Optimizing Breeding Program Design

Marker Assisted Selection

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Effect of new technologies

DNA technologies

» Parentage testing

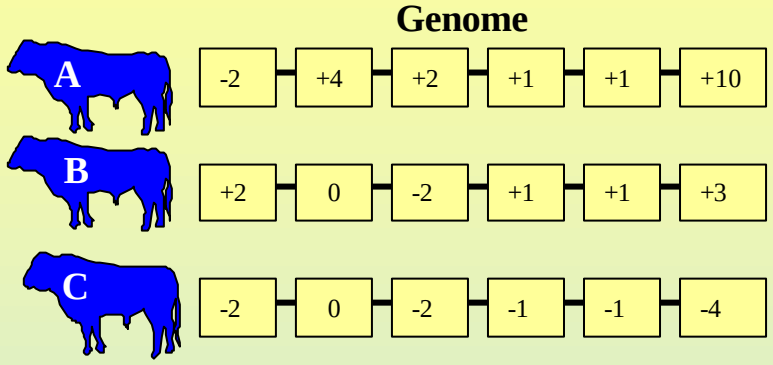
» Marker Assisted Selection

» Marker Assisted Introgression

Selection for Quantitative Traits

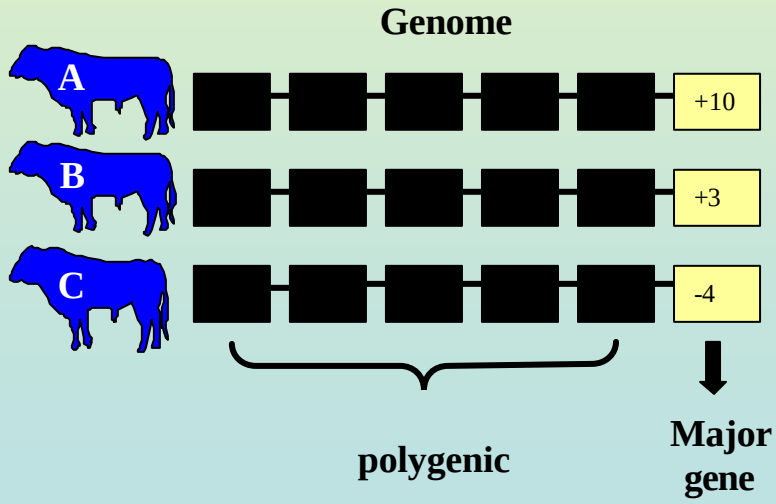
polygenes and major genes

True situation



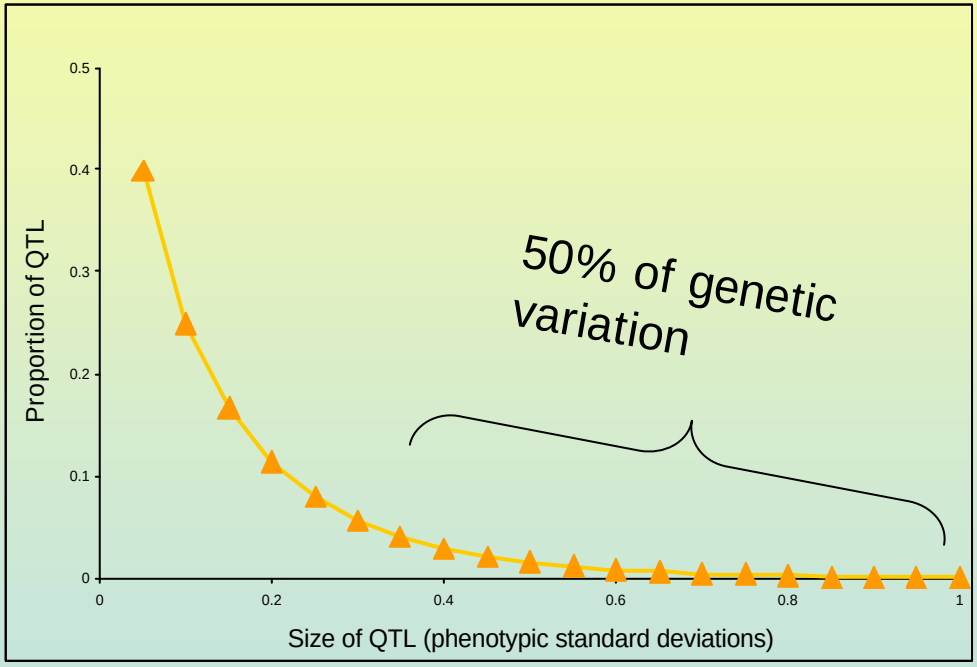
	Effects		
	Genetic	**Environment**	**Phenotype**
A	+16	-10	**+6**
B	+5	+9	**+14**
C	-10	+20	**+10**

Observed situation



Phenotype
+6
+14
+10

How many genes?



- Maybe 5-10 large QTL explain the majority of the genetic variance.
- Mapping experiments should be able to detect these large QTL

Many small genes with small effect,

few with large effect

Marker Asssisted Selection

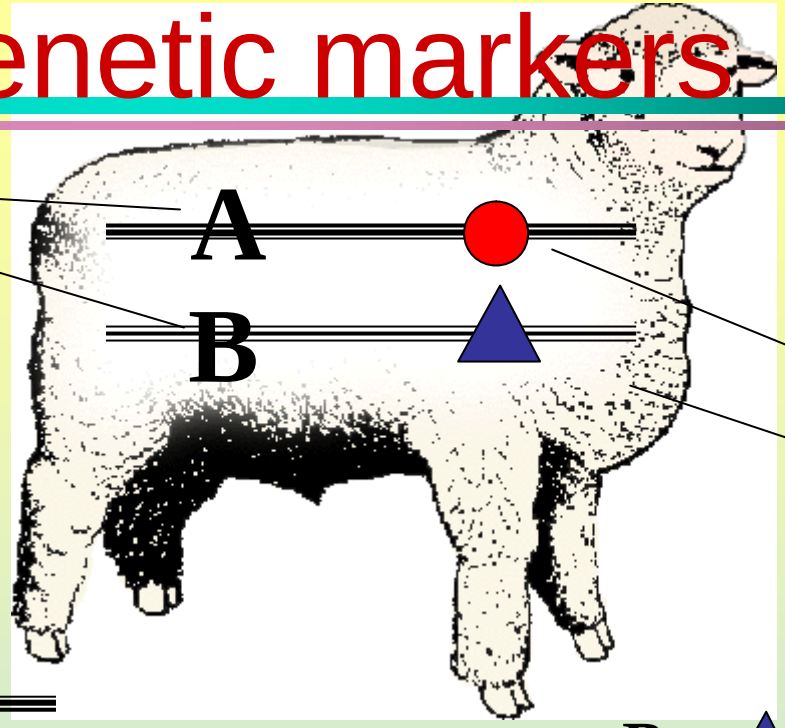
How it works

- Indirect markers
- Direct markers

Indirect genetic markers

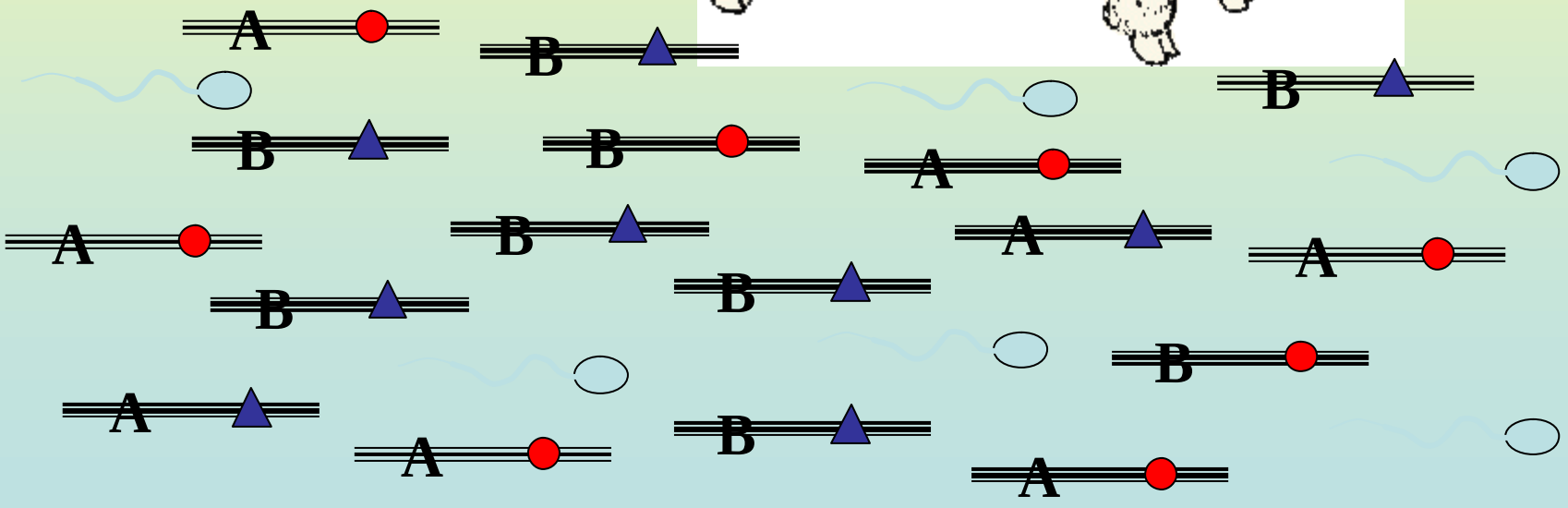
Marker gene alleles

A Ram:



