

Single and Multiple-Breed Genomic Predictions for Conformation Traits of Canadian Dairy Goats

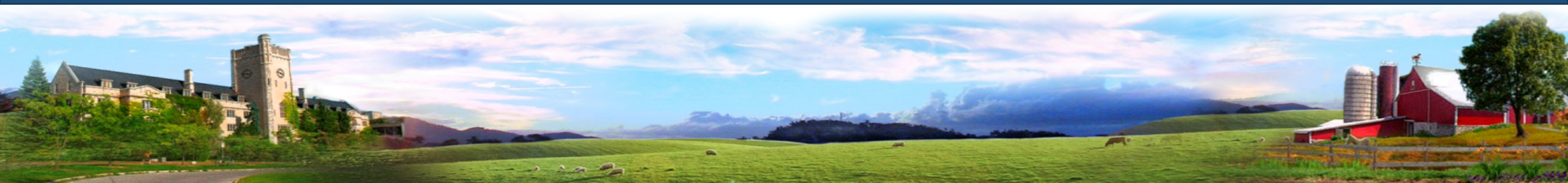
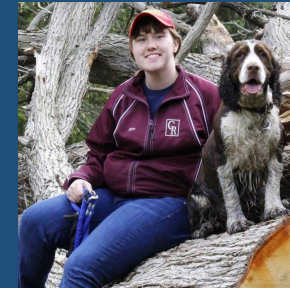
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Dairy Goat Classification System

- Managed by the CGS for Canadian dairy goat breeds
- Non-selective system, all first lactation does in participating herds
 - Later lactation does and bucks are optional
- Traits are scored on a 1 to 9 scale by trained classifiers



Canadian Goat
Society

Traits Classified

- Traits and sub-indexes scored have changed over time
- Genetic evaluation system uses traits equivalent to the original classification system

Original	Pre-2012	Current
• General Appearance • Feet & Legs • Body Capacity • Dairy Character • Suspensory Ligament • Fore Udder • Rear Udder • Teats	• Structure • Rump • Feet & Legs • Body Capacity • Dairy Character • Mammary System • Fore Udder • Rear Udder • Teats	• Rump • Dairy Strength • Feet & Legs • Mammary System

Canadian Goat Society Type Classification Report

Reg. No. _____ Tattoo Rt. _____ Lt. _____ Birth Date _____
Barn Name _____ Owner _____ Location _____

Linear Appraisal Type Traits (desired ranges are)

Structure (Frame) Head _____ Shoulder _____ smooth _____
Strength of Loin _____ reached _____
Stature _____ breed standard _____
Size _____ breed standard _____

Comment: _____

Rump _____ Width _____ wide _____
Slope _____ steep _____

Comment: _____

Feet & Legs Bone Quality _____ flat _____
Rear Leg Set _____ sickled _____
Pastern Strength _____ straight _____
Balance, Front Feet _____ balanced _____
Balance, Rear Feet _____ balanced _____

Comment: _____

Body Capacity _____ Chest Width _____ wide _____
Depth of Heart _____ deep _____
Body Depth _____ deep _____
Body Length _____ long _____

Comment: _____

Dairy Character _____ Dairy Form _____ angular _____

Comment: _____

Mammary System Ligament _____ excessive _____ weak _____
Depth _____ deep _____ shallow _____
Texture _____ soft _____ meaty _____

Comment: _____

Fore Udder Attachment _____ strong _____ weak _____
Length _____ long _____ short _____
Width _____ wide _____ narrow _____

Comment: _____

Rear Udder Height _____ high _____ low _____
Width _____ wide _____ narrow _____
Profile _____ bulgy _____ flat _____

Comment: _____

Teats Placement _____ inside _____ outside _____
Size _____ small _____ large _____

Comment: _____

Mammary Score _____ Final Score _____ Classification Date _____ Classifier _____ Owner/Agent _____
py/mm/dd

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CLASSIFICATION REPORT
DAIRY SENIOR DOE

Owner: _____
Classification Date: 2019-04-25
Classifier: _____

NAME: _____ Registration # _____ Fresh Date: 2019-02-31
DOB: _____ Breed: NIDEPAN DWARF Lactation: 2
SIRE: _____ Days Fresh: 88
DAM: _____ Age: 2-4

