TECHNICAL BULLETIN

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INHERIT SELECT TECHNICAL REPORT

INHERIT Select Product Features for North America

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TECHNICAL SUMMARY

- INHERIT Select is a genomic test and genetic evaluation for commercial crossbred replacement females (heifers and cows) that provides: Genomic Expected Progeny Differences (GEPD) and Percentile Rankings for twenty-seven traits and seven economic indexes (three optional); sire and dam parentage discovery; genomic approximations of breed composition; genotypes for black/red/wild-type and dilution color, and horned/polled; to inform more effective selection, breeding and marketing decisions.
- INHERIT Select trait predictions and indexes are updated weekly through the Zoetis Multi-Breed Genetic Evaluation (ZMBE) that currently includes over 1.6 million animals – and an expanding database of traditional and unique phenotypes intended to comprehensively inform profit functions for commercial cow-calf producers.
- INHERIT Select results are easy to use because of seven economic indexes – Zoetis Cow-Calf; Zoetis Feedlot | Carcass; Zoetis Total Return; Dollar Bovine Respiratory Disease ($BRD), and optional Leachman Cattle of Colorado dollar Ranch, Feeder and Profit – all of which help simplify proper multiple-trait selection for net return.
- INHERIT Select is exclusively for genomic determined females, with maternal trait results not reported for genomic males.
- INHERIT Connect is a companion test to INHERIT Select, that enables testing of A.I. sires, bull batteries and cows to determine progeny parentage, genomic breed composition, color and polled genotypes – connects candidate sires and dams to tested daughters – no trait or index results are reported for INHERIT Connect, with the exception that BRD Health, BRD Survival and $BRD may be ordered as an add-on.
- INHERIT Select is intended for use in crossbred Bos Taurus females comprised of the following British and Continental breeds: Angus, Red Angus, South Devon, Hereford, Shorthorn, Simmental, Gelbvieh, Limousin and Charolais. Genomic breed composition is reported for these target breeds, plus dairy, indicus, and Wagyu – however, British and Continental must be ≥75%, and Brahman must be ≤50%, to be eligible for trait and index predictions.
- Customers with groups of females that are predominantly 75% and greater black Angus breed composition are advised to use GeneMax® Advantage™ offered through collaboration between Angus Genetics Inc. (AGI) and Zoetis[1].
- Optional add-ons to INHERIT Select include Bovine Viral Diarrhea Virus (BVDV), various genetic conditions, GEPD and Ranks for Pulmonary Arterial Pressure (PAP) and access to Leachman Cattle of Colorado dollar Ranch, Feeder and Profit indexes.
- INHERIT Insights reports are generated monthly and primarily serve to benchmark customers' tested females against the INHERIT reference population to help illustrate genetic strengths and weaknesses for more informed future bull and heifer selection and breeding decisions.

INHERIT SELECT PRODUCT FEATURES

ZOETIS MULTI-BREED EVALUATION

The Zoetis Multi-Breed Evaluation (ZMBE) is a proprietary engine that generates INHERIT Select results using software and ssGBLUP[3] methodology (single-step Genomic Best Linear Unbiased Prediction) developed by the University of Georgia, as well as proprietary Zoetis procedures. This analysis of phenotype, pedigree and genomic data simplifies evaluation processes as compared to conventional approaches and yields superior accuracy, especially for non-parent animals. These innovations are what makes INHERIT Select possible – namely, genetic predictions in the form of genomic expected progeny differences (GEPD) using genomic information, effectively informed through large pedigree, breed composition and phenotypic performance databases from genetically related, connected seedstock populations. What's more, these sources of information are ever expanding, so on a weekly basis, the proprietary ZMBE is executed and INHERIT Select results are updated.

While the data resources that fuel the ZMBE and INHERIT predictions are ever expanding, information from roughly 1.6 million animals currently contribute. These data originate from a variety of sources, including Leachman Cattle of Colorado (LCoC) and associated Cooperators as well as Dollar ($) Profit Share Partners, along with Zoetis company-owned resources from collaborating cow-calf, feedyard and beef-dairy crossbreeding entities. Just over half of the animals are relatively straight-bred, while the remainder are crossbred representing various combinations of breed composition. The six most influential breeds, ranked in descending order of prevalence among both straight-bred and crossbred animals included in the ZMBE are Angus, Red Angus, Simmental, South Devon, Gelbvieh and Hereford. Although less influential, Limousin, Charolais, Shorthorn and Brahman composition are also represented in the evaluated population. It follows that the target spectrum of breed composition to qualify for INHERIT Select testing is currently confined to crosses of these ten breeds, and especially crosses anchored by black and red Angus (see genomic breed composition section below).

