



PURDUE
UNIVERSITY

Characterization of genomic diversity in sheep populations based on complementary metrics and its implications in genomic selection

Dr. Luiz F. Brito

Department of Animal Sciences, Purdue University



1

Diverse Production Systems

A collage of six images illustrating diverse sheep production systems: 1) Sheep in a snowy, mountainous landscape. 2) A large flock of sheep in a lush green field. 3) Sheep in a valley with snow-capped mountains in the background. 4) Sheep in a field with a large pile of hay. 5) Sheep in a large, modern indoor facility with a high ceiling and metal railings. 6) Sheep grazing in a dry, hilly landscape.

PURDUE | ANIMAL SCIENCES
AGRICULTURE

2

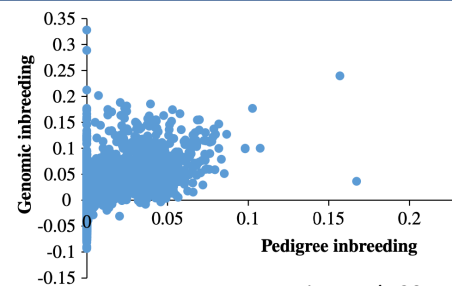
Genetic Diversity in Sheep Populations

- ✓ There are >600 sheep breeds around the world (FAO, 2021)
- ✓ Less-intensive “bottlenecks” during domestication (in comparison to other ruminant species): N_e ranging from 50 to 1,500 (Kijas et al., 2012; Brito et al., 2015, 2017)
- ✓ Recent formation of various composite breeds (e.g. Katahdin, Focus Prime)
- ✓ Many relatively-small breeds and flocks: higher risk of inbreeding
- ✓ Less-intensive production systems: greater environmental exposure
- ✓ **It is critical to maintain genetic diversity in sheep populations!**

3

Assessing Genetic Diversity: Challenges

- ✓ Pedigree recording and errors
 - Multiple-sire mating
 - Pasture-based lambing (over a short period)
 - Lower AI efficiency (need for “tailup rams”)
 - Pedigree incompleteness or lower pedigree depth
- ✓ Limited adoption of parentage testing and genomic data in many breeds/flocks
- ✓ Lower connection among sheep flocks



4

Main Goals of This Presentation

- ✓ Describe genomic diversity metrics that can be used for characterizing sheep populations (based on examples from our research group)
- ✓ Discuss the implications and applications of genetic diversity when designing genomic breeding programs in sheep

5

Genomic Inbreeding

- ✓ **Inbreeding coefficient** (Wright, 1922): probability that two base pairs at a randomly chosen position in the genome (locus) are **identical by descent**.

✓ Pedigree inbreeding

- Assumes all individuals in the base population are unrelated
- It does not account for Mendelian Sampling
- Highly influenced by the quality of the pedigree data
- Expected inbreeding values

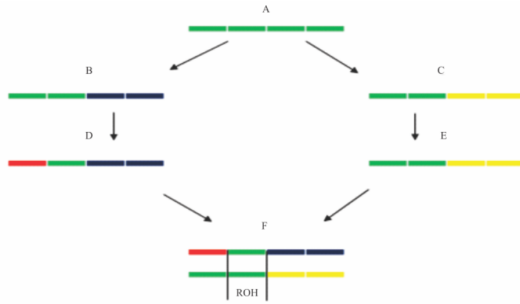
✓ Genomic inbreeding

- Accounts for Mendelian sampling between individuals
- Differentiate old from recent inbreeding
- Localized inbreeding in the genome
- Realized inbreeding values

6

ROH-based Inbreeding

- ✓ **Runs of homozygosity (ROH):** Contiguous lengths of homozygous genotypes that are present in an individual due to parents transmitting identical haplotypes to their offspring

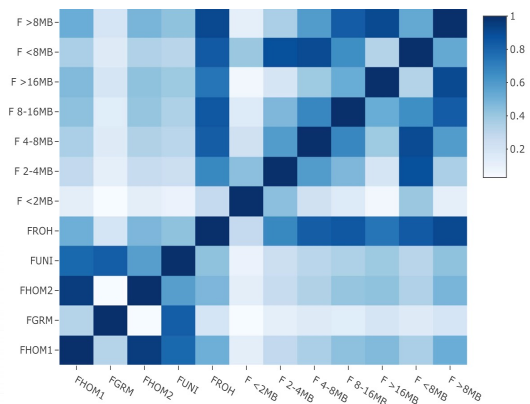


$$F_{ROH_L} = \frac{\sum L_{ROH}}{L_{AUTO}}$$

7

ROH-based Inbreeding

- ✓ Identification of inbreeding age:
- More ancient inbreeding: based on shorter ROH segments
 - More recent inbreeding: based on larger ROH segments **(of greater concern)**



Mulim et al., 2022

8

Study 1

Article

Detection and Visualization of Heterozygosity-Rich Regions and Runs of Homozygosity in Worldwide Sheep Populations

Alana Selli ^{1,*}, Ricardo V. Ventura ^{1,*}, Pablo A. S. Fonseca ², Marcos E. Buzanskas ³, Lucas T. Andrietta ¹, Júlio C. C. Balieiro ¹ and Luiz F. Brito ⁴