Section	Descriptive Trait	Code	1	2	3	4	5	6	7	8	9	(Ideal)	Defects
Rump (10%)													
90	Rump Angle (47%)	5											Low (46)
	Thurl Width (31%)	9											Narrow (8-9)
	Loin Strength (22%)	6											Weak (8-9)
	Thurl Placement (Research)	6											Back (8)
Dairy Strength (22%)													
82	Stature (12%)	5											Tall (7-9)
	Height at Front End (3%)	5											High (5-7)
	Chest Width (23%)	6											Narrow (7-8)
	Body Depth (17%)	6											Shallow (7-8)
	Angularity (28%)	6											Coarse (6)
	Body Condition Score (5%)	9											Low (6-7)
Feet & Legs (26%)													
86	Pastern Strength (20%)	6											Weak (7-8)
	Heel Depth (20%)	6											Shallow (8-9)
	Bone Quality (12%)	6											Coarse (7)
	Rear Legs-Side View (17%)	6											Straight (4-5)
	Rear Legs-Rear View (31%)	6											Hocked-in (6)
Mammary System (42%)													
88	Udder Depth (14%)	6											Deep (4-6)
	Udder Texture (10%)	5											Soft (9)
	Medial Suspensory Ligament (20%)	6											Weak (8)
	Fore Attachment (20%)	6											Weak (9)
	Rear Attachment Height (14%)	9											Low (9)
	Rear Attachment Width (12%)	8											Narrow (9)
	Teat Placement (8%)	6											Wide (8-8)
	Teat Length (2%)	3											Short (5-6)

Final Score: VERY GOOD 86

Highest Scoring Traits **Lowest Scoring Traits**

Rump Angle **Body Condition Score**
Rear Attachment Height **Loin Strength**

2020

Pre-2012

Genetic Evaluation System

- Genetic evaluations are computed by the Canadian Centre for Swine Improvement (CCSI) and available through GoatGenetics.ca
- Multiple-breed evaluations
- Single-trait animal models for conformation traits
 - **Fixed effects** – breed, parity, age class, days in milk
 - **Random effects** – herd-year-classifier and animal additive genetic



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GoatGenetics.ca
GénétiqueCaprine.ca

Multiple-Breed Genetic Evaluations

- **Common for small ruminant populations**
 - Many breeds and small populations for individual breeds
 - High use of crossbreeding and ancestral relationships between breeds
- **May increase the accuracy of single-step GEBV when:**
 1. **Genomic training populations are small**
 2. **Limited phenotypes are recorded**
- **The benefits of multiple-breed genomic evaluation models may vary, depending on the consistency of gametic phase between breeds**
 - Brito et al. (2015) – Low consistency of gametic phase for Canadian Alpine and Saanen breeds
 - Carillier et al. (2014) – Higher theoretical accuracies observed for multiple-breed models for French Alpine and Saanen breeds

Objective

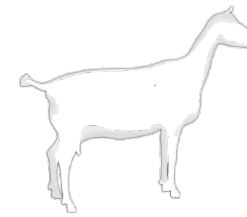
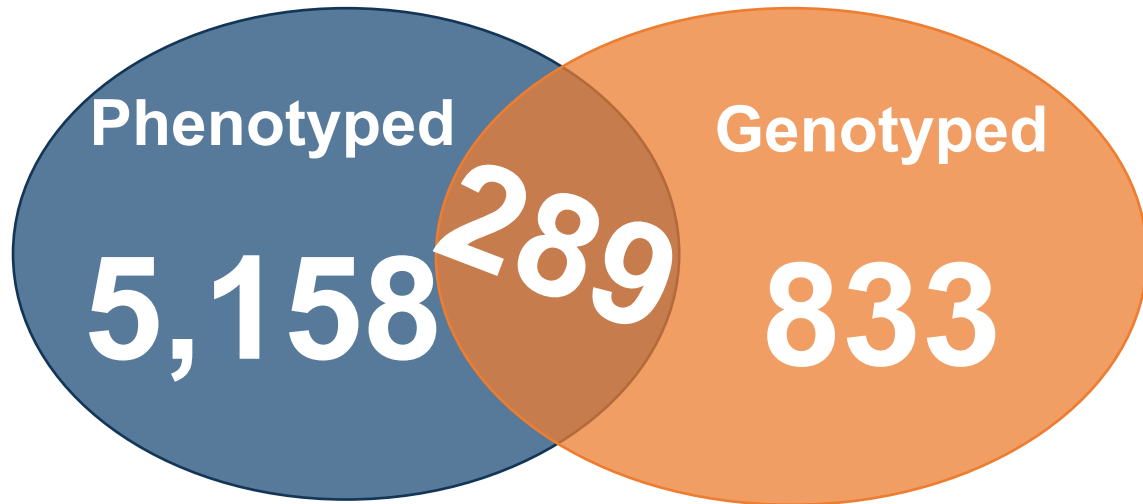
Compare the theoretical accuracy of single and multiple-breed single-step genomic evaluations for conformation traits of Canadian Alpine and Saanen goats.