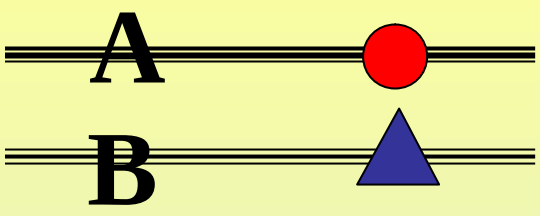
Major gene alleles

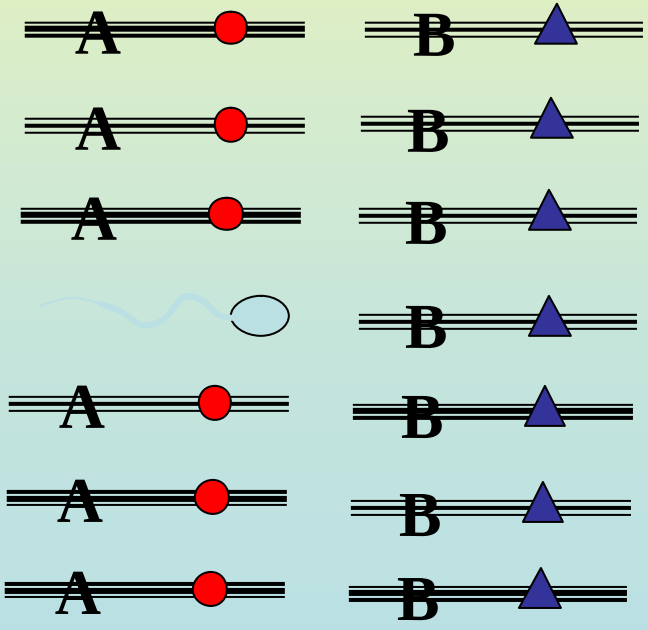
His semen:

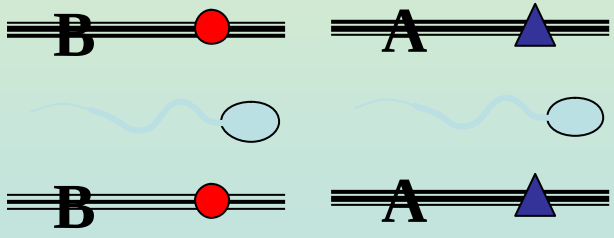


Indirect genetic markers

Can select among offspring ...



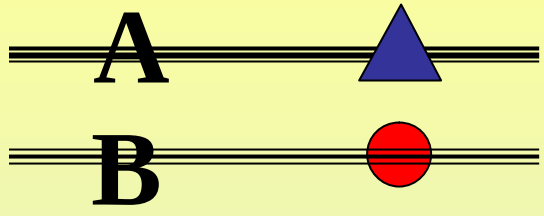


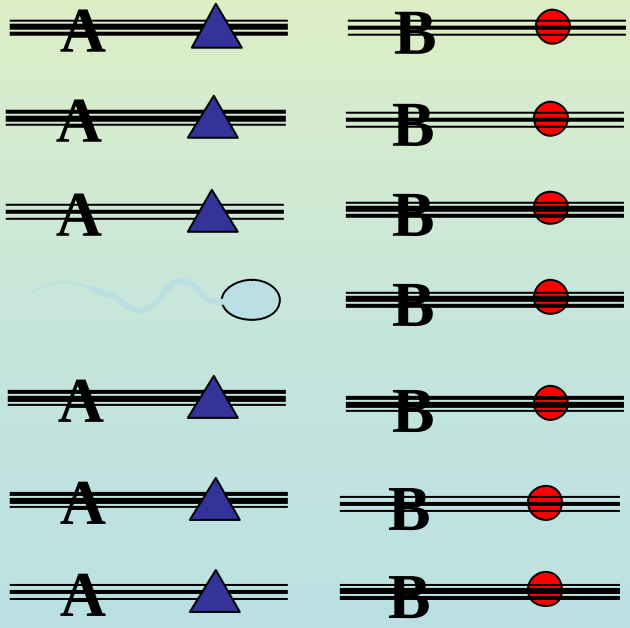


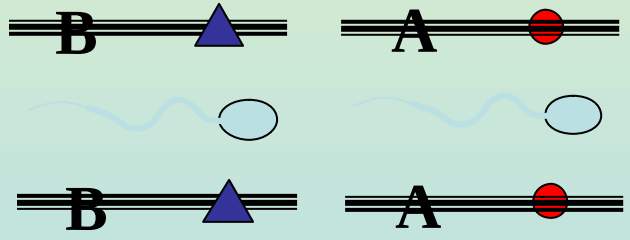
‘recombinants’

Indirect genetic markers

Phase can be opposite

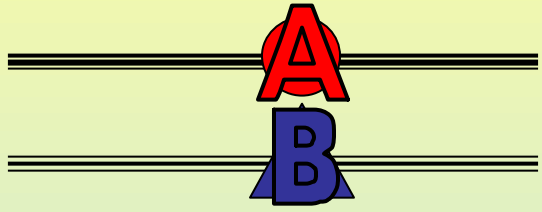






‘recombinants’

Direct genetic markers



We like to find the actual mutations!

A **- always circle, always good**

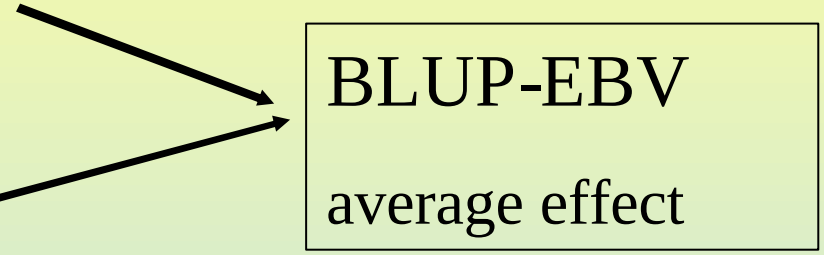
B **- always triangle, always bad**

Selecting for QTL genotypes

- Increase desired allele frequency at QTL
- Introgressing them into lines
- In addition to polygenic selection

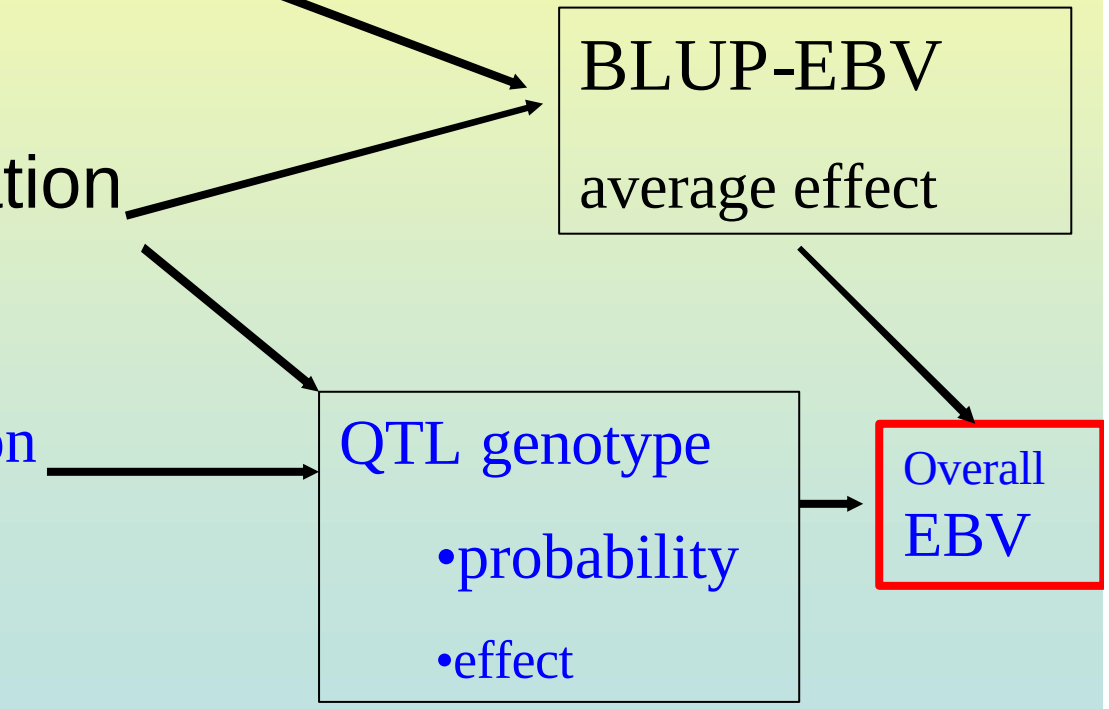
Normal Genetic Evaluation

- Performance information
- Pedigree information



Genetic Evaluation with QTL

- Performance information
- Pedigree information
  - Marker information



Effect of MAS on rate of genetic gain

	Selection *after* recording		Selection *before* recording	
	Gen 1	Gen 5	Gen 1	Gen 5
$h^2 = 0.11$, $V_{QTL}=0.33$	+21%	+6%	+45%	+23%

