GENETIC IMPROVEMENT OF DISEASE TRAITS IN DAIRY CATTLE

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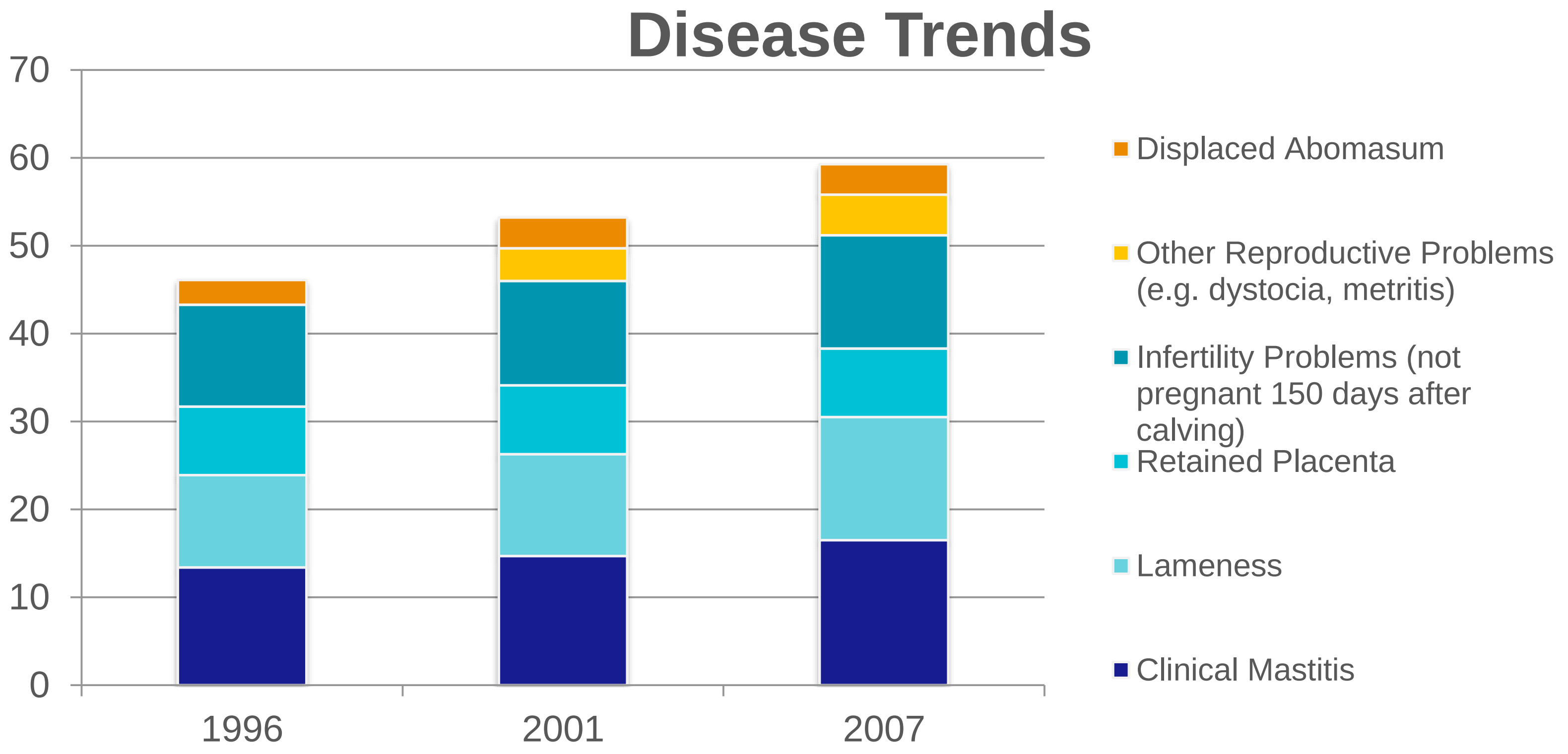
NBCEC Brown Bagger Webinar
October 9 of 2019