Phenotypes and Genotypes

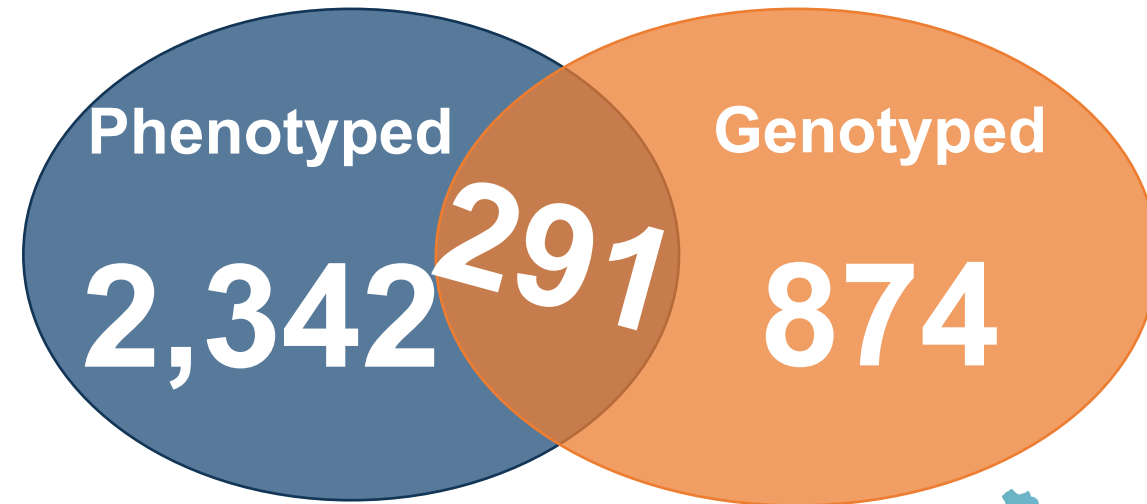
- Registered Alpine and Saanen bucks and does from across Canada were genotyped



Alpine



Saanen



Methods – Genetic Evaluations

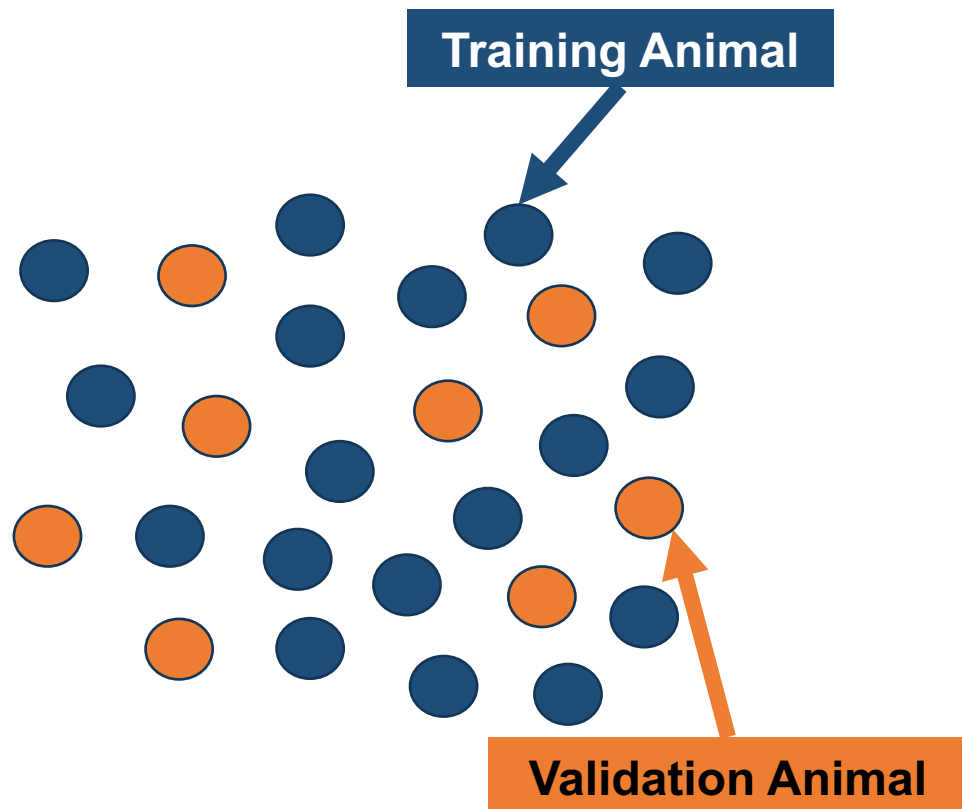
- BLUPf90 family programs used to estimate genetic parameters and predict (G)EBV
 - Optimal scaling parameters: $\tau = 1.0$ and $\omega = 0.8$
- **Genetic Evaluation Models:**
 - Single-trait animal models, with effects as in routine genetic evaluations
 - (G)EBV were predicted with full datasets and validation datasets, where phenotypes were removed for selection candidates and their descendants
- **Single-Breed and Multiple-Breed Models:**
 - Genetic parameters were calculated across breeds for the multiple-breed analyses
 - Breed was modelled as a fixed effect

