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SALMON BREEDING PROGRAM IN THE GENOMIC ERA, QTLS OR GENOMIC SELECTION ?

Sergio Vela Avitúa

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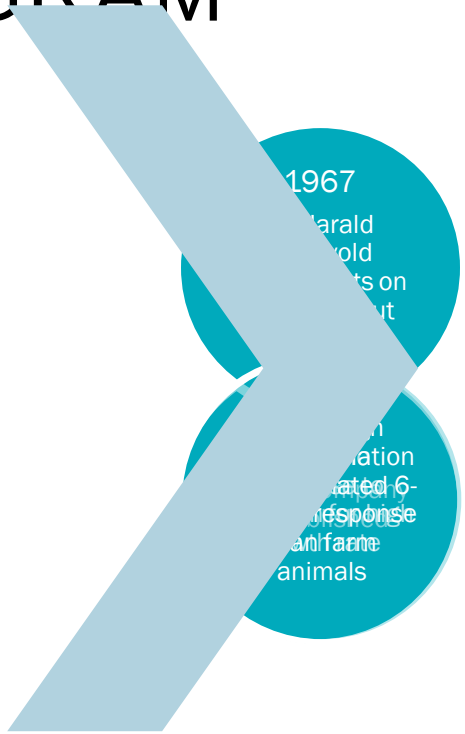
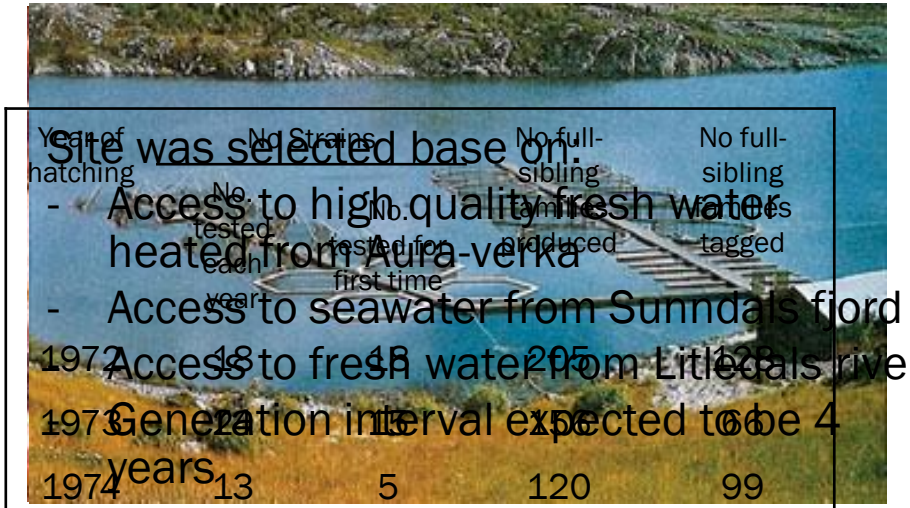
THE FIRST SALMON BREEDING PROGRAM



1973



Site was selected base on:

- Access to high quality fresh water heated from Aura-verka
- Access to seawater from Sunndals fiord
- Access to fresh water from Litledals river
- Generation interval expected to be 4 years

Year of hatching	No. Strains tested each year	No. tested for first time	No full-sibling families produced	No full-sibling families tagged
1972	18	18	205	128
1973	24	16	156	66
1974	13	5	120	99
1975	8	3	240	149
Total	63	41	721	442

Sunndalsøra Andelslag

Gjedrem, 2010

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THE FIRST SALMON BREEDING PROGRAM: LEARNING THE BASICS

- Broodstock was obtained from diferent rivers
- Each male fertilized 3-4 females (full and paternal half sibs)
- Approx. 12 full-sibling families per river
- Number of individuals standardized
- Common rearing up to marking (10-15g)
    - Common rearing represented 2.5%-6.4% of total variance in body weight and less than 1% of total variance at market size

Gjedrem, 2010

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THE FIRST SALMON BREEDING PROGRAM: LEARNING THE BASICS

Evaluations

- Phenotypic variation
- Heritabilities
- Heterosis
- Inbreeding
- Genotype-environment
- Survival and product quality
- Feed conversion rate