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Meuwissen and Goddard, 1996

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$h^2 = 0.27$, $V_{QTL}=0.11$	+1.3%	+1.3%	+8%	+6%

Meuwissen and Goddard, 1996

Conditions that are good for Marker Assisted Selection

- Where heritability is low
  - e.g. fertility, nr. of lambs
- Where the trait is sex limited.
  - e.g. maternal effects, fertility, nr. of lambs
- Trait not measurable before first selection
  - e.g. longevity, micron blowout, fertility.
  - Most traits when using juvenile selection.
- Trait is difficult to measure.
  - e.g. disease resistance, recessive conditions, feed efficiency pigmented fibres, carcass traits

Discussion on simulation studies

- They assume response in one trait
  - Need whole breeding objective context
  - More a matter of *shifting response between traits* rather than increasing overall response

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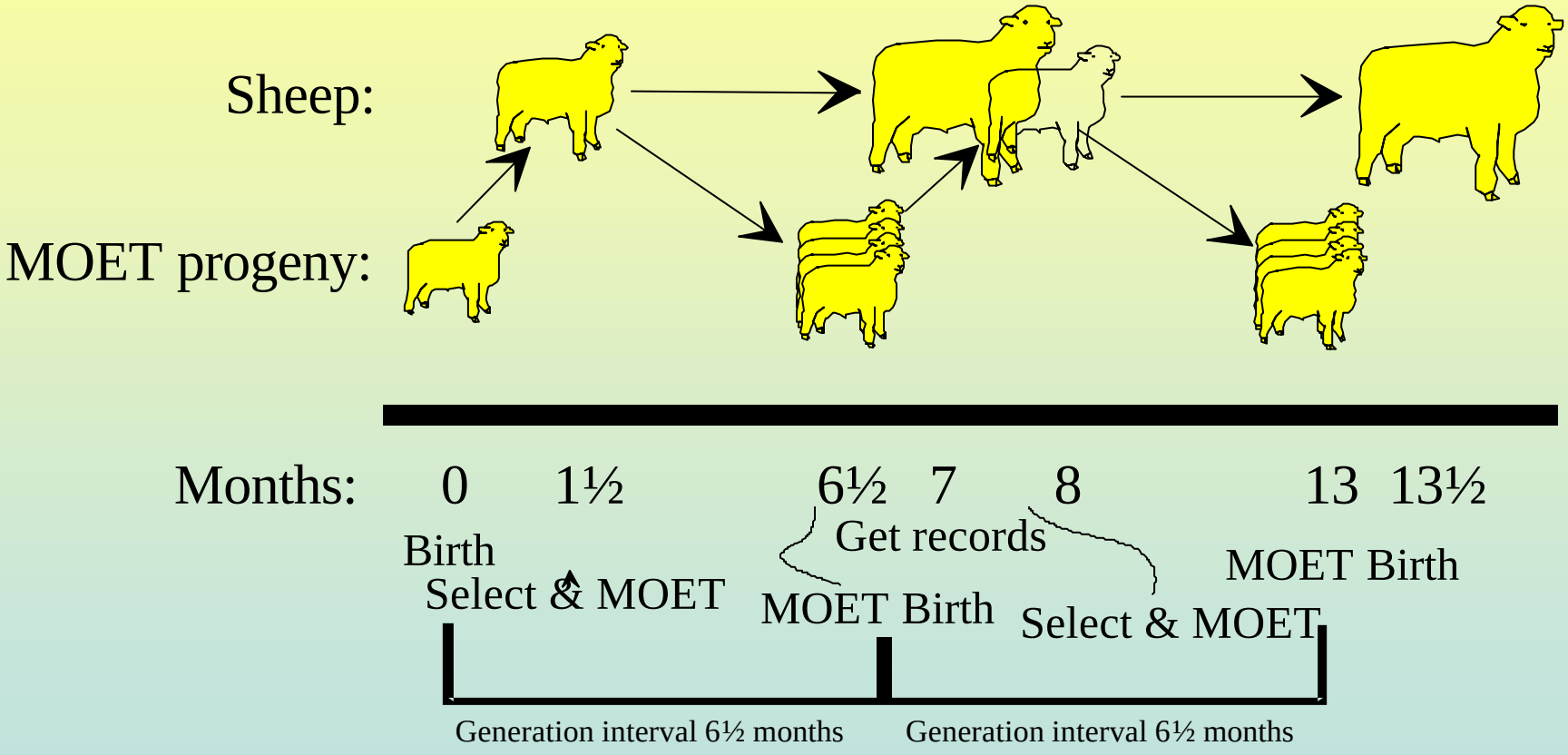
- They assume response in one trait
  - Need whole breeding objective context
  - More a matter of *shifting response between traits* rather than increasing overall response
- They assume abundant recording of pedigree and gene testing
  - Will we have cheap DNA testing available?
  - We can apply strategies to save on genotyping.
  - Some degree of phase-testing is needed
- They assume gene effects are known
  - Need monitoring by measurement

Conclusion on MAS

- Effect on extra gain in breeding programs maybe limited to cases where
  - There are special genes with large effect
    - Disease resistance, Booroola, etc.
  - Breeding objective traits are difficult to measure
    - Carcass Traits, Feed Efficiency, Disease
  - When reproductive technologies are used

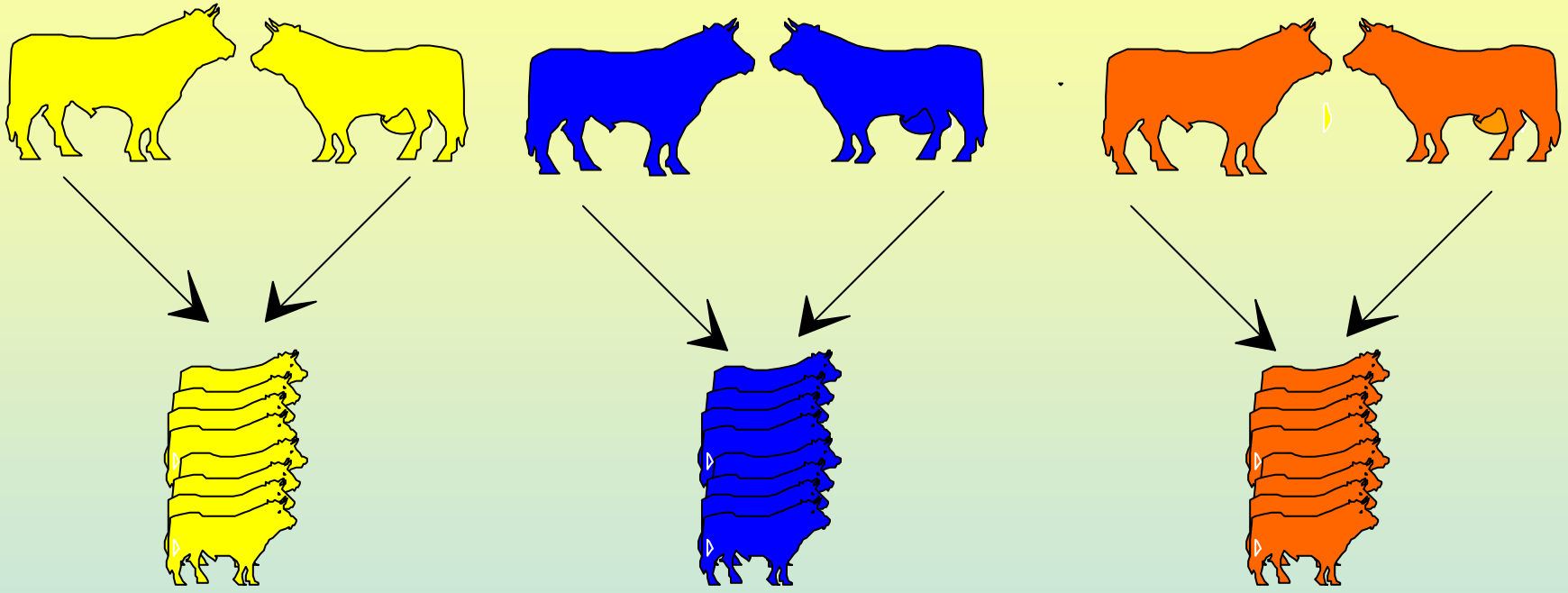
Juvenile sheep MOET/JIVET



More offspring of top ewe *before* testing it

Select based on parent average

Between versus within family selection



No own information (performance or genotype):