Methods - Validation Design

Forward Validation

- All animals born > 2012 with average full dataset EBV accuracy > 0.40

All Genotyped Animals



Forward Cross-validation

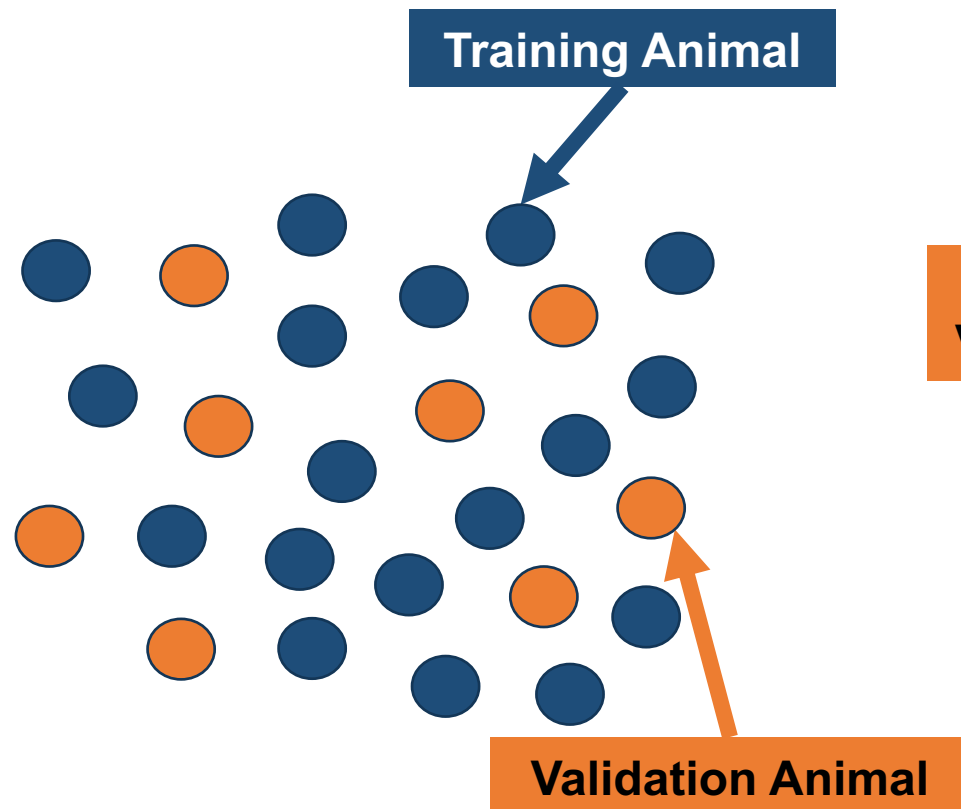
- Subsets of 100 animals eligible for validation population
- Results averaged over 10 replicates

