Accelerating Goat Genetic Improvement with Genomic Selection

Erin Massender

Acting Small Ruminant Specialist, OMAFRA
Ph.D. Candidate, University of Guelph

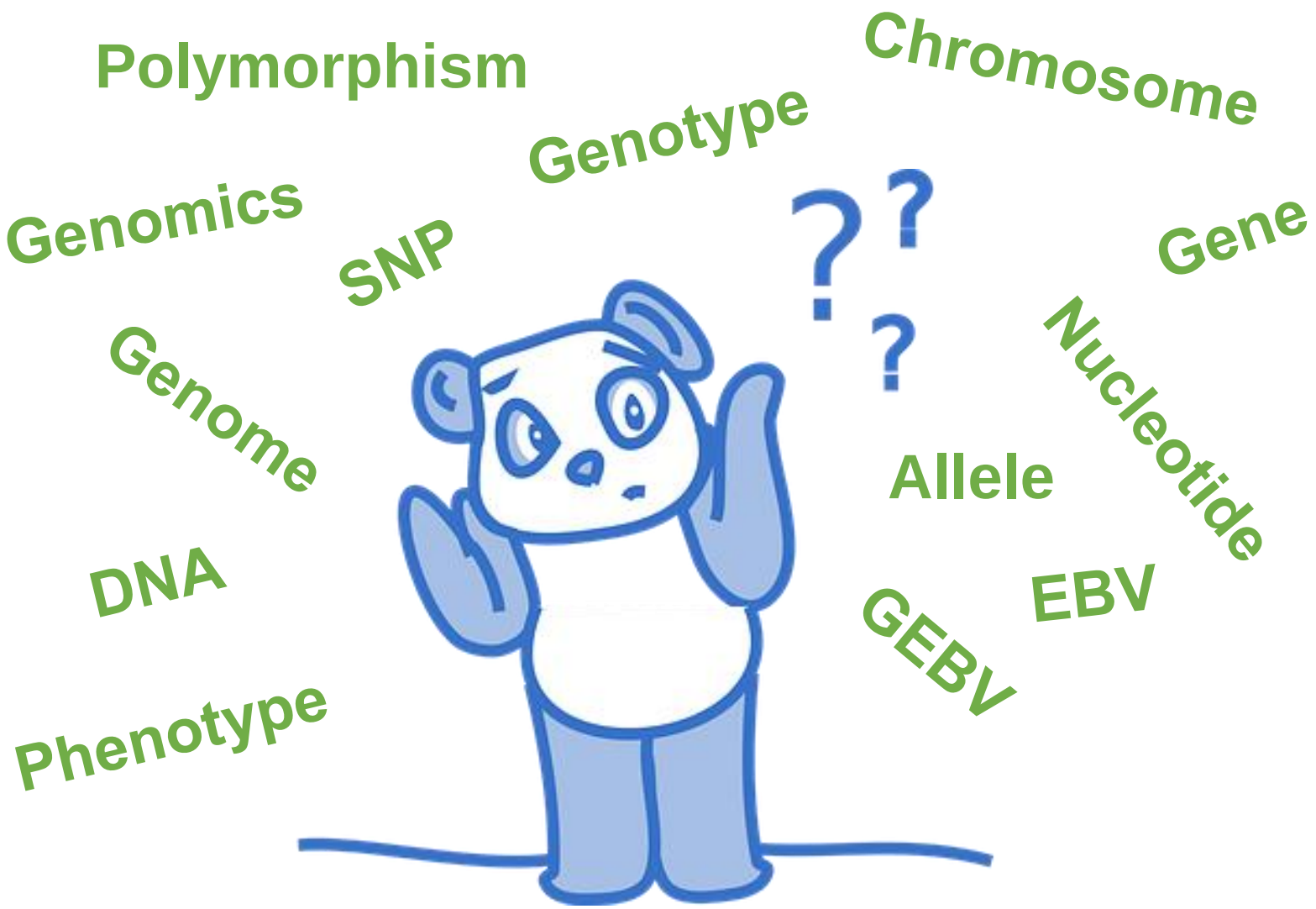
OMAFRA Goat Genetic Improvement Webinar Series

July 22nd, 2021

Erin Massender
emassend@uoguelph.ca

A Bit About Genomics

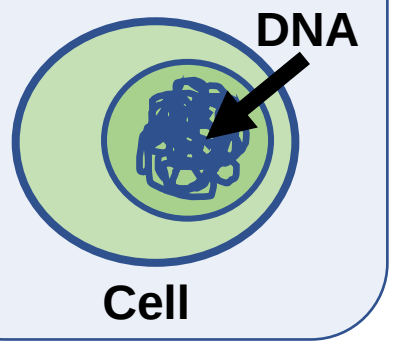
Some Genomics Lingo



Some Genomics Lingo – An Example

Genome

All of an animal's genetic material or DNA



Harry Potter and the Philosopher's Stone

\- CHAPTER ONE –

The Boy Who Lived

Mr. and Mrs. Dursley, of number four, Privet Drive, were proud to say that they were perfectly normal, thank you very much. They were the last people you'd expect to be involved in anything strange or mysterious, because they just didn't hold with such nonsense….

Chromosome

One partition of the DNA, chromosomes come in pairs

XX XX XX XX XY

1 2 3 4 … 30

Some Genomics Lingo – An Example

Harry Potter and the Philosopher's Stone

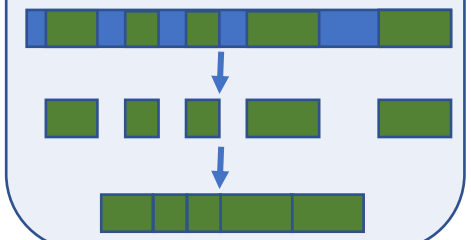
\- CHAPTER ONE –

The Boy Who Lived

Mr. and Mrs. Dursley, of number five, Privet Drive, were proud to say that they were perfectly normal, thank you very much. They were the last people you'd expect to be involved in anything strange or mysterious, because they just didn't hold with such nonsense….

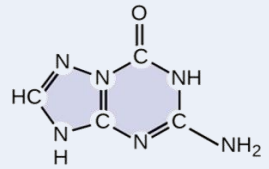
Gene

A region of DNA with a functional impact on the animal, alternate forms of a gene are called **alleles**



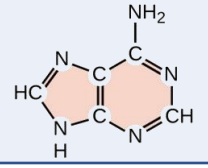
Nucleotide

An individual unit of the genetic code



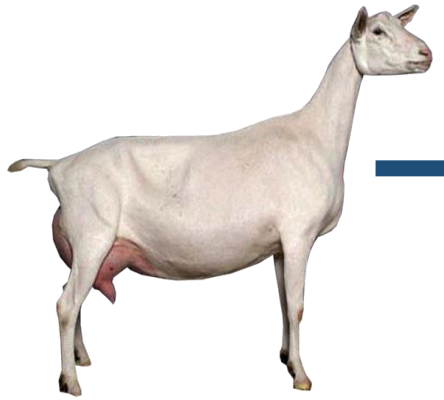
SNP

A **S**ingle **N**ucleotide **P**olymorphism is a typo, or mutation, that changes a single nucleotide in the DNA



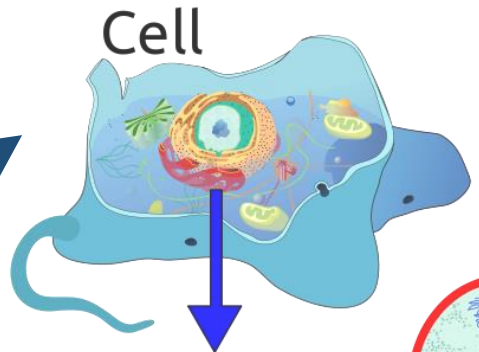
What is Genomic Selection?