Overview

Objective and contents

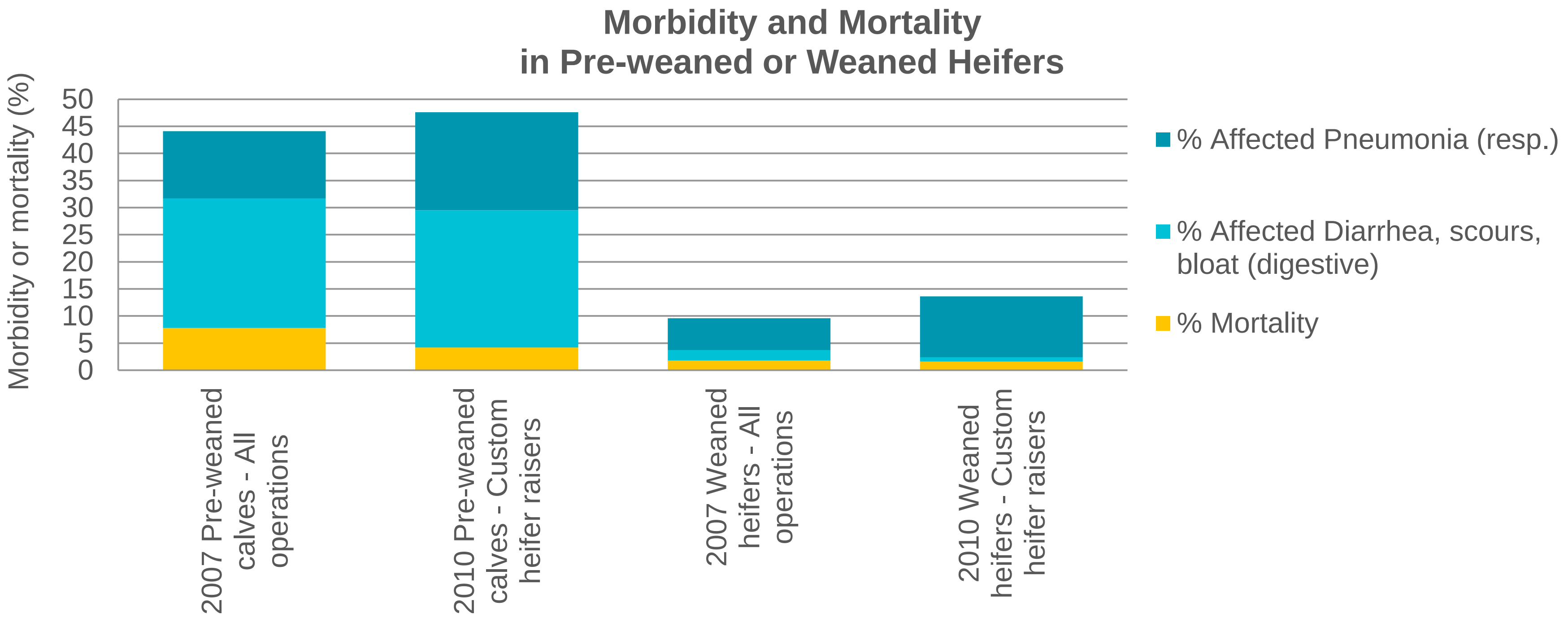
- The need for healthier cows and calves
- Creating genetic predictions for health traits in cows and calves
- Achieving genetic progress in health traits through multi-trait selection indexes
- Remarks and conclusions

Dairy cow morbidity trends



USDA. 2008. Dairy 2007, Part II: Changes in the U.S. Dairy Cattle Industry, 1991–2007 USDA-APHIS-VS, CEAH. Fort Collins, CO #N481.0311.

No improvement in dairy Calf/Heifer Health trends



USDA. 2008. Dairy 2007, Part II: Changes in the U.S. Dairy Cattle Industry, 1991–2007 USDA-APHIS-VS, CEAH. Fort Collins, CO #N481.0311.
USDA. NAHMS Dairy Heifer Raiser 2011: A Study of Operations that Specialize in Raising Dairy Heifers

Impact of morbidity is significant in dairy cows

	Incidence per Lactation Range	Cost ($) per Case	Culling Risk[1] (%)
Displaced Abomasum	3-5% [1,2,3,4,13]	$494 [4]	26.9
Ketosis	5-14% [1,3,4,13]	$117-289 [4,5]	32.5
Lameness	10-48% [2,4,6,13]	$177-469 [4,7]	16 [2]
Mastitis	12-40% [1,2,3,4,8,13]	$155-224 [4,8,9]	32.7
Metritis	2-37% [1,3,10,11,13]	$300-358 [10,11]	17.1
Retained Placenta	5-15% [1,2,3,4,11,12]	$206-315 [4,12]	31.7

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DAIRY WELLNESS TRAITS FOR HOLSTEIN AND JERSEY

Cow and Calf Health Predictions

Single Step (SS-BLUP) Genetic Evaluation for Health Traits

- One-step analysis procedure for Zoetis Wellness Traits
- 100 most highly cited papers published in JDS since the beginning of 2016.