PURDUE
AGRICULTURE

ANIMAL SCIENCES

9

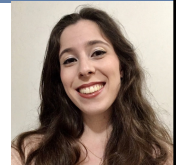
9

Detection and Visualization of ROH and HER

Article

Detection and Visualization of Heterozygosity-Rich Regions and Runs of Homozygosity in Worldwide Sheep Populations

Alana Selli ^{1,*}, Ricardo V. Ventura ^{1,*}, Pablo A. S. Fonseca ², Marcos E. Buzanskas ³, Lucas T. Andrietta ¹, Júlio C. C. Balieiro ¹ and Luiz F. Brito ⁴



- ✓ Runs of homozygosity (ROH): can also be informative of population's history, structure, demography events, and overall genetic diversity
- ✓ Heterozygosity enriched regions (HER): regions of high heterozygosity, which can harbor important genes associated with key functional traits (e.g., immune response and disease resilience)

PURDUE
AGRICULTURE

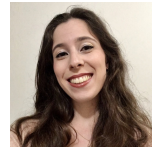
ANIMAL SCIENCES

10

10

Visualization of ROH and HER

✓ 50K genotypes for 1,186 sheep from eight breeds (Merino, Rambouillet, Suffolk, Texel, Lacaune, Churra, East Friesian, Soay, and Tibetan)

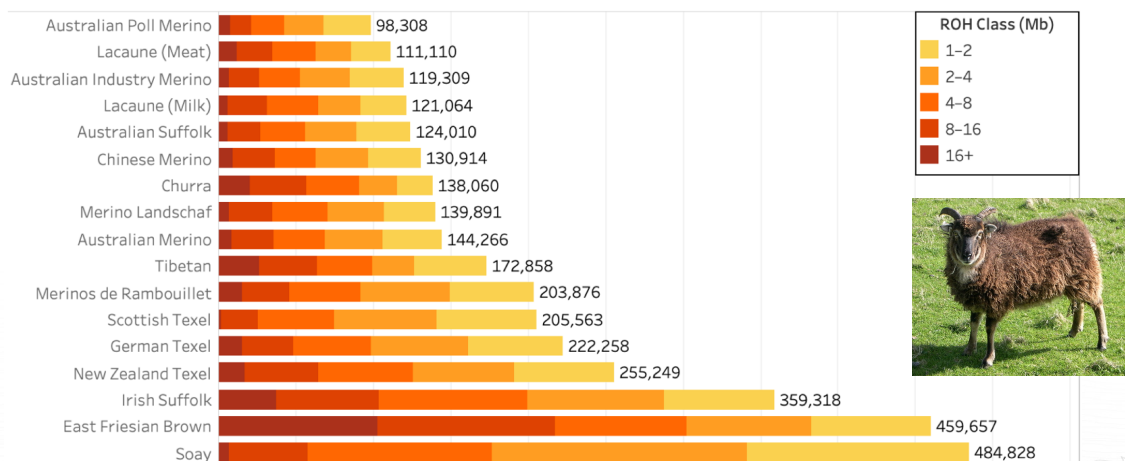


✓ Business Intelligence (BI; Software Tableau V. 2020.1.14): combine results from multiple analyses and create dynamic visualization schemes integrating different information:

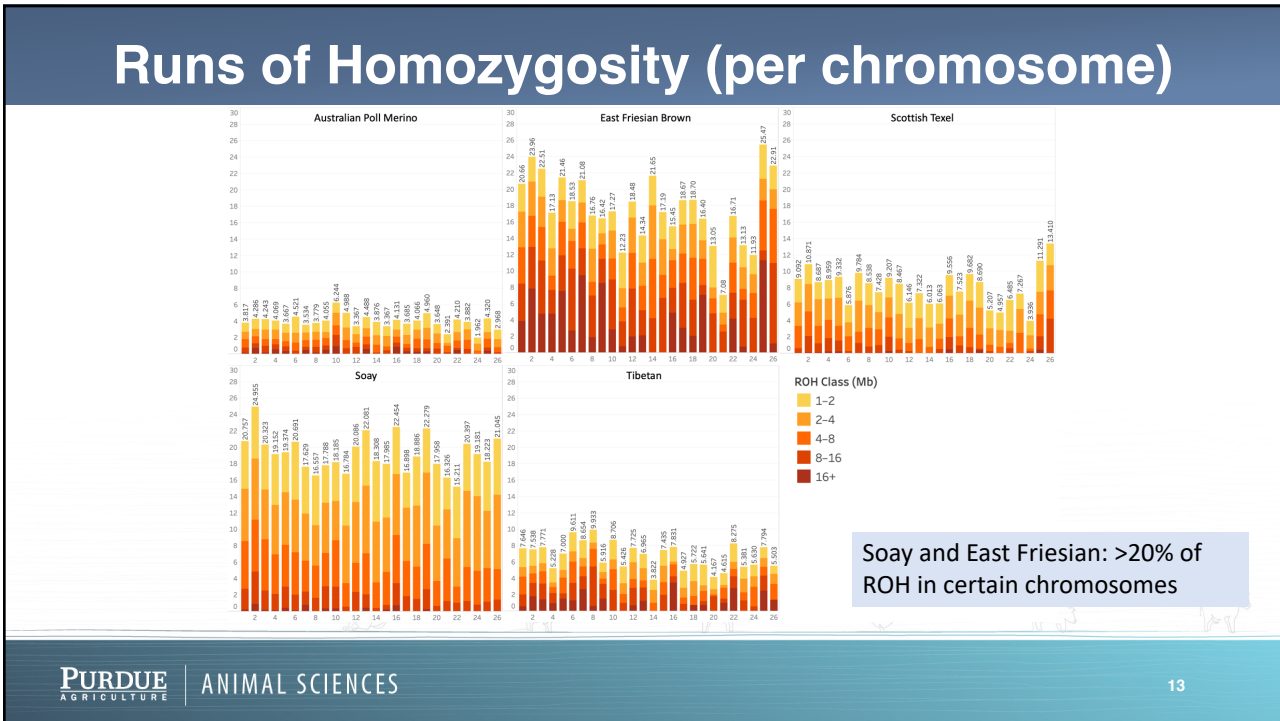
- ROH, HER, linkage disequilibrium, allele frequency, QTL location