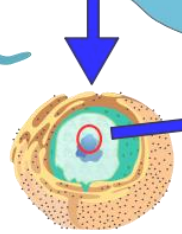
Genomic Selection: The use of information on an animal's DNA to select breeding candidates



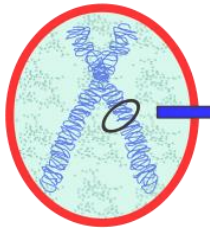
Breeding Candidate

Tissue Sample



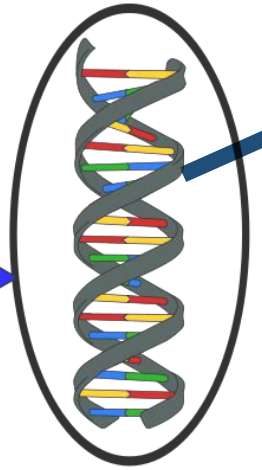


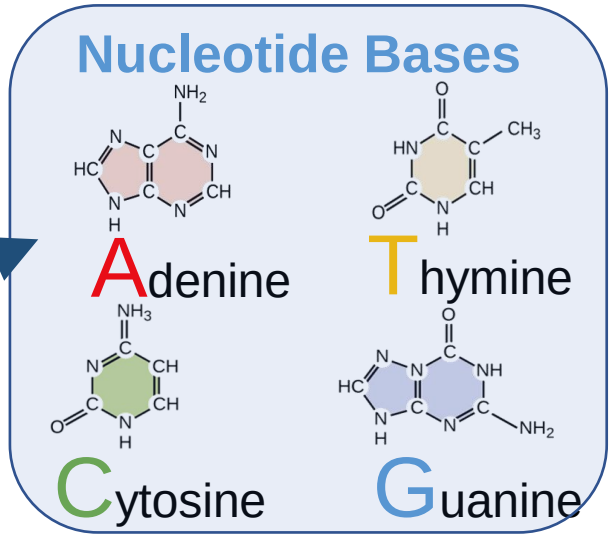
Nucleus



Chromosome

(Source: Wikimedia Commons)





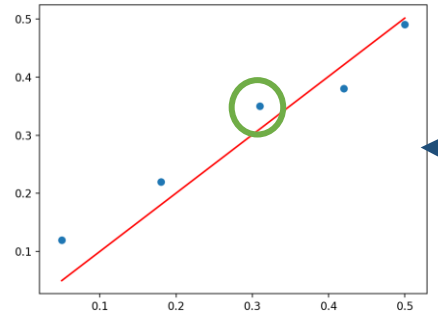
(Source: OpenStax College Microbiology)

DNA Extraction

ATGAAAACGCGTCATAATTAG
TGCGCGCAAAATTCCGCTCA
TAGGGATACTAAAGAGCCGC
GCTAGGGGCATAAAAACTGC
GAGCGCTAGATATATTTCACT

Genotype

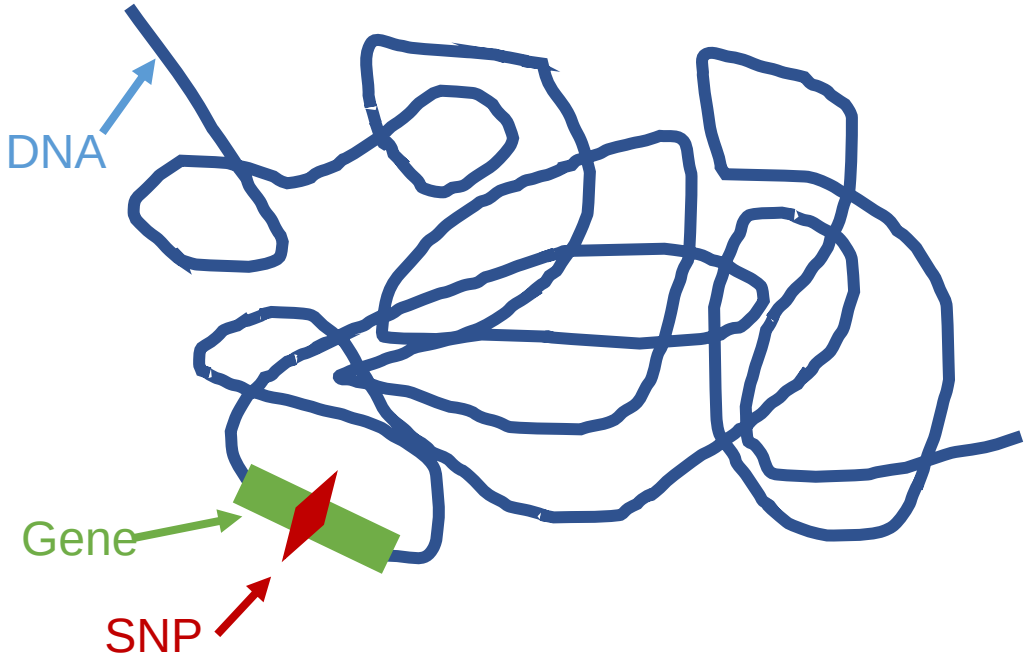
SNP Chip

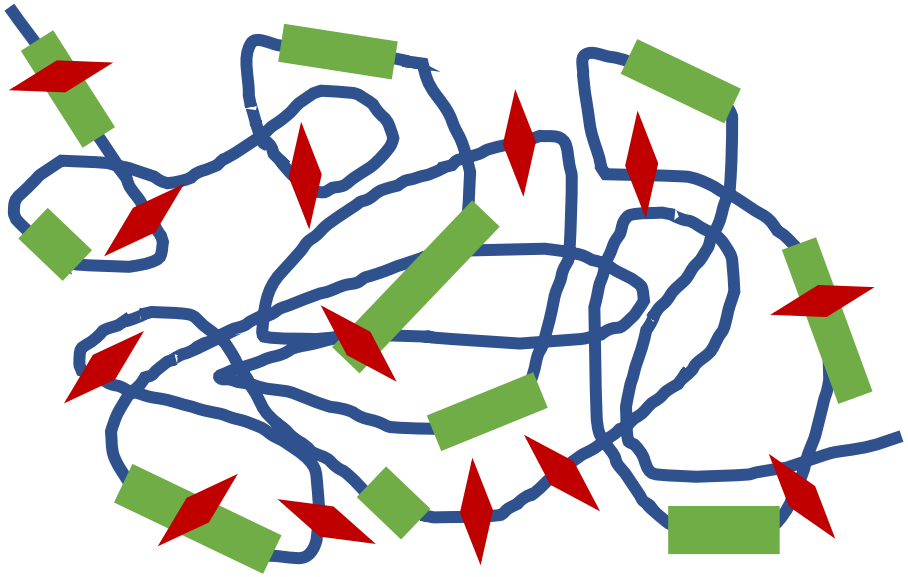


Predict Genetic Merit

Selection Decision

Genetic Testing vs. Genomic Selection





Genetic Testing:

- Identify alleles that can reliably predict phenotype
- Useful for simple traits
- Traits controlled by one or a few major genes
- Ex. *PrP* (Scrapie), *Alpha S1 Casein*

Genomic Selection:

- Genetic merit is predicted based on many markers (SNP) across the genome
- Useful for complex traits
- Traits controlled by many genes with a small effect
- Ex. reproduction, disease resistance, production

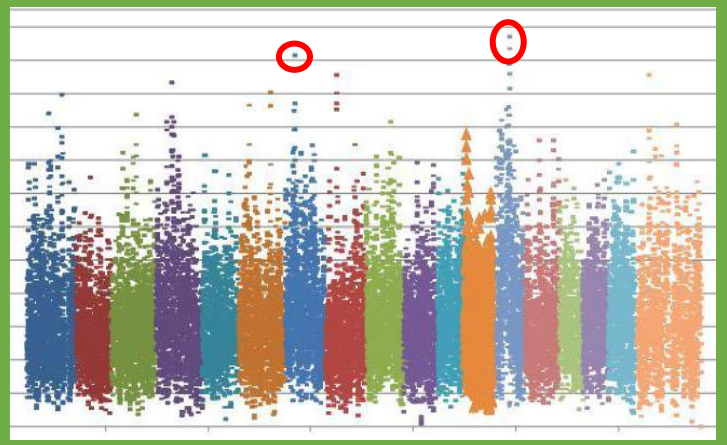
How Does Genomic Selection Work?

