ADSA Annual Meeting Louisville, Kentucky June 23rd, 2026

Managing genetic diversity: Strategies for sustainable livestock improvement

C.F. Baes, G. Condello, B. Makanjuola, S. Duggan, J.B. Cole, C. Maltecca, R.E. Jahnel, F. Malchiodi, P. Stothard, F.S. Schenkel, F. Miglior

Abstract #: 1115

UNIVERSITY OF GUELPH

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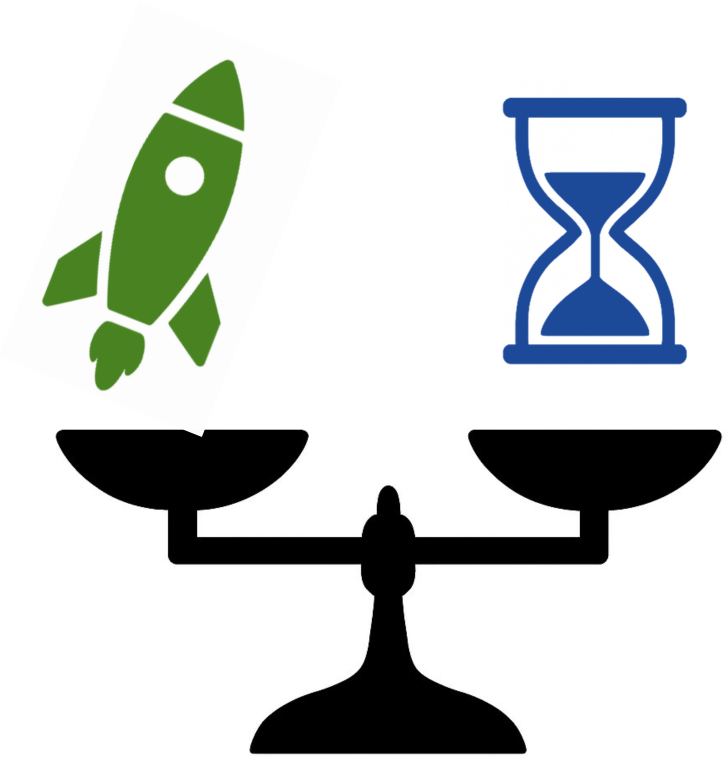
DAIRY at GUELPH
CANADA'S DAIRY UNIVERSITY

Genomic selection: Progress and pitfalls

Key benefits:

- Genomic selection allows increased accuracy and genetic gain
- Reduced generation interval

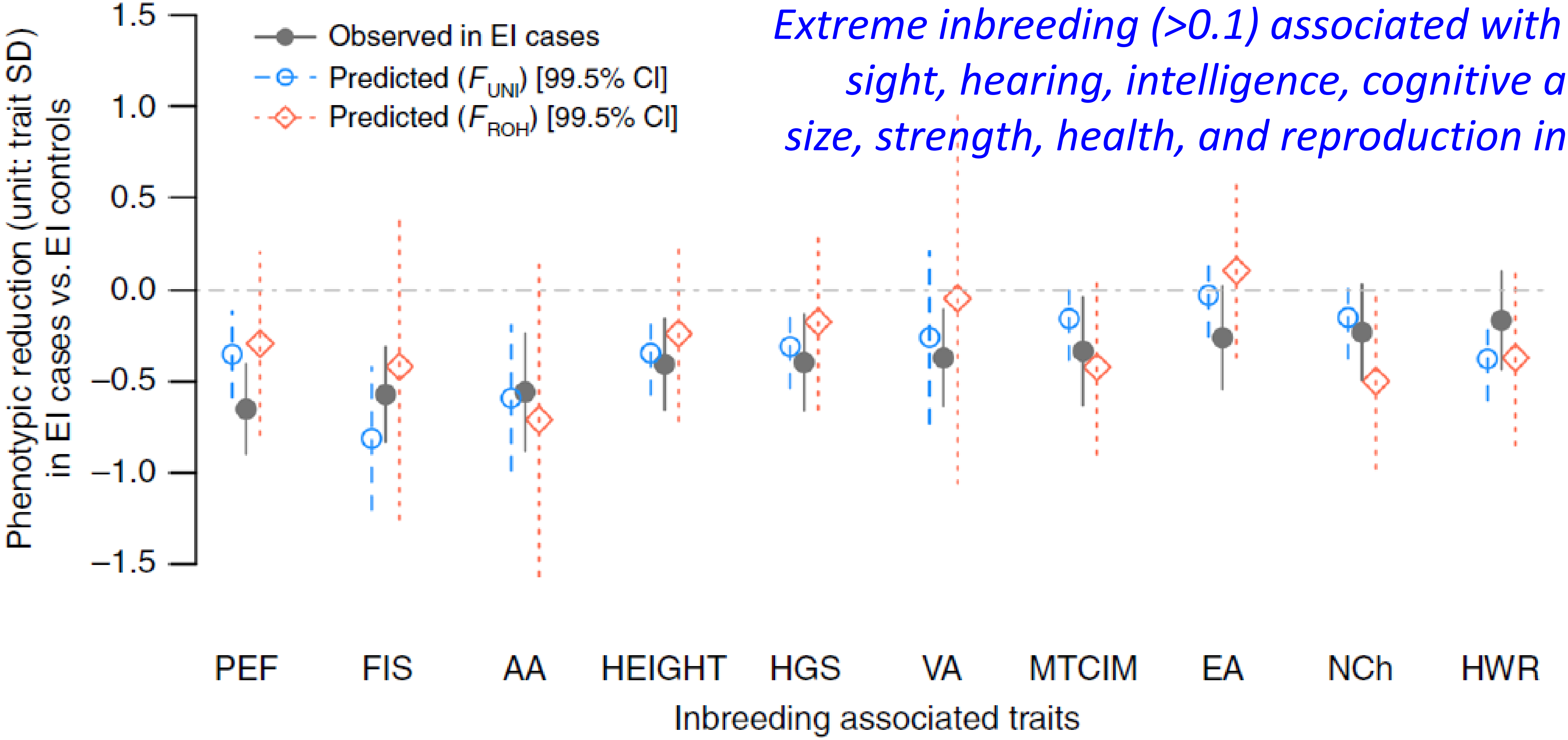


Key Challenges:

- Accelerated increase in inbreeding
- Increased homozygosity
- Emergence of recessive disorders

Need to balance fast progress / short-term gain with sustainable improvement

Why genetic diversity matters



Extreme inbreeding (>0.1) associated with impaired sight, hearing, intelligence, cognitive ability, size, strength, health, and reproduction in humans

Yengo, L., N. R. Wray, and P. M. Visscher. 2019. Extreme inbreeding in a European ancestry sample from the contemporary UK population. Nature Communications 10:3719.

Why genetic diversity matters

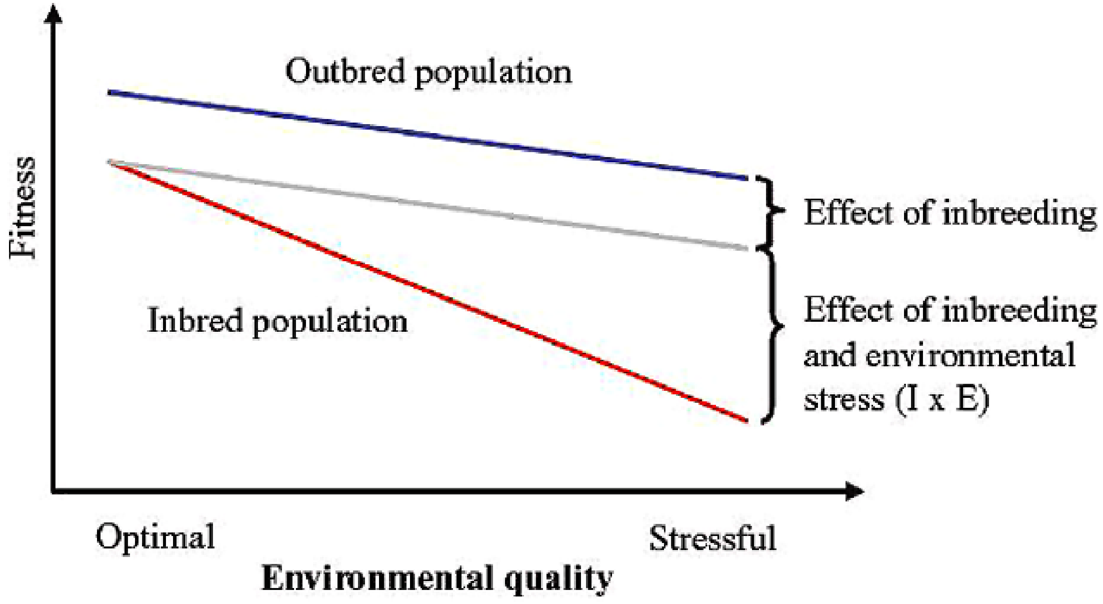


FIGURE 2 | Schematic illustration of fitness effects of inbreeding by environment interactions. Assuming the effect of inbreeding is independent of the environment, the reduction in fitness as a result of reduced environmental quality will be equal for outbred and inbred populations. The blue and gray lines illustrate fitness of an outbred and an inbred population, respectively, in the absence of inbreeding by environment interactions. Inbreeding depression is, however, often more severe under stressful environmental conditions. Thus, the red line illustrates fitness of an inbred population taking into account the effect of inbreeding by environment interactions (redrawn from Kristensen et al., 2010).