11

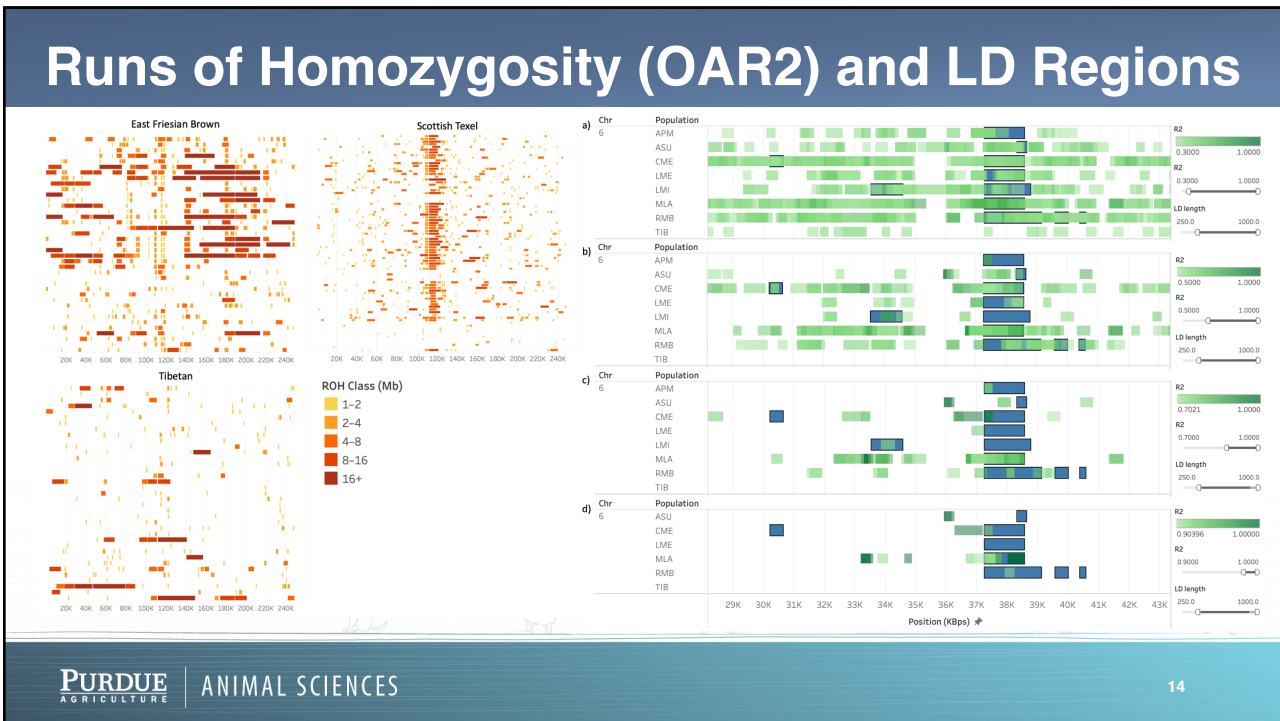
Runs of Homozygosity (total length in kb)



12



13



14

ROH Islands

✓ Main HERs islands: genes previously associated with adaptation traits

ANIMAL SCIENCES
15

15

Study 2

BMC Genetics

RESEARCH ARTICLE

Open Access

CrossMark

Genetic diversity of a New Zealand multi-breed sheep population and composite breeds' history revealed by a high-density SNP chip

Luiz F. Brito^{1,2*}, John C. McEwan², Stephen P. Miller^{1,2}, Natalie K. Pickering³, Wendy E. Bain², Ken G. Dodds², Flávio S. Schenkel¹ and Shannon M. Clarke²