Step 1: Build a Reference Population

Phenotype
Measure Various Traits

Genotype
Read the Animal's Genetic

Analysis
Estimate the impact of SNPs on the different traits



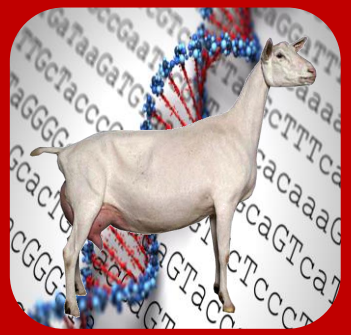
Reference Population: A group of animals with both phenotypes and genotypes

How Does Genomic Selection Work?

Step 2: Predict Genetic Merit of Breeding Candidates

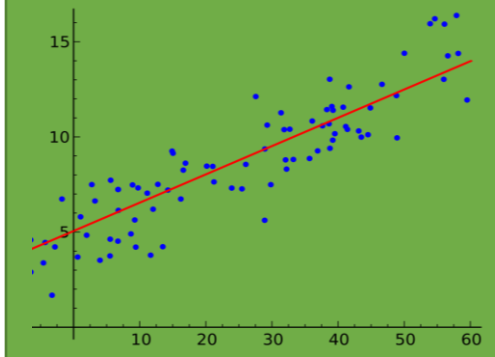
Genotype

Read the Animal's Genetic



Analysis

Predict Genetic Merit for Traits



$GEBV = \beta_1 X_1 + \beta_2 X_2 + \ldots\ldots + \beta_{nl} X_{nl}$

Accelerating Genetic Gain with Genomics

- Greater accuracy = greater genetic gain
- Greater selection accuracy for breeding candidates

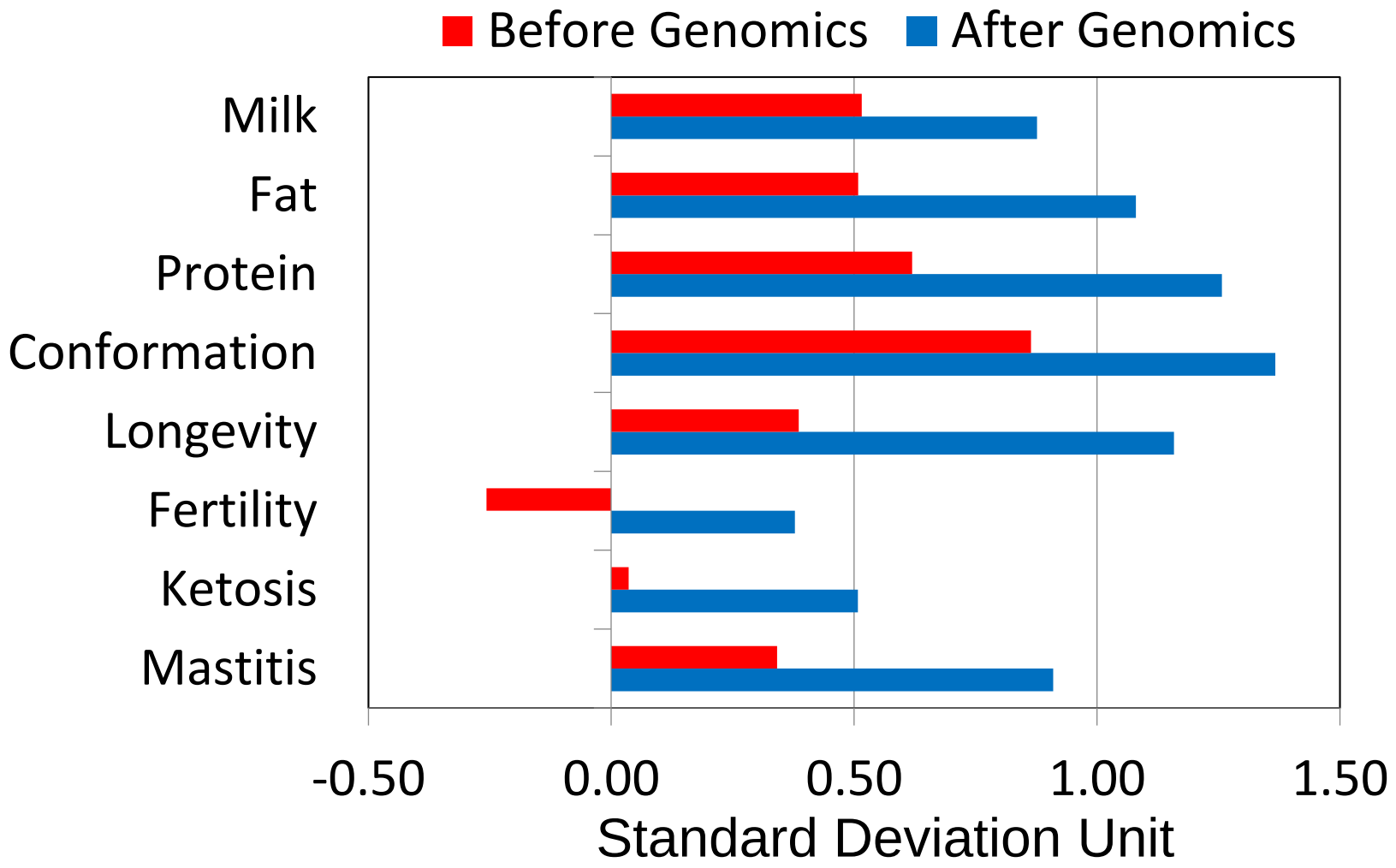
- Greater intensity = greater genetic gain
- Enables testing of more animals for expensive to measure traits

$$\text{Genetic Gain / yr} = \frac{\text{Accuracy} * \text{Intensity} * \text{Genetic SD}}{\text{Generation Interval}}$$

- Shorter generation interval = greater genetic gain
- Allows rapid selection of young animals

- Need variability for selection
- Limited impact in the short term, but intense selection could reduce variability