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Development of genetic and genomic evaluation for wellness traits in US Holstein cows

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ABSTRACT

In March 2016, Zoetis Genetics offered the first commercially available evaluation for wellness traits of Holstein dairy cattle. Phenotypic data on health events, pedigree, and genotypes were collected directly from producers upon obtaining their permission. Among all recorded health events, 6 traits were chosen to be included in the evaluation: mastitis, metritis, retained placenta, displaced abomasum, ketosis, and lameness. Each trait was defined as a binary event, having a value of 1 if a cow has been recorded with a disorder at any point during the lactation and zero otherwise. The number of phenotypic records ranged from 1.8 million for ketosis to 4.1 million for mastitis. Over 14 million pedigree records and 114,216 genotypes were included in the evaluation. All traits were analyzed using univariate threshold animal model with repeated observations, including fixed effect of parity and random effects of herd by year by season of calving, animal, and permanent environment. A total of 45,425 single nucleotide polymorphisms were used in the genomic analyses. Animals genotyped with low-density chips were imputed to the required number of single nucleotide polymorphisms. All analyses were based on the single-step genomic BLUP, a method that combines phenotype, pedigree, and genotype information. Predicted transmitting abilities were expressed in percentage points as a difference from the average estimated probability of a disorder in the base population. Reliabilities of breeding values were obtained by approximation based on partitioning of a function of reliability into contributions from records, pedigree, and genotypes. Reliabilities of genomic predicted transmitting abilities for young genotyped and pedigreed females without recorded health events had average values between 50.2% (displaced abomasum) and 51.9% (mastitis). Genomic predictions for wellness traits can provide new information about an animal's genetic potential for health and new selection tools for dairy wellness improvement.
Key words: wellness traits, dairy cattle, single-step genomic BLUP, reliability

INTRODUCTION

Interest is growing in the use of genetic improvement strategies as a component to the management of health in dairy cattle. Breeding strategies that incorporate information on health traits have the potential to improve animal well-being and overall effectiveness of dairy operations. Dairy animals that experience health events have a negative effect on herd profitability through increased culling, veterinary expenses, and labor, as well as monetary losses through reduced milk sales (Parker Gaddis et al., 2014). Guard (2009) estimated the expenses related to the common dairy cow diseases to range from $181 per case of ketosis to $391 per case of displaced abomasum. Dairy researchers and producers have focused on providing the best environment to reduce health events through nutrition, management, and housing. However, improving functional traits genetically presents a challenge, because health traits have low heritability and may be difficult and expensive to measure and record.

Genetic evaluation of health traits has a long tradition in countries with routine health data recording. In Scandinavian countries, health traits have been included in breeding programs since the mid-1970s (Heringstad and Østerås, 2013); currently, over 97% of Norwegian dairy cows are included in the recording system (Heringstad, 2010; Haugaard et al., 2012). In other countries, the use of direct health data in genetic evaluation is progressing rapidly. Routine data collection and genetic evaluation for health traits in Germany and Austria started in 2006 (Fuerst et al., 2011). In France, clinical mastitis has been included in routine genetic evaluation since 2010 (Govignon-Gion et al., 2012). In 2014, genetic evaluation for mastitis resistance was introduced for Canadian dairy cows; the evaluation is based on clinical mastitis incidence recorded in the first and second lactation and SCS (Koeck

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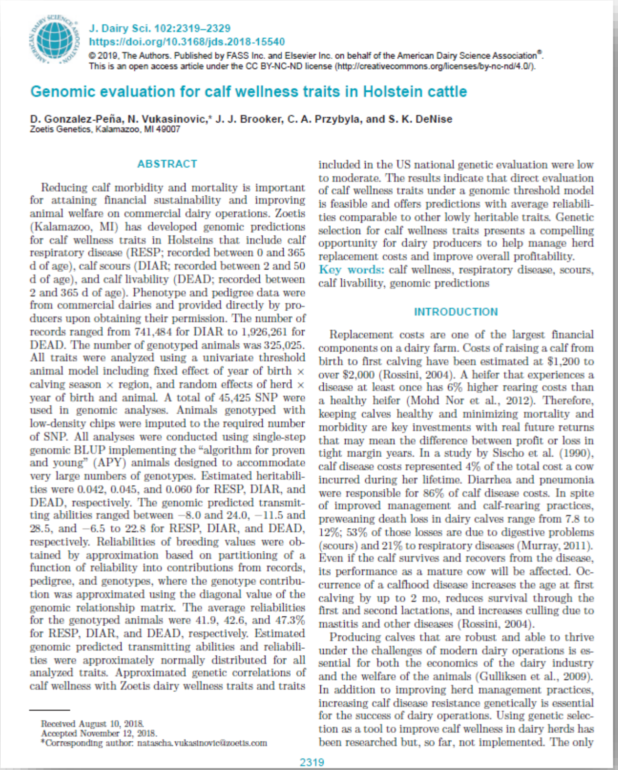
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Genomic evaluation for calf wellness traits in Holstein cattle