Gjedrem, 2010

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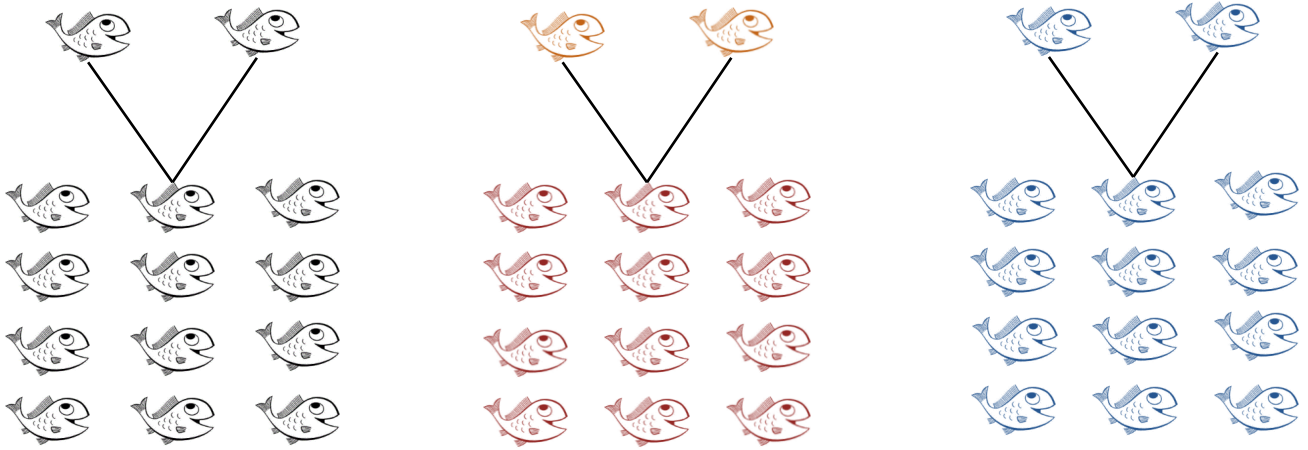
FAMILY BASED BREEDING PROGRAMS



Select candidates based on the performance of their relatives

Test for diferent traits

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FAMILY BASED BREEDING PROGRAMS

- Reduced generation interval when compared to progeny test
- Allow to select for traits not possible to evaluate in candidates:
    - Disease related traits (biosecure)
    - Quality traits
- Makes use of the high fecundity of fish
- Requires special facilities (expensive)
- Exploids only between family differences

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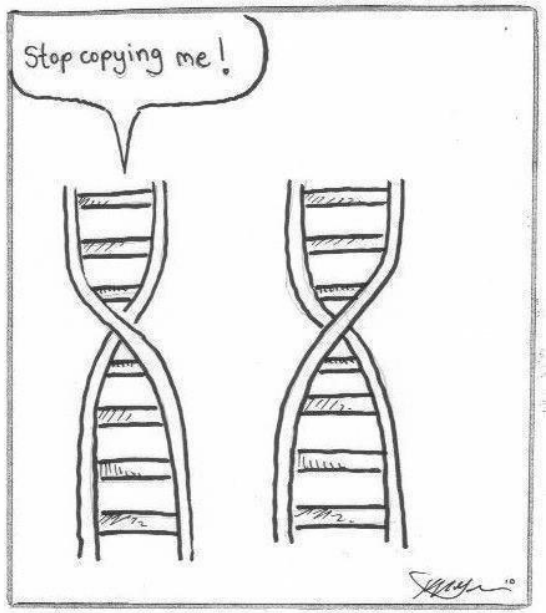
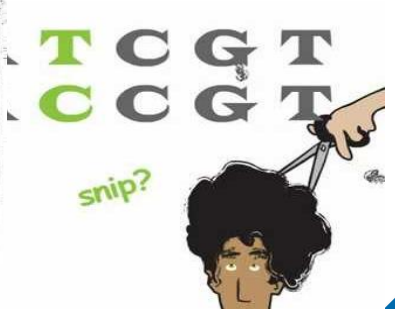
GENOTYPING, DNA SEQUENCING AND GENOMIC REVOLUTION

- Allozymes
- PCR based methods
  - Microsat
  - Restrictic
    polymorp
  - Randoml
    Polymorp
  - Amplifiec
    Polymorp
- Single Nucleotid





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MARKER-ASSISTED SELECTION:

Uses markers throughout the genome to estimate gene effects to identify Quantitative trait locus (QTLs), which are genes that explains most or a large proportion of the variation.