Methods - Validation Design

Forward Validation

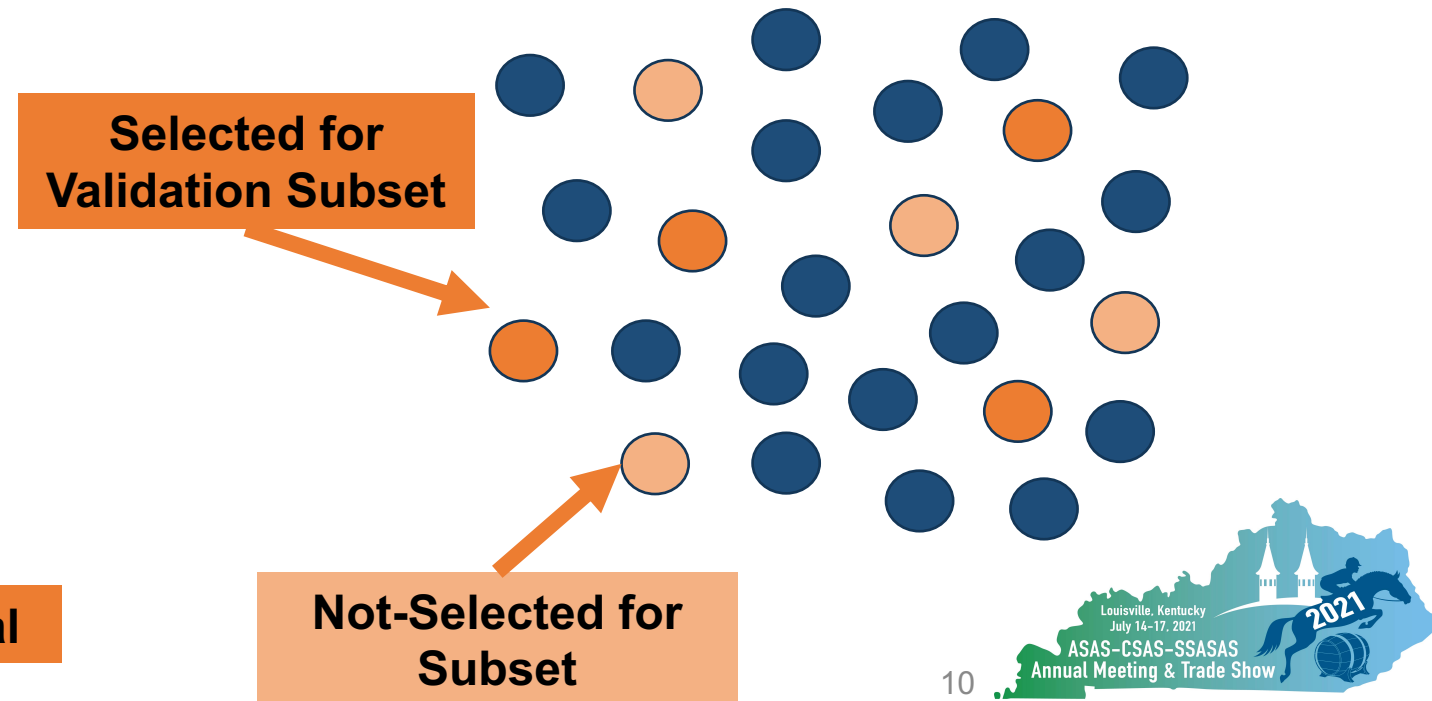
- All animals born > 2012 with average full dataset EBV accuracy > 0.40

All Genotyped Animals



Forward Cross-validation

- Subsets of 100 animals eligible for validation population
- Results averaged over 10 replicates



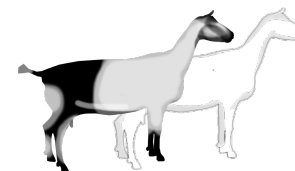
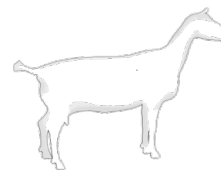
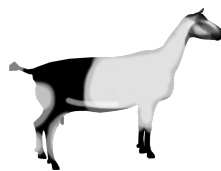
Methods – Theoretical Accuracy

- Theoretical accuracy (ACC) of (G)EBV was calculated from the standard error of prediction (s), accounting for inbreeding (f):

$$ACC_i = \sqrt{1 - \frac{(s_i)^2}{(1 + f_i)\sigma_a^2}} \quad (\text{Van Vleck, 1993})$$