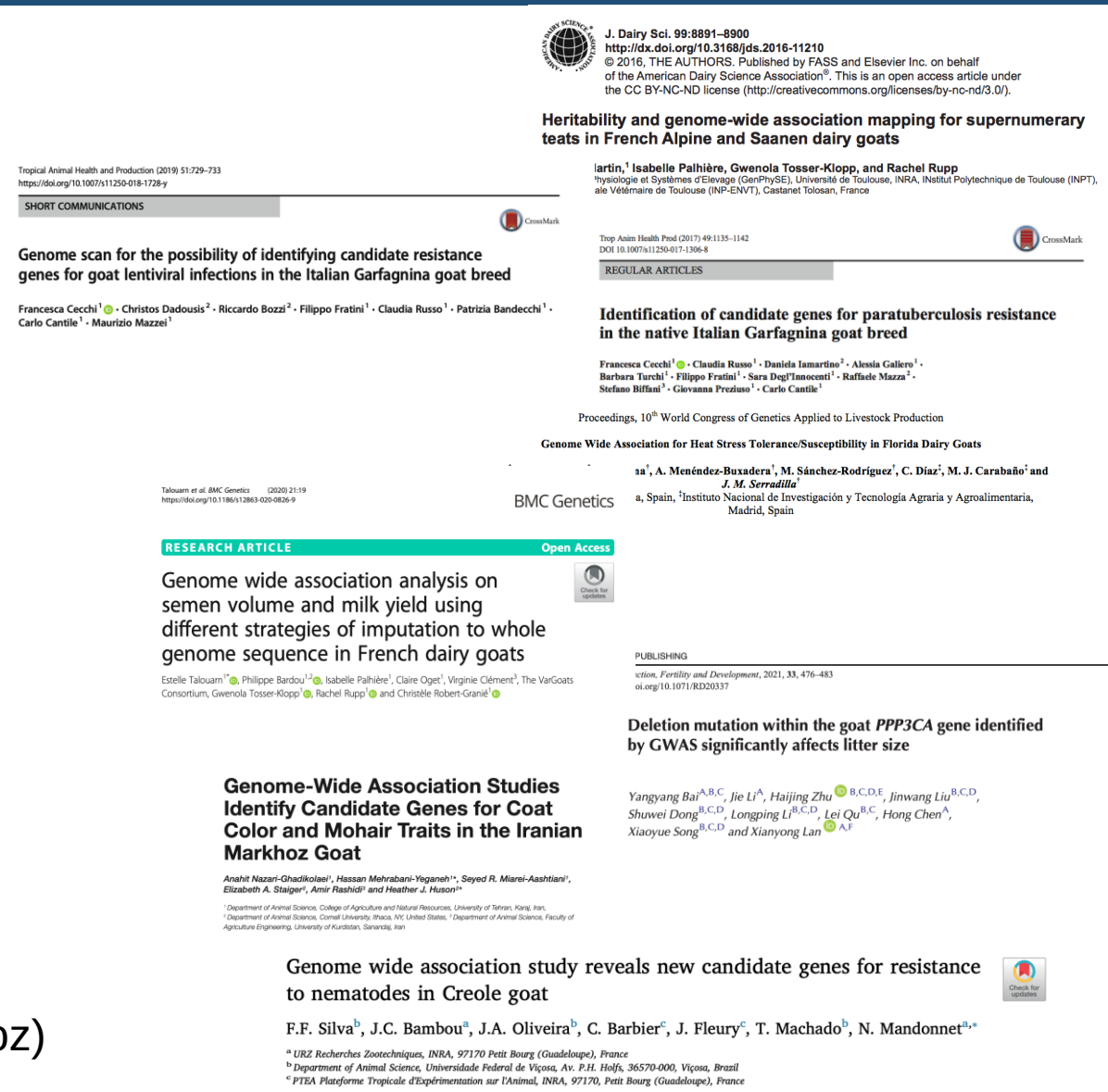
An Example of Accelerating Genetic Gain



(Adapted from Brito, 2018)

Enables Selection for Novel Traits

- Supernumerary Teats (French Alpine and Saanen)
- Semen Volume (French Alpine and Saanen)
- Litter Size (Chinese Cashmere)
- Heat Stress (Spanish Florida)
- Johne's Disease (Italian Garfagnina)
- Parasite (GIN) Resistance (Guadeloupian Creole)
- CAEV Resistance (Italian Garfagnina)
- Mohair Colour, Yield and Quality (Iranian Markhoz)



J. Dairy Sci. 99:8891–8900
http://dx.doi.org/10.3168/jds.2016-11210
© 2016, THE AUTHORS. Published by FASS and Elsevier Inc. on behalf of the American Dairy Science Association®. This is an open access article under the CC BY-NC-ND license (http://creativecommons.org/licenses/by-nc-nd/3.0/).

Heritability and genome-wide association mapping for supernumerary teats in French Alpine and Saanen dairy goats

Tropical Animal Health and Production (2019) 51:729–733
https://doi.org/10.1007/s11250-018-1728-y

SHORT COMMUNICATIONS

Genome scan for the possibility of identifying candidate resistance genes for goat lentiviral infections in the Italian Garfagnina goat breed

Francesca Cecchi · Christos Dadousis · Riccardo Bozzi · Filippo Fratini · Claudia Russo · Patrizia Bandecchi · Carlo Cantile · Maurizio Mazzei

Trop Anim Health Prod (2017) 49:1135–1142
DOI 10.1007/s11250-017-1306-8

REGULAR ARTICLES

Identification of candidate genes for paratuberculosis resistance in the native Italian Garfagnina goat breed

Francesca Cecchi · Claudia Russo · Daniela Iamartino · Alessia Galiero · Barbara Turchi · Filippo Fratini · Sara Degl'Innocenti · Raffaele Mazza · Stefano Biffani · Giovanna Preziuso · Carlo Cantile

Proceedings, 10th World Congress of Genetics Applied to Livestock Production

Genome Wide Association for Heat Stress Tolerance/Susceptibility in Florida Dairy Goats

Talouarn et al. BMC Genetics (2020) 21:19
https://doi.org/10.1186/s12863-020-0826-9

BMC Genetics

RESEARCH ARTICLE Open Access

Genome wide association analysis on semen volume and milk yield using different strategies of imputation to whole genome sequence in French dairy goats

Estelle Talouarn, Philippe Bardou, Isabelle Palhière, Claire Oget, Virginie Clément, The VarGoats Consortium, Gwenola Tosser-Klopp, Rachel Rupp and Christèle Robert-Granié

PUBLISHING

Deletion mutation within the goat *PPP3CA* gene identified by GWAS significantly affects litter size

Genome-Wide Association Studies Identify Candidate Genes for Coat Color and Mohair Traits in the Iranian Markhoz Goat

Genome wide association study reveals new candidate genes for resistance to nematodes in Creole goat

F.F. Silva, J.C. Bambou, J.A. Oliveira, C. Barbier, J. Fleury, T. Machado, N. Mandonnet

Cost-Benefit Considerations for Genomic Selection in Goats

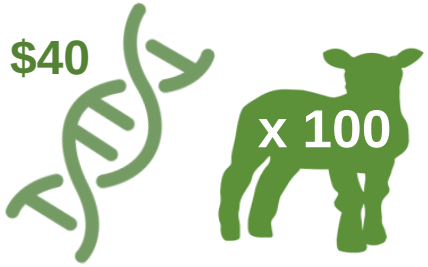
Genotyping Costs

Traditional Selection

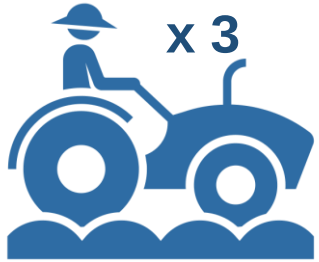
= $ 0

Current genotyping costs are less than $40 per animal!

Genomic Selection



+



2 Hours @ $25/hr

= $ 4,150

<u>Assumptions:</u>

- **# of doelings to genotype: 100**

Image Source: Tractor Icon created by Symbolon from the Noun Project

Replacement Rearing Costs

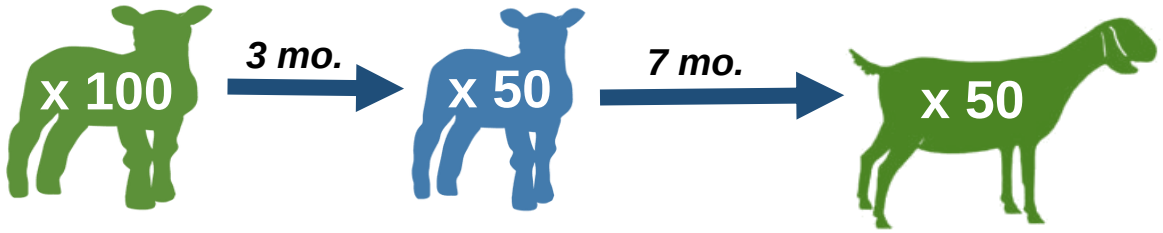
Traditional Selection

= $ 21,500

Assumptions:

- # of doelings Born: 100
- 50% of doelings selected
- Doeling Feed Costs: $20/month[1]
- First Kidding: 15 mo.