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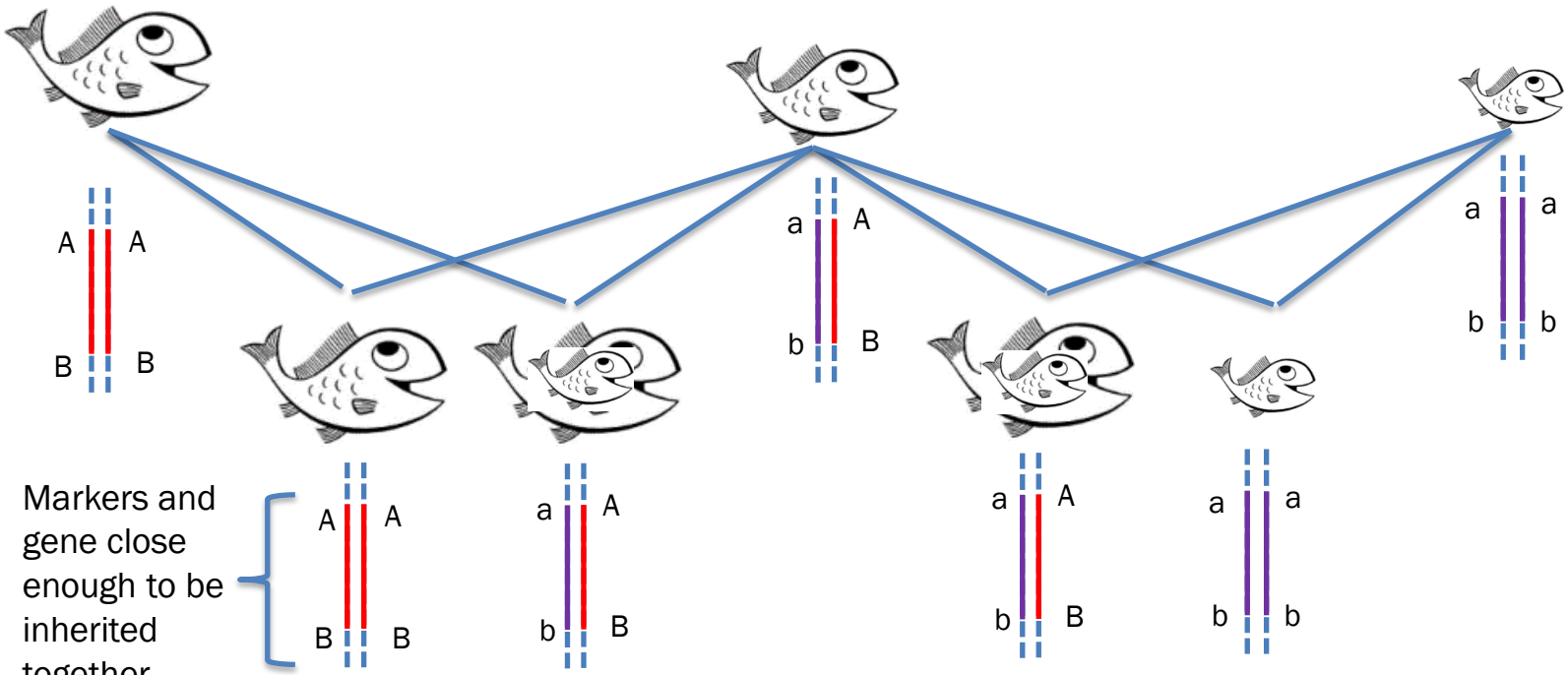
QUANTITATIVE TRAIT LOCI



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QUANTITATIVE TRAIT LOCI

The susceptibility of Atlantic salmon fry to freshwater infectious pancreatic necrosis is largely explained by a major QTL

R D Houston, C S Haley, A Hamilton, D R Guy, J C Mota-Velasco, A A Gheyas, A E Tinch, J B Taggart,

- Both studies coincide on the location of the QTL (linkage group 21)

- QTL explained most of variance for IPN-resistance
  - 23% to 51% of phenotypic variance
  - 83% to 99% of the genetic variance

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QUANTITATIVE TRAIT LOCI

Marine Biotechnology

Original Article | OPEN

Mapping and validation of a major QTL affecting resistance to pancreas disease (salmonid alphavirus) in Atlantic salmon (*Salmo salar*)

S Gonen, M Baranski, I Thorland, A Norris, H Grove, P Arnesen, H Bakke, S Lien, S C Bishop & R D Houston

