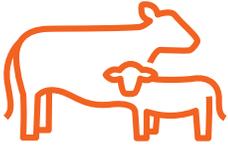


# TECHNICAL REPORT

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## DEVELOPMENT OF GENOMIC EXPECTED PROGENY DIFFERENCES (GEPD) AND AN ECONOMIC INDEX FOR BOVINE RESPIRATORY DISEASE (BRD) USING FEEDLOT CATTLE<sup>1</sup>

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### **Introduction and Background**

Bovine Respiratory Disease (BRD) is the most prevalent illness affecting feedlot cattle in the United States, responsible for approximately 80% of all morbidity (sickness) and 50-70% of finishing mortality (death)<sup>2,3</sup>. The economic impact is substantial, resulting from death loss, treatment costs, reduced feed efficiency and gain, lighter carcass weight, and diminished carcass quality.

Healthy cattle not afflicted by BRD tend to have better performance during backgrounding and finishing, as well as more valuable carcass outcomes. While BRD-related traits are generally low in heritability, previous studies have shown that genetic selection is possible, with heritability estimates ranging from 0.01 to 0.26 depending on methodology, breed, and trait definition<sup>4, 5, 6, 7</sup>. Together, vaccination, management, and genetic improvement programs for BRD health can favorably contribute to animal wellbeing, antibiotic stewardship, and economic sustainability.

## DEVELOPMENT OBJECTIVES

The genetics of BRD project aimed to develop genomic expected progeny differences (GEPD) for BRD using high density genotypes, available discovered parentage, and recorded health events in beef feedlot cattle, specifically defined as:

- **BRD-Health (BRDH) GEPD:** Predicted genetic differences in the probability that progeny stay healthy from arrival at backgrounding yards to harvest and do not require pull and treatment for BRD.
- **BRD-Survival (BRDS) GEPD:** Predicted genetic differences in probability that progeny survive from arrival at backgrounding yards to harvest without dying from BRD.
- **Dollar BRD (\$BRD):** Predicted differences in the impact on revenue (direct and indirect) from progeny due to combined genetic merit for BRDH and BRDS as defined above.

These genetic predictions for BRD were deployed within the Zoetis' INHERIT Franchise genetic improvement programs (weekly genetic evaluations) – specifically INHERIT Select for replacement females and as an INHERIT Connect Upgrade primarily for beef seedstock - enabling producers to evaluate and select for animals with improved BRD health and survival, thereby reducing adverse economic impacts.

## MATERIALS AND METHODS

Ongoing collaborations with large US feedlot operations provided a robust dataset. The development and evaluation population included roughly 50,000 commercial beef feeder cattle consisting of mostly moderate or higher BRD-risk crossbred steers. The cattle were a commercially representative population from across North America, that were finished and harvested from 2021 to 2025. The average genomic breed composition was 66% Angus, 5% Red Angus, 9% Simmental, 4% Hereford, 4% Gelbvieh, 4% Limousin, 3% Charolais, and other breeds that comprised 5%.

High density genomic data underwent rigorous quality control on SNP call rates, heterozygosity, sex/breed conflicts, genomic breed composition and parentage discovery. Phenotypic performance data included arrival weights, BRD treatment and BRD mortality records (binary), and carcass weight, fat thickness, ribeye area, yield grade, marbling and quality grade.

Statistical models for analysis of BRD included single-trait animal mixed models with fixed effects (arrival weight, retained heterozygosity, sex, contemporary group) and random genetic effects using genomic relationship matrices. Variance components and heritabilities were estimated using threshold models and transformed to linear scales for validation and deployment<sup>8,9</sup>. Using these genetic parameters, available pedigree and genomic information, together with BRD morbidity and mortality events, GEPD values were calculated as traits included in weekly Zoetis Multi-Breed Evaluations (ZMBE).

The ZMBE is a proprietary engine that generates INHERIT results using software and ssGBLUP<sup>10,11</sup> methodologies (single-step Genomic Best Linear Unbiased Prediction;

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Aguilar et al., 2010), as well as proprietary Zoetis procedures. This analysis of phenotype, pedigree and genomic information simplifies evaluation processes as compared to conventional approaches and yields superior accuracy, especially for non-parent animals. These sources of information are ever expanding, so on a weekly basis additional animals are evaluated, and predictions are updated and enhanced across non-parent and parent commercial and seedstock animals.

The \$BRD index was developed to help simplify selection and management for combined BRD Health and Survival. The assumed incidences of morbidity (13.5% treated) and mortality (3.8% death) were the same as those in the population described above that was used to develop genetic parameters for BRDH and BRDS GEPD.