BMC Genetics

RESEARCH ARTICLE

Open Access

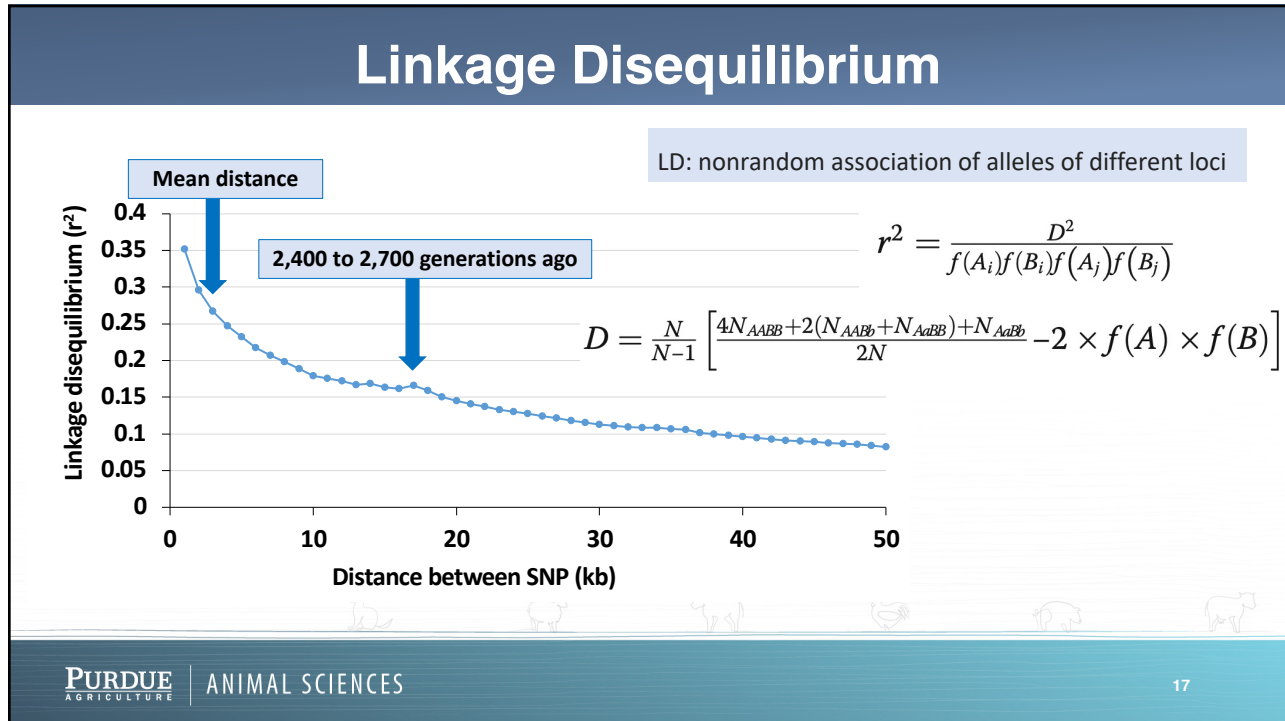
CrossMark

Prediction of genomic breeding values for growth, carcass and meat quality traits in a multi-breed sheep population using a HD SNP chip

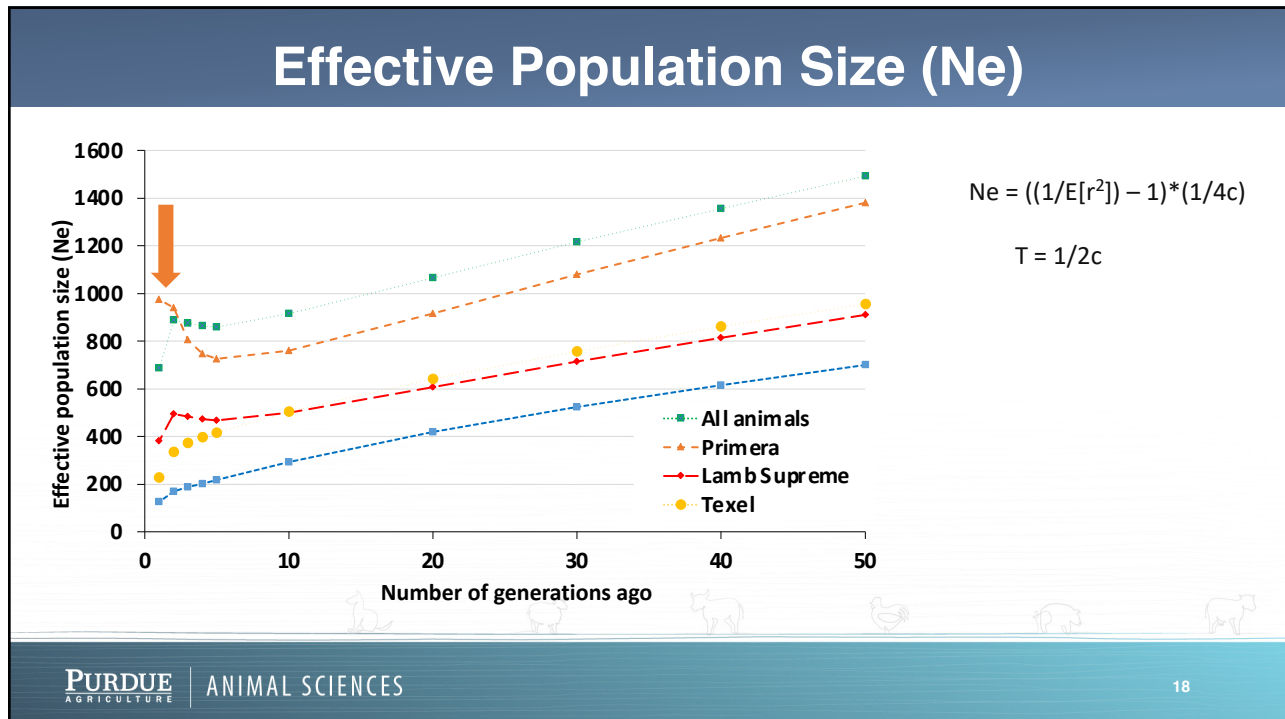
Luiz F. Brito^{1,2*}, Shannon M. Clarke², John C. McEwan², Stephen P. Miller^{1,2}, Natalie K. Pickering³, Wendy E. Bain², Ken G. Dodds², Mehdi Sargolzaei^{1,4} and Flávio S. Schenkel¹

