Reducing Dairy Cattle Lameness with Improved Genetic Understanding and Selection for Digital Cushion Thickness

Stambuk, C.[1], Bicalho, R.[2], Huson, H.J.[1]

[1]College of Agriculture and Life Sciences, Cornell University
[2]College of Veterinary Medicine, Cornell University

Digital Cushion

- Extends forward beneath the pedal bone and is made up of three cylindrical parallel oriented bodies each with a capsule of connective tissue filled with soft adipose tissue
- It has been shown that:
  - The digital cushion (DC) of primiparous (first lactation animals) animals is thinner than that of multiparous cows
  - Increased digital cushion thickness (DCT) is highly associated with body condition score (BCS)
  - DCT is a strong predictor of lameness
  - DCT is moderately heritable and has a strong negative genetic correlation with claw horn disruption lesions
    - Genetic selection for thicker digital cushion is possible and should lead to an increased genetic resistance to claw horn lesions and lameness

Impact of Lameness on Industry

- Lameness in dairy cattle is a serious animal welfare issue and a significant cause of economic loss.
  - It causes reduced reproductive efficiency and milk production, which increases cull rates
  - It can be caused by a wide variety of diseases, such as claw horn lesions
- Preventing lameness is important to reduce the negative welfare implications for cows and lessen costs for the farmers

Hypothesis

- Cows that are able to maintain increased DCT throughout lactation will have reduced incidence of lameness and lesions
- There is an underlining genetic component associated with DCT

Objective

Phase 1: Longitudinal cohort study

- Phenotypic characterization of DCT over lactation, parturition, and age
- Determine 1 to 2 critical time points for further investigation

Acknowledgements

This project was funded by NIFA Federal Formula Funds Hatch Project, the American Jersey Cattle Association, and the American Simmental Association. A special thank you to the labs of Dr. Huson and Dr. Bicalho, as well as, the farmers.

Materials and Methods

200 U.S Holstein dairy cows in upstate New York phenotypically characterized for DCT at four time points throughout lactation

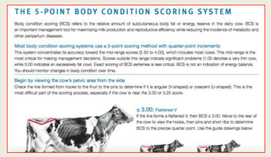
	Sample Event 1 245-266 DCC	Sample Event 2 1-30 DIM	Sample Event 3 91-120 DIM	Sample Event 4 271-300 DIM
Blood	X			
BCS	X	X	X	X
Lesion	X	X	X	X
Locomotion	X	X	X	X
Ultrasound	X	X	X	X
Height	X			X

Genotype

Blood

Phenotype

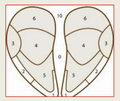
BCS

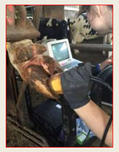


Lesion

Locomotion

Ultrasound





Height

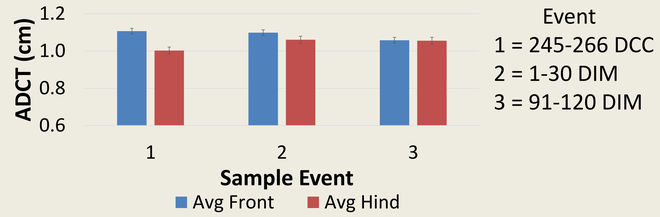
Cow Records

DairyCOMP 305

Future: Genome-wide association study (GWAS) will be conducted using the genetic information from the Illumina Bovine High-density beadchip with 777K single-nucleotide polymorphisms (SNPs) spanning the entire genome. Phenotypic data will be analyzed for correlations and genetic association.

Preliminary Data

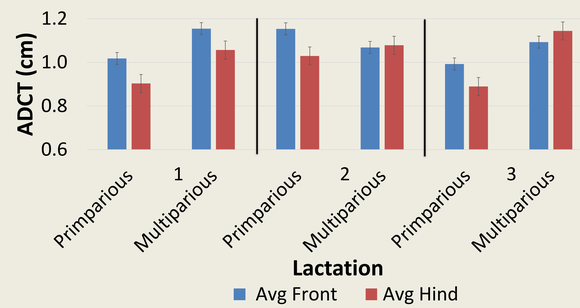
Average Digital Cushion Thickness by Sample Event



Significant difference between:

- Sample event 1 and 2 in the average of the hind digits
- Sample event 1 and 3 in both the average front and hind digits

Average Digital Cushion Thickness by Lactation



Significant difference between primiparous and multiparous for:

- All averages except the average hind in Sample event 2

Discussion and Future Directions

Current Data:

- Significant difference in DCT between:
  - Sample event 1 and 2 in the average hind digits
  - Sample event 1 and 3 both the average front and hind digits
  - Primiparous and multiparous for all averages except average hind in Sample event 2
- According to the current data, BCS and DCT are not correlated (R^2= 0.056).

Future Directions:

- Perform Phase 1 on another 80 U.S Holsteins from second farm
- Begin genetic analysis on Phase 1 data
- Phase 2:
  - Add 200 more U.S Holsteins and 200 U.S Jerseys using the critical time point(s) determined from Phase 1
  - Conduct a GWAS for DCT to identify regions of the genome associated with DCT