Heredity (2015) **115**, 405–414 (2015)
doi:10.1038/hdy.2015.37

Received: 21 October 2014
Revised: 22 February 2015

94, 166–172 (2005)
doi:10.1038/sj.hdy.6800590

Accepted: 21 July 2004

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GENOTYPING DNA SEQUENCING AND GENOMIC REVOLUTION

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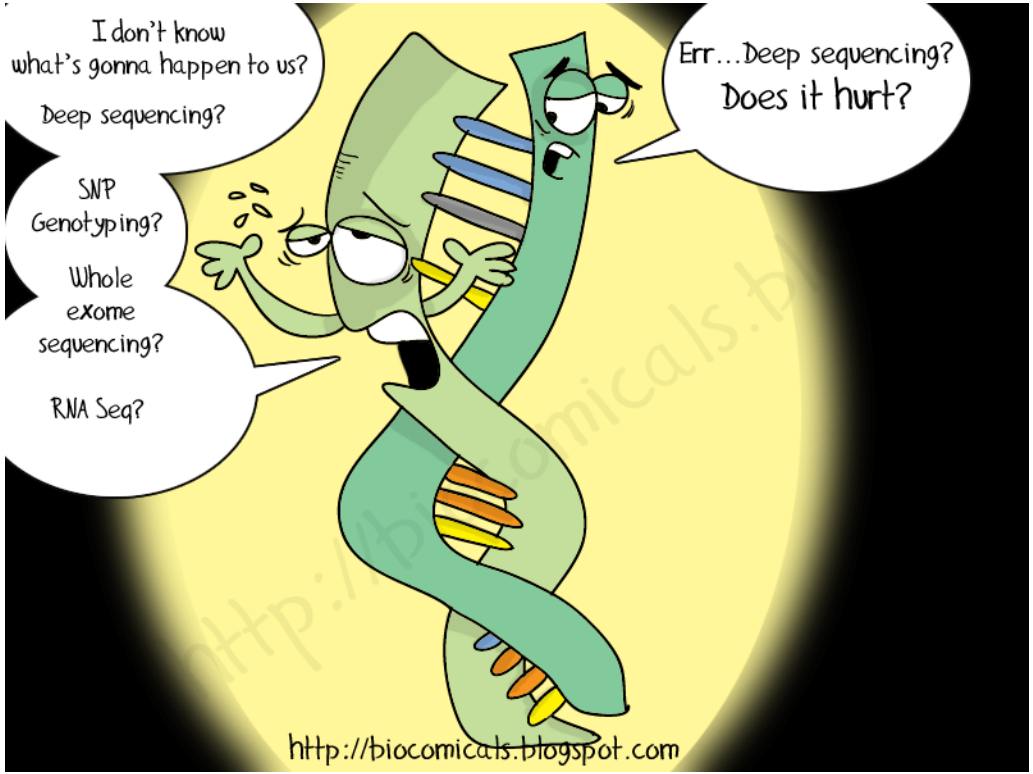

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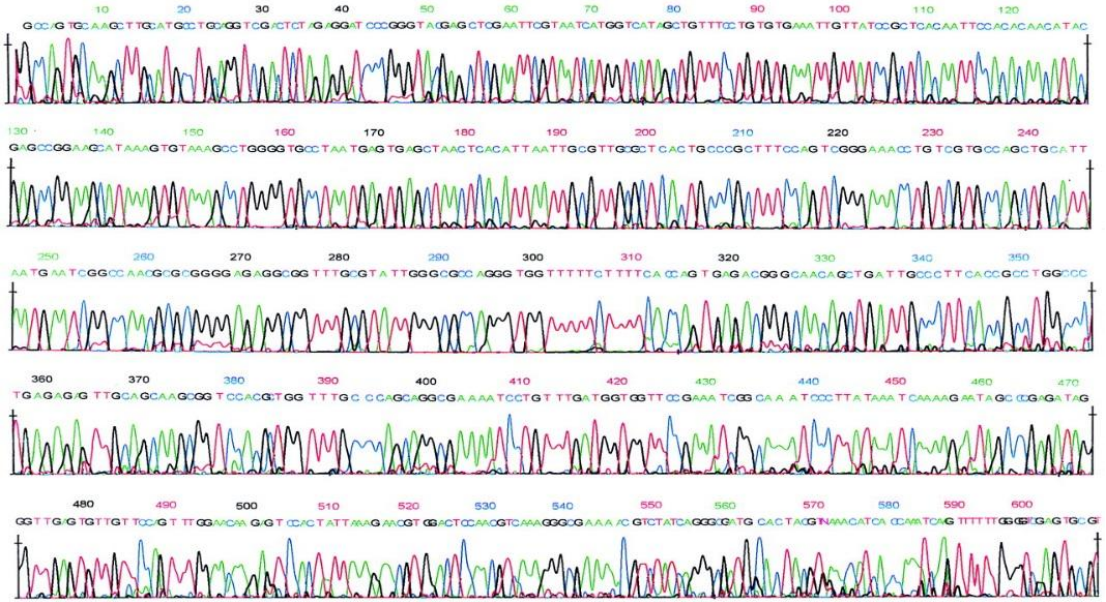
GENOMIC SELECTION