Selection based on parent average

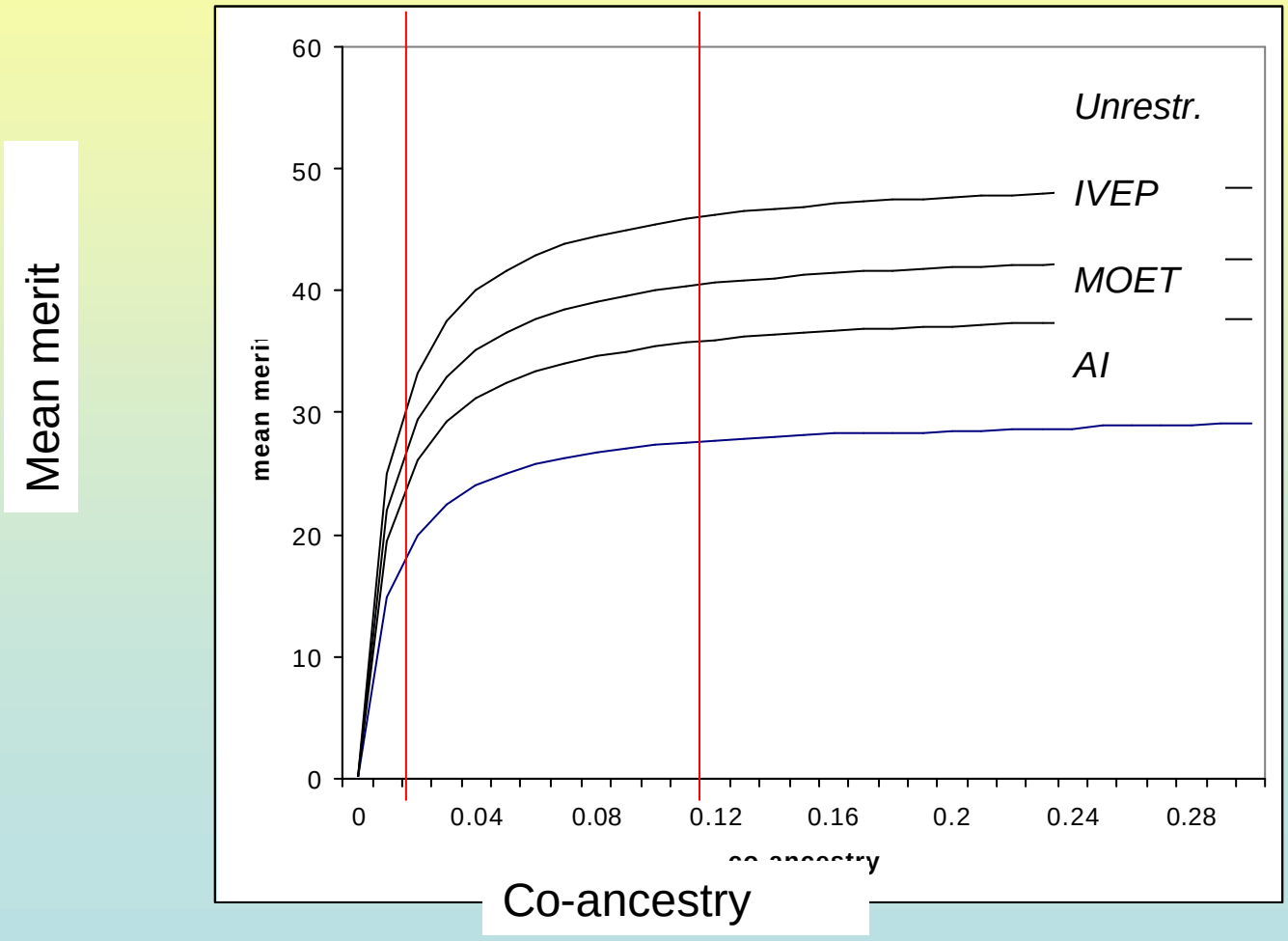
More between-family selection - ***more inbreeding***

Genetic gain versus genetic diversity

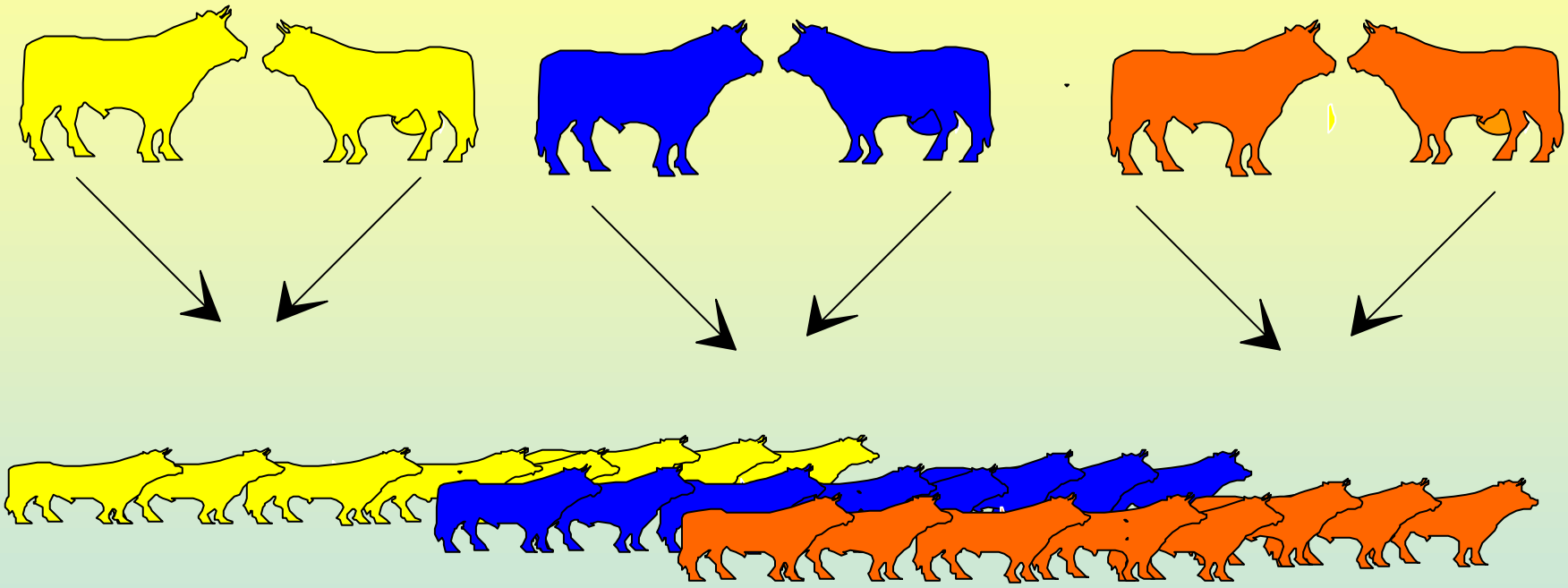
- Sustainable breeding programs require optimal selection balancing genetic gain and genetic diversity

- Potential short term benefits from reproductive technologies are inhibited by the need to maintain diversity

The balance between increased merit and inbreeding



Between versus within family selection



Own information (performance or genotype):

More variation within families

More within-family selection – ***less inbreeding***

MAS combined with reproductive technologies

- Genotype testing provides within family information

- Exploiting this variation allows early selection and genetic gain without jeopardizing inbreeding

Modelling Genotype Information in Beef Cattle Selection for RFI

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Australian Beef Breeding Objectives

- Growth
- Reproduction
- Feed Efficiency - RFI
- Carcass quality characteristics
  - MARBLE SCORE
  - TENDERNESS/PALATABILITY