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ABSTRACT

Reducing calf morbidity and mortality is important for attaining financial sustainability and improving animal welfare on commercial dairy operations. Zoetis (Kalamazoo, MI) has developed genomic predictions for calf wellness traits in Holsteins that include calf respiratory disease (RESP; recorded between 0 and 365 d of age), calf scours (DIAR; recorded between 2 and 50 d of age), and calf livability (DEAD; recorded between 2 and 365 d of age). Phenotype and pedigree data were from commercial dairies and provided directly by producers upon obtaining their permission. The number of records ranged from 741,484 for DIAR to 1,926,261 for DEAD. The number of genotyped animals was 325,025. All traits were analyzed using a univariate threshold animal model including fixed effect of year of birth × calving season × region, and random effects of herd × year of birth and animal. A total of 45,425 SNP were used in genomic analyses. Animals genotyped with low-density chips were imputed to the required number of SNP. All analyses were conducted using single-step genomic BLUP implementing the "algorithm for proven and young" (APY) animals designed to accommodate very large numbers of genotypes. Estimated heritabilities were 0.042, 0.045, and 0.060 for RESP, DIAR, and DEAD, respectively. The genomic predicted transmitting abilities ranged between −8.0 and 24.0, −11.5 and 28.5, and −6.5 to 22.8 for RESP, DIAR, and DEAD, respectively. Reliabilities of breeding values were obtained by approximation based on partitioning of a function of reliability into contributions from records, pedigree, and genotypes, where the genotype contribution was approximated using the diagonal value of the genomic relationship matrix. The average reliabilities for the genotyped animals were 41.9, 42.6, and 47.3% for RESP, DIAR, and DEAD, respectively. Estimated genomic predicted transmitting abilities and reliabilities were approximately normally distributed for all analyzed traits. Approximated genetic correlations of calf wellness with Zoetis dairy wellness traits and traits included in the US national genetic evaluation were low to moderate. The results indicate that direct evaluation of calf wellness traits under a genomic threshold model is feasible and offers predictions with average reliabilities comparable to other lowly heritable traits. Genetic selection for calf wellness traits presents a compelling opportunity for dairy producers to help manage herd replacement costs and improve overall profitability.
Key words: calf wellness, respiratory disease, scours, calf livability, genomic predictions

INTRODUCTION

Replacement costs are one of the largest financial components on a dairy farm. Costs of raising a calf from birth to first calving have been estimated at $1,200 to over $2,000 (Rossini, 2004). A heifer that experiences a disease at least once has 6% higher rearing costs than a healthy heifer (Mohd Nor et al., 2012). Therefore, keeping calves healthy and minimizing mortality and morbidity are key investments with real future returns that may mean the difference between profit or loss in tight margin years. In a study by Sischo et al. (1990), calf disease costs represented 4% of the total cost a cow incurred during her lifetime. Diarrhea and pneumonia were responsible for 86% of calf disease costs. In spite of improved management and calf-rearing practices, preweaning death loss in dairy calves range from 7.8 to 12%; 53% of those losses are due to digestive problems (scours) and 21% to respiratory diseases (Murray, 2011). Even if the calf survives and recovers from the disease, its performance as a mature cow will be affected. Occurrence of a calfhood disease increases the age at first calving by up to 2 mo, reduces survival through the first and second lactations, and increases culling due to mastitis and other diseases (Rossini, 2004).

Producing calves that are robust and able to thrive under the challenges of modern dairy operations is essential for both the economics of the dairy industry and the welfare of the animals (Gulliksen et al., 2009). In addition to improving herd management practices, increasing calf disease resistance genetically is essential for the success of dairy operations. Using genetic selection as a tool to improve calf wellness in dairy herds has been researched but, so far, not implemented. The only

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Development of the Genetic Evaluation for Wellness Traits

- Mastitis
- Lameness
- Metritis
- Retained Placenta
- Displaced Abomasum
- Ketosis
- Milk Fever
- Calf Livability
- Calf Respiratory
- Calf Scours

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Development of genetic and genomic evaluation for wellness traits in US Holstein cows

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Table 1. Number of records (after editing), phenotypic means (average incidence per lactation), and SD of the wellness traits used in genetic and genomic evaluation (GE)

Trait[1]	No. of records in GE	Mean	SD
MAST	4,102,518	0.25	0.43
METR	2,966,946	0.10	0.30
RETP	3,330,123	0.05	0.23
DA	3,015,132	0.02	0.15
KETO	1,841,446	0.05	0.22
LAME	3,400,015	0.12	0.33
Pedigree	14,339,576		
Genotypes	114,216		

[1]MAST = mastitis; METR = metritis; RETP = retained placenta; DA = displaced abomasum; KETO = ketosis; LAME = lameness.

