Opportunities offered by dense marker maps for local breeds

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Agrobiodiversity

- Local breeds
- Worth to conserve
  - Beautiful
  - Cultural Heritage
  - Contain unique genetic diversity
- National and international efforts for conservation
  - E.g. gene banks
  - Genomics helpful?

Unique traits of local breeds

- Adapted to local environment
- Generally low input – low output
  - Can survive in harsh conditions or periods
    - Dry areas
    - Mountain areas
    - Poor soils
    - High disease pressure
    - Etc.
  - High input – high output -> global breeds
- Slow food – better taste

Local breeds under threat

- Few breeds dominate the world more and more
  - E.g. Holstein Friesians
  - Superior production
  - Superior breeding programs
- Can Genomic Selection help in local breeding programs?

Options for local breeding

- Improve local traditional breeds
- Cross with improved / exotic breeds
- Replace with exotic high production breeds
  - Loss of diversity
  - Limited success
  - May not reach local farmers

Breeding program components

- Determine breeding goal
- Collect data
    - Phenotype recording
    - Pedigree recording
- Estimate breeding values
- Selection and mate
- Disseminate improved genotypes

Data collection

- Poor infrastructure
  - No or limited pedigree recording
  - No (regular) phenotype recording
- Recording in research herd
  - More optimal conditions than in field
  - Other genotypes or small sample of genotypes in the field
  - Limited herd size

Pedigree estimation

- What is the relationship of animals with unknown or incomplete ancestry
- Is the research herd a representative sample of all the genotypes in the breed?
- Limited number of markers
  - E.g. 30 micro satellite markers
  - Within breed (e.g. Oliehoek et al. 2006 Genetics)
  - Across breeds (e.g. Eding 2002 GSE)
- Dense marker maps
  - E.g. 10 000 SNPs
  - Relationship of specific parts of the genome

Genomic selection

- Pedigree estimation and breeding value (BV) estimation combined
  - Also for populations of 1000 Animals
  - Genomic EBV ≈ BLUP EBV with 10 daugthers
- G*E interaction research herd - field
- Multiple traits some in research herd some in field
- Estimate BV in research herd – select in field
- Cross breeding