Short-term: as populations become smaller and less diverse, relative fitness decreases (i.e., survival and fertility, etc.)

Long-term consequences: lower gene diversity means less raw material for adaptations to changing environments, which may affect long-term survival

Also: Increased risk of nasty recessives

Assessment of genetic diversity in (Canadian) dairy cattle


J. Dairy Sci. 103
https://doi.org/10.3168/jds.2019-18013
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Effect of genomic selection on rate of inbreeding and coancestry and effective population size of Holstein and Jersey cattle populations

Bayode O. Makanjuola,[1] Filippo Miglior,[1,2] Emhimad A. Abdalla,[1] Christian Maltecca,[1,3] Flavio S. Schenkel,[1] and Christine F. Baes[1,4*]


RESEARCH ARTICLE Open Access

Inbreeding and runs of homozygosity before and after genomic selection in North American Holstein cattle

Mehrnush Forutan[1,2*], Saeid Ansari Mahyari[1*], Christine Baes[2], Nina Melzer[3], Flavio Schramm Sch
and Mehdi Sargolzaei[2,4,5]


RESEARCH ARTICLE Open Access

Identification of unique ROH regions with unfavorable effects on production and fertility traits in Canadian Holsteins

Bayode O. Makanjuola[1*], Christian Maltecca[1,2], Filippo Miglior[1], Gabriele Marras[3], Emhimad A. Abdalla[1], Flavio S. Schenkel[1] and Christine F. Baes[1,4]


J. Dairy Sci. 103:5302–5313
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Symposium review: **Exploiting homozygosity in the era of genomics—Selection, inbreeding, and mating programs***

C. Maltecca,[1]† F. Tiezzi,[1] J. B. Cole,[2] and C. Baes[3,4]


J. Dairy Sci. 102:2807–2817
https://doi.org/10.3168/jds.2018-15520
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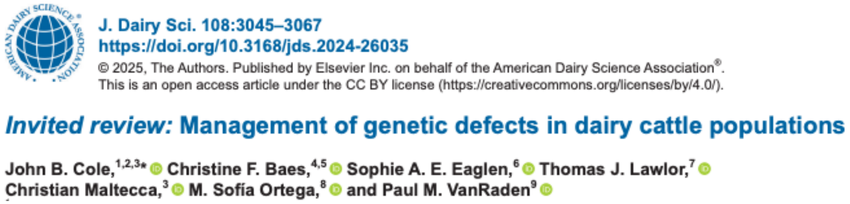
Symposium review: **The genomic architecture of inbreeding: How homozygosity affects health and performance***

Christine F. Baes,[1,2]† Bayode O. Makanjuola,[1] Filippo Miglior,[1,3] Gabriele Marras,[1,4] Jeremy T. Howard,[5,6] Allison Fleming,[1,3] and Christian Maltecca[6]


RESEARCH ARTICLE

Effect of recent and ancient inbreeding on production and fertility traits in Canadian Holsteins

Bayode O. Makanjuola[1*], Christian Maltecca[1,2], Filippo Miglior[1], Flavio S. Schenkel[1] and Christine F. Baes[1,3]


J. Dairy Sci. 108:3045–3067
https://doi.org/10.3168/jds.2024-26035
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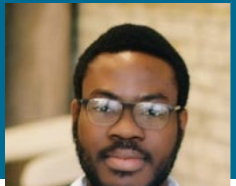
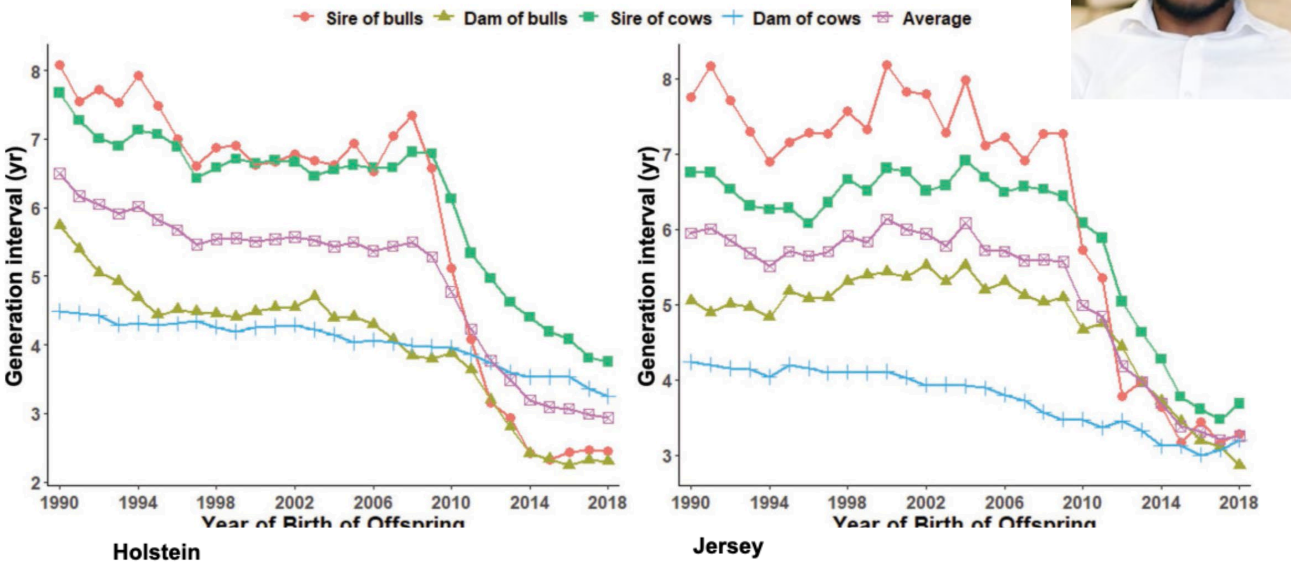
Invited review: **Management of genetic defects in dairy cattle populations**

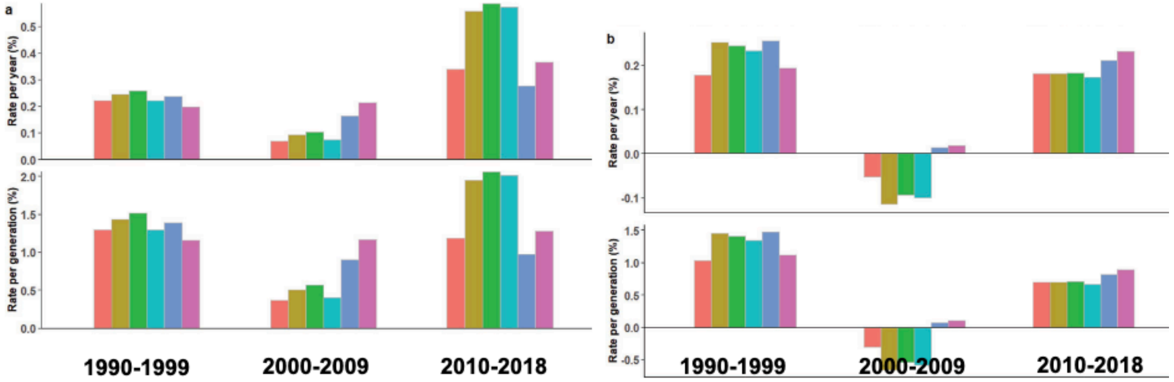
John B. Cole,[1,2,3*] Christine F. Baes,[4,5] Sophie A. E. Eaglen,[6] Thomas J. Lawlor,[7] Christian Maltecca,[3] M. Sofía Ortega,[8] and Paul M. VanRaden[9]

Evidence: inbreeding trends



- Estimate the rate of inbreeding and effective population size using both pedigree and genomic information for animals born between 1990 and 2018
- Evaluate the changes in effective population size following genomic selection
- Compare genetic diversity pre and post genomics



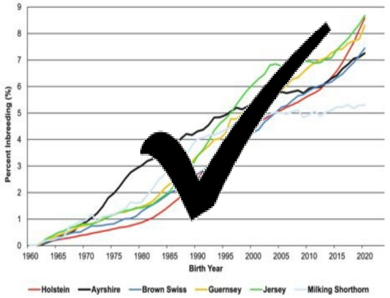


Effective population size	Estimated values
Pedigree (Ne_{PED})	66
Runs of Homozygosity ($Ne_{ROH\_SNP1101}$)	46

Makanjuola et al., 2020

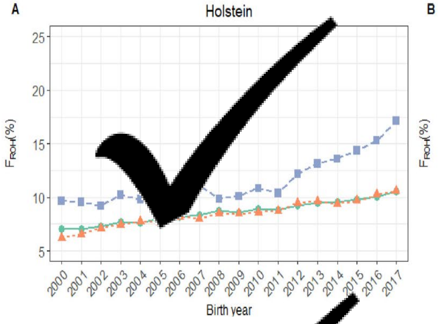
Rate of Inbreeding is increasing (fact check)

Is the rate of inbreeding increasing in the US? In all breeds?



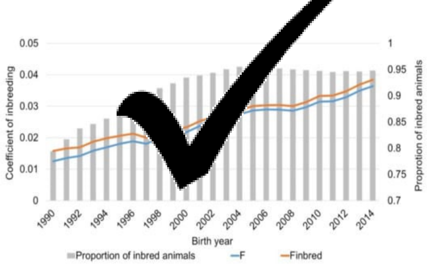
L.F. Brito, N. Bedere, F. Douhard, H.R. Oliveira, M. Arnal, F. Peñagaricano, A.P. Schinckel, C.F. Baes, F. Miglior, (2021) Genetic selection of high-yielding dairy cattle toward sustainable farming systems in a rapidly changing world. Animal,(15, 1)

How about in Australian cows?