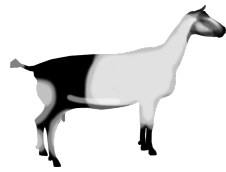
- Average (G)EBV accuracy of each trait was calculated for selection candidates, using the reduced validation datasets
- The average expected gain in theoretical accuracy of GEBV compared to EBV was assessed for various subsets of the population for both genotyped and non-genotyped animals

Heritability Estimates

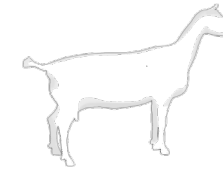


Trait	Abr.	Alpine	Saanen	Both
Body Capacity	BC	0.22 ± 0.02	0.11 ± 0.03	0.19 ± 0.02
Dairy Character	DC	0.16 ± 0.02	0.16 ± 0.04	0.17 ± 0.02
Feet and Legs	FL	0.17 ± 0.03	0.11 ± 0.03	0.16 ± 0.02
Fore Udder	FU	0.28 ± 0.03	0.23 ± 0.04	0.26 ± 0.02
General Appearance	GA	0.31 ± 0.03	0.21 ± 0.04	0.27 ± 0.02
Rear Udder	RU	0.22 ± 0.03	0.14 ± 0.03	0.19 ± 0.02
Suspensory Ligament	SL	0.18 ± 0.02	0.13 ± 0.04	0.15 ± 0.02
Teats	TE	0.18 ± 0.03	0.12 ± 0.04	0.16 ± 0.02