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Phenotypic means, standard deviations, and heritabilities in the analyses

Trait	Unit	Mean	SD	h^2
Mastitis	Case per animal/lactation	0.25	0.42	0.069
Lameness	Case per animal/lactation	0.20	0.40	0.063
Metritis	Case per animal/lactation	0.10	0.30	0.059
Retained placenta	Case per animal/lactation	0.05	0.22	0.073
Displaced abomasum	Case per animal/lactation	0.02	0.15	0.081
Ketosis	Case per animal/lactation	0.05	0.22	0.059

- Each trait was defined as a Holstein female recorded with the presence or absence of a disease/disorder in a given lactation
- Every cow was assigned with 0 (no incidence) or 1 (recorded one or more incidences) per lactation

Source: Data on file, Zoetis internal data, August 2015, Zoetis Inc.

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Development of the Genomic Evaluation for Calf Wellness Traits

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Genomic evaluation for calf wellness traits in Holstein cattle

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Table 1. Calf wellness trait definitions and characteristics of the data

Trait	Acronym	Description	Records	Incidence (%)	No. of herds	Average herd size[1]	G+P[2]	Pedigree[3]
Calf respiratory disease	RESP	RESP + PNEU[4] 0–365 d of age	1,331,626	21.0	188	7,083	67,289	2,310,723
Calf scours	DIAR	DIAR 2–50 d of age	741,484	26.1	118	6,283	70,275	1,583,960
Calf livability	DEAD	DEAD 2–365 d of age	1,926,261	4.7	233	8,267	105,012	2,923,038

[1]Average number of phenotypic records per herd across all years of data.
[2]Number of animals with a genotype that also had a phenotype for each trait.
[3]Number of animals in the final pedigree for each trait.
[4]Pneumonia.

Gonzalez -Pena et al 2019. JDS

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Calf Wellness Traits

Trait	Recording period	Incidence (%)	Number of records	Heritability (h^2)
Z_Calf_LIV	2-365 days of age	4.7	1,926,261	0.060
Z_Calf_RESP	0-365 days of age	21.0	1,331,626	0.042
Z_Calf_SCOUR	2-50 days of age	26.1	741,484	0.045

More than 451,000 genotypes were available for consideration as of January 2018

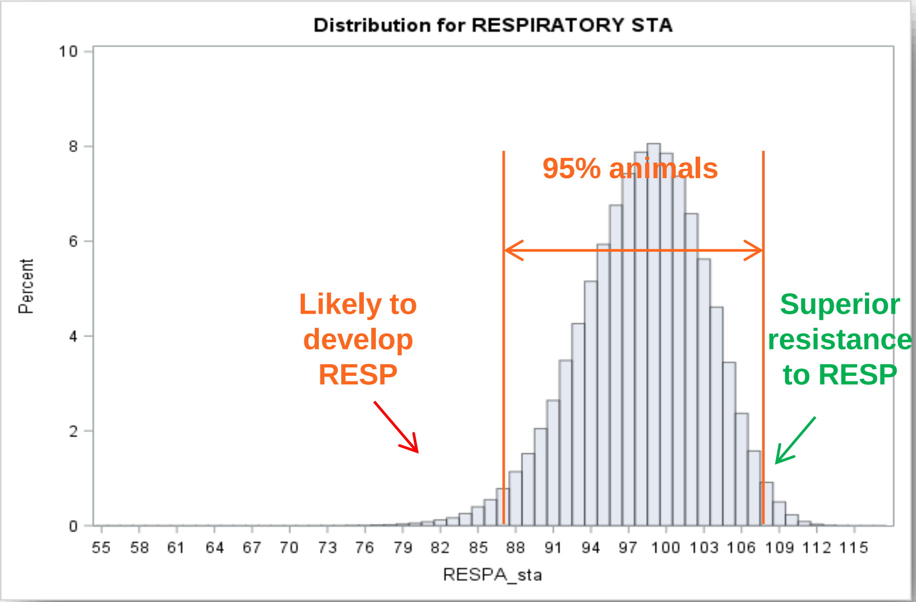
Data on file, Zoetis internal data, January 2018, Zoetis Inc.