ANIMAL SCIENCES
16

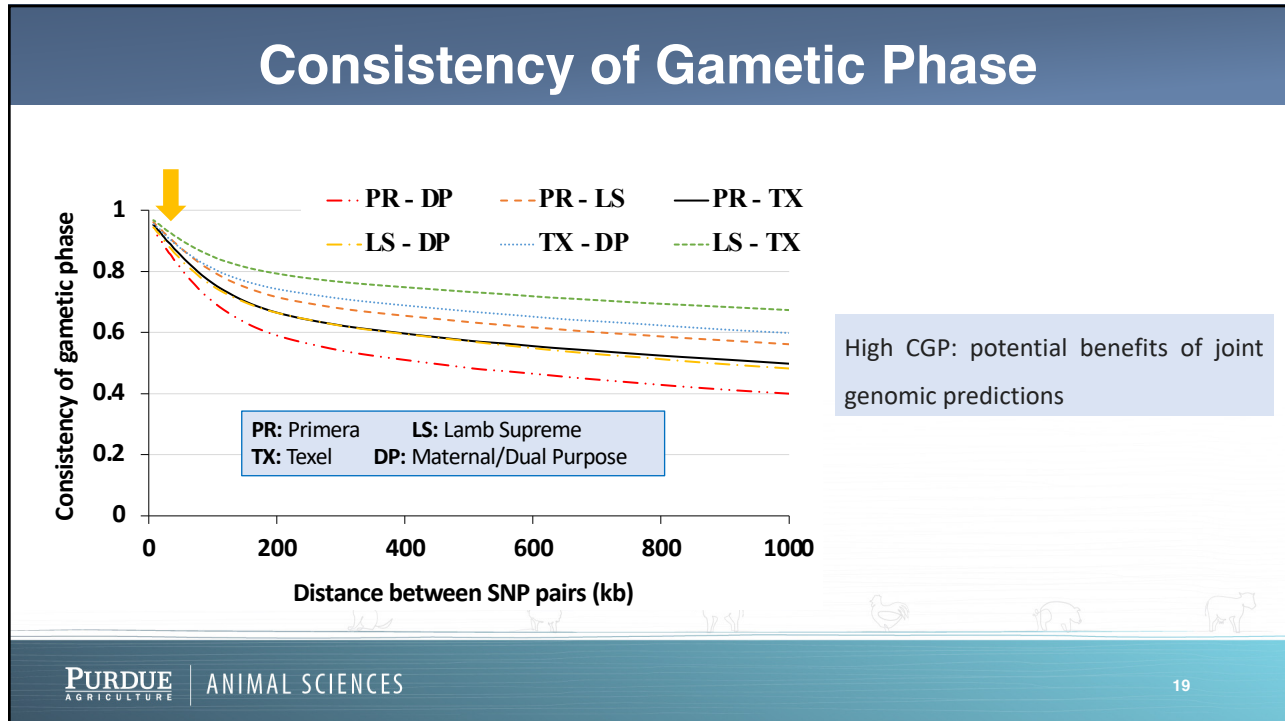
16



17



18



19

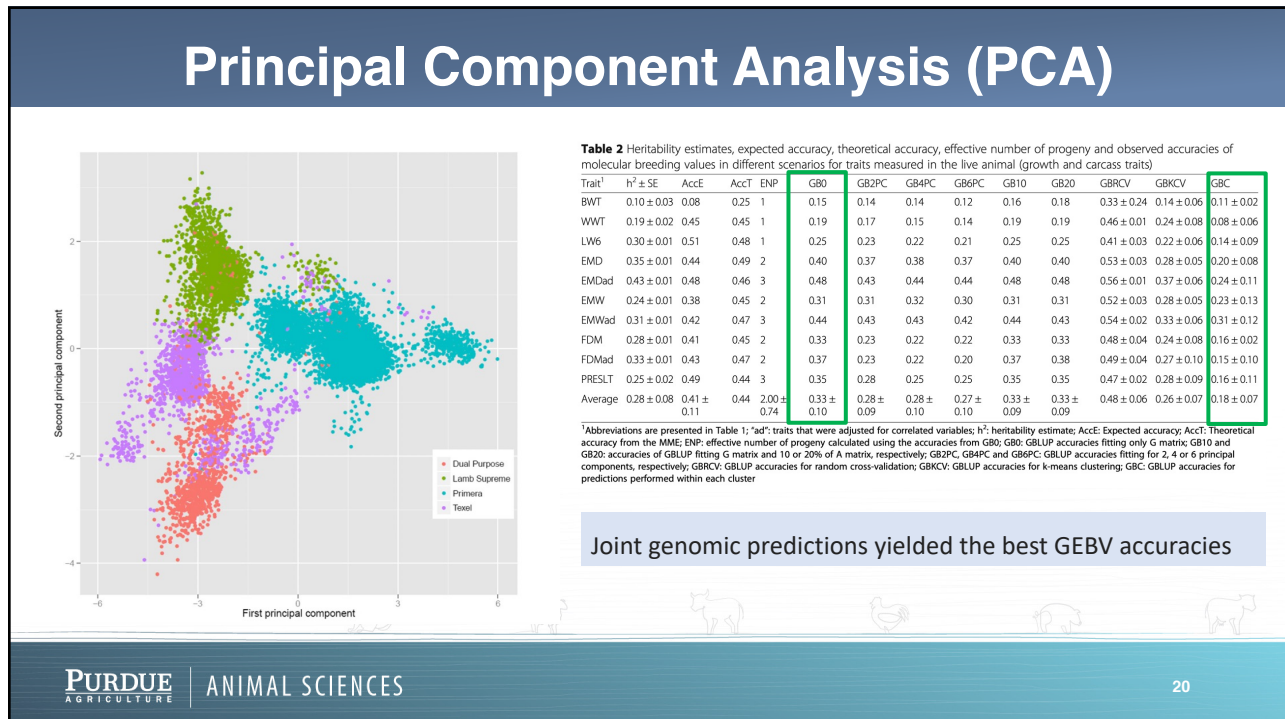


Table 2 Heritability estimates, expected accuracy, theoretical accuracy, effective number of progeny and observed accuracies of molecular breeding values in different scenarios for traits measured in the live animal (growth and carcass traits)


Trait ¹	$h^2 \pm SE$	AccE	AccT	ENP	GBO	GB2PC	GB4PC	GB6PC	GB10	GB20	GBRCV	GBKCV	GBC
BWT	0.10 ± 0.03	0.08	0.25	1	0.15	0.14	0.14	0.12	0.16	0.18	0.33 ± 0.24	0.14 ± 0.06	0.11 ± 0.02
WWT	0.19 ± 0.02	0.45	0.45	1	0.19	0.17	0.15	0.14	0.19	0.19	0.46 ± 0.01	0.24 ± 0.08	0.08 ± 0.06
LW6	0.30 ± 0.01	0.51	0.48	1	0.25	0.23	0.22	0.21	0.25	0.25	0.41 ± 0.03	0.22 ± 0.06	0.14 ± 0.09
EMD	0.35 ± 0.01	0.44	0.49	2	0.40	0.37	0.38	0.37	0.40	0.40	0.53 ± 0.03	0.28 ± 0.05	0.20 ± 0.08
EMDad	0.43 ± 0.01	0.48	0.46	3	0.48	0.43	0.44	0.44	0.48	0.48	0.56 ± 0.01	0.37 ± 0.06	0.24 ± 0.11
EMW	0.24 ± 0.01	0.38	0.45	2	0.31	0.31	0.32	0.30	0.31	0.31	0.52 ± 0.03	0.28 ± 0.05	0.23 ± 0.13
EMWad	0.31 ± 0.01	0.42	0.47	3	0.44	0.43	0.43	0.42	0.44	0.43	0.54 ± 0.02	0.33 ± 0.06	0.31 ± 0.12
FDM	0.28 ± 0.01	0.41	0.45	2	0.33	0.23	0.22	0.22	0.33	0.33	0.48 ± 0.04	0.24 ± 0.08	0.16 ± 0.02
FDMad	0.33 ± 0.01	0.43	0.47	2	0.37	0.23	0.22	0.20	0.37	0.38	0.49 ± 0.04	0.27 ± 0.10	0.15 ± 0.10
PRESLT	0.25 ± 0.02	0.49	0.44	3	0.35	0.28	0.25	0.25	0.35	0.35	0.47 ± 0.02	0.28 ± 0.09	0.16 ± 0.11