GENOMIC DETERMINED GENDER

INHERIT Select is designed for commercial females – replacement heifers and cows – and not intended for use in bulls. To effectively manage such use, genomic information is utilized to determine the sex of animals tested with INHERIT Select. In cases where samples are inadvertently submitted, tested, and identified as genomic males, maternal trait predictions are not reported, but predictions are reported for health, feedlot and carcass traits, as well as associated indexes.

The reason INHERIT Select maternal trait predictions are exclusively for females, is because the essential pedigree, performance and genomic resources used to inform such predictions, comes from significant long-term financial, labor and innovations made by seedstock partners of Zoetis. The core business of these partners is to breed and market dependably evaluated, genetically superior bulls for commercial cow-calf producers. The policy that INHERIT Select maternal trait predictions are only reported for commercial females recognizes the vast ongoing investments in pedigree, performance data collection and genotyping made by these seedstock partners. Importantly, results from INHERIT Select, and better understanding of genetic strengths and weaknesses, as well as sire parentage and breed composition of commercial cow herds, informs and complements bull-buying decisions based on information provided by seedstock producers.

PARENTAGE DISCOVERY

Sire and/or dam parentage discovery are included features of INHERIT Select and are updated weekly. An essential prerequisite for parentage discovery, is that candidate parents must have HD50K® or qualifying High Density (HD) genotypes included in the **Zoetis** parentage HD archive. Since the evaluation is executed weekly, genotypes for parents or progeny may enter parentage discovery any time. Updated parentage and other results are reported via secured customer login to the Zoetic genetics reporting platform called SearchPoint®, whether parents are submitted prior to, at the same time (with these two options recommended), or after parents or progeny are tested.

INHERIT Select parentage discovery is flexible, and both 1) verifies presumed sires and dams of record, as well as 2) identifies the specific sire and dam from tested bull batteries and cow inventories, without having to nominate defined groups of candidate parents. If sires and/or dams of record exist for specific animals, based on A.I. breeding and calving records, single sire breeding pastures, or observed services, the presumed parent registration number and breed association, or ZID numbers, may be included on the order form. Alternatively, if sire and/or dam of record are unknown, typically due to multiple sire breeding programs, the sire and/or dam identity of record should be left blank.

There are five possible Parentage Status outcomes – detailed separately for sire and dam – reported by INHERIT Select. These outcomes apply to the reported Sire and Dam of Evaluation, and are reported in the Sire and Dam Status fields as follows:

1. **Genomically confirmed**
   The listed 'Sire or Dam of Evaluation' is genomically confirmed.

2. **Submitted sire | dam excluded, alternative sire | dam genomically confirmed**
   The alternative listed Sire or Dam was identified and genomically confirmed, while the submitted sire or dam was excluded.

3. **Submitted sire | dam excluded, no alternative sire | dam found**
   The Sire or Dam of Evaluation field is blank, because the submitted sire or dam was excluded, and no qualifying alternative sire or dam was identified.

4. **Submitted sire | dam not genotyped, unable to genomically confirm**
   The Sire or Dam of Evaluation field contains the recorded parent submitted on the order form, but since the sire or dam does not have genotypes available, the evaluation was unable to genomically confirm.

5. **No sire | dam found**
   The Sire or Dam of Evaluation field is blank because such was not submitted on the order form and there was no sire or dam found by the evaluation.

INHERIT CONNECT

Recognizing that INHERIT Select customers may have portions of their bull battery or cow herds that do not have HD50K genotypes included in the ZMBE, INHERIT Connect is available as a stand-alone or companion product to enable such testing. As the name indicates, the purpose is to discover and connect candidate parents to tested progeny as well as connect sires, dams and progeny to other genotyped animals in the evaluation. When ordering INHERIT Connect, if animals are registered, available registration number and breed association information should be provided to enable Zoetis to add external pedigree information.

INHERIT connect thus enables more complete sire and dam discovery across groups of tested heifers, as well as improves the dependability of trait and index predictions through strengthened genetic connections to animals in the ZMBE. Other than confirmation of successful genotyping and entry into the evaluation, as well as genomic predictions of breed composition, available parentage, color and polled genotypes, the only result delivered for INHERIT Connect is parentage determination for progeny tested with INHERIT Select and Optimize – no trait and index predictions are reported. The exception is that trait and index predictions for Bovine Respiratory Disease (BRD) may be ordered as an add-on to INHERIT Connect (more information provided below).

TRAIT PREDICTIONS – GENOMIC EXPECTED PROGENY DIFFERENCES (GEPD)

Predictions of genetic merit from beef genetic evaluations for individual traits are typically expressed as either Expected Progeny Differences (EPD) or Estimated Breeding Values (EBV). These two measures are alike in that one-half of an animal's EBV is represented in the animal's EPD, where the former (EBV) pertains to the animal itself and the latter (EPD) to genetic differences transmitted to the animal's progeny. Regardless, the primary functions of both EPD and EBV are to rank animals for predicted genetic merit of evaluated traits and hence inform selection, mating and marketing decisions.