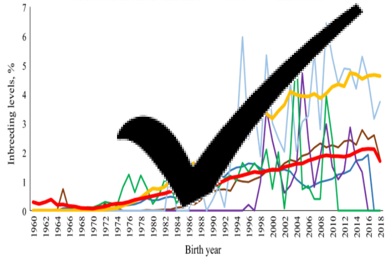
Scott, B. A., M. Haile-Mariam, B. G. Cocks, and J. E. Pryce. 2021. How genomic selection has increased rates of genetic gain and inbreeding in the Australian national herd, genomic information nucleus, and bulls. Journal of Dairy Science 104:11832-11849.

What about German cows?



Wirth A, Duda J, Distl O. Genetic Diversity and the Impact of the Breed Proportions of US Brown Swiss in German Brown Cattle. Animals. 2021; 11(1):152

But what about red cows?



Nyman, S., Johansson, A.M., Palucci, V. *et al.* Inbreeding and pedigree analysis of the European red dairy cattle. *Genet Sel Evol* **54**, 70 (2022). https://doi.org/10.1186/s12711-022-00761-3

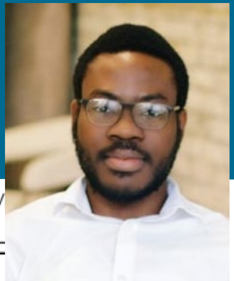
(…etc)

Rates of inbreeding are increasing faster in the genomic era

Implementation of genomic selection decreasing effective population size

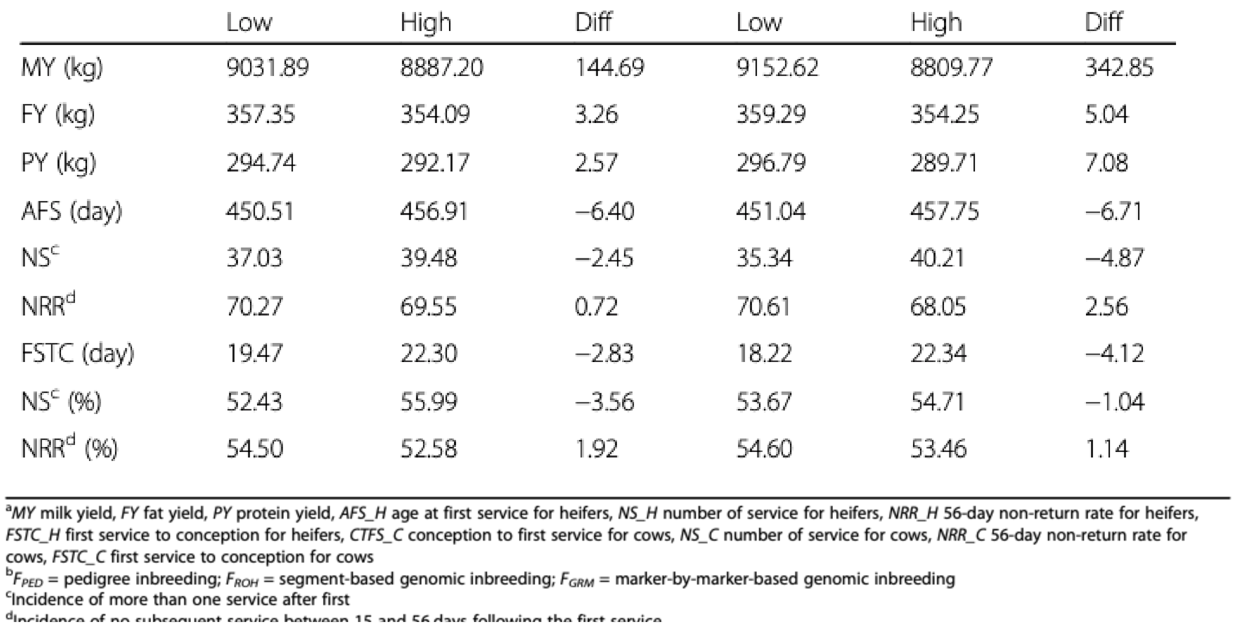
Not sure what long-term implications are

Evidence: inbreeding trends



- Estimate the effect of inbreeding on production and fertility traits
- Assess the effect of recent and ancient inbreeding on production and fertility traits

Table 4 Estimates of inbreeding depression for all significant traits, expressed as the difference (Diff) in predicted phenoty between lowly inbred (5% percentile) and highly inbred (95% percentile) from the mean for F_{PED}, F_{ROH} and F_{GRM}



Traits[a]	F_{PED}[b]			F_{ROH}[b]		
	Low	High	Diff	Low	High	Diff
MY (kg)	9031.89	8887.20	144.69	9152.62	8809.77	342.85
FY (kg)	357.35	354.09	3.26	359.29	354.25	5.04
PY (kg)	294.74	292.17	2.57	296.79	289.71	7.08
AFS (day)	450.51	456.91	−6.40	451.04	457.75	−6.71
NS[c]	37.03	39.48	−2.45	35.34	40.21	−4.87
NRR[d]	70.27	69.55	0.72	70.61	68.05	2.56
FSTC (day)	19.47	22.30	−2.83	18.22	22.34	−4.12
NS[c] (%)	52.43	55.99	−3.56	53.67	54.71	−1.04
NRR[d] (%)	54.50	52.58	1.92	54.60	53.46	1.14

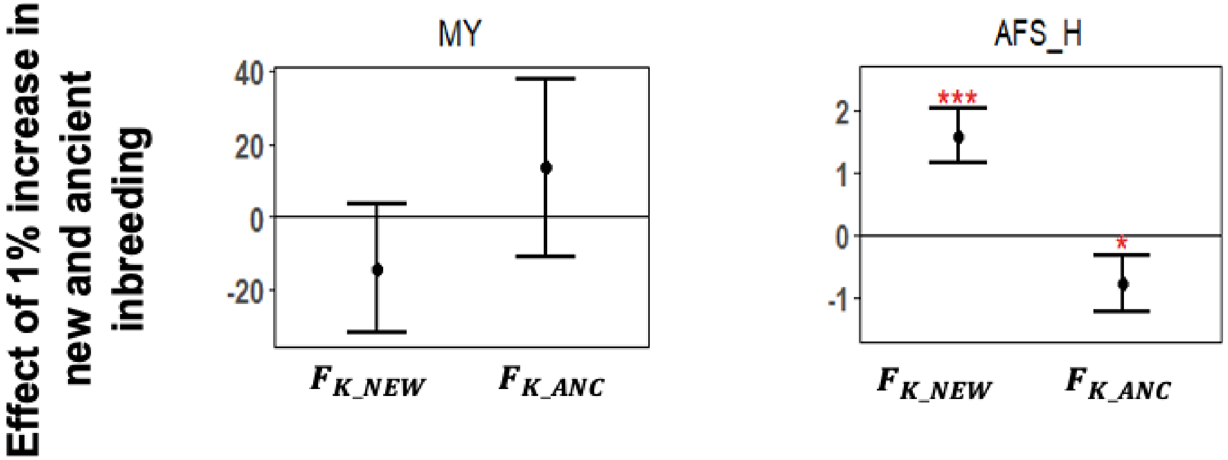
---

[a] *MY* milk yield, *FY* fat yield, *PY* protein yield, *AFS_H* age at first service for heifers, *NS_H* number of service for heifers, *NRR_H* 56-day non-return rate for heifers, *FSTC_H* first service to conception for heifers, *CTFS_C* conception to first service for cows, *NS_C* number of service for cows, *NRR_C* 56-day non-return rate for cows, *FSTC_C* first service to conception for cows

[b] F_{PED} = pedigree inbreeding; F_{ROH} = segment-based genomic inbreeding; F_{GRM} = marker-by-marker-based genomic inbreeding

[c] Incidence of more than one service after first

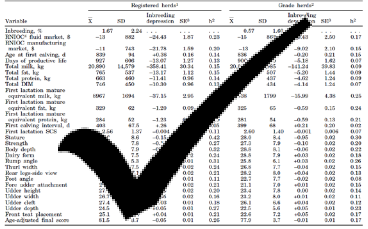
[d] Incidence of no subsequent service between 15 and 56 days following the first service



Makanjuola et al., 2021

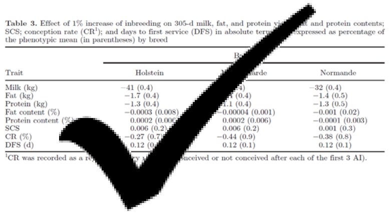
Estimated inbreeding depression (fact check)

Were there detrimental effects of inbreeding in American Holsteins in the 90's?



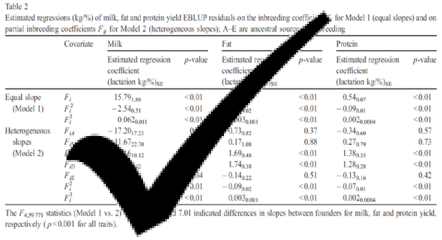
Smith, L. A., B. G. Cassell, and R. E. Pearson. 1998. The effects of inbreeding on the lifetime performance of dairy cattle. Journal of Dairy Science 81:2729-2737

How about in French cows?