Average	0.28 ± 0.08	0.41 ± 0.11	0.44 ± 0.11	2.00 ± 0.74	0.33 ± 0.10	0.28 ± 0.09	0.28 ± 0.10	0.27 ± 0.10	0.33 ± 0.09	0.33 ± 0.09	0.48 ± 0.06	0.26 ± 0.07	0.18 ± 0.07

¹Abbreviations are presented in Table 1; ²ad: traits that were adjusted for correlated variables; h^2 : heritability estimate; AccE: Expected accuracy; AccT: Theoretical accuracy from the MME; ENP: effective number of progeny calculated using the accuracies from GBO; GBO: GBLUP accuracies fitting only G matrix; GB10 and GB20: accuracies of GBLUP fitting G matrix and 10 or 20% of A matrix, respectively; GB2PC, GB4PC and GB6PC: GBLUP accuracies fitting for 2, 4 or 6 principal components, respectively; GBRCV: GBLUP accuracies for random cross-validation; GBKCV: GBLUP accuracies for k-means clustering; GBC: GBLUP accuracies for predictions performed within each cluster

Joint genomic predictions yielded the best GEBV accuracies

20

Study 3



ORIGINAL RESEARCH
published: 24 April 2021
 doi: 10.3389/fgene.2020.02031

Received: 25 February 2021 | Revised: 29 May 2021 | Accepted: 6 August 2021
 DOI: 10.1111/fg.12642

ORIGINAL ARTICLE

Animal Breeding and Genetics | **WILEY**



Genetic Connectedness Between Norwegian White Sheep and New Zealand Composite Sheep Populations With Similar Development History

Hinayah Rojas de Oliveira^{1,2}, John Colin McEwan³, Jette Jakobsen⁴, Thor Blichfeldt⁴, Theodor Meuwissen⁵, Natalie Pickering⁶, Shannon Marie Clarke³ and Luiz F. Brito^{1,2}*