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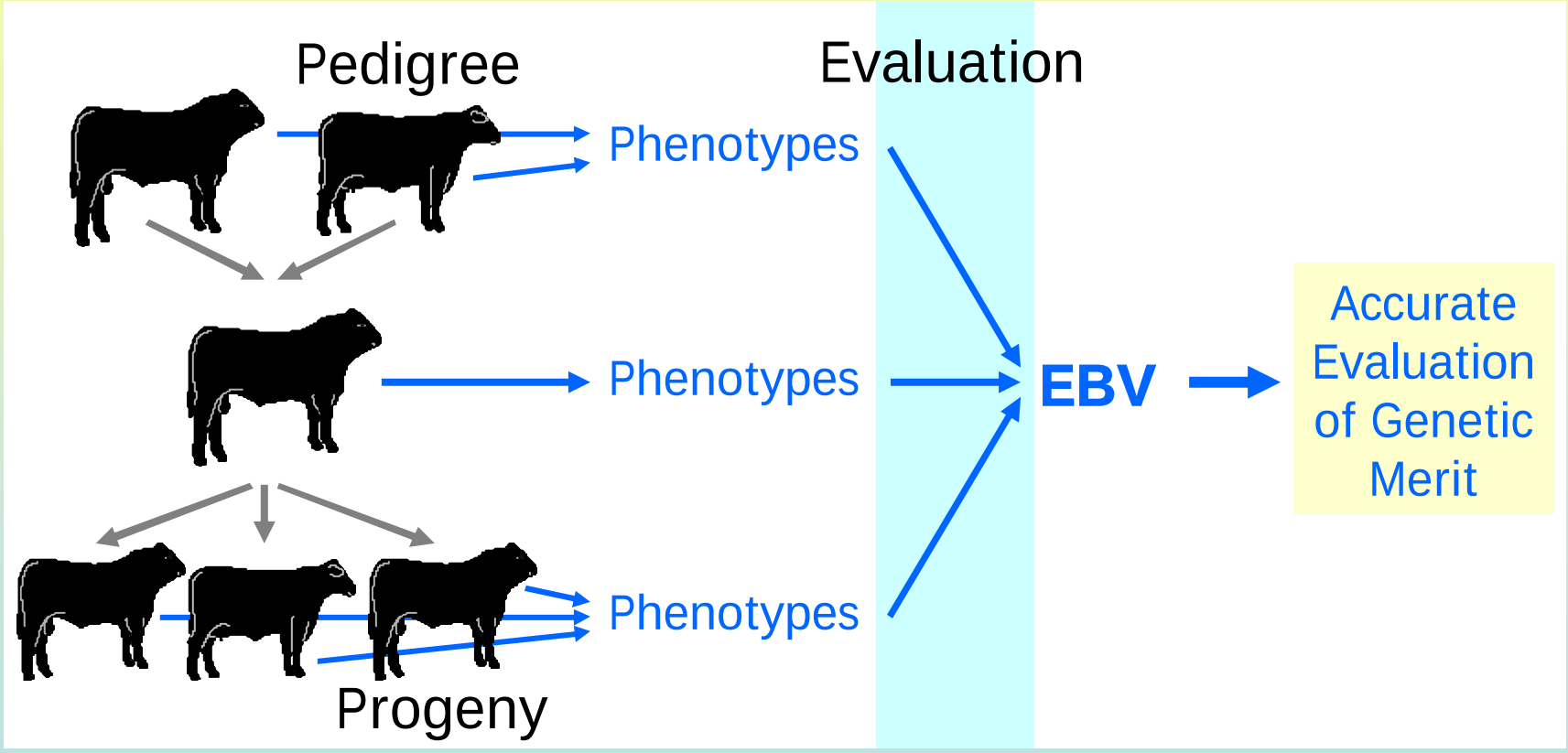
Residual Feed Intake (RFI)

Aim :

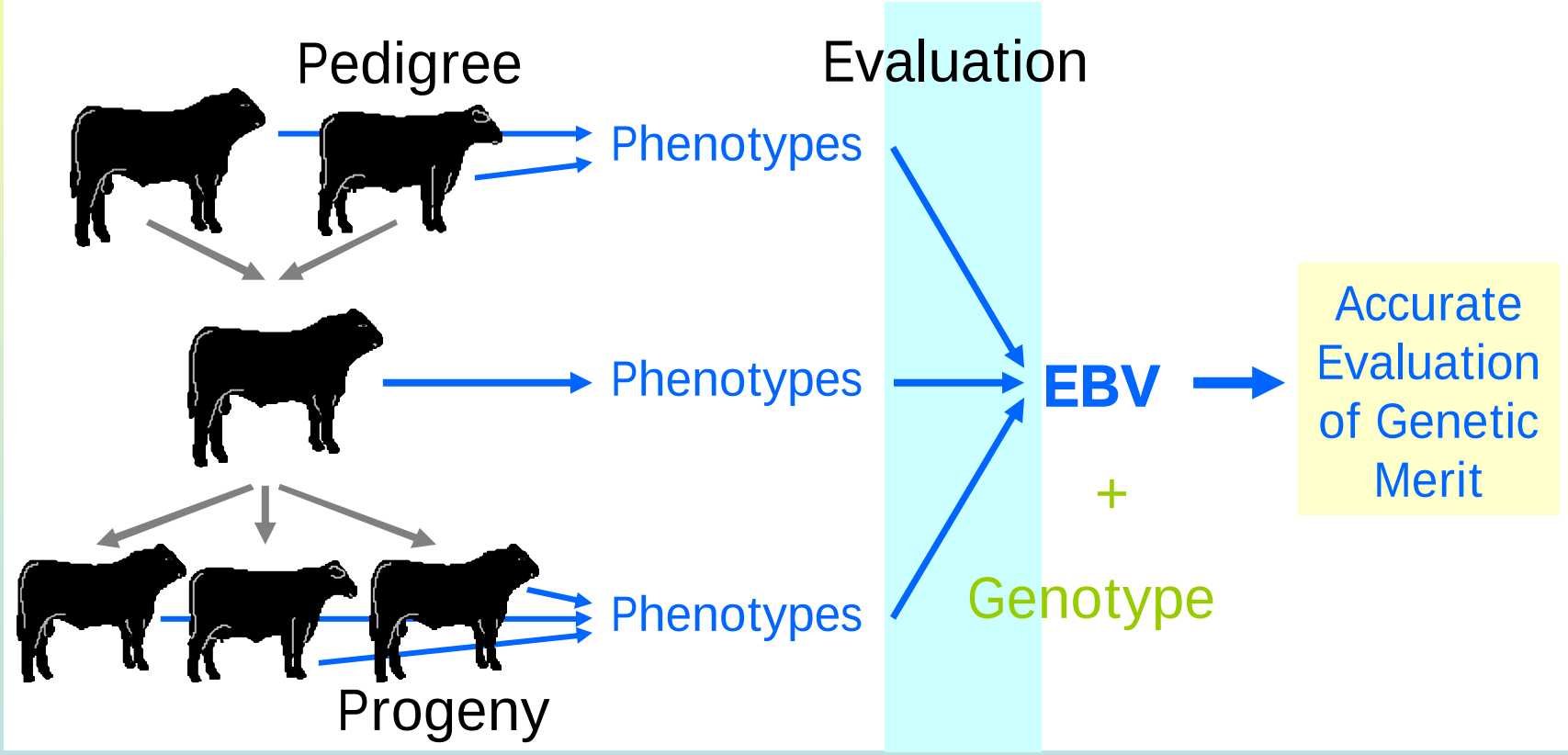
To model the change in response due to RFI QTL and model different selection strategies

- Residual feed intake – measure of the efficiency of an animal
- Heritable (0.39)
- Expensive to measure
  - 71 day feeding trial

