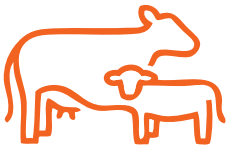


TECHNICAL BULLETIN



Building a Healthier Herd with CLARIFIDE® PLUS

Dairy producers can use CLARIFIDE Plus to select animals based on wellness and fertility traits with a goal of a healthier, more productive herd.

Zoetis

10 Sylvan Way
Parsippany, NJ 07054

KEY POINTS

- CLARIFIDE Plus is the first commercially available dairy genetic evaluation in the US for abortion, twinning, cystic ovary, and cow respiratory disease in dairy cattle.
- As longevity and productivity in dairy herds increases, the risk of adverse health and fertility events also increases. Incorporating selection for lower risk of these adverse events into genetic programs will help cows to achieve their profitability potential.
- CLARIFIDE Plus genomic predictions for fertility and wellness traits provide reliable assessments of genetic risk factors for economically relevant reproductive health challenges in Jersey cattle.
- CLARIFIDE Plus provides an expanded suite of genetic selection tools that provide highly relevant information to dairy producers that seek to continue to improve the health, productivity, and profitability of the dairy cattle they care for.

Introduction

Profitable dairy cows are more fertile, productive, healthy and long lived. They generally require fewer veterinary treatments and are less likely to be prematurely culled. Due to the impact of health and fertility on profitability, dairy farmers seek to incorporate improvement for these key areas in their breeding programs. In 2016, Zoetis Genetics developed direct genetic predictions for six common Holstein cow disease conditions¹ and in 2018 Zoetis

developed three common calf disease and mortality genetic predictions.² In 2019, Zoetis introduced these predictions to the Jersey Breed. Zoetis Genetics is continuing this commitment to providing direct genetic predictions for additional wellness and new fertility traits that impact profitability with the development of abortion, twinning, cystic ovary, milk fever (added to Holsteins now), and cow respiratory disease genetic evaluations. Abortion among dairy cows, which occurs at 42 to 260 days of gestation,

represents a major economic burden to the dairy industry. The average cost of pregnancy loss by abortion was estimated at \$555 in a herd based on Holstein cow performance and prices in the United States.³ The risk of abortion can result in an increased risk of other diseases as well as increased risk of premature culling. In addition, twinning in dairy cattle is an undesirable reproductive outcome because it reduces the overall profitability of a dairy operation through negative effects on cows having twins as well as on calves born as twins.⁴ Twinning can result in an increased risk of dystocia, retained placenta, metritis, abortion, and culling. The event of twinning can be costly not only to the cow but to the calf she produces. The mortality rate for twins is two to three times greater than that of a single calf.⁵ As dairy producers strive to improve the longevity of their dairy herd in order to capture more milk from mature cows, there is an increased risk of twinning, as multiparous cows have a higher twinning rate than 1st lactation cows. Additionally, the incidence of twinning increases with increasing milk production.⁶ There is a need to balance increased milk production and longevity with the corresponding increased risk of twinning and other adverse health and fertility events. Today, dairy producers have another tool to help control these costly diseases by directly selecting for improvement with these new fertility traits. Genetic improvement programs that incorporate risk of disease and adverse fertility events into selection and breeding strategies have the potential to improve profitability of dairy production through improved prevention and control of economically relevant diseases and fertility events as well as enhanced animal productivity.

Development of Jersey wellness and fertility predictions

Genomic predictions for Jersey wellness and fertility traits were developed by Zoetis based on an independent database

of pedigrees, genotypes and production records assembled from commercial dairies.

Cow health and fertility events were assembled from on-farm dairy production records with consent by commercial dairy producers. Data editing procedures to condense recorded disease and fertility incidence to a common format were developed based on review of event codes in on-farm software and consultation with dairy production and veterinary experts.⁶

Targeted phenotypes included:

- Cow Abortion (Z_ABRT)
- Twinning (Z_TWIN)
- Cow Respiratory Disease (Z_RESP)
- Cystic Ovary (Z_CYST)

All diseases and conditions were defined as a Jersey female diagnosed with the respective disease or condition one or more times in a given lactation on the basis of qualifying event codes in on-farm dairy software, or clinical research records. Table 1 shows the approximate number of phenotypic records in the database used to derive CLARIFIDE Plus for Jersey predictions as of December 2019. Records are continuously added to this database on a monthly basis from producer supplied farm records.

Genomic data was obtained from commercially tested animals or available genotypes within Zoetis research databases. More than 96,000 genotypes were available for consideration as of December 2019. Additional commercial genotypes are added on a weekly basis. Animals included in the evaluation were genotyped with low and medium density chips and imputed to Illumina BovineSNP50v2 using FImpute.⁷

CLARIFIDE Plus predictions are derived from a weekly internal genetic evaluation that employs single-step statistical methods for estimating genomic breeding values. This method for genetic evaluation derives a joint relationship matrix based on pedigree and genomic relationships and provides

Table 1 – Number of records, incidence, and heritability for Jersey Traits as of December of 2019.