- With markers accross all genome, chances are that QTLs are close enough (in likage disequilibrium) with at least one marker



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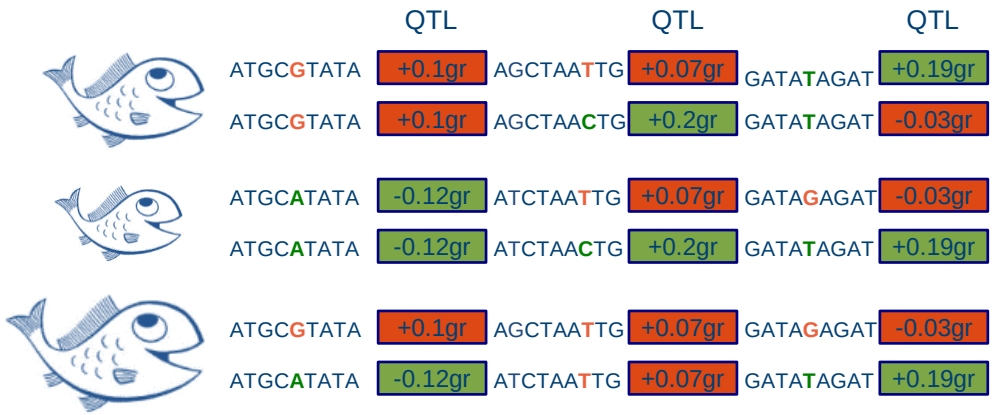
GENOMIC SELECTION



Then the sum of effects of all SNPs is the genetic value of the individual

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GENOMIC SELECTION

- Methods
  - BLUP
    - GBLUP: No marker effects estimated
  - Bayesian alphabet

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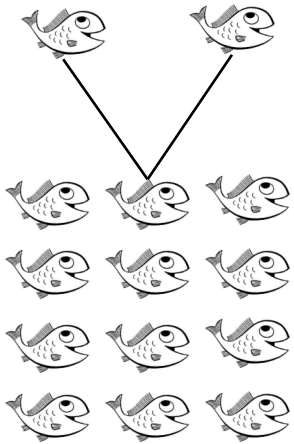
BREEDING PROGRAMS USING GENOMIC SELECTION



Individual genetic values are calculated for the candidates

Marker effects are calculated

Test for diferent traits
+
Genotypes

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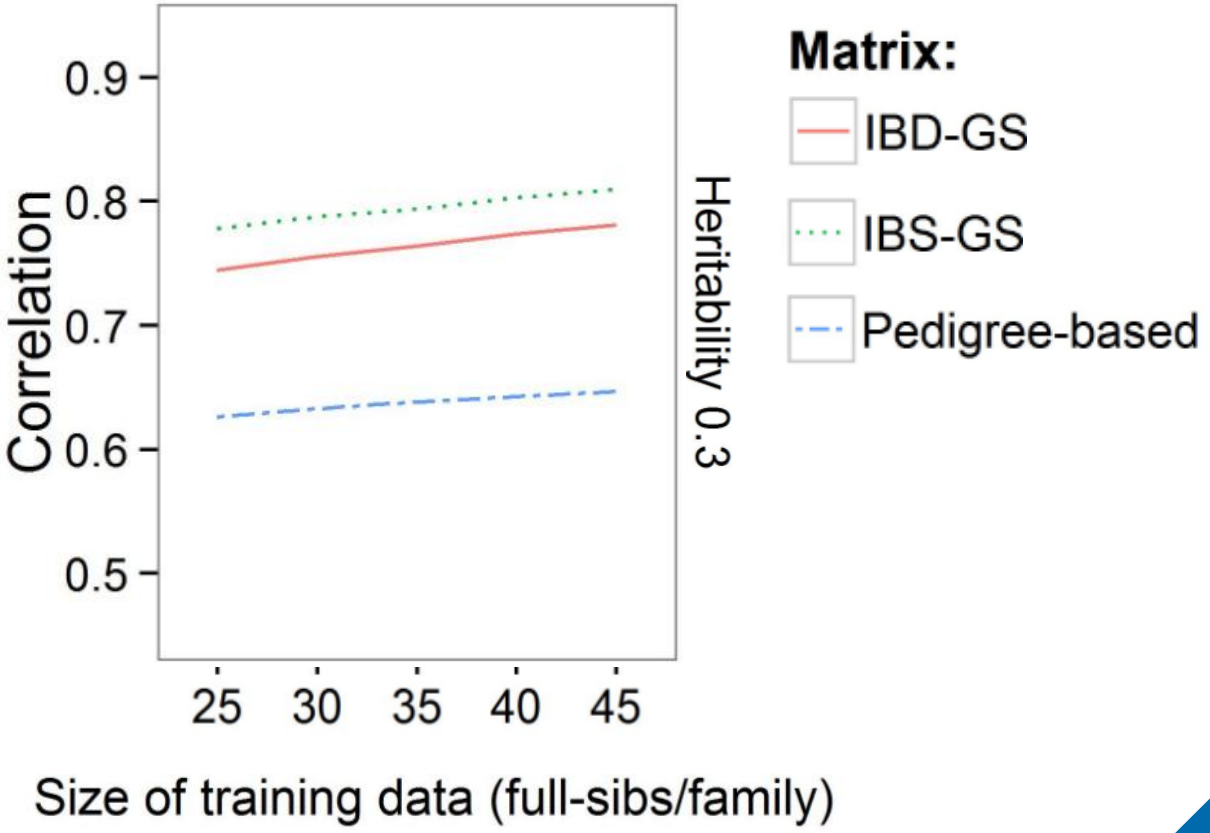
GENOMIC SELECTION: GBLUP SIMULATIONS