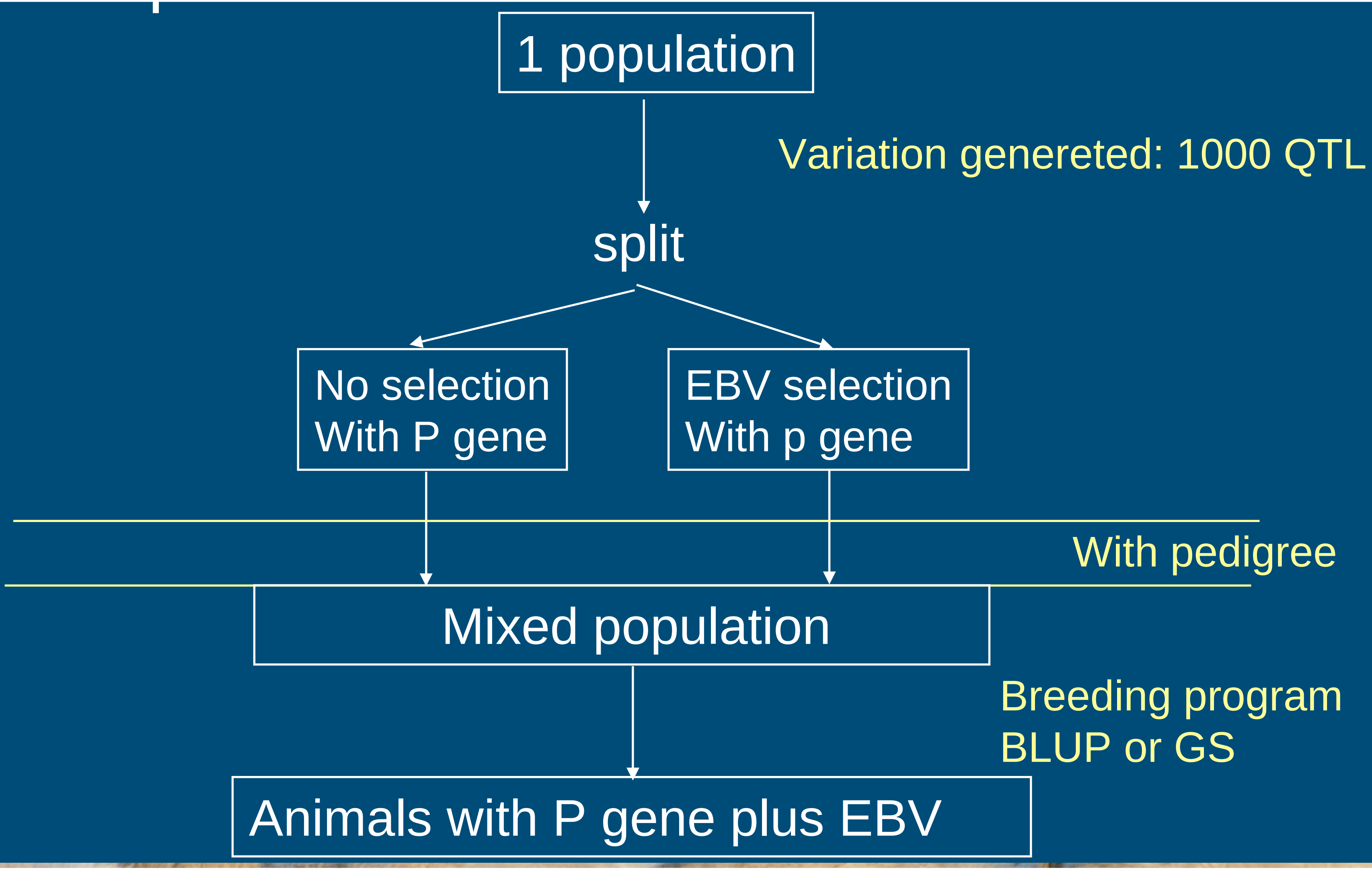
Introgression of single genes

- Interesting traits of local breeds for high production breeds
  - Disease resistance
  - Polledness
  - Etc. etc.
- And the other way around
  - QTLs

Can genomic selection help?

- Classical program: backcross
  - Selection for gene + rest original population
  - No selection for breeding values
- BLUP program
  - Selection for gene + BLUP EBV
  - May take long (e.g. > 4 generations)
- Genomic selection
  - Selection for gene + Genomic EBV

Computersimulation



1 population

Variation genereted: 1000 QTL

split

No selection
With P gene

EBV selection
With p gene

With pedigree

Mixed population

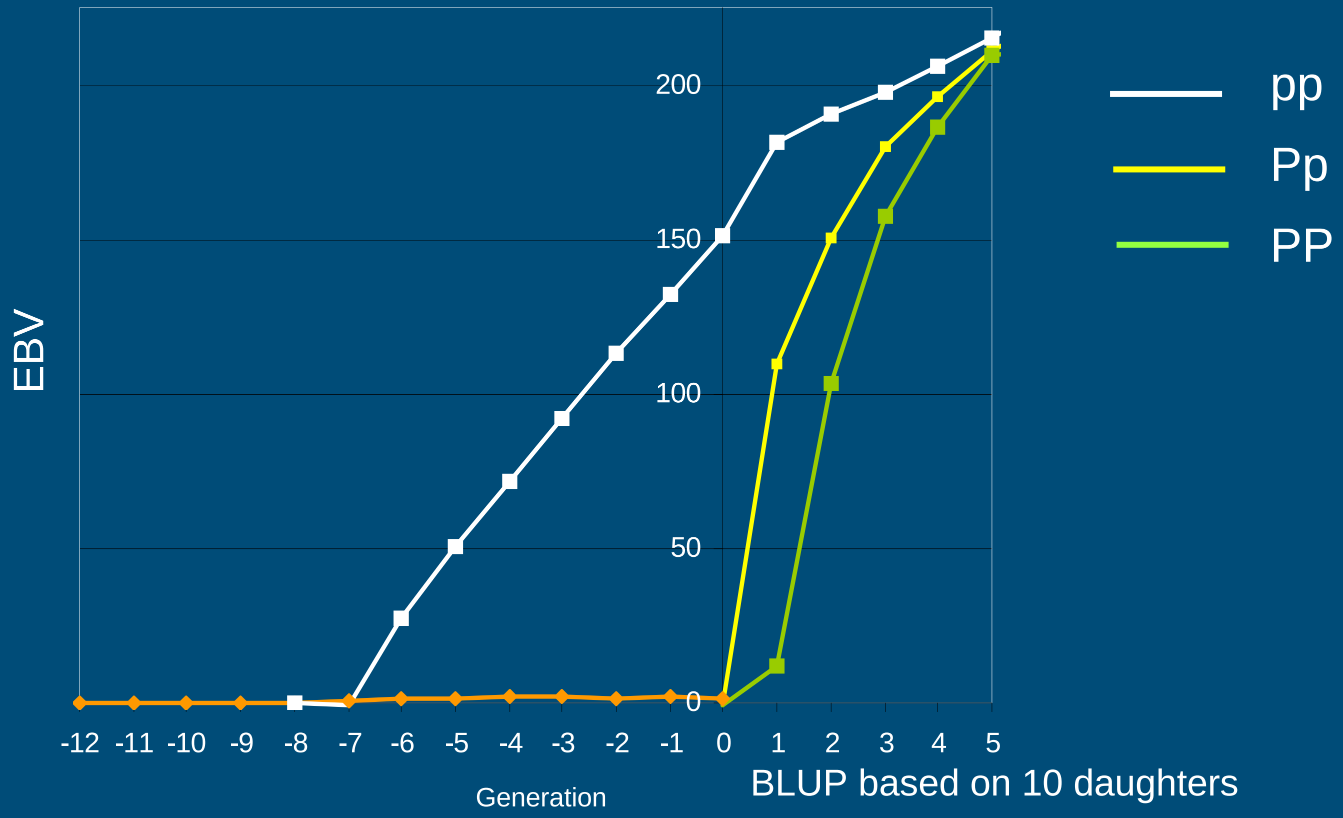
Breeding program
BLUP or GS

Animals with P gene plus EBV

Breeding programs

- 100 males, 900 females
- Breeding value estimation (index value)
  - GS
  - BLUP: 100 daughters (r = 70%)
  - BLUP: 10 daughters (r = 50%)
  - BLUP: No daughters (r = 30%)
- 10 best males selected
  - At least 1 male with P gene (homo- or heterozygote)
  - At least 5
  - 0 or more