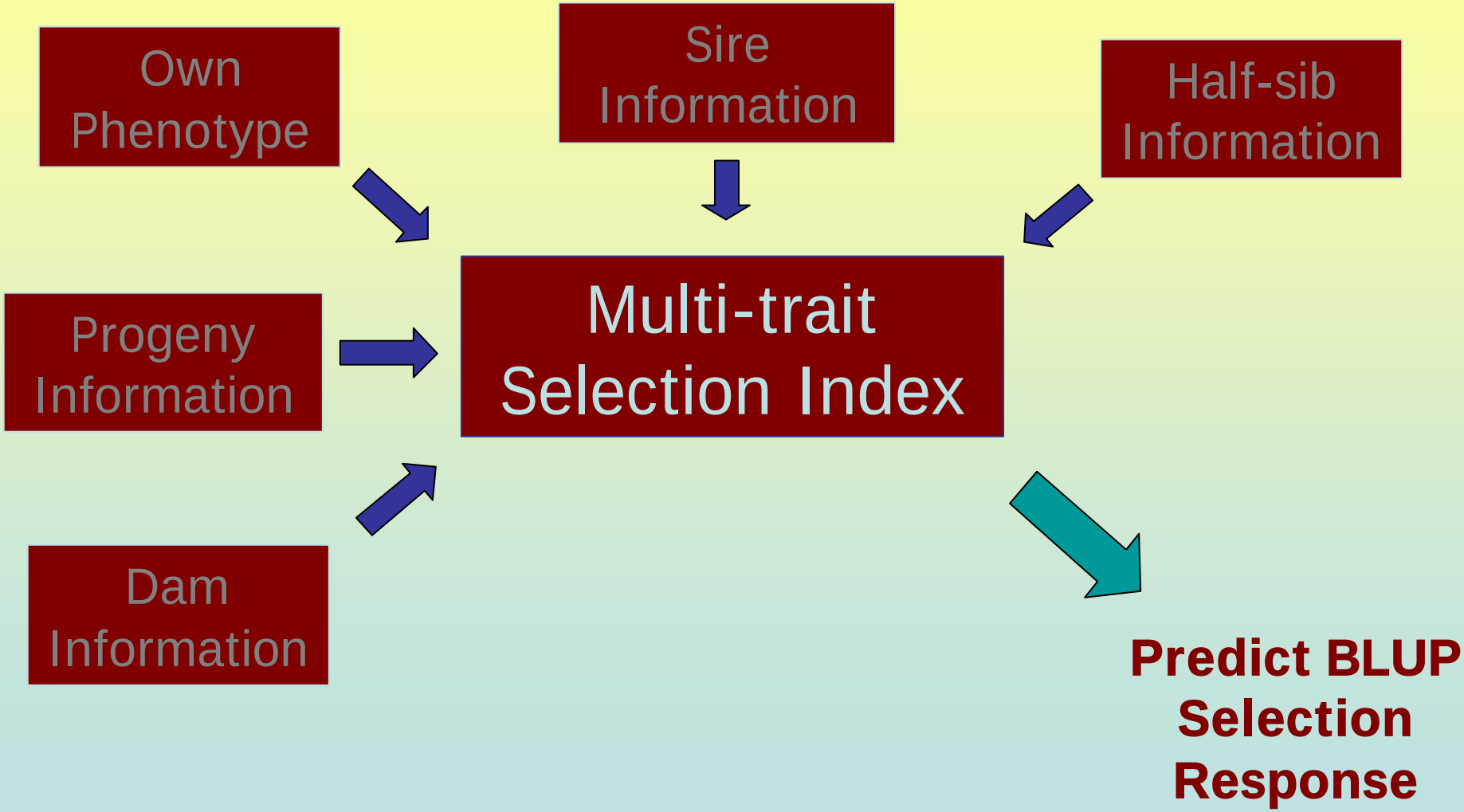
Current Genetic Evaluation



Genotype Notification



Method: Pseudo-BLUP Selection Index



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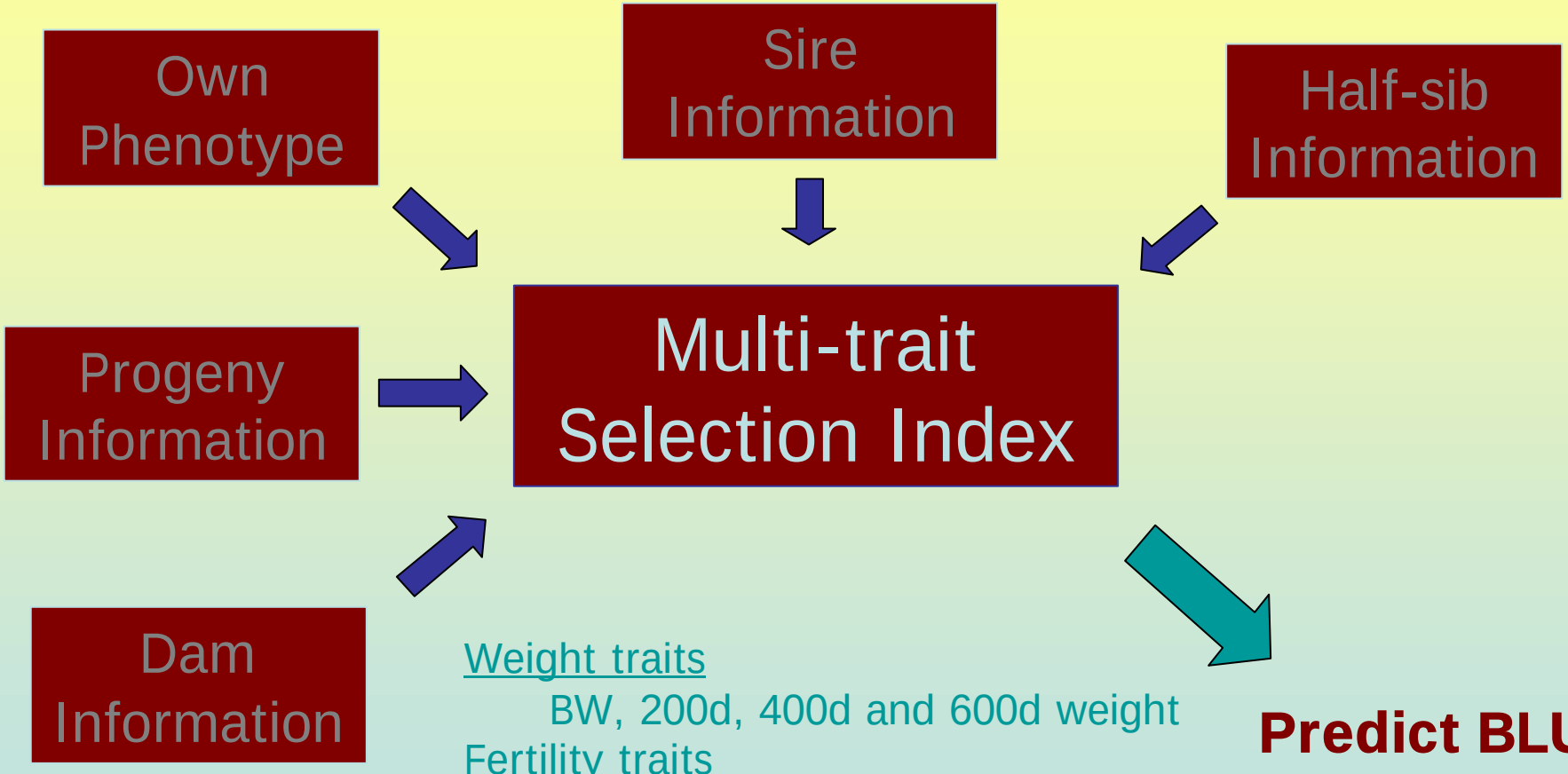