Genomic Selection



= $ 18,000

19% Savings in Feed

+ Labour Savings
+ Housing Savings
+ Veterinary Savings

[1]Approximated based on Delaney (2012) with adjustment for inflation and currency

Genetic Gain

Traditional Selection

0.52

10% of Bucklings
50% of Doelings

208 L

4 years

= 34.6 L/doe/year

28% gain

Genomic Selection

0.67

10% of Bucklings
50% of Doelings

208 L

4 years

= 44.4 L/doe/year

Image Source: Bullseye created by Edwin PM from the Noun Project, Volume Icon by Vectors Market, Weight Mikicon, Turnover Icon by Jerry Kim

Genetic Gain

Traditional Selection

0.52

10% of Bucklings
50% of Doelings

208 L

4 years

= 34.6 L/doe/year

47% gain

Genomic Selection

0.67

10% of Bucklings
50% of Doelings

208 L

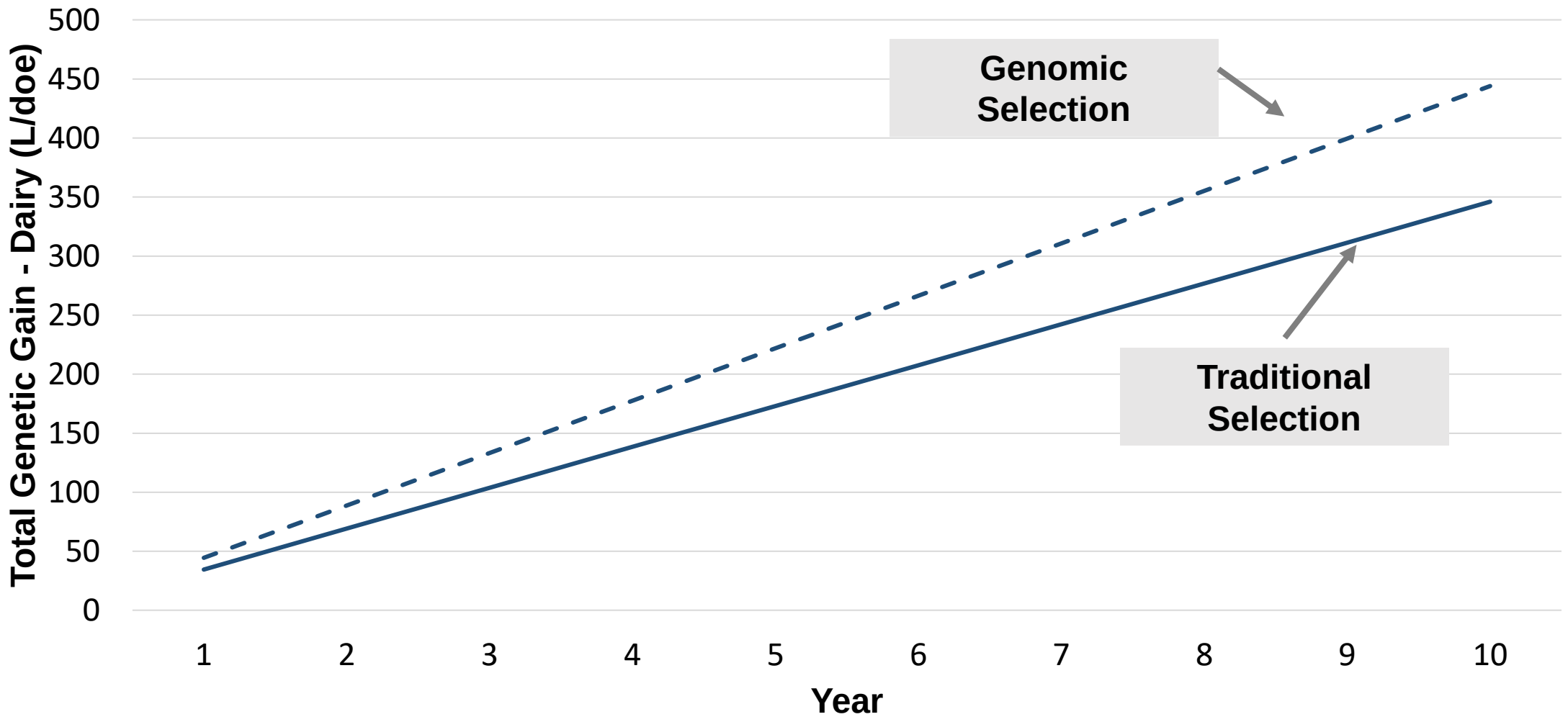
3.5 years

= 51.0 L/doe/year

Shorter generation interval

Image Source: Bullseye created by Edwin PM from the Noun Project, Volume Icon by Vectors Market, Weight Mikicon, Turnover Icon by Jerry Kim

Accelerating Genetic Gain: It Adds Up



Remember: Genetic gain is cumulative!

Small differences in yearly genetic gain lead to big changes overtime!

Other Considerations for Implementation

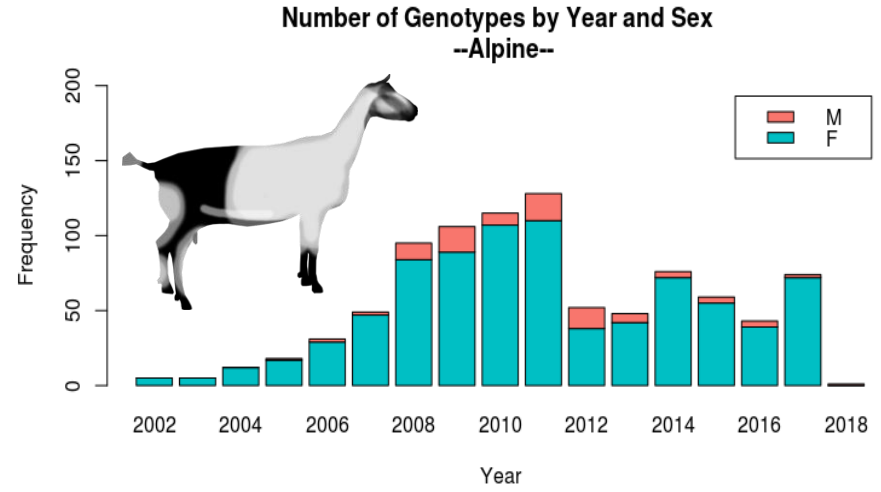
1. **Genomic predictions are breed-specific**
   - Funds and industry coordination are needed to build reference populations for each breed of interest
2. **Genomic selection is limited by the availability of phenotypic information**
   - Participation in industry-wide genetic improvement programs is needed to continue to capture phenotypic data for both common and novel traits
3. **Enables new herds to participate in the genetic evaluation program**
   - Genomic evaluations available for large commercial herds without registration or pedigree-recording
4. **Genotypes can be used to fix pedigree errors**
5. **Selective genotyping, such as only genotyping bucks, could be used to reduce costs at a farm level**

University of Guelph's Dairy Goat Genomics Project

Samples & Genotyping

- **Genotypes**
  - **1,267** Alpine and Saanen goats from **13** herds across Canada
  - **720** genotypes from a previous project

- **Criteria for Sampling:**
  - Herds participating in milk testing
  - Registered bucks
  - Registered does with milk and/or classification records



