 | Rym4 Rym9 Rym11 Rym4 Rym9 Rym11 | (rym4) (rym9) Rym11 Rym4 Rym9 Rym11 |
| (rym4) (rym11) Rym9 | (rym4) Rym9 Rym11 (rym4) Rym9 (rym11) | Rym4 (rym9) Rym11 (rym4) Rym9 (rym11) | Rym4 Rym9 Rym11 (rym4) Rym9 (rym11) | (rym4) (rym9) Rym11 (rym4) Rym9 (rym11) |

Pyramiding virus resistances - 3



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* r=allele of the resistant parent, s=allele of the susceptible parent

rym = resistance encoding allele; *Rym* = susceptibility encoding allele