Trait	Phenotype time period	Incidence (%)	Number of records	Heritability (h ²)
Z_ABRT	Lactation	8.7	423,464	0.0396
Z_TWIN	Lactation	2.2	734,029	0.1069
Z_RESP	Lactation	2.2	188,857	0.0487
Z_CYST	Lactation	1.5	71,329	0.0541

Table 2 –Reliabilities of Genomic Predictions for Dairy Wellness traits based on a subset of the reference population of approximately 37,227 Jersey heifers not contributing phenotypes to the genetic evaluation.

Traits	Average Reliability	Standard Deviation	Minimum	Maximum
Z_ABRT	30%	5%	13%	47%
Z_TWIN	44%	5%	26%	58%
Z_RESP	27%	5%	11%	46%
Z_CYST	25%	5%	11%	45%

a unified framework that eliminates several assumptions and parameters, thus enabling more accurate genomic evaluations.⁸

Table 2 shows the average reliability of genomic predictions for wellness traits in CLARIFIDE Plus. Among approximately 37,227 Jersey heifers born without phenotypes in 2018 and 2019 within the reference dataset, the average reliability ranged from 25% to 44% across all traits. Notably, as direct predictions for Jersey abortion, twinning, cow respiratory, and cystic ovary are not presently available, this represents a substantial increase in reliability from zero. Reliabilities below the average can be explained by several factors such as a lack of phenotype or pedigree information or limited relationship with the genetic evaluation population. Further, the average reliability of genomic predictions for these traits will continue to increase as more records are added to the evaluation.

Reporting of Jersey traits in CLARIFIDE Plus

CLARIFIDE Plus predictions for these additional Jersey traits are expressed as genomic standardized transmitting abilities (STA), similar to how other Zoetis Wellness Traits (i.e. Zoetis Mastitis) are expressed. Values are centered at 100 with a standard deviation of 5 (Table 3). For all Jersey trait predictions, a value of 100 represents average expected risk and values of greater than 100 reflect animals with lower expected average risk relative to herdmates with lower STA values. Higher values are more desirable for all traits, thus selecting for a high STA will apply selection pressure for reduced risk of cow disease or cow fertility issue.

Table 3 – Genomic standardized transmitting abilities (STA) for Jersey Traits based on a reference population of approximately 10,711 head born in 2015.

Wellness Traits	Average	Standard Deviation	Minimum	Maximum
Z_ABRT	100	5	77	118
Z_TWIN	100	5	72	112
Z_RESP	100	5	79	117
Z_CYST	100	5	80	118

Summary

Due to the impact of wellness and fertility performance on profitability, dairy farmers seek to incorporate improvement for these key areas in their breeding programs. CLARIFIDE® Plus now provides accurate genetic predictions for more wellness and new fertility traits including Cow Respiratory, Cow Abortion, Twinning, and Cystic Ovary. The result is an expanded suite of genetic selection tools that provide highly relevant information to dairy producers that seek to continue to improve the health, fertility, longevity, productivity, and profitability of the dairy cattle in their care.

NOTICES:

- Data incorporated in this document include tested U.S. females and males genotyped by Zoetis using low and moderated density panels and is based on data obtained from the December 2019 Zoetis Dairy Genetic Evaluation for Wellness Traits.
- The reported averages and standard deviations (SDs) of the Zoetis population may not reflect industry averages or trends.

References

1. Gonzalez-Peña, D., et al. *Genomic evaluation for calf wellness traits in Holstein cattle*. Journal of dairy science, 2019. 102(3): p. 2319-2329.
2. De Vries, A. *Economic value of pregnancy in dairy cattle*. Journal of dairy science, 2006. 89(10): p. 3876-3885.
3. Fricke, P.M. *Twinning in dairy cattle*. The professional animal scientist, 2001. 17(2): p. 61-67.
4. Del Río, N.S., et al. *An observational analysis of twin births, calf sex ratio, and calf mortality in Holstein dairy cattle*. Journal of dairy science, 2007. 90(3): p. 1255-1264.
5. Lopez, H., et al. *Relationship between level of milk production and multiple ovulations in lactating dairy cows*. Journal of dairy science, 2005. 88(8): p. 2783-2793.
6. Vukasinovic, N., et al. *Development of genetic and genomic evaluation for wellness traits in US Holstein cows*. Journal of dairy science, 2017. 100(1): p. 428-438.
7. Sargolzaei, M., J.P. Chesnais, and F.S. Schenkel. *A new approach for efficient genotype imputation using information from relatives*. BMC genomics, 2014. 15(1): p. 478.
8. Aguilar, I., et al. *Hot topic: A unified approach to utilize phenotypic, full pedigree, and genomic information for genetic evaluation of Holstein final score*. Journal of Dairy Science, 2010. 93(2): p. 743-752.