Across-country genomic predictions in Norwegian and New Zealand Composite sheep populations with similar development history

Hinayah Rojas de Oliveira^{1,2} | John C. McEwan³ | Jette H. Jakobsen⁴ | Thor Blichfeldt⁴ | Theo H. E. Meuwissen⁵ | Natalie K. Pickering⁶ | Shannon M. Clarke³ | Luiz F. Brito^{1,2}






ANIMAL SCIENCES

21







21


Across-country Genomic Predictions

- ✓ Norway: 792 Norwegian White Sheep genotyped animals (606k SNP panel)
- ✓ New Zealand: 16,912 genotyped animals (606k SNP panel)





Finn	Primera	Texel	Dual Purpose	Lamb Supreme	Terminal Sire
N = 50	N = 8,554	N = 220	N = 1,831	N = 6,092	N = 165












ANIMAL SCIENCES









22

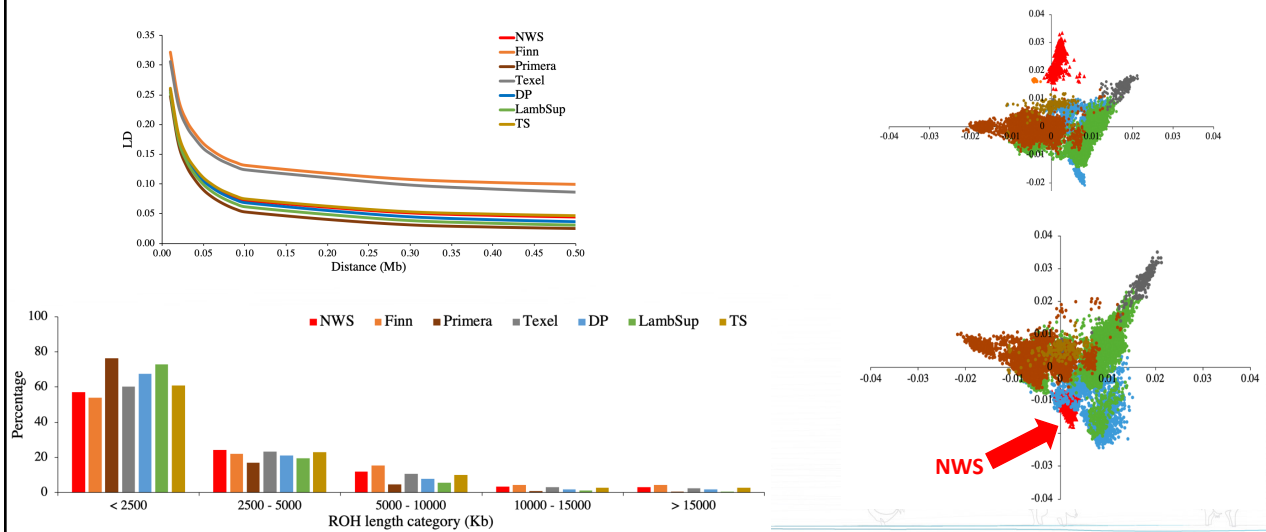
22

Population Characterization

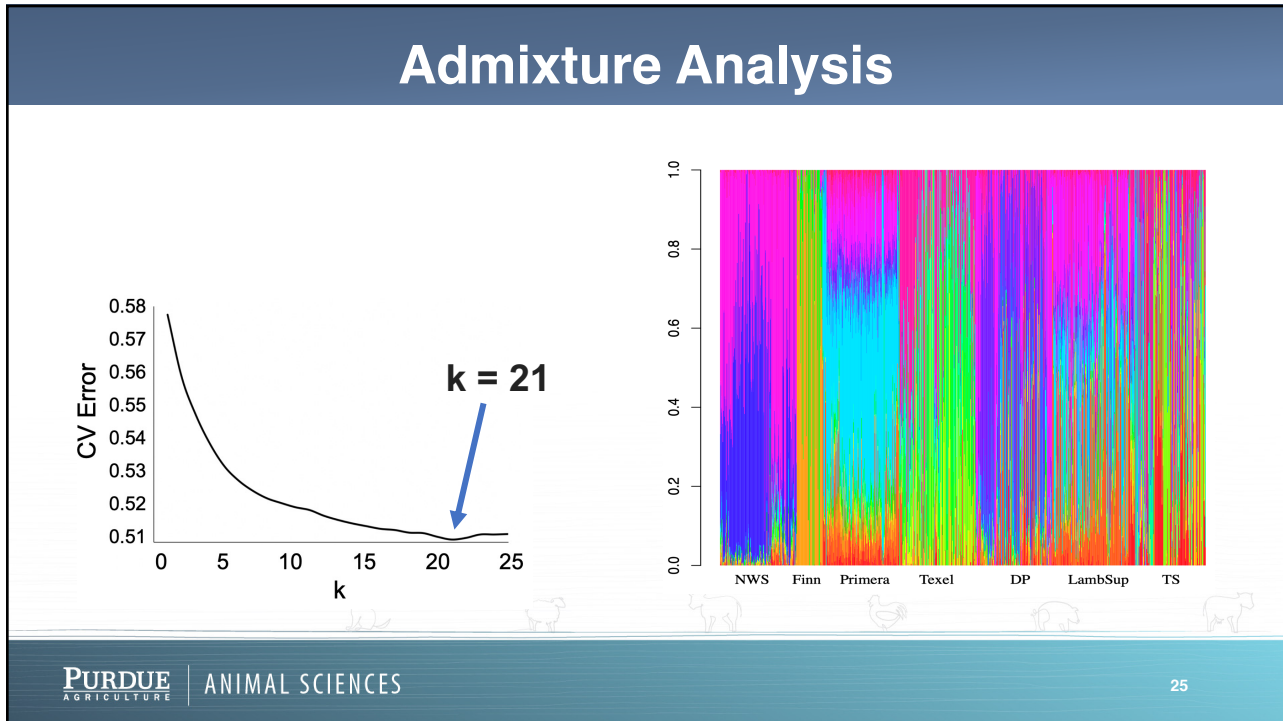
- ✓ Linkage disequilibrium
- ✓ Runs of homozygosity
- ✓ Consistency of gametic phase
- ✓ Principal component analysis
- ✓ Admixture analysis