Economic assumptions for the \$BRD index were also consistent with those incurred in the resource population, including the direct cost of BRD treatment estimated as \$15 per treatment for medicine and chute charges, and indirect cost of reduced carcass value for treated vs untreated animals of \$60 per head. This indirect cost was mostly from lighter average carcass weight and standardized 2025 carcass price/CWT, and to a lesser extent grid price due to lower quality grade. Hence, the index assumed that healthy animals had an estimated \$75/head advantage as compared to animals treated once or more for BRD. The average estimated cost per mortality of \$2,500 was based on the average arrival weight and associated standardized 2025 price/CWT for animals that died, as well as their average days-on-feed and related estimated feed and yardage costs.

## **RESULTS & INTERPRETATION OF BRD GENETIC PREDICTIONS**

Estimated heritability, on the threshold scale for BRDH was 0.13 and for BRDS was 0.16. These values, while relatively low, are consistent with other BRD health trait heritability estimates and indicate potential for genetic selection and improvement<sup>4, 5, 6, 7</sup>. The correlation between GEPD for BRDH and BRDS was .74, substantiating an expected strong relationship between genetic merit for BRD health and survival. The fixed effects in the model were all significant, including heterosis which was beneficial for BRDH and BRDS, with up to 9.1% and 7.7% greater probability of BRD Health and Survival, respectively.

Higher GEPDs for BRDH and BRDS are desirable and indicate greater likelihood of health (not requiring treatment) and survival (not dying). Using the population of nearly 200,000 INHERIT Select tested commercial females that do not have BRD health events contributing to the evaluation (only genotypes), ranking in the top 25% versus bottom 75%, equated to progeny that on average: are genetically 24% more likely to stay healthy; 13% more likely to survive from feedlot arrival to harvest; and have \$14 per calf advantage in net return from predicted differences in genetic merit from BRDH and BRDS (Table 1).

If this same contrast were for bulls tested using INHERIT Connect + BRD and they produce an assumed 100 calves during their lifetimes, there's a \$1400 predicted advantage to top versus bottom 25<sup>th</sup> percent rank for \$BRD. It's also meaningful to note that tested feeder cattle are predicted to express their Estimated Breeding Values

(EBV = 2 X EPD) for BRD traits. Thus, pens of cattle that on average rank in the top versus bottom genetic quartiles for \$BRD are predicted to have roughly a \$28/head advantage in lower combined treatment and mortality expense. Especially high BRD genetic risk feeder cattle in the least desirable decile rank for \$BRD (pink highlighted in Figure 1) are predicted to possess upwards to \$30/head or more health liability as compared to feeder cattle in the top quartile for \$BRD.

**Figure 1. Percent ranks and associated GEPD and index values for BRDH, BRDS and \$BRD for INHERIT Select tested females as of February 19, 2026 (n=208,926).**

### INTERPRETATION & VALUE OF BRD GEPD & \$BRD

Females		BRD Traits		
Top %	BRDH	BRDS	\$BRD	
Rank	%	%	\$	
1	28	16	17.50	As parents, the difference in GEPD between the top (green and above) and bottom (yellow and below) 25% for BRDH, BRDS and \$BRD means progeny that <b>genetically</b> are...
5	24	14	15.10	
10	22	12	13.70	
20	18	11	11.90	
25	17	10	11.15	
30	15	10	10.45	• 24% more likely to stay healthy • 13% more likely to survive • \$14 /calf more revenue (less costly)
40	12	8	9.10	
50	10	7	7.80	
60	7	6	6.40	
70	4	4	4.85	
75	3	4	3.95	
80	1	3	3.00	
90	-3	1	0.55	
95	-6	-1	-1.25	
99	-11	-4	-4.15	

As parents, the difference in GEPD between the top (green and above) and bottom (yellow and below) 25% for BRDH, BRDS and \$BRD means progeny that **genetically** are...

- 24% more likely to stay healthy
- 13% more likely to survive
- \$14 /calf more revenue (less costly)

### PREDICTIVE PERFORMANCE

The efficacy of GEPD for BRDH and BRDS were evaluated in three different case groups, representing populations of varying breed composition and disease risk. In cases 1 and 2, BRD health event phenotypes were masked in randomly chosen groups of 500 steers from the development population described above, and groups of 1,000 steers from roughly 3,000 new beef crossbreds added to the development population, respectively.

The top, middle and bottom GEBV groups for BRDH and BRDS based only on genomic information (health events not included in the evaluations) were compared to their associated observed incidences of health and survival. This process was repeated five times for each of these cases and associated BRD traits. In case 3, the top, middle and bottom GEBV groups based only on genomic information were compared to observed incidences in a population of just over 5,200 beef-dairy crosses.