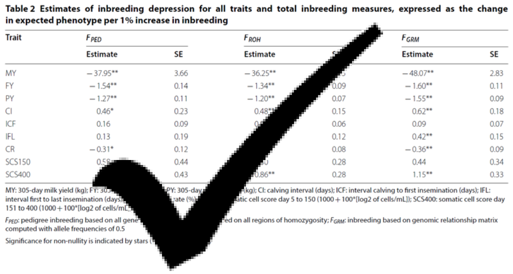
Dezetter, C., H. Leclerc, S. Mattalia, A. Barbat, D. Boichard, and V. Ducrocq. 2015. Inbreeding and crossbreeding parameters for production and fertility traits in Holstein, Montbéliarde, and Normande cows. Journal of Dairy Science 98:4904-4913.

What about Jerseys?



Gulisija, D., D. Gianola, K. A. Weigel, and M. A. Toro. 2006. Between-founder heterogeneity in inbreeding depression for production in Jersey cows. Livestock Science 104:244-253.

Surely not in Dutch cows, though, right?



Doekes, H. P., R. F. Veerkamp, P. Bijma, G. de Jong, S. J. Hiemstra, and J. J. Windig. Inbreeding depression due to recent and ancient inbreeding in Dutch Holstein-Friesian dairy cattle. Genetics Selection Evolution (2019) 51:54.

(etc…)

Negative effect of inbreeding observed on many traits

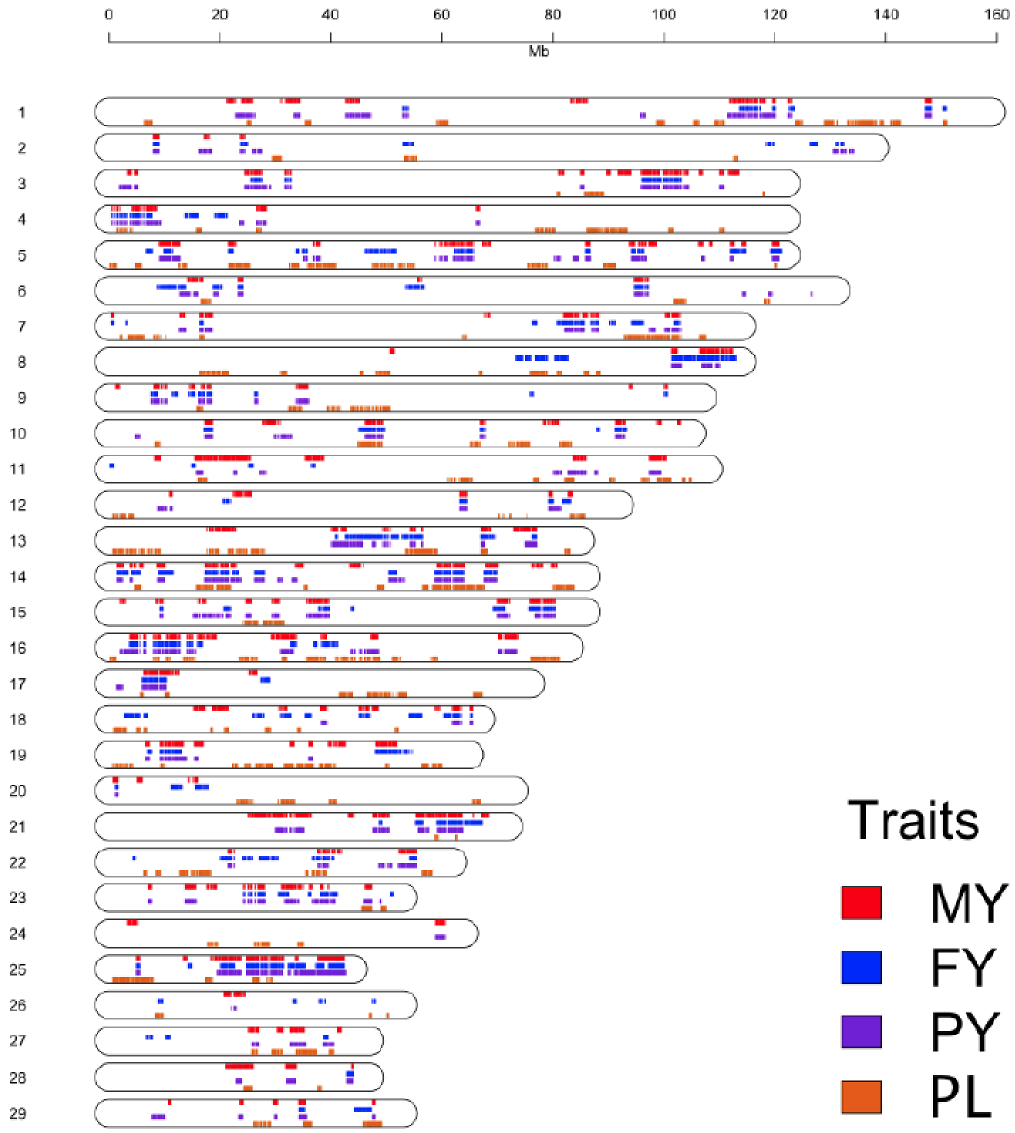
Recent inbreeding had more detrimental effect compared to ancient inbreeding

Little evidence of purging due to selection

(Gulisija, Crow and Weigel 2006 is an exception… others?)

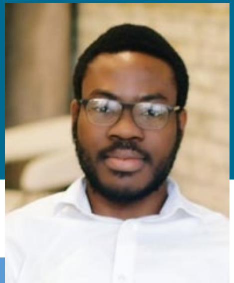
ROH used to find undesireable (not lethal) regions

- Some mutations in the population are sub-lethal: they harm performance but don’t kill animals
- They are more difficult to find than lethal haplotypes
- May appear in ROH



Maltecca et al., 2019

Evidence: inbreeding trends



- Identify specific genetic regions where homozygosity has negative effects on production and fertility traits
- Identify unique ROH with unfavorable effects across multiple traits

Trait	BTA	ROH effects	$-\log_{10}$ (P value)
MY (kg)	8	-545.69	6.64
FY (kg)	14	-23.59	6.65
PY (kg)	8	-16.34	6.25
NS	6	0.23	5.40
NRR	1	-0.10	3.41
FSTC (day)	6	7.80	4.84

Unique ROH regions with unfavorable effects within and across traits identified

Candidate genes with negative association detected

Measures to manage the frequency of detrimental regions need to be considered

Makanjuola et al., 2021

Haplotype frequencies by year (2008–2023)

- Genomics facilitates identification of recessive defects
- Impacts: pregnancy loss, malformations, early mortality, etc.
- Examples: Cholesterol Deficiency, Brachyspina, etc.