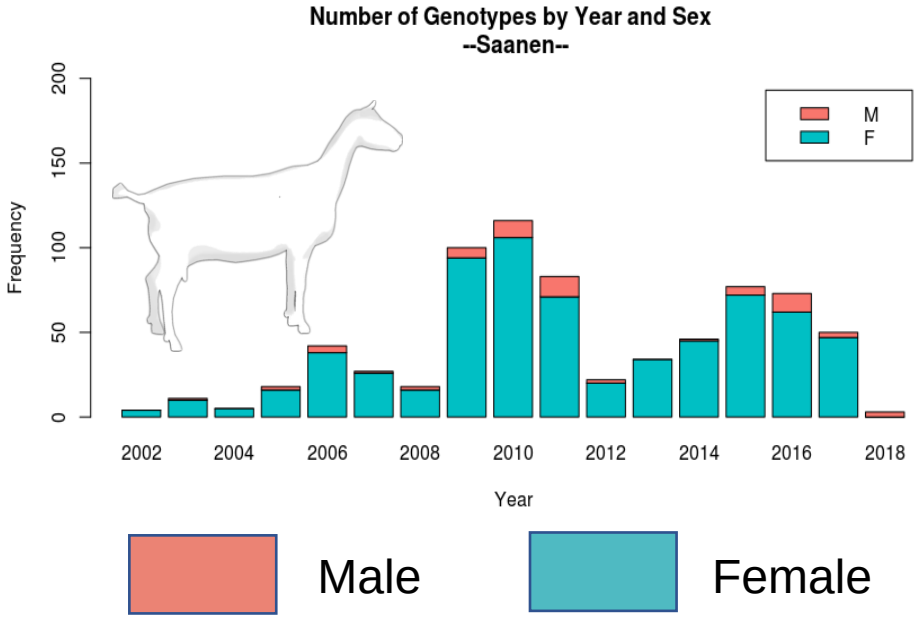


Image source: Canadian Goat Society, 2020 Classification Manual

Sample Collection Methods

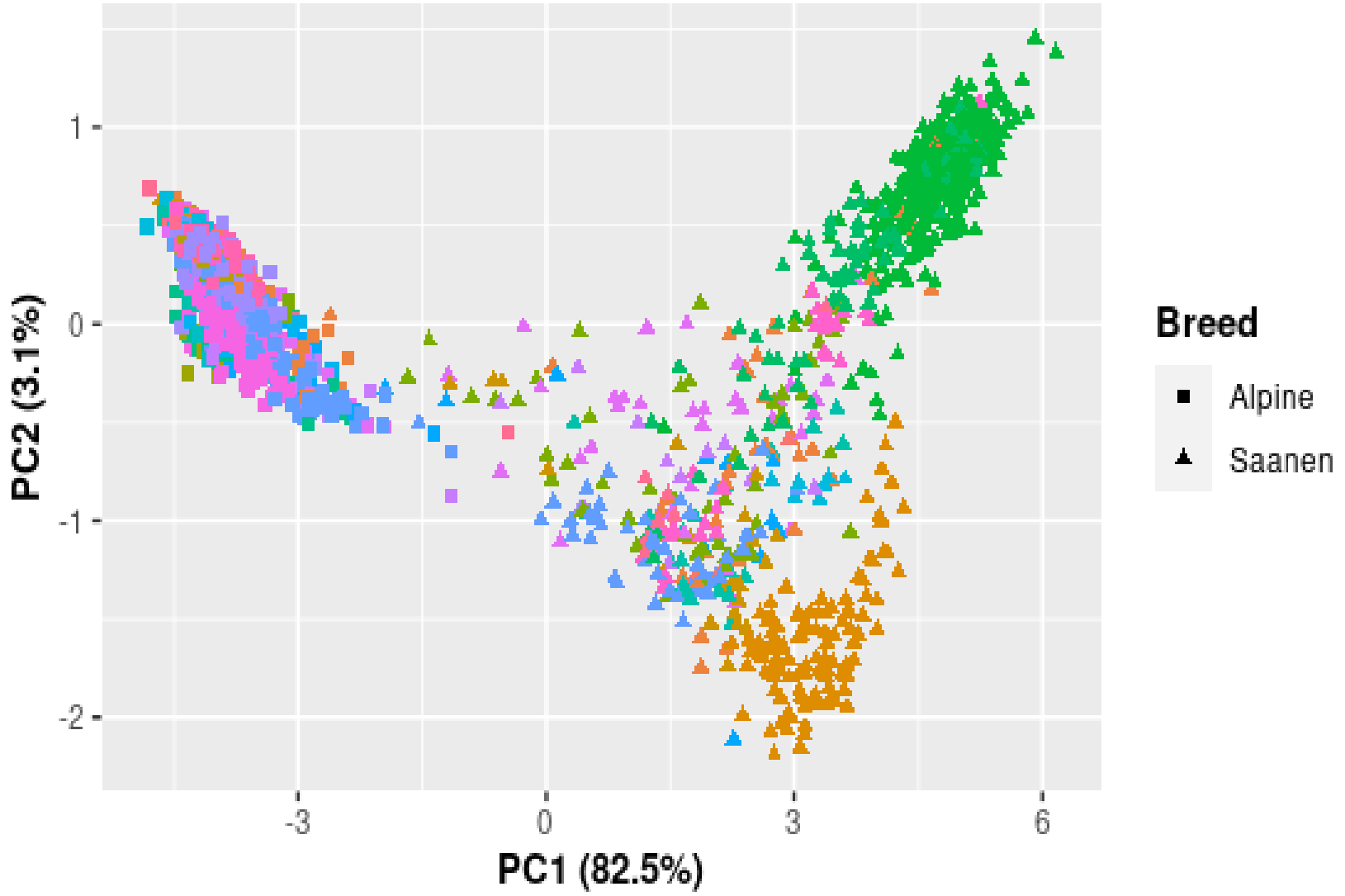
Nasal Swabs

Blood

Allflex Tissue Sampling Units (Ear Hole Punch)

Semen

Relatedness of Genotyped Animals



Genotyped animals are coloured by herd of origin.

Summary of Data

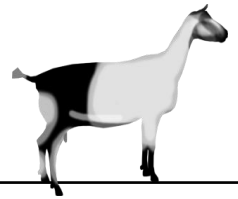
Animal Group	Breed	
	Alpine	Saanen
Does with Milk Records	13,939	8,179
Does with Classification Records	5,158	2,342
Animals Genotyped	833	874

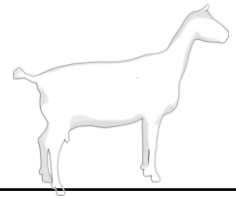
CCSI CCAP

GoatGenetics.Ca
GénétiqueCaprine.Ca

CGS

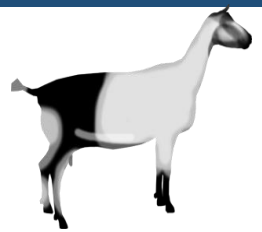
Milk Production Traits

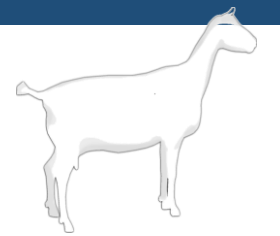




			Alpine		Saanen	
Lactation	**Trait**	**Abr.**	**Mean ± SD**	**h^2**	**Mean ± SD**	**h^2**
First	Milk Yield	MY1	887 ± 168	0.33 ± 0.03	890 ± 223	0.35 ± 0.04
	Protein Yield	PY1	27 ± 5	0.36 ± 0.03	28 ± 7	0.36 ± 0.04
	Fat Yield	FY1	30 ± 6	0.32 ± 0.03	30 ± 8	0.38 ± 0.04
	Protein Percentage	PP1	3 ± 0.2	0.66 ± 0.02	3 ± 0.2	0.55 ± 0.04
	Fat Percentage	FP1	3 ± 0.4	0.57 ± 0.03	3 ± 0.5	0.43 ± 0.04
Later	Milk Yield	MY2+	888 ± 194	0.21 ± 0.02	885 ± 242	0.17 ± 0.03
	Protein Yield	PY2+	28 ± 6	0.24 ± 0.02	27 ± 7	0.18 ± 0.03
	Fat Yield	FY2+	30 ± 7	0.22 ± 0.02	30 ± 9	0.20 ± 0.03
	Protein Percentage	PP2+	3 ± 0.2	0.61 ± 0.02	3 ± 0.2	0.61 ± 0.03
	Fat Percentage	FP2+	3.4 ± 0.4	0.55 ± 0.02	3 ± 0.5	0.44 ± 0.03