Reporting Approach (Expression)

Reported as Standardized Transmitting Ability (STA)

- Genomically enhanced PTA's were converted into STA's using the equation

$$STA = \{[(gPTA - \mu)/\sigma] \times -5\} + 100$$



McNeel AK, et al. (2017) *Validation of genomic predictions for wellness traits in US Holstein cows*. Journal of Dairy Science. https://doi: 10.3168/jds.2016-12323

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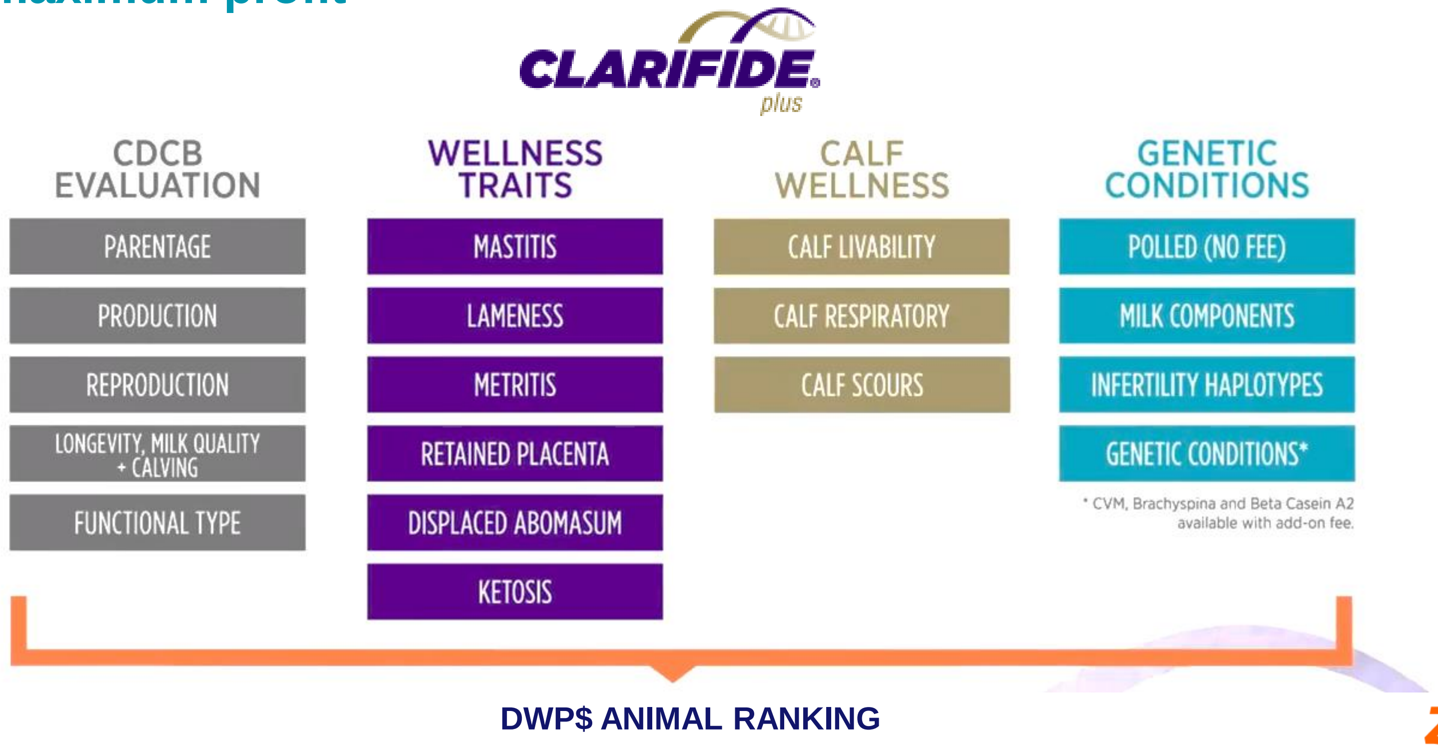
Wellness Traits - CLARIFIDE Plus

A balance of production, fertility, longevity, type and health traits to deliver maximum profit



Validation of genomic predictions for wellness traits in US Holstein cows

Evaluate the efficacy of wellness trait genetic predictions in commercial herds of US Holstein cows

- 3,400 randomly selected pregnant Holstein females in 11 herds and 2 age groups (69% nulliparous, 31% primiparous)

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Validation of genomic predictions for wellness traits in US Holstein cows

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Table 1. Standardization of on-farm codes used to record the 6 health events analyzed in this study

Health event	Standardized abbreviation	Farm term
Retained placenta	RETP	RETP, RP, RETAINP, RETPLACENT, RET PLACENT, RET_PLACEN
Metritis	METR	METR, METRHR, MET, UTERUS, PYO, METRITIS
Ketosis	KETO	KETOSIS, KETO
Displaced abomasum	DA	DA, LDA, RDA, LDA/RDA
Mastitis	MAST	MAST, MASTITIS, EXTMAST, EXMAST2, MAST., MAST.RR, MAST.RF, MAST.LR, MAST.LF, HMAST
Lameness	LAME	LAME, TRIMLAME, LAME2, HOOFROT, FOOTROT, TRIM_WRAPP, LOCOMO