Generally, the genetic predicted and expressed one-third groups for BRD health and survival across the three cases were directionally aligned (Table 1). Cases 1 and 2 that included beef crossbred steers showed better line up of magnitude of predicted and expressed health and survival than case 3 that included beef-dairy crosses that had a very low incidence of mortality. These cases support favorable relationships between genetic predicted and expressed BRD health and survival, although the magnitude of underlying predicted genetic potentials may not be fully expressed due to variation in breed type as compared to the reference population, health management (i.e. vaccination history) and environment (i.e. weather).

**Table 1. BRD GEPD efficacy evaluation case groups and observed incidence outcomes.**

BRD GEPD Efficacy Evaluation Groups									
BRDH & BRDS GEPD Groups	Case 1 - Beef Crossbred (n = 500) x 5 <sup>1</sup>			Case 2 - Beef Crossbred (n = 1,000) x 5 <sup>1</sup>			Case 3 - Beef-Dairy Cross Steers (n = 5,232)		
	Count	Observed Incidence		Count	Observed Incidence		Count	Observed Incidence	
		Healthy	Survival		Healthy	Survival		Healthy	Survival
Top Third	167	97.6%	97.0%	333	87.7%	89.5%	1744	87.7%	99.8%
Middle Third	167	94.6%	96.4%	333	85.9%	88.6%	1744	86.6%	99.7%
Bottom Third	166	68.7%	93.4%	334	81.7%	84.7%	1744	85.1%	99.6%
Difference Top - Bottom		28.9%	3.6%		6.0%	4.8%		2.6%	0.2%

<sup>1</sup>Random withholding of health events for five different groups and incidences averaged across groups.

### **CORRELATIONS BETWEEN BRD AND OTHER TRAIT GEPD:**

Overall, Pearson correlations between the BRD trait GEPD defined herein and calving, maternal and carcass quality trait GEPDs were relatively low but favorable, however unfavorable with carcass yield. The strongest set of correlations were with YG (.42 to .48 for BRDH and BRDS), Fat Thickness (.45 and .47), Yearling Height (-.37 and -.45), Liver Health (.32 and .38), Ribeye Area (-.27 and -.34), and Marbling (.31 and .24), indicating that some of the same genes for BRD health and survival also contribute to increased fat deposition and earlier compositional maturity.

There were lower but favorable correlations between GEPD for BRD health and calving ease traits (.31 and .32 for Calving Ease Direct; .29 and .31 for Calving Ease Maternal; -.30 and -.28 for Gestation Length, -.19 and -.14 for Birth Weight), as well as mature cow frame size (-.28 and -.32 for Mature Height), cow fleshing ability (.16 and .24 for cow Body Condition Score), Teat and Udder Composite (.21 and .32), Scrotal Circumference (.11 and .15), and cow Fertility (.11 and .22).

There were low, unfavorable correlations between GEPD for BRD health and Milk (-.13 and -.29), Weaning Weight (-.02 and -.09), and Carcass Weight (-.10 and -.09). Conversely, favorable correlations were documented with Yearling Weight (.12 and .07) and Feed-to-Gain (-.07 and -.10). Thus, these correlations suggest that simultaneous selection for BRD Health, post-weaning gain, feed efficiency, marbling and most maternal traits are generally complementary. It follows that GEPD for BRD health help enable selection of animals that bend apparent genetic antagonisms with traits such as carcass weight, fatness, muscularity and resultant carcass yield grade.

### **CONCLUSIONS**

The genetics of BRD project successfully developed genomic predictions in the form of GEPD for BRD Health and Survival in beef cattle, demonstrated predictive power in commercial datasets, and established a pathway for integrating these predictions into genetic selection programs through INHERIT Select and INHERIT Connect. Despite relatively low heritability (expected for health traits) the models and resultant BRD GEPD can differentiate animals at lower versus higher genetic risk for related

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health and survival, enabling targeted breeding that effectively manages correlated traits. As with other lowly heritable traits, heterosis for BRD health and survival from crossbreeding, and importantly vaccination and management practices that support immunity are advised. The inclusion of a \$BRD index simplifies selection for respiratory health and survival and helps quantify related economic differences.

*This technical report synthesizes the methodology, main findings, and implications of the internal Zoetis Genetics R&D Technical Report on genomic predictions for BRD in beef cattle, which provides a more comprehensive description for researchers. This report also summarizes development of an economic selection index to help simplify multiple trait selection for favorable BRD health and productivity outcomes.*

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