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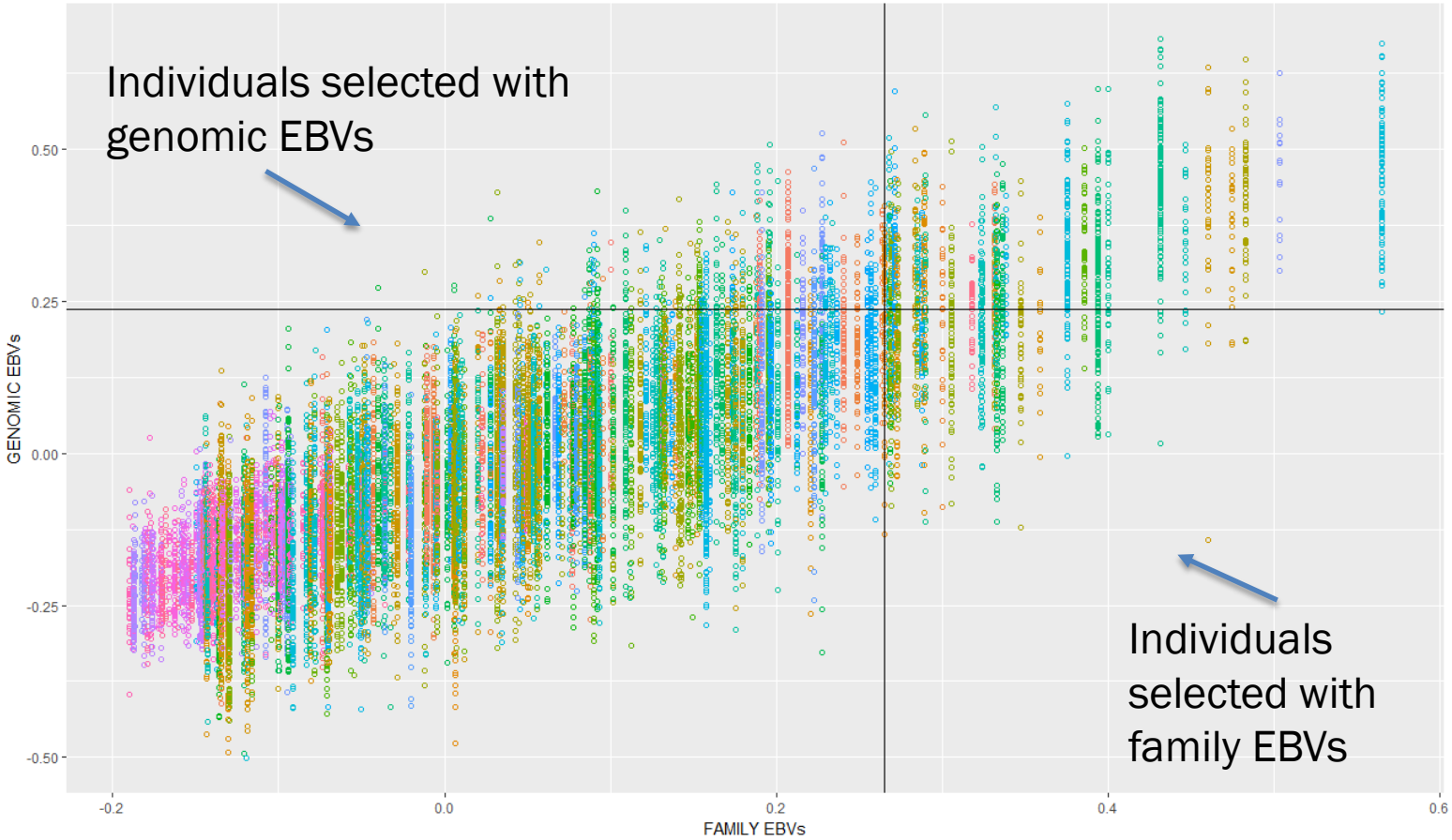
GENOMIC SELECTION VS FAMILY SELECTION IN ACTION