23

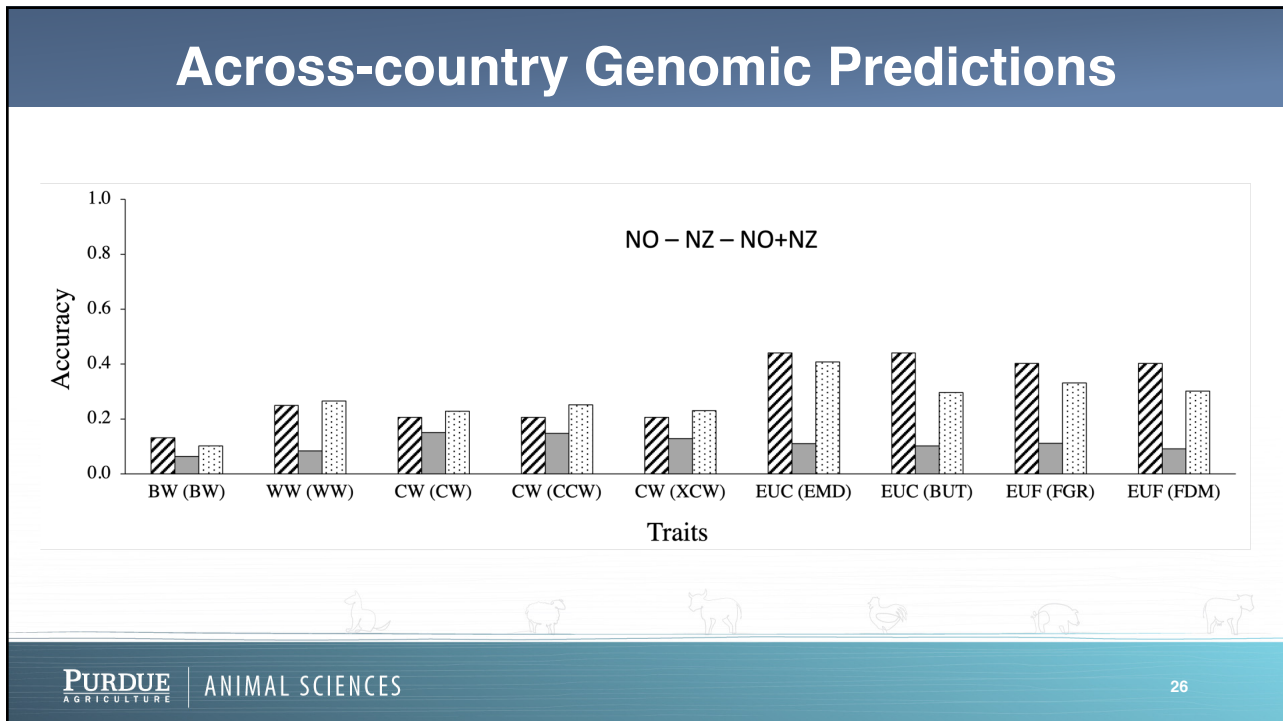
Population Characterization



24



25



26

Key Messages

- ✓ Highly-variable genetic diversity levels across sheep populations
- ✓ Multiple genetic diversity metrics can be used, including the more recent ROH and HER
- ✓ Genomics is a powerful tool for assessing genetic diversity in sheep populations
- ✓ Genetic diversity metrics can determine the feasibility of developing joint genomic evaluations

27

Next Steps

- ✓ **USDA-NIFA: 2022-67015-36073 (Improving robustness and climatic resilience in U.S. sheep populations through genomics)**
- ✓ Team: Drs. Ron Lewis, Luiz Brito, Joan Burke, Brad Freking, Tom Murphy, and Bret Taylor
- ✓ Objective #1: Generate genomic datasets and estimate genomic diversity metrics essential for the successful implementation of genomic selection
- ✓ Objective #2: Build reference populations for key robustness and climatic resilience traits and understand their underlying genomic background
- ✓ Objective #3: Evaluate genotyping strategies and methods for genomic prediction of breeding values in the main U.S. sheep breed-types



28



agresearch
āta mātai, mātai whetū

PURDUE UNIVERSITY

NSG
Norwegian University of Life Sciences

FOCUS GENETICS

FARM IQ | SYSTEMS LIMITED

Thank You!

Smarter
SMALL Ruminant's breeding for Efficiency and Resilience

britol@purdue.edu




PURDUE AGRICULTURE | ANIMAL SCIENCES