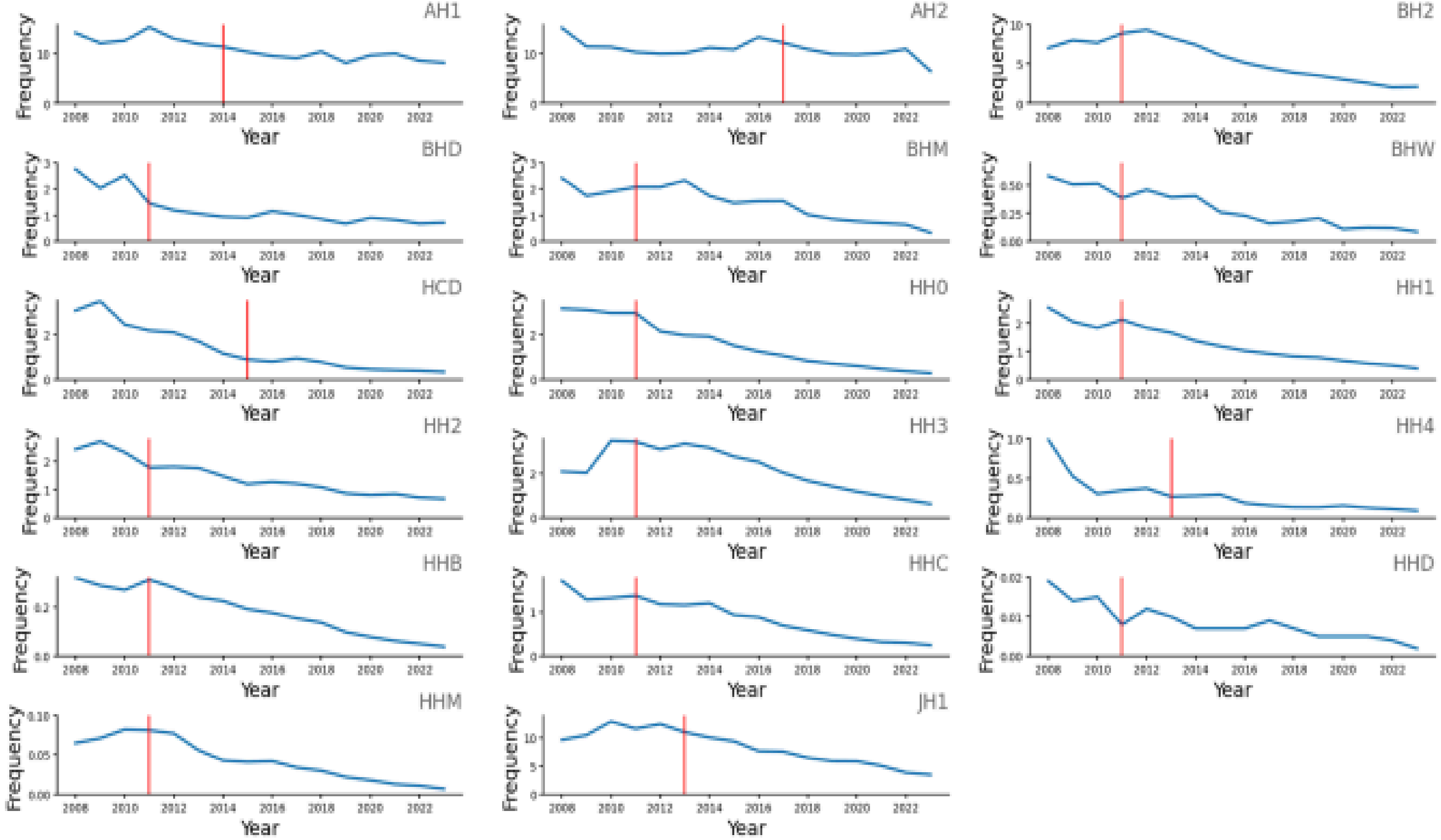


Figure 2. Haplotype frequencies by year (2008–2023) for recessive genetic defects in US Ayrshire, Brown Swiss, Holstein, and Jersey cattle, tracked by the Council on Dairy Cattle Breeding, that are under control (Al-Khudhair et al., 2024a). Vertical red lines indicate the year each haplotype was first published. AH1 = Ayrshire Haplotype 1 (PIRM/*UBE3B*), AH2 = Ayrshire Haplotype 2 (*RPAP2*), BH2 = Brown Swiss Haplotype 2 (*TUBD1*), BHD = spinal dysmyelination (SDM; *SPAST*), BHM = spinal muscular atrophy (SMA; *KDSR/FVT1*), BHW = Weaver (*PNPLA8*), HCD = cholesterol deficiency (*APOB*), HH0 = Holstein Haplotype 0 (brachyspina/*FANCI*), HH1 = Holstein Haplotype 1 (*APAF1*), HH2 = Holstein Haplotype 2 (*IFT80*), HH3 = Holstein Haplotype 3 (*SMC2*), HH4 = Holstein Haplotype 4 (*GART*), HHB = bovine leukocyte adhesion deficiency (*ITGB2*), HHC = complex vertebral malformation (*SLC35A3*), HHD = deficiency of uridine monophosphate synthase (*UMPS*), HHM = mulefoot (syndactyly; *LRP4*), and JH1 = Jersey haplotype 1 (*CWC15*). The year the haplotype test was introduced is not the time of initial discovery of a genetic defect; some defects were discovered decades before haplotype tests became available.

Cole et al., 2025

Haplotype frequencies by year (2008–2023)

- Higher homozygosity unmasks recessive defects
- Impacts: pregnancy loss, malformations, early mortality, etc.
- Examples: Cholesterol Deficiency, Brachyspina, etc.

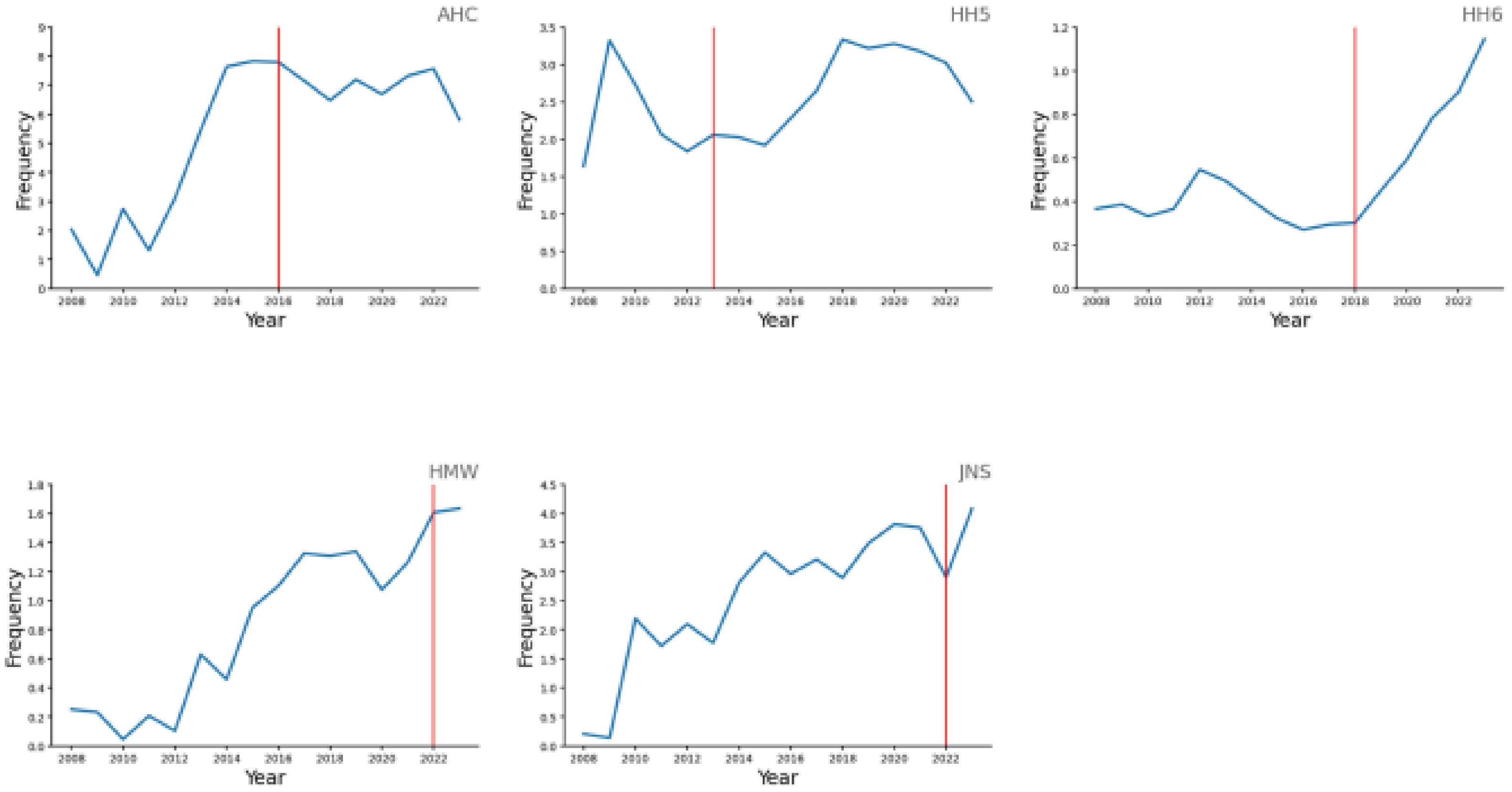


Figure 3. Haplotype frequencies by year (2008–2023) for recessive genetic defects in US Ayrshire, Holstein, and Jersey cattle, tracked by the Council on Dairy Cattle Breeding, which have unfavorable trends (Al-Khudhair et al., 2024a). Vertical red lines indicate the year the haplotype test associated with each defect was first published. AHC = Ayrshire Haplotype C (*CHRNB1*), HH5 = Holstein Haplotype 5 (*TFB1M*), HH6 = Holstein Haplotype 6 (*SDE2*), HMW = early-onset muscle weakness (*CACNA1S*), and JNS = Jersey neuropathy with splayed forelimbs (*UCHL1*). The year the haplotype test was introduced is not the time of initial discovery of a genetic defect; some defects were discovered decades before haplotype tests became available.

Cole et al., 2025

“We don’t have a way to quickly identify if a bull has a bad mutation we don’t know about”

“Are our top 10 and 100 lists doing us any favours?”

“My cows milk a lot already – do I really have to push them more?

“The client is responsible for mating decisions, we just help them choose bulls.”

“We can always crossbreed, but we haven’t reached that level of pain yet”

“I sit down with my rep and he gives me a list to choose from”

“How do producers make decisions?”