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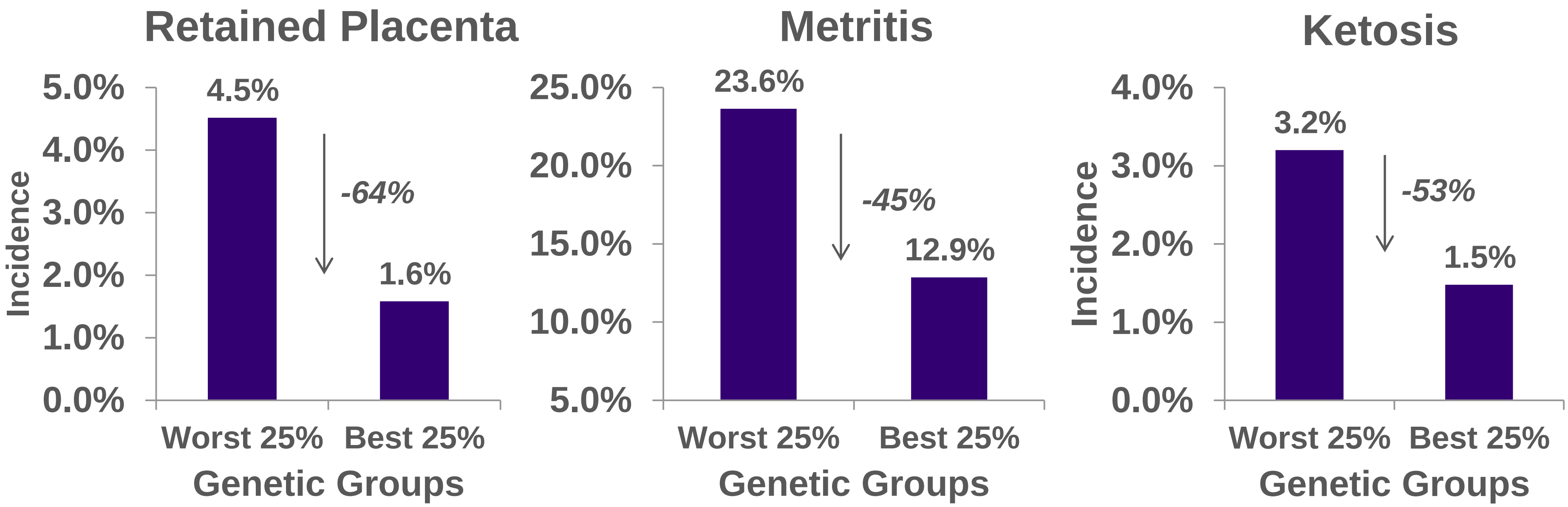
US HOLSTEIN EXTERNAL FIELD TRIAL PERCENT DIFFERENCE IN DISEASE: YEAR 1

Difference Between Best and Worst Quartile



McNeel AK, Reiter BC, Weigel D, Osterstock J, Di Croce FA. Validation of genomic predictions for wellness traits in US Holstein cows. *J Dairy Sci*. 2017;100:9115–9124.

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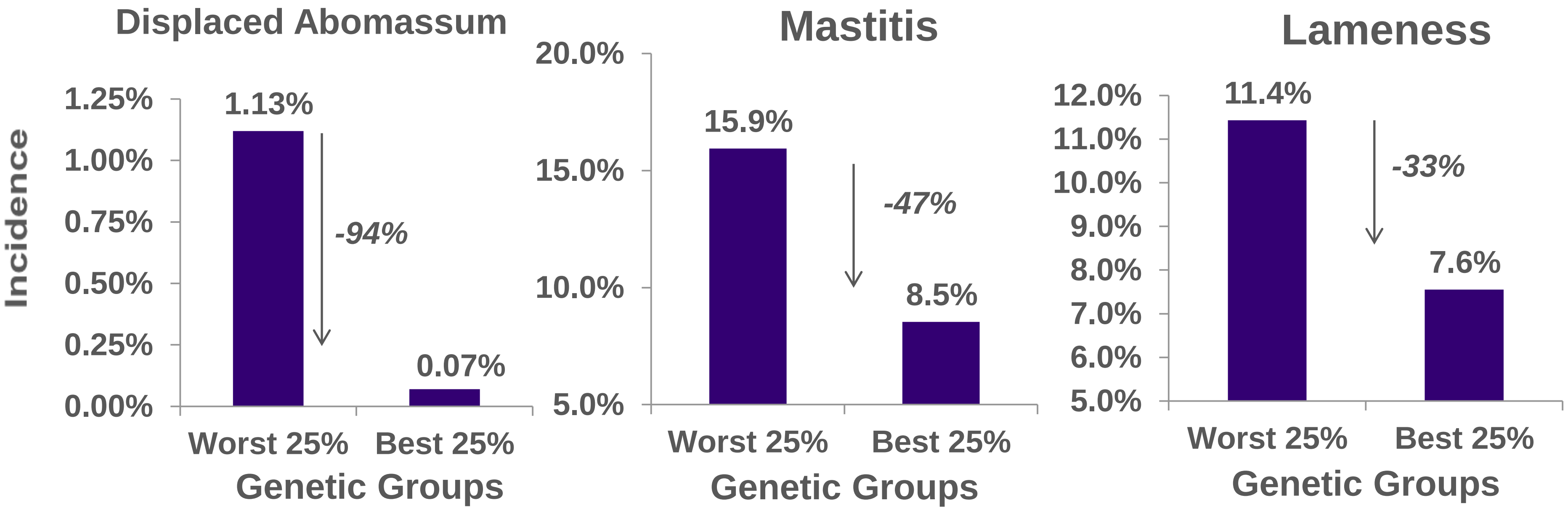
US HOLSTEIN EXTERNAL FIELD TRIAL PERCENT DIFFERENCE IN DISEASE: YEAR 1