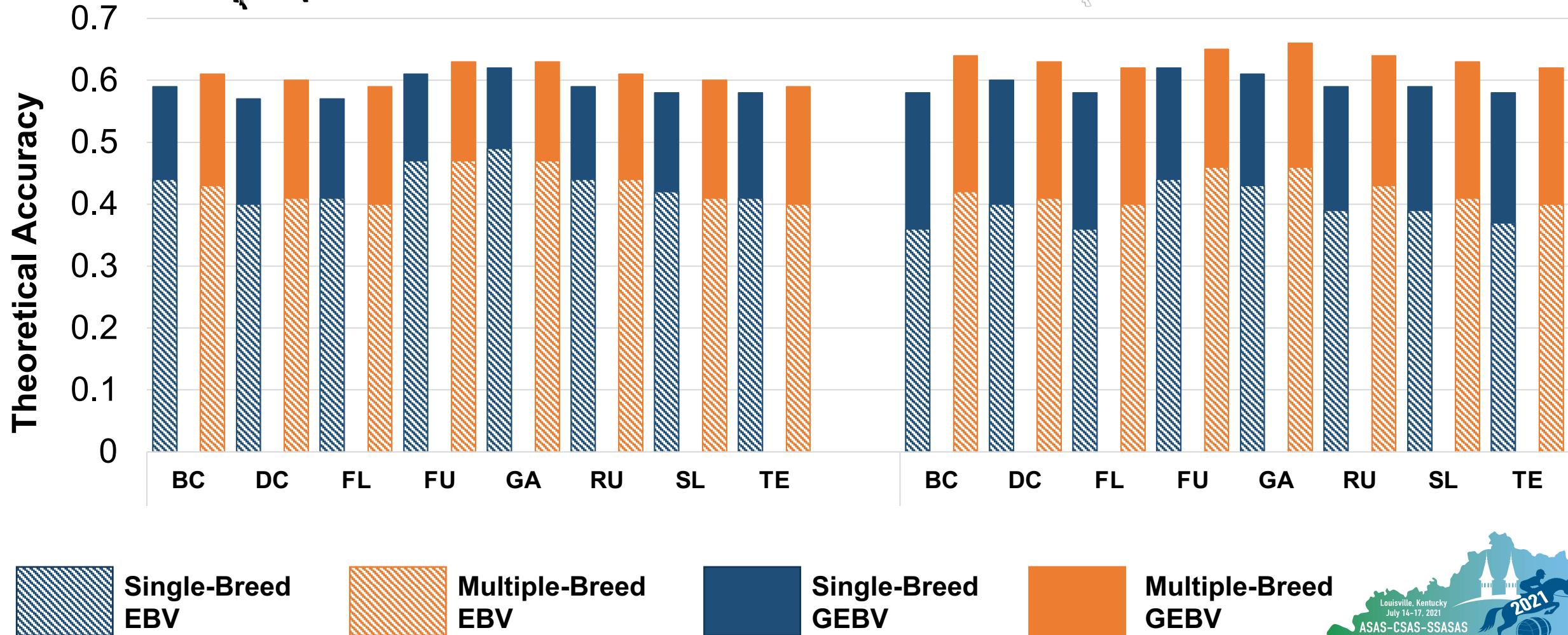
Accuracy of Selection Candidates



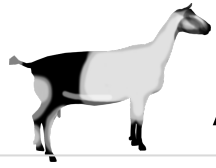
Alpine



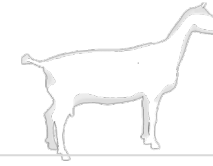
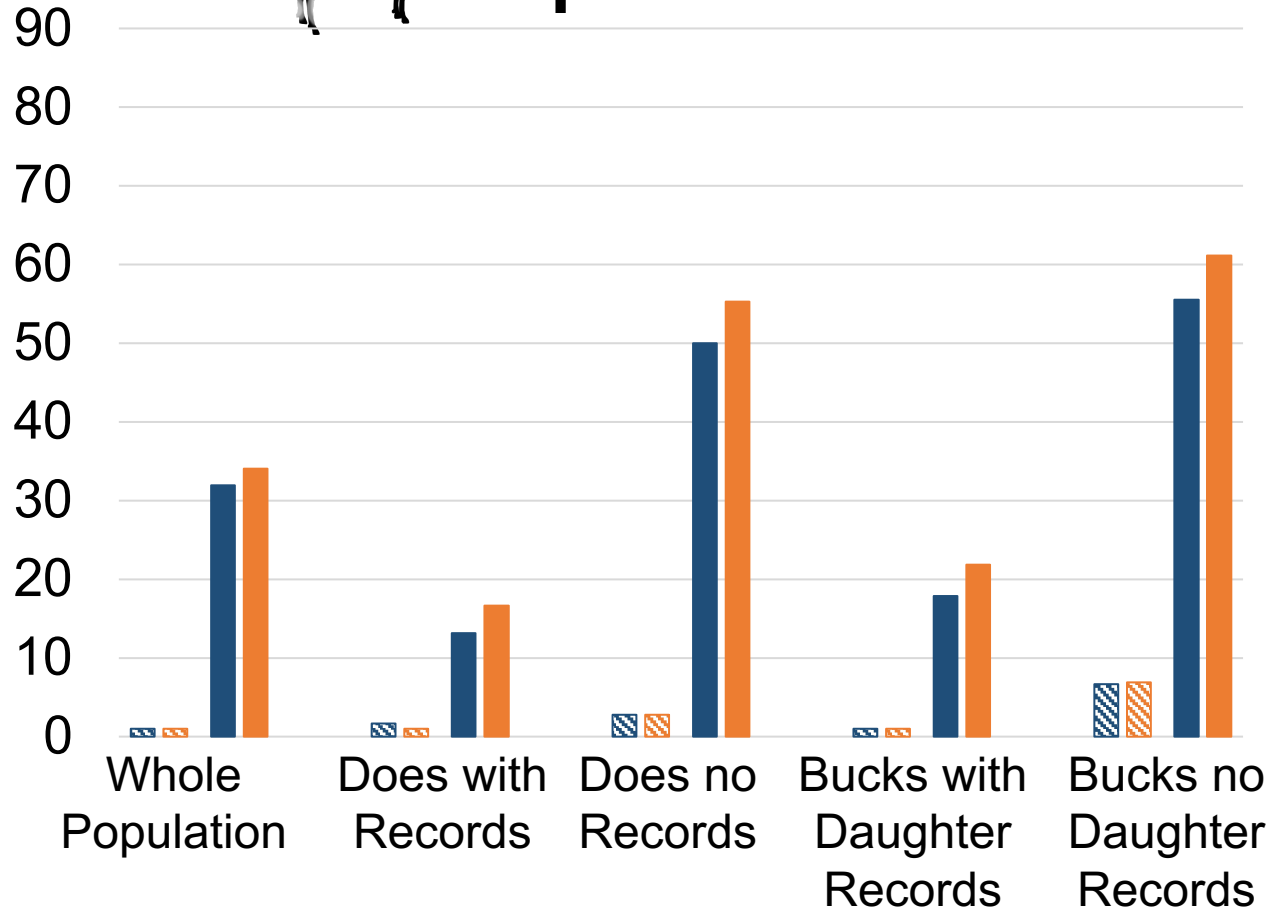
Saanen