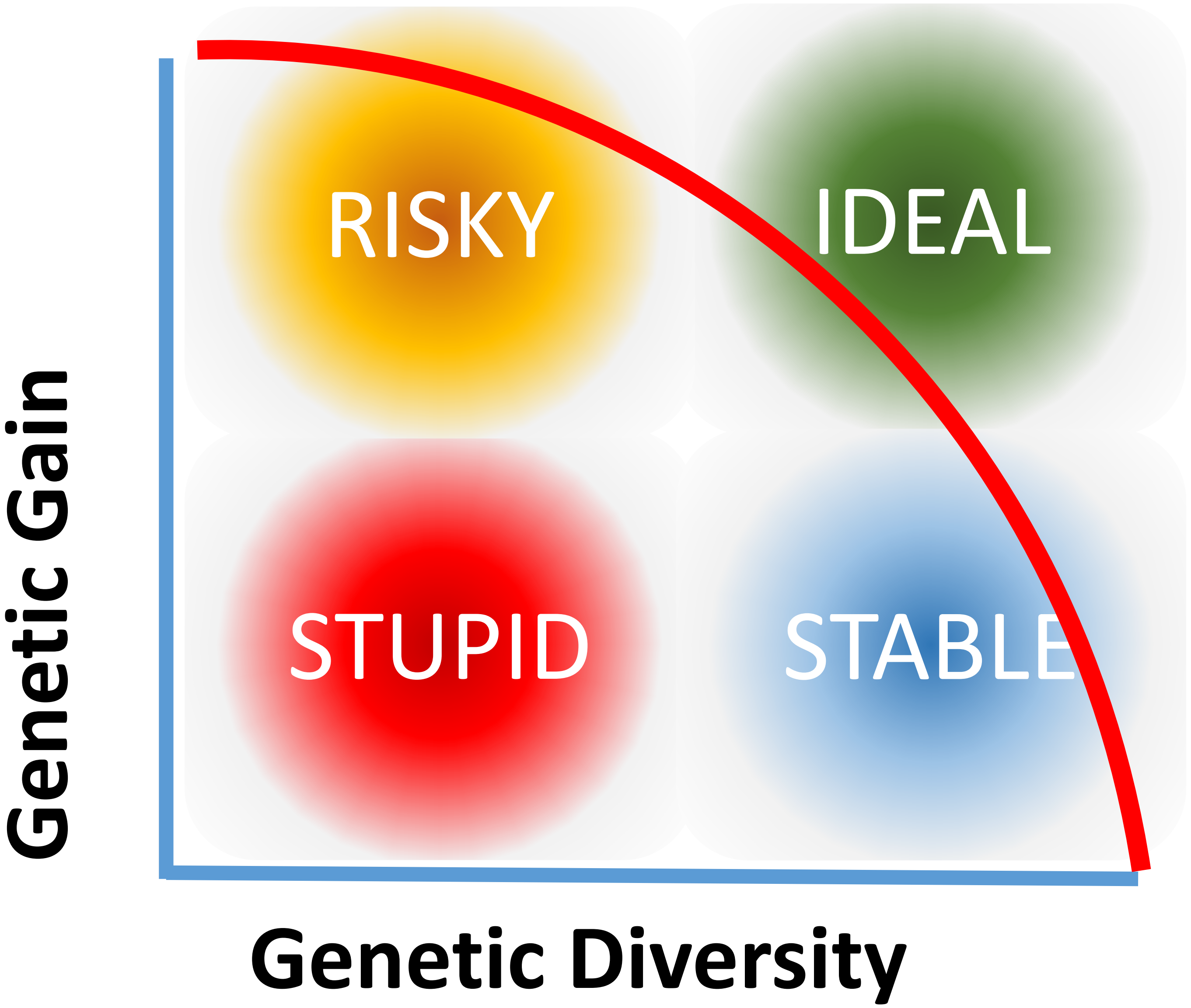
“I don’t want malformed calves”

“How do we create demand for outcross bulls?”

“All bulls are good these days, I just need healthy cows”

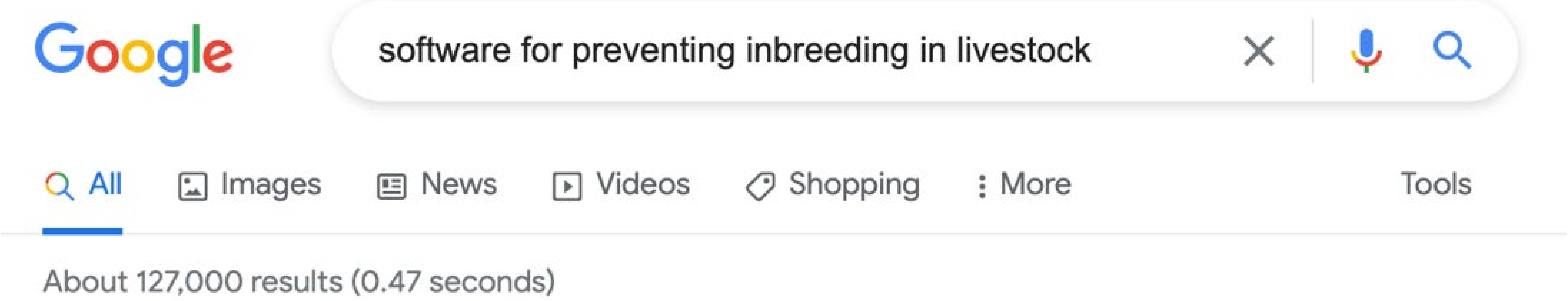
What should we do now?

The breeders dilema



Adapted from Gorjanc et al., 2019

Tools / strategies currently available

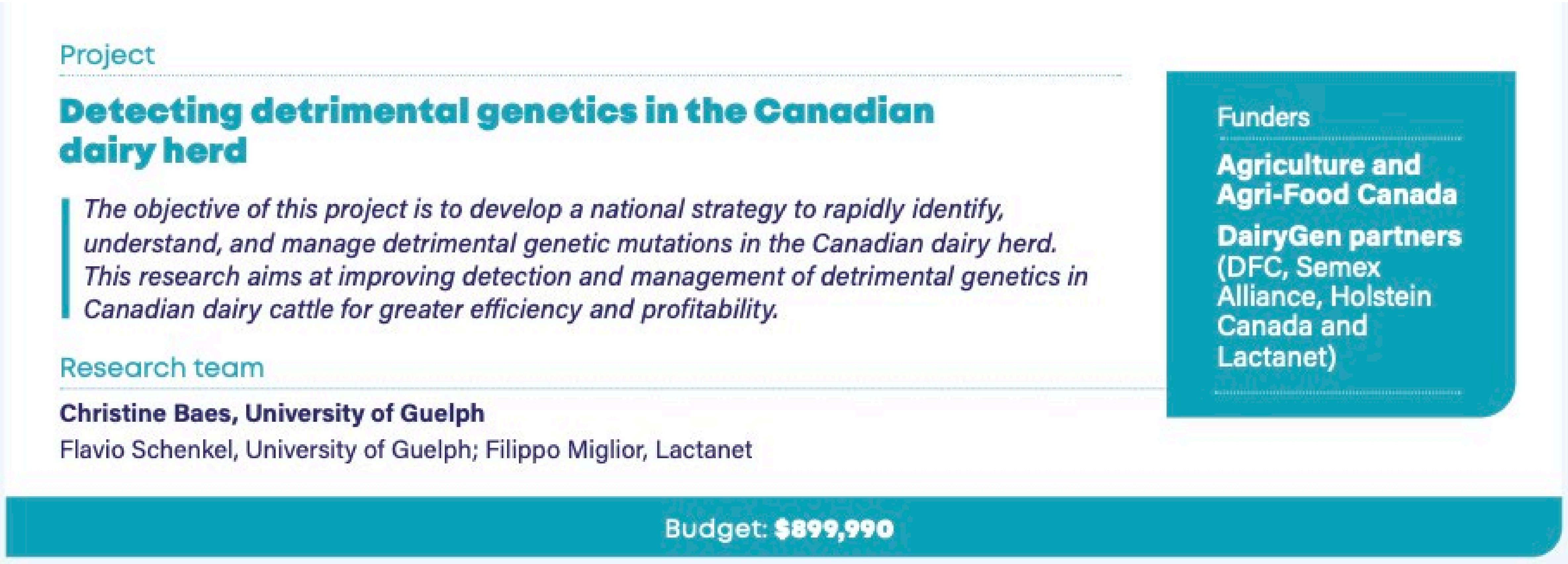


software for preventing inbreeding in livestock

About 127,000 results (0.47 seconds)

Reality:

- Optimal Contribution Selection rarely used in practice
- Top lists dominate conversations / decisions / semen tanks
- ”outcrosses” interesting, but generally unpopular
- Cross breeding, etc. mainly seen as ”Experimenting”



Project

Detecting detrimental genetics in the Canadian dairy herd

> *The objective of this project is to develop a national strategy to rapidly identify, understand, and manage detrimental genetic mutations in the Canadian dairy herd. This research aims at improving detection and management of detrimental genetics in Canadian dairy cattle for greater efficiency and profitability.*

Research team

Christine Baes, University of Guelph

Flavio Schenkel, University of Guelph; Filippo Miglior, Lactanet

Funders

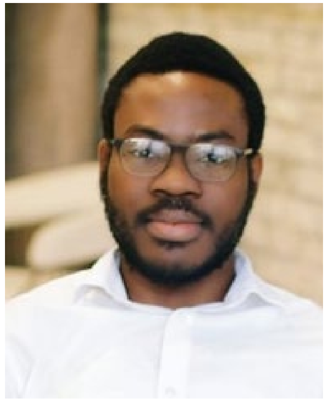
Agriculture and Agri-Food Canada

DairyGen partners (DFC, Semex Alliance, Holstein Canada and Lactanet)

Budget: **$899,990**

Shelby Duggan
(Undergrad)

Gabriella Condello
(PhD Student)

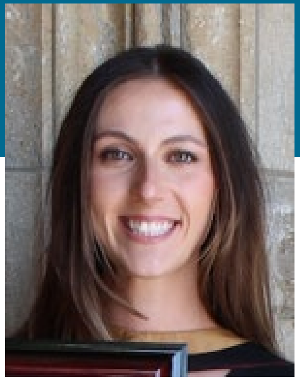


Bayode Makanjuola
(Research Associate)

Ricarda Jahnel
(Project Manager)

Colin Lynch
(Lactanet, Brian Wickam Young Person Exchange Program))

Survey producers to understand needs



Survey to ensure the developed reporting system meets the needs of the Dairy Industry:

1. Understand current limitations affecting reporting genetic conditions

2. Experience with suspected genetic conditions and reporting

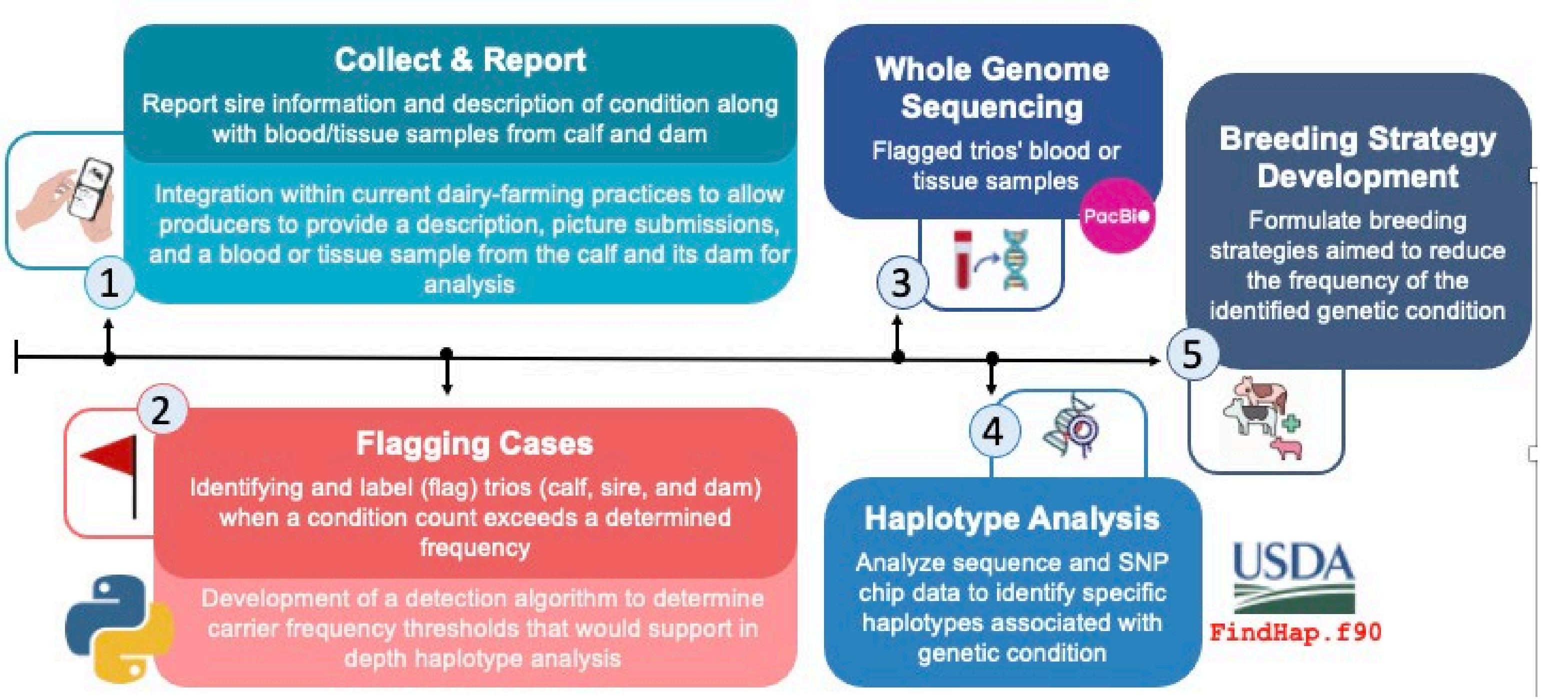
3. Outlook on genetic testing for health traits

<u>Poster 2350</u>: Developing a Rapid Monitoring System to Identify Genetic Conditions in Dairy Cattle

Survey approved by University of Guelph Research Ethics Board, Approval #64

Developing a monitoring system

- Industry portal: report photo, description, tissue sample
- Not all congenital defects are genetic in nature: Auto-flag cases beyond threshold →WGS + haplotype mapping
- Breeding recommendations fed back to AI companies & producers



1

Collect & Report

Report sire information and description of condition along with blood/tissue samples from calf and dam

Integration within current dairy-farming practices to allow producers to provide a description, picture submissions, and a blood or tissue sample from the calf and its dam for analysis

2

Flagging Cases

Identifying and label (flag) trios (calf, sire, and dam) when a condition count exceeds a determined frequency

Development of a detection algorithm to determine carrier frequency thresholds that would support in depth haplotype analysis

3

Whole Genome Sequencing

Flagged trios' blood or tissue samples

PacBio

4

Haplotype Analysis

Analyze sequence and SNP chip data to identify specific haplotypes associated with genetic condition

USDA

FindHap.f90

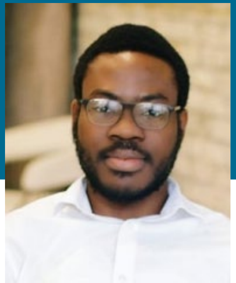
5

Breeding Strategy Development

Formulate breeding strategies aimed to reduce the frequency of the identified genetic condition

<u>Poster 2350</u>: Developing a Rapid Monitoring System to Identify Genetic Conditions in Dairy Cattle

Measuring relatedness



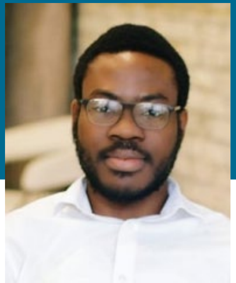
- **Relationship value (R-Value)** represents the percentage of DNA a sire shares with active females within a given population *(Van Doormaal et al., 2003)*

- Pedigree relationship (R) vs. Genomic relationship (GR)
- Expected Future Inbreeding (EFI/GFI) = ½ × R-Value
- Genomic R-Value ≈ 1.5 × R-Value in modern populations
- Diversity KPI for AI companies?

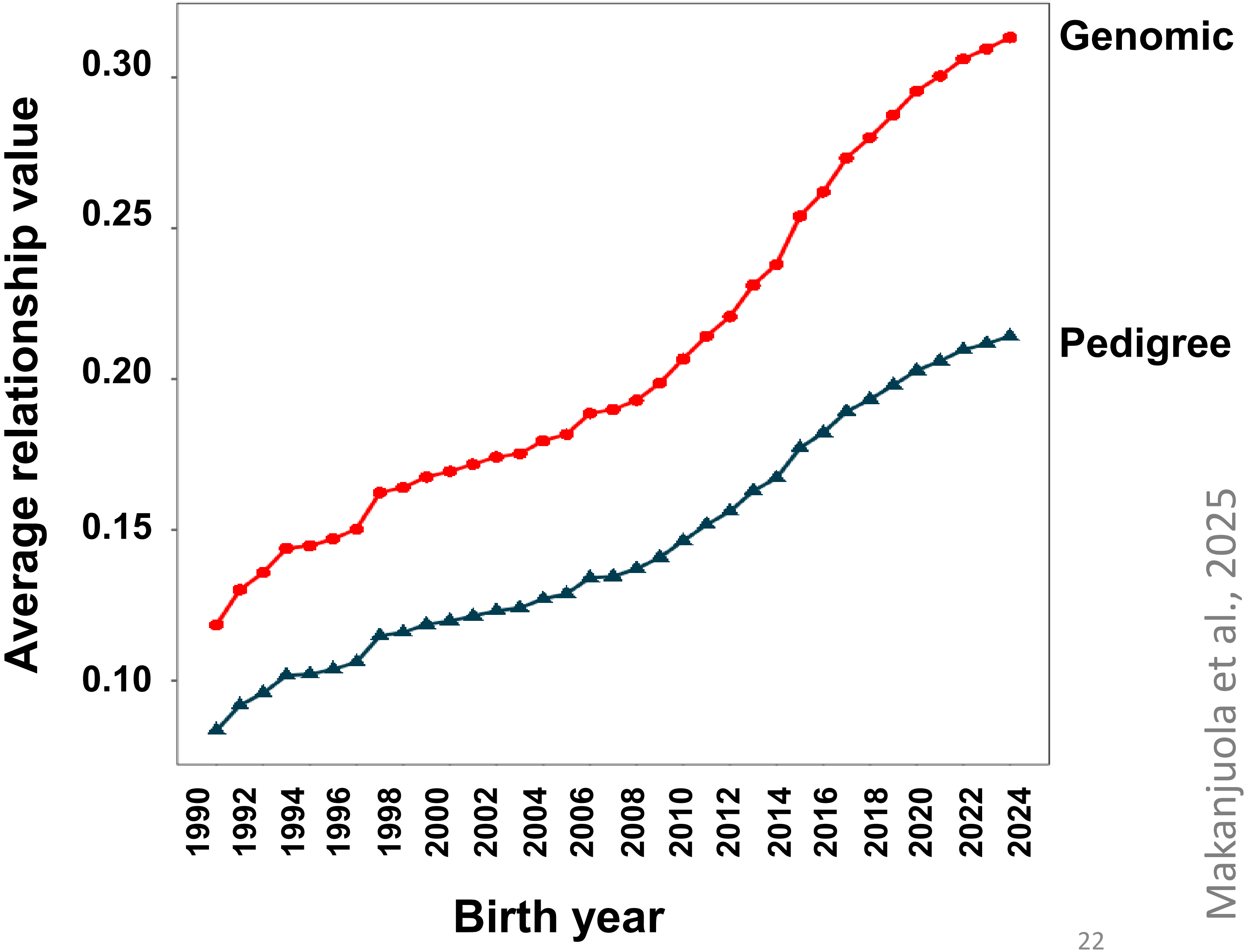
- Can calculate R-Vales for a bull with:
    - A population of females
    - All females in a herd

Makanjuola et al., 2025

Measuring relatedness



- Average R-Value increasing over time
  - ~50 % since 2000
- Increase mirrors the observed increase in inbreeding
- Genomic R-Values ≈ 1.5 × R in modern populations



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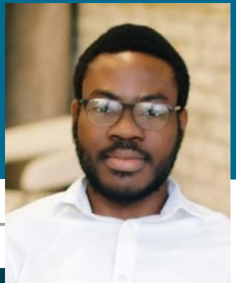
A herd-level tool to guide sire selection?