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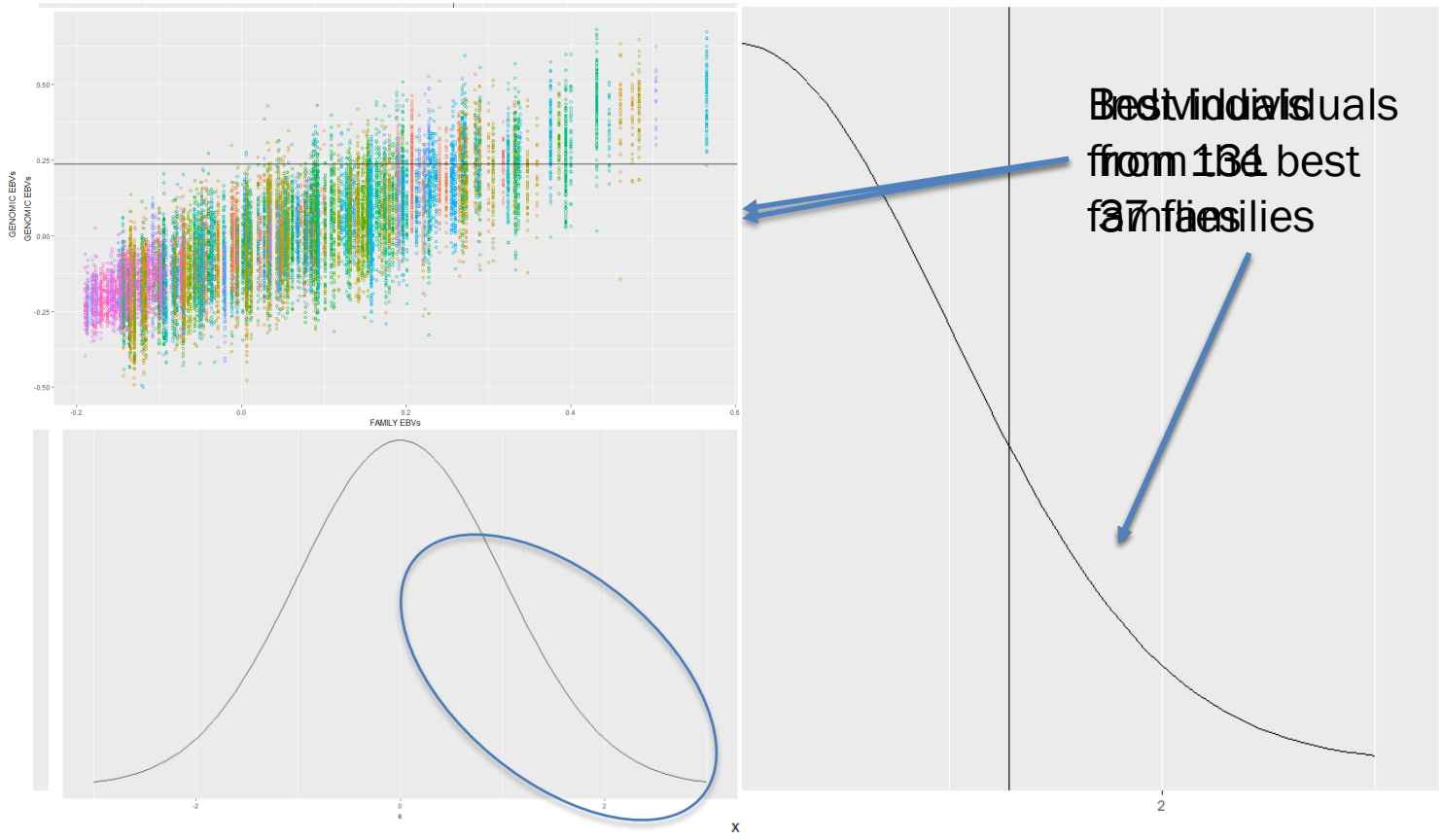
GENOMIC SELECTION VS FAMILY SELECTION: SELECTION DIFERENTIAL