Difference Between Best and Worst Quartile



McNeel AK, Reiter BC, Weigel D, Osterstock J, Di Croce FA. Validation of genomic predictions for wellness traits in US Holstein cows. *J Dairy Sci*. 2017;100:9115–9124.

Profitable Dairy Cows

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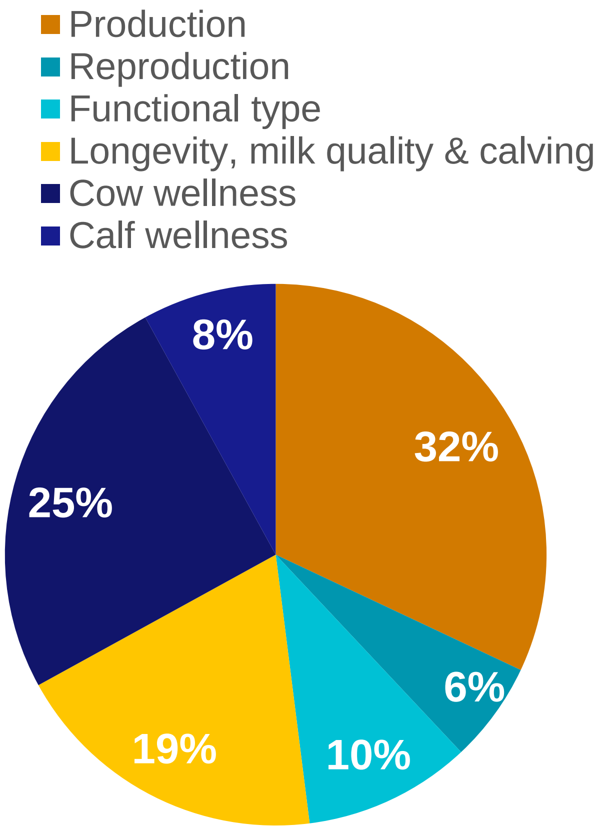
Dairy Wellness Profit Index® (DWP$®)

- Comprehensive selection index
  - Production, reproduction, longevity, milk quality, calving, functional type, cow and calf wellness, plus polled
  - Developed using standard selection index theory

- Economic index describing differences in lifetime profitability
  - Same economic assumptions as Net Merit (NM$) for core traits
  - Economic values from scientific literature for cow and calf wellness traits
  - Economic incentive for selection of animals with polled genotype



Remarks and Conclusions

- Direct selection for health and wellness traits is possible.

- Millions of records from lactating dairy cows in U.S. dairies were evaluated to deliver accurate genomic predictions for wellness traits
  - Data pipelines for continuous flow of health event phenotypes have been established
  - Single Step Genetic Evaluation is running weekly

- New wellness traits for Holsteins have similar or higher average Reliabilities (50% or greater) as some traditional CDCB traits (i.e. HCR and DSB)

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Remarks and Conclusions

- Marginal milk is king
  - Mature cows give 25% more milk than 1st calf heifers
  - Cows/heifers that avoid health events net more milk than those that don't
- Wellness Traits (e.g. CLARIFIDE Plus predictions) translate to real performance differences
- Improving health/wellness traits, through direct genetic selection presents a compelling opportunity for dairy producers to help manage disease incidence and improve profitability when coupled with sound management practices

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