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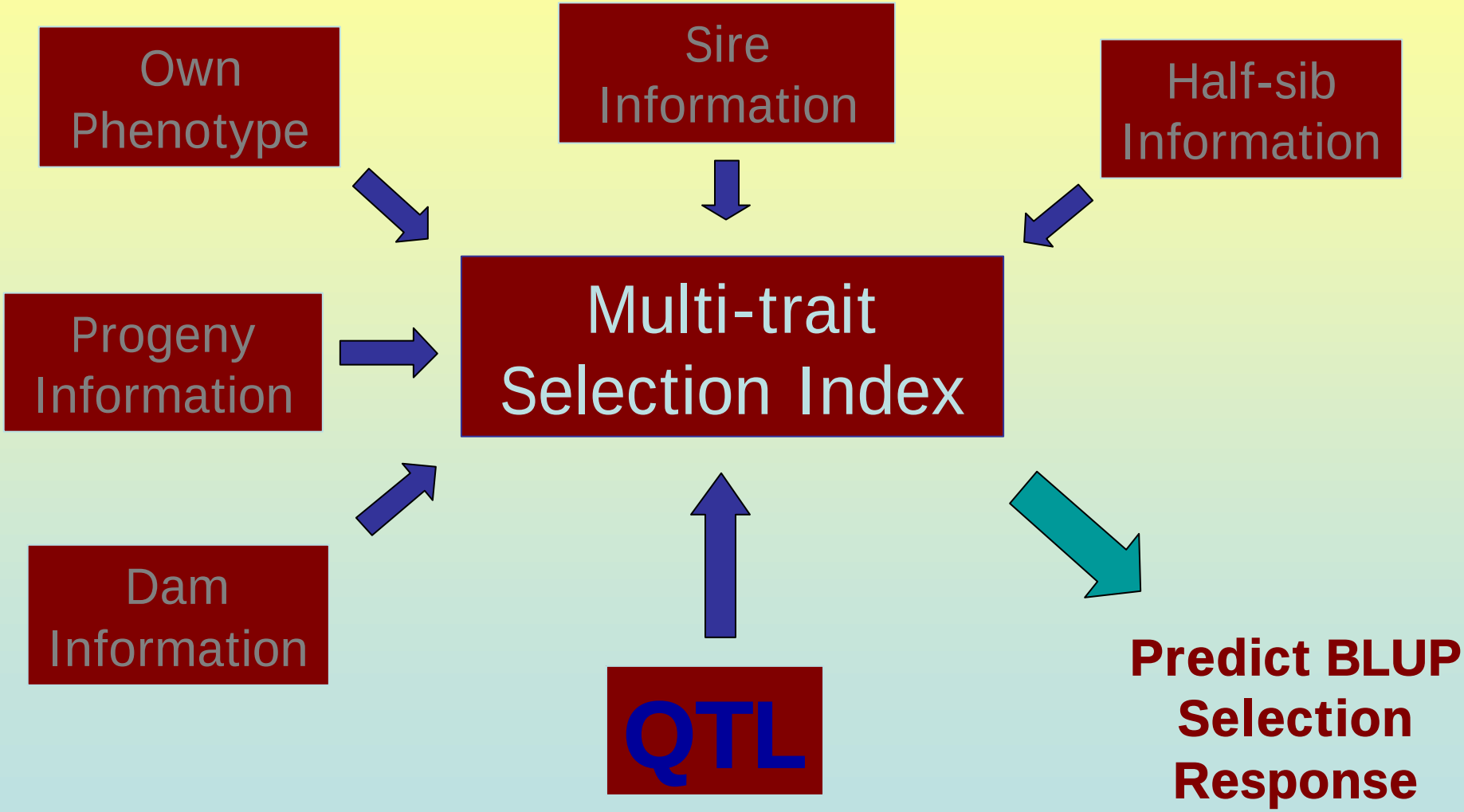
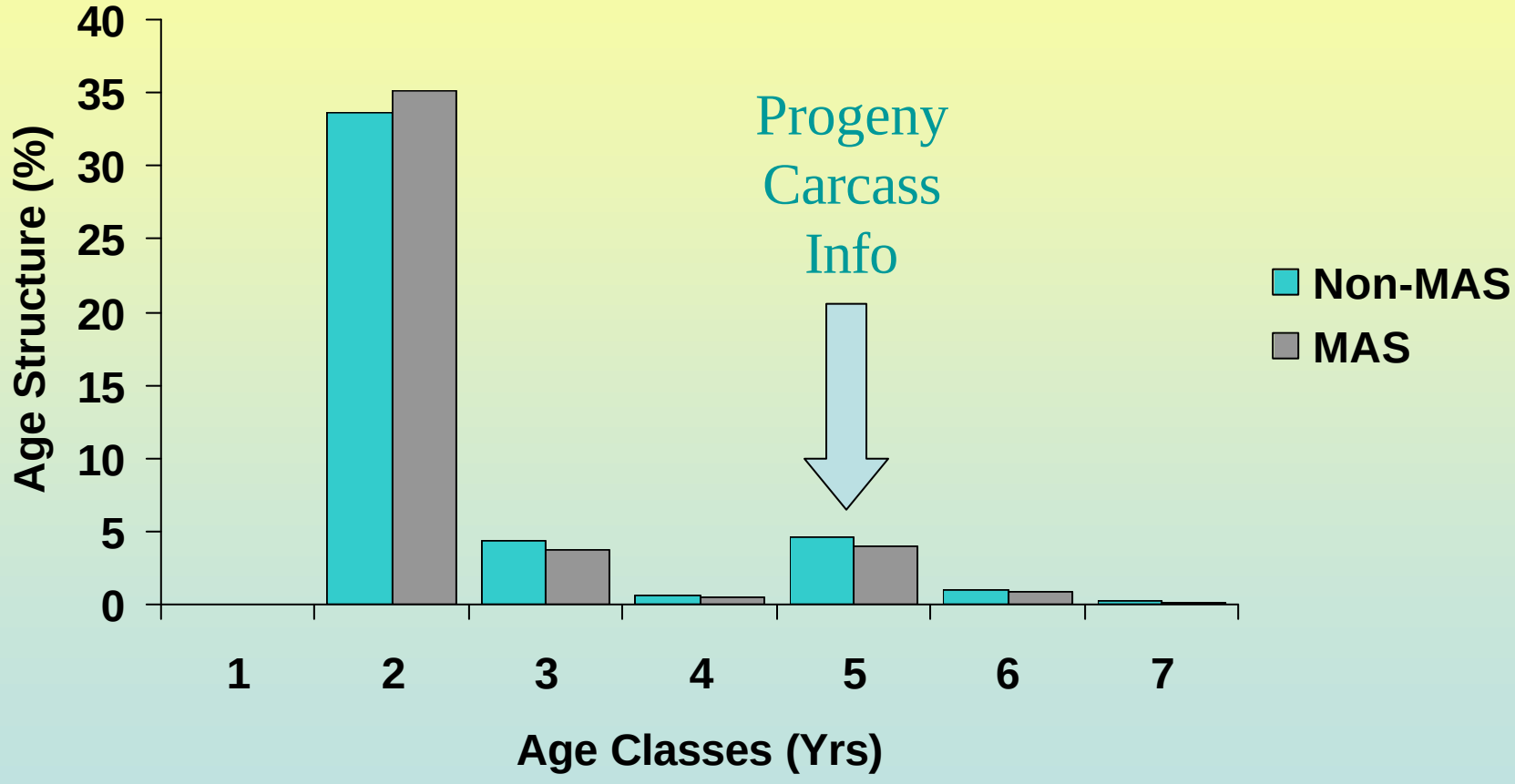
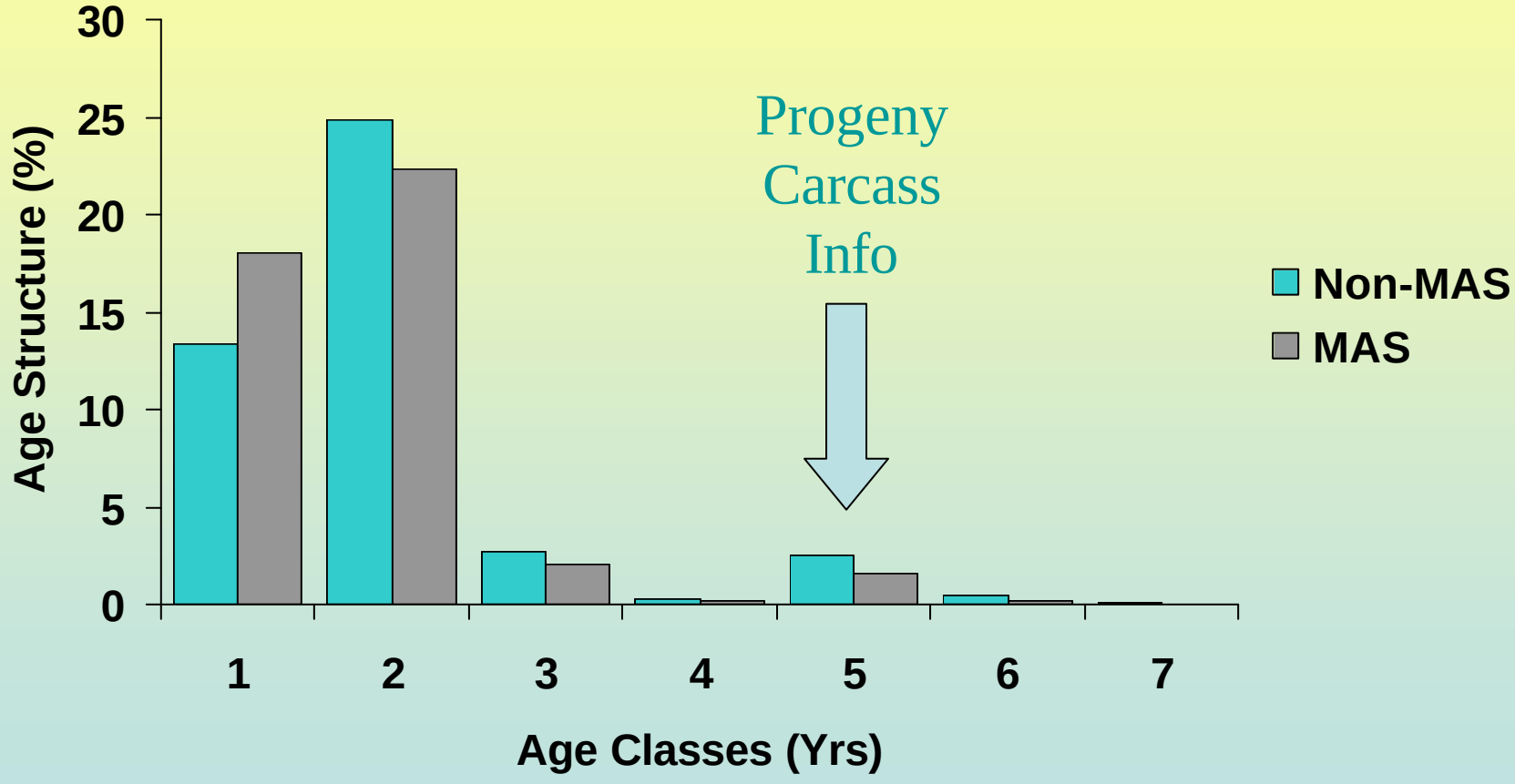