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GENOMIC SELECTION VS FAMILY SELECTION

- Exploids the whitin family genetic component compared with family selection which cannot differentiate between relatives from the same family
- Higher genetic gain due stronger selection diferential
- Increased accuracy
- Reduce inbreeding: Individuals of families previously not selected can be selected due individual genetic values

- Requires large sets of individuals with both genotype and measured traits (phenotype)
- Genotyping is costly
- Benefits reduce if the trait is measure on candidates
- Questionable cost-benefit when applied to many traits

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GENOMIC SELECTION VS QTLS

- Prefered for polygenic traits
- Training data needs to be updated often (preferable every generation)
- GBLUP can use genotyped and ungenotyped data
- Requires dense genotyping of reference and candidate individuals

- Prefered for traits influenced by a small number of genes
- Estimated effects don’t need to be updated as often as in GS
- In theory selection can be done in one generation
- Only training population need to be dense genotyped
- Candidates genotyped only for markers linked to the QTL

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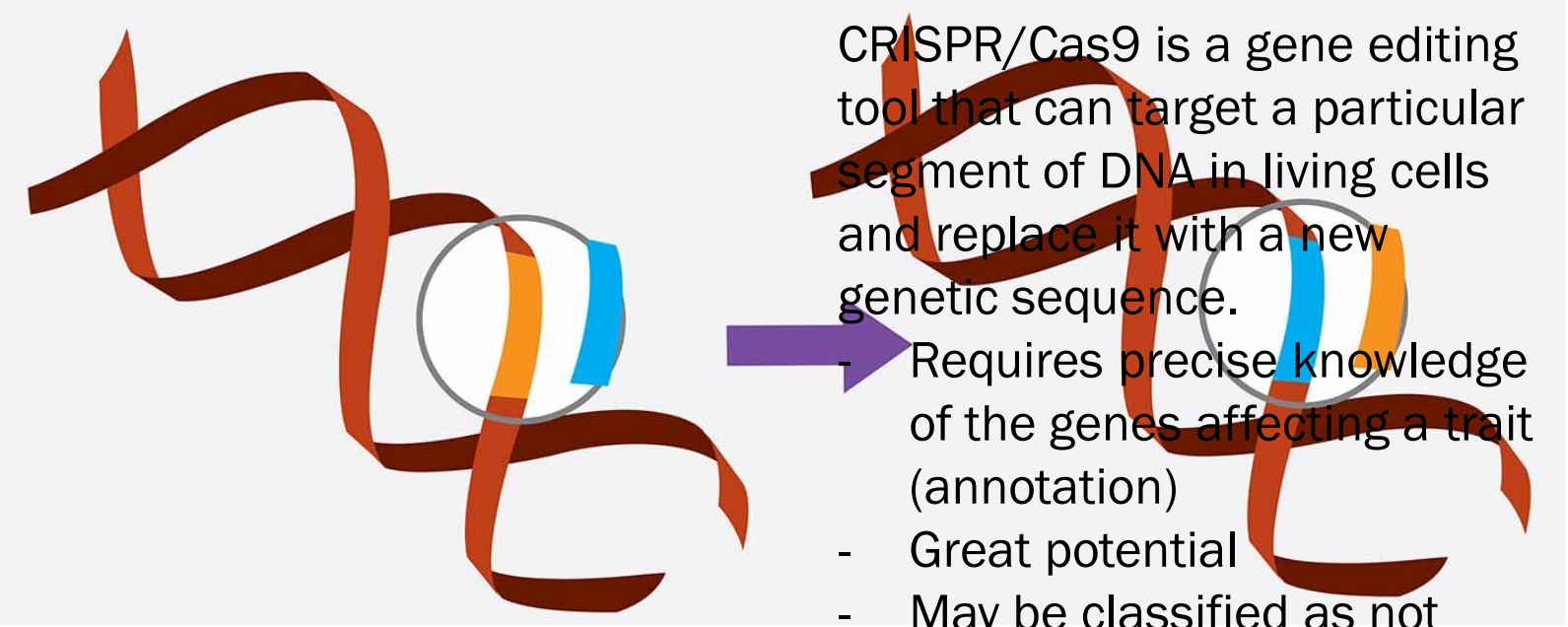
GENE EDITING



CRISPR/Cas9 is a gene editing tool that can target a particular segment of DNA in living cells and replace it with a new genetic sequence.

- Requires precise knowledge of the genes affecting a trait (annotation)
- Great potential
- May be classified as not GMO as normal variants are used and not new genes inserted

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