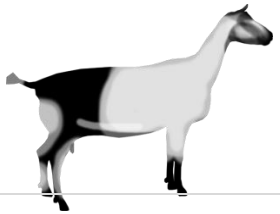
Conformation Traits



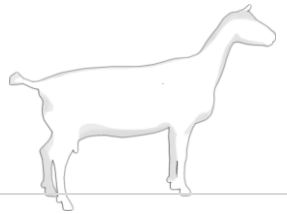


		Alpine		Saanen	
Trait	**Abr.**	**Mean ± SD**	**h^2**	**Mean ± SD**	**h^2**
Body Capacity	BC	5.78 ± 1.23	0.22 ± 0.02	6.16 ± 1.17	0.11 ± 0.03
Dairy Character	DC	6.38 ± 1.09	0.16 ± 0.02	6.59 ± 1.18	0.16 ± 0.04
General Appearance	GA	5.51 ± 1.17	0.31 ± 0.03	5.78 ± 1.16	0.21 ± 0.04
Feet and Legs	FL	4.98 ± 1.51	0.17 ± 0.03	5.58 ± 1.41	0.11 ± 0.03
Fore Udder	FU	5.81 ± 1.30	0.28 ± 0.03	6.14 ± 1.27	0.23 ± 0.04
Rear Udder	RU	5.48 ± 1.44	0.22 ± 0.03	5.81 ± 1.41	0.14 ± 0.03
Suspensory Ligament	SL	5.87 ± 1.35	0.18 ± 0.02	6.27 ± 1.36	0.13 ± 0.04
Teats	TE	5.09 ± 1.85	0.18 ± 0.03	5.47 ± 1.36	0.12 ± 0.04

Selection Accuracy for Breeding Candidates



Milk Production



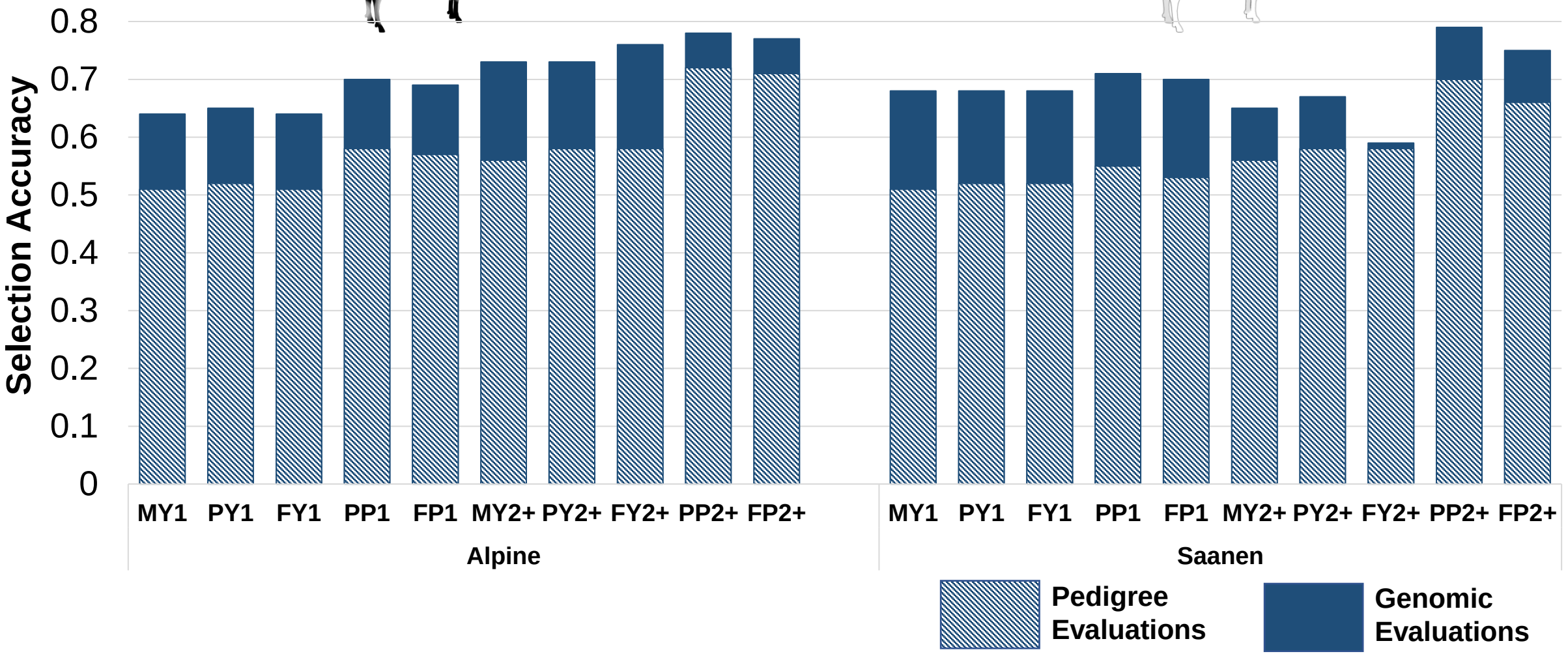
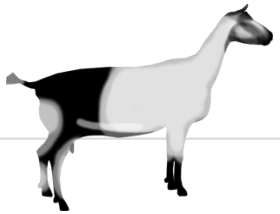
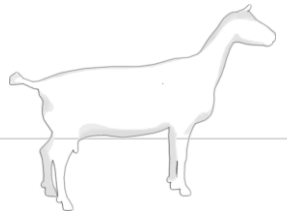


Image source: Canadian Goat Society, 2020 Classification Manual

Selection Accuracy for Breeding Candidates



Conformation



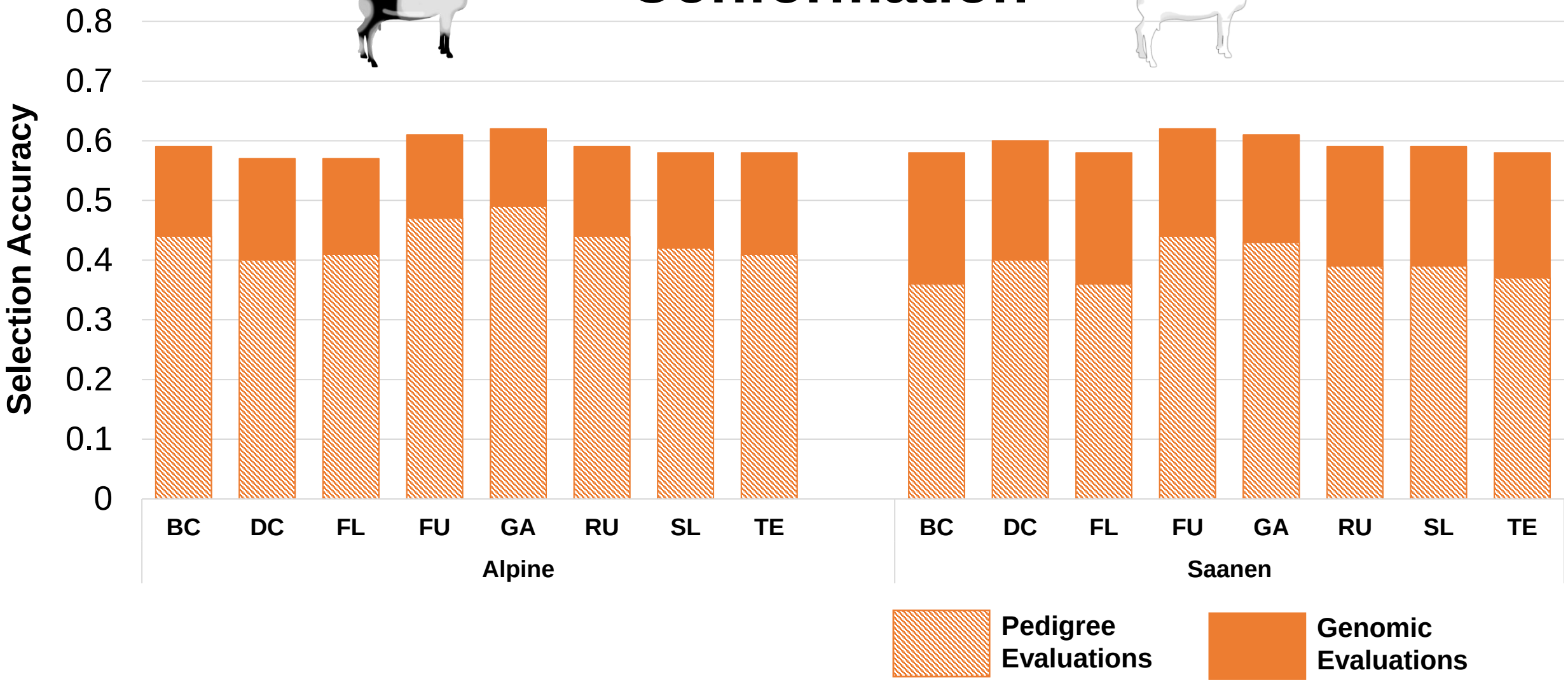
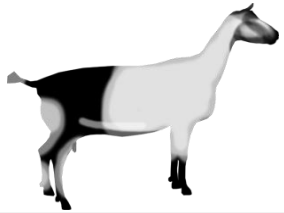
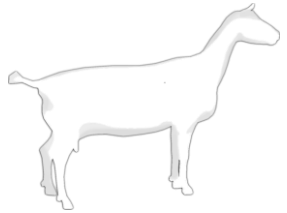