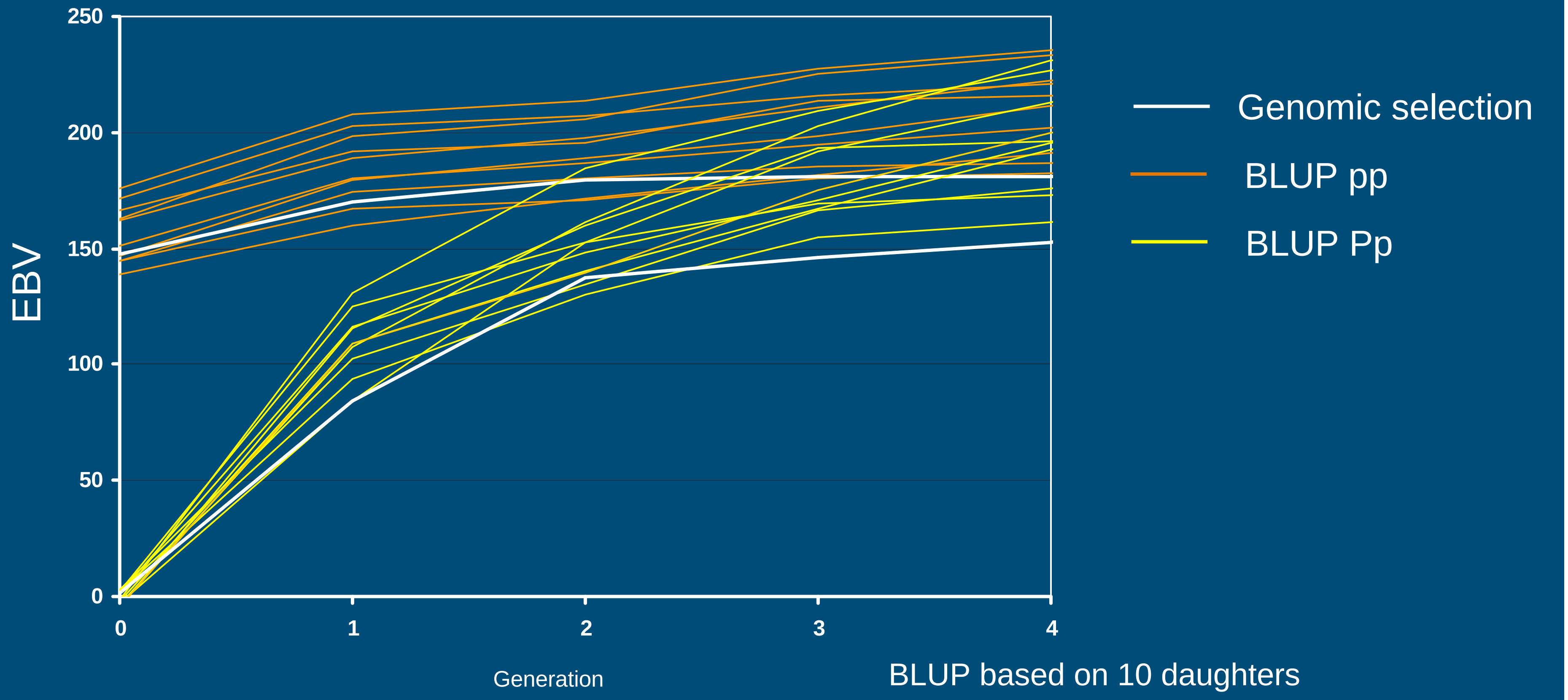
Results simulation program



BLUP based on 10 daughters

Each generation at least one Pp male selected

GS vs. BLUP



BLUP based on 10 daughters

Each generation at least one Pp male selected

Conclusions introgression

- GS better than BLUP with 10 daughters
  - Progress in EBV comparable
  - But: generation interval shorter
- In 4 generations homozygote animals with high EBVs can be bred
  - Re-estimation of marker effects each 2-3 generations?

Gene banking

- Now based on average relationship
- With the help of markers
  - Target specific areas for conservation
  - Monitor loss in other diversity if specific alleles (or traits) are targeted

General conclusion

- Dense marker maps provide the opportunity to incorporate specific diversity into conservation
  - (Single) traits, QTLs, Alleles
  - Breeding in small populations
  - Introgression
  - Gene banking