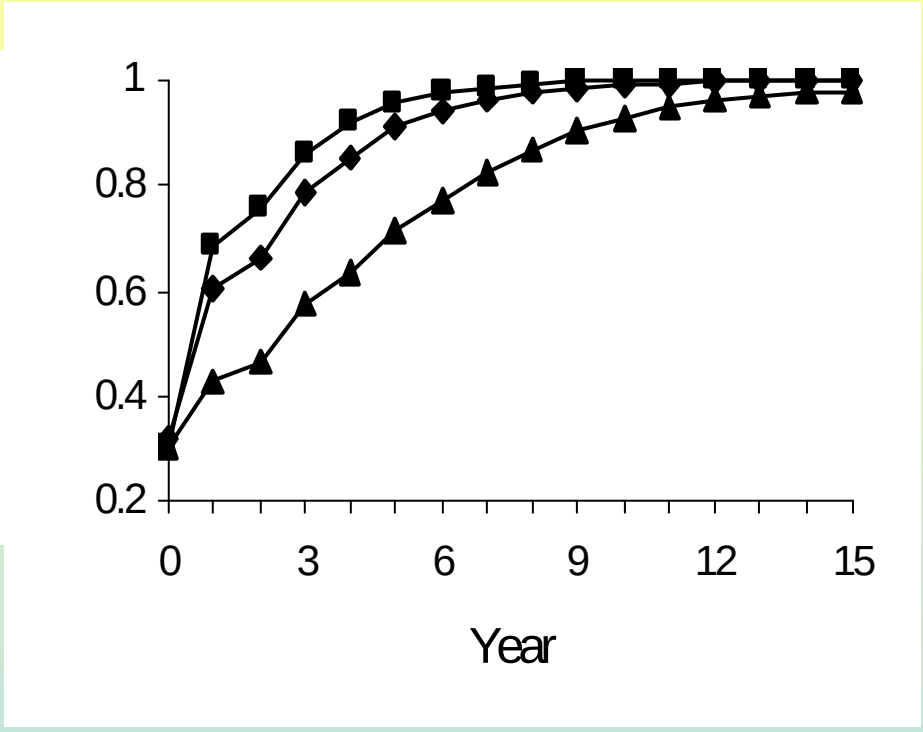
Population Structure – Selection from 2 years



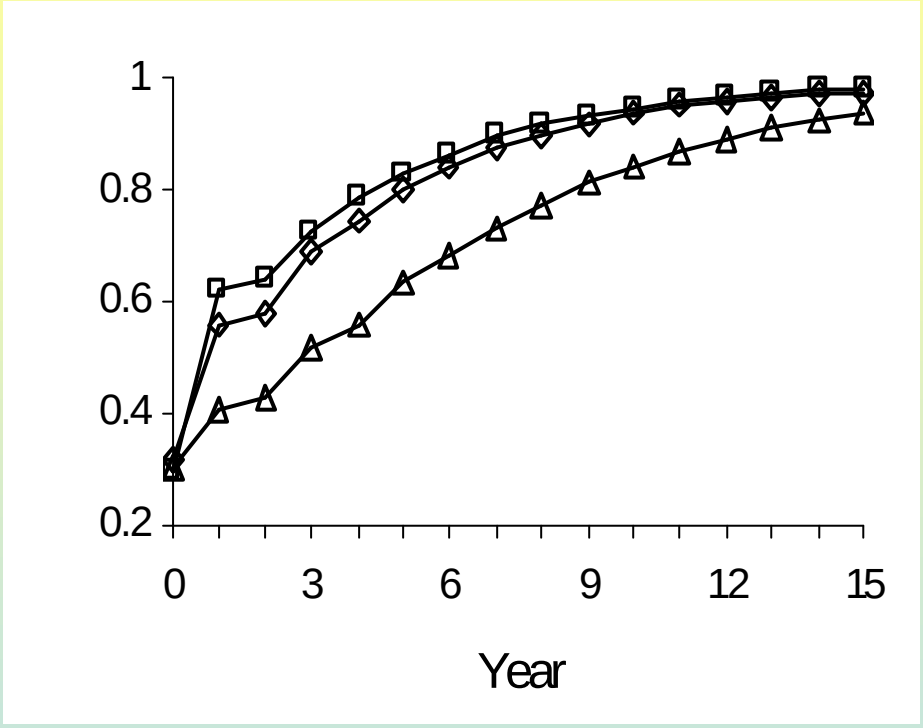
Population Structure – Availability Year 1 = 30%



Change in Gene Frequency



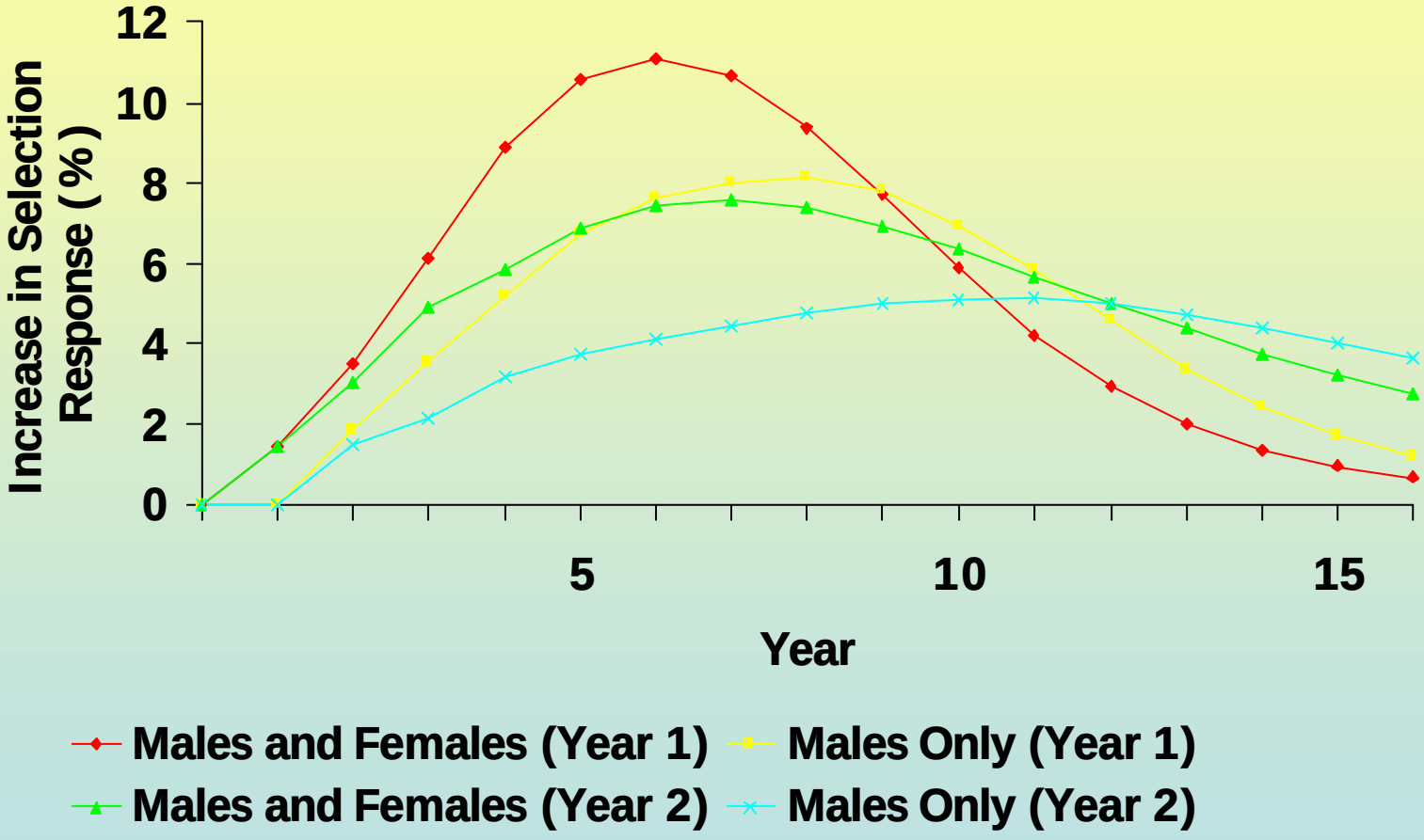
Male and Female Genotyping



Male Only Genotyping

Available for selection from 1 Year of Age

Increase in Annual Selection Response – Large QTL



Take home message

- Genotyping benefits depend on:
  - Gene inheritance
  - Genotype costs
  - Size of the gene effect
- As RFI is moderately heritable QTL the value of marker is decreased considerably if early selection not used.
- Optimisation of age structure is important