Image source: Canadian Goat Society, 2020 Classification Manual

Overall Gain in Accuracy from Genomic Selection





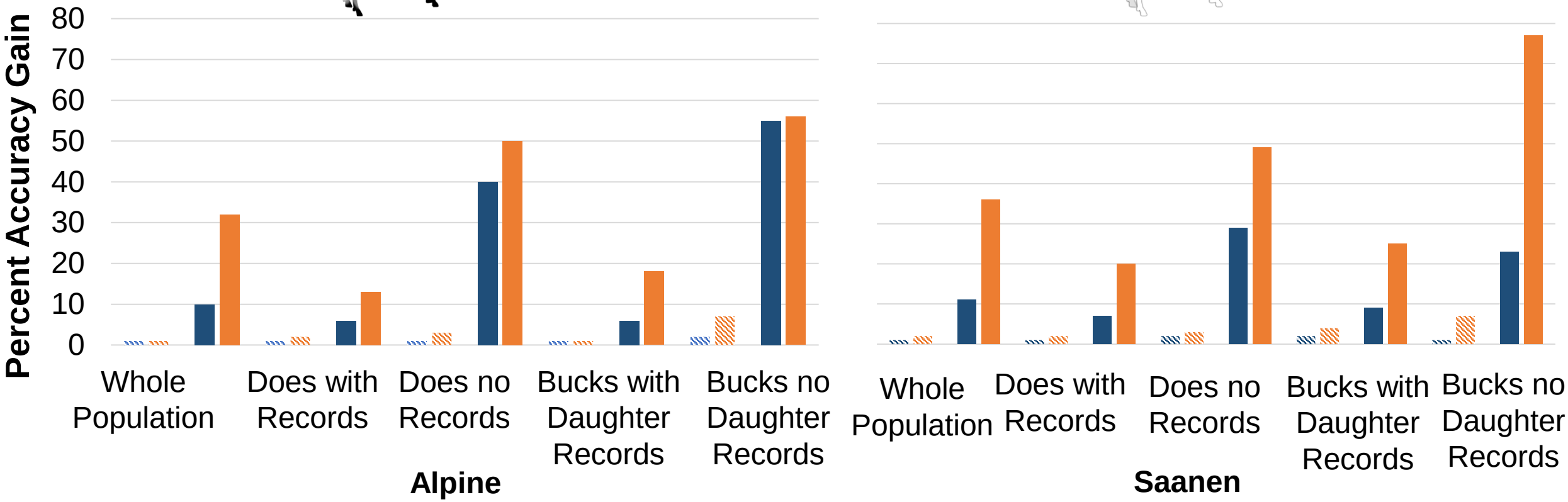


Image source: Canadian Goat Society, 2020 Classification Manual

Take Home Messages

1. Genomic selection utilizes small differences in the DNA of individual animals in order to more accurately predict genetic merit of young breeding candidates.

2. It has been proven to rapidly accelerate genetic improvement and enable selection on expensive and difficult to measure traits in many species.

3. Substantial gains to selection accuracy are expected from its implementation for the Canadian Alpine and Saanen breeds, especially for does without records (29 to 50%) and bucks without daughter records (23 to 77%).

Acknowledgements

Project Team:

CGIL:
Erin Massender
Hinayah Rojas de Oliveira
Flavio Schenkel

Purdue University:
Luiz Brito

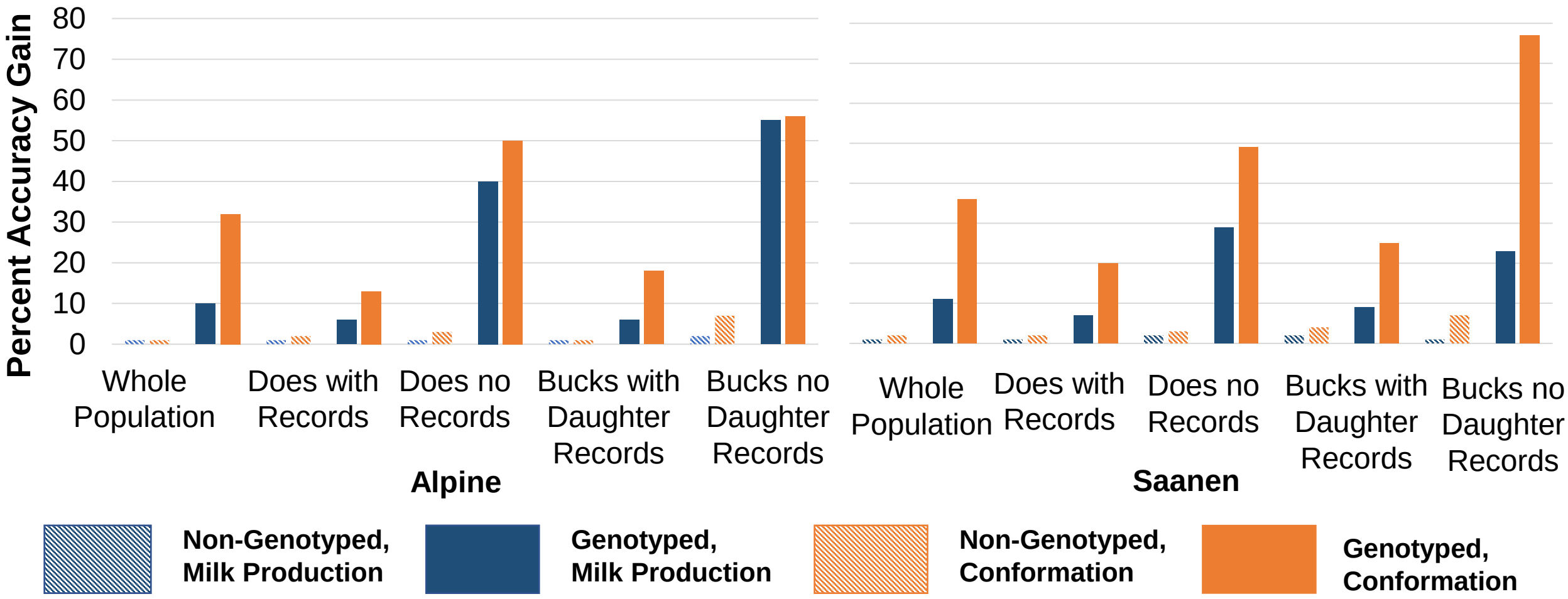
Canadian Centre for Swine Improvement:
Laurence Maignel
Mohsen Jafarikia
Brian Sullivan

Data Provision:

We thank the Canadian Goat Society and CCSI for providing data and all producer herds that participated in collecting samples for this project.

Funding:

This research is funded by the Ontario Ministry of Agriculture, Food and Rural Affairs (OMAFRA), through the Ontario Agri-Food Innovation Alliance.

Thank YOU!

Overall Gain in Accuracy from Genomic Selection