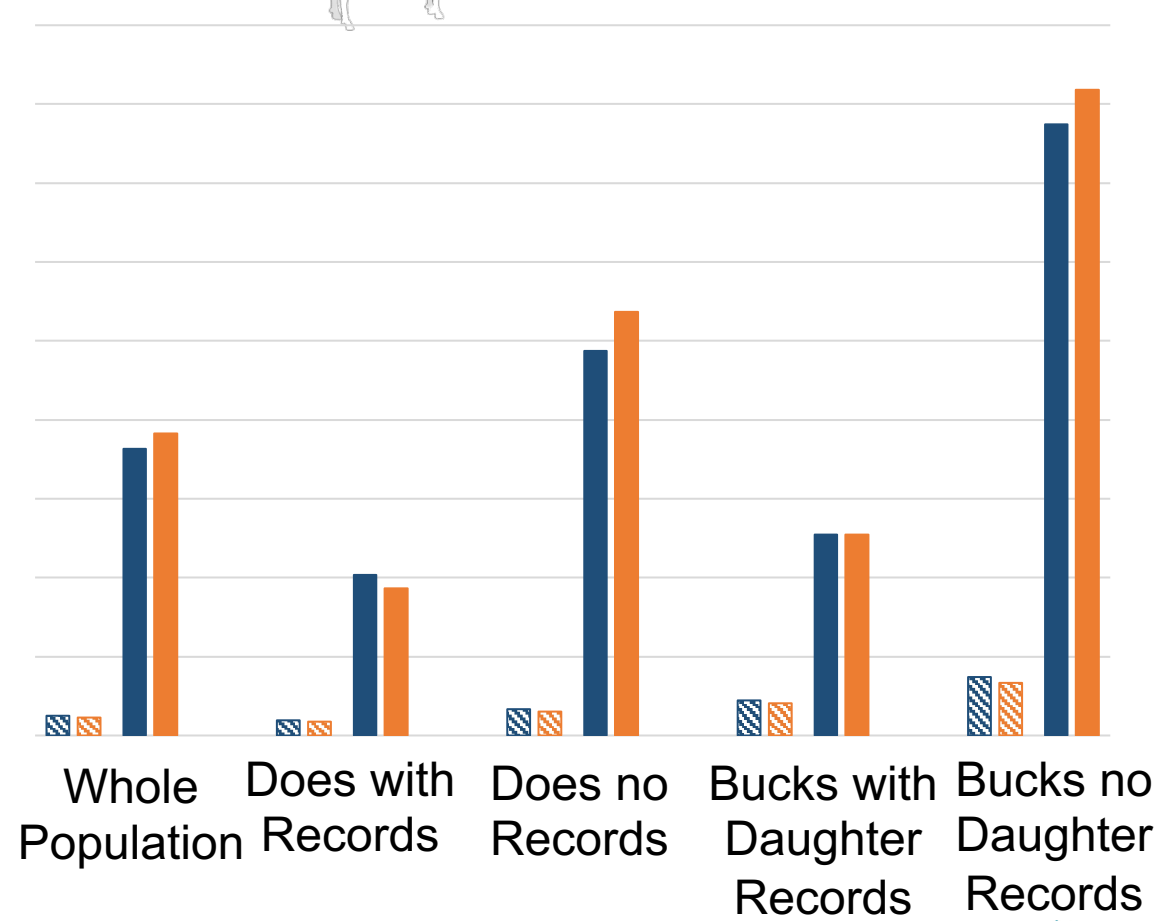
Gain in Accuracy from GEBV



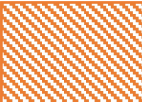
Alpine



Saanen



 Single-Breed, Non-Genotyped

 Multiple-Breed, Non-Genotyped

 Single-Breed, Genotyped

 Multiple-Breed, Genotyped

Conclusions

1. GEBV for selection candidates from multiple-breed analyses were consistently more accurate than single-breed analyses.
2. Substantial gains to selection accuracy are expected from the implementation of genomic evaluations for conformation traits, especially for unclassified does (49 to 55%) and bucks without daughter classification records (56 to 82%).

Acknowledgements

Project Team:

Centre for Genetic Improvement of Livestock:

Erin Massender
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Flavio Schenkel
Christine Baes

Purdue University:

Luiz Brito

Canadian Centre for Swine Improvement:

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Brian Sullivan

Data Provision:



GoatGenetics.Ca
GénétiqueCaprine.Ca

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Thank You!

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