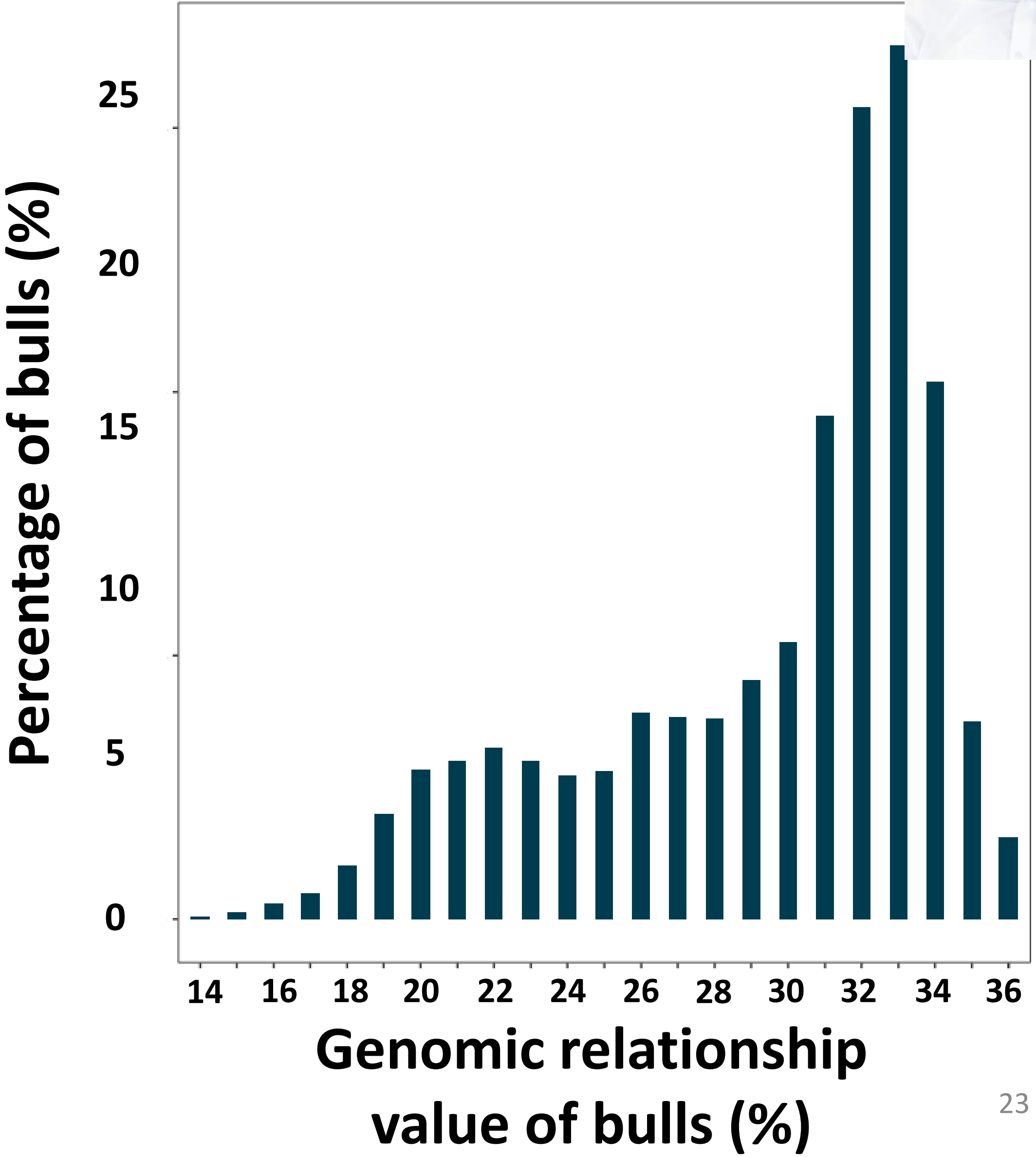


- R-values: 10% to 25%
- Genomic R-values: 14% to 36%

- For top 100 LPI bulls:
  - R-values: 19% to 25%
  - Genomic R-values: 28% to 36%

- Relationship dashboards to guide sire selection
- Encourage AI companies to publish diversity KPIs

Highlights opportunity to select less related bulls



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Other approaches / safeguards

Genetic conservation toolbox

- Gene banks: semen, embryos, somatic cells
- Strategic crossbreeding / introgression for rare alleles
- Monitor Effective Population Size (Ne) to guide action

Future-proofing with new technology?

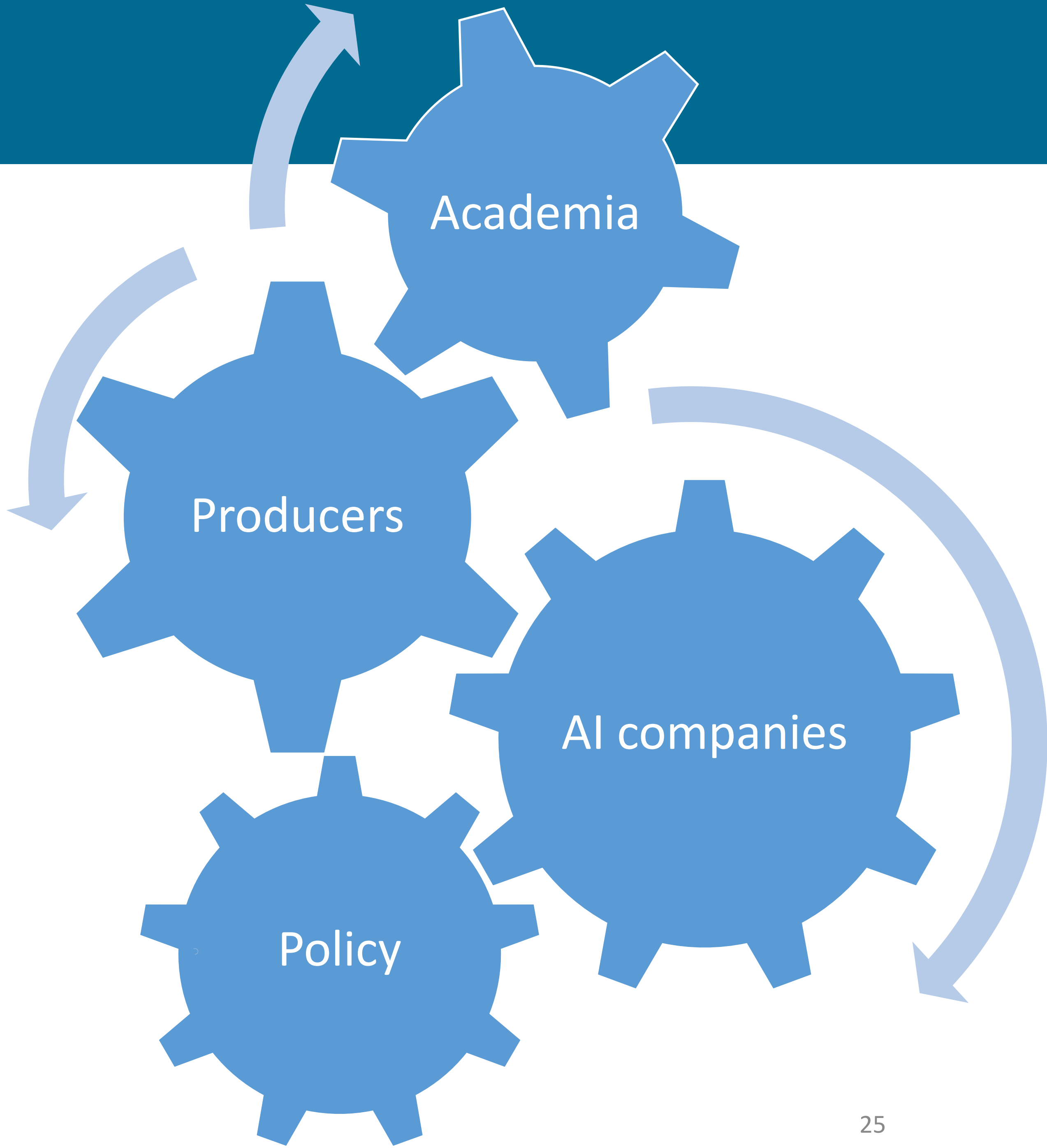
- CRISPR knock-in of favourable alleles w/out added Genomic R
- Targeted recombination to de-intensify ROH blocks
- Regulatory & societal considerations ahead

Roadmap for stakeholders

Understand and **acknowledge** that this is **our collective responsibility,**

-but there are already great tools we can use to do better!

- Academia: develop technology, metrics & algorithms
- AI companies: publish diversity KPIs, diversify sire teams
- Producers & Associations: adopt mate-selection tools, report defects
- Policy: incentive programs for conservation & transparency (Gene banks: semen, embryos, somatic cells)



Key messages

- Genetic diversity is our insurance for climate & market change
- Need to balance fast progress / short-term gain with sustainable improvement
- Genomics offers a lot of opportunities to manage genetic conditions
- Collaboratively Monitor • Manage • Innovate

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