Beyond ranking, in the context of comparing animals as parents, EPDs predict the magnitude of difference in the average performance of progeny due to genetics and are typically expressed in units of the given trait. While INHERIT Select reports GEPD, in the trait descriptions below there are instances where differences among GEBV – two times the GEPD – are more indicative of differences in expected expressed female productivity.

For example, differences in observed progeny weaning weights are a function of both the GEBV of the female for milk and the GEPD for weaning weight of the female that describes differences in genetics for growth transmitted to progeny. Finally, for tenderness, predictions are in the form of Molecular Value Predictions (MVP), which are synonymous with GEBV, but derived exclusively from marker effects that impact the Calpain and Calpastatin enzyme systems.

PERCENTILE RANKINGS

Percentile rankings (%) associated with GEPD and indexes from INHERIT Select are reported for individual animals, for the purpose of easy benchmarking against representative commercial crossbred heifers, across the global beef industry (females from the U.S., Canada, Australia, New Zealand, Argentina, and the United Kingdom). For most traits, lower percentile rank values generally indicate "top" or more favorable genetic merit (i.e. top 5%), while higher values usually represent undesirable merit (i.e. top 95%, which means most animals are better).

For some traits such as milking ability and mature cow size, intermediate levels of GEPD and rank are optimum for most production systems and are discussed below in the trait GEPD explanations. It should be noted that while GEPD reported for females tested with INHERIT Select are generally comparable to GEPD for seedstock animals included in the ZMBE, the reference populations for percent rank benchmarking are different to enable more appropriate comparisons. As of December 2025, the INHERIT Select reference population for computing percent ranks included 198,909 females, which expands and is updated with each weekly ZMBE (Table 1).

DESCRIPTION OF TRAIT PREDICTIONS

Birth Weight (BW) GEPD are expressed in pounds and predict genetic differences in the average birth weight of future progeny, as compared to other animals in the evaluation. Lower and moderate BW GEPD values – as well as lower and moderate percentile rankings – generally indicate genetics for lower and moderate progeny birth weights and more desirable calving ease.

Weaning Weight (WW) GEPD are in units of pounds and predict genetic differences in the average adjusted 205-day weaning weight of future progeny, as compared to other animals in the evaluation. Higher WW GEPD values – and lower percentile ranks – translate to genetic merit for heavier and generally more desirable progeny weaning weights.

Yearling Weight (YW) GEPD are in units of pounds and predict genetic differences

Table 1. Percentile ranking table for INHERIT Select as of December 13, 2025.

INHERIT descriptive statistics for beef females as of 12-13-2025 (n = 198,909 with trait and index predictions).																																	
Females	INDEX						EPD														EPD+ HET	EPD							MVP	EPD			INDEX
Top % Rank	ZTR	ZCC	ZFC	$P	$R	$F	BW	WW	YW	DMI	F:G	YH	MW	MH	BCS	CEM	MILK	TUC	DOC	FRT	PP	SC	FSC	CW	FAT	REA	YG	MARB	PAP	HSHED	BRDH	BRDS	$BRD
	$	$	$	$	$	$	lbs	lbs	lbs	lbs	ratio	in	lbs	in	score	%	lbs	score	score	prog	prog	cm	score	lbs	in	in2	score	score	mm	score	%	%	$
1	380	205	200	25000	120	252	-3.4	73	127	-75	-0.39	1.4	95	1.00	0.36	16	32	0.59	0.16	3.19	6.62	1.78	0.33	74	-0.119	1.47	-0.14	1.30	-2.41	-0.47	28.30	15.93	14.25
5	342	183	178	23152	120	202	-1.9	65	113	-42	-0.27	1.1	76	0.80	0.29	13	29	0.46	0.11	2.68	5.58	1.43	0.37	64	-0.084	1.19	0.01	1.06	-1.76	-0.29	24.41	13.74	12.33
10	322	172	167	20141	109	175	-1.1	61	106	-25	-0.20	0.9	67	0.70	0.25	12	27	0.40	0.08	2.41	5.03	1.25	0.40	58	-0.065	1.04	0.09	0.93	-1.36	-0.21	21.80	12.48	11.21
20	299	158	153	16609	88	143	-0.2	56	97	-4	-0.12	0.7	55	0.50	0.21	10	25	0.32	0.05	2.10	4.38	1.03	0.42	52	-0.043	0.86	0.17	0.78	-0.79	-0.13	18.12	10.81	9.72
25	291	153	147	15304	80	130	0.1	54	94	4	-0.09	0.6	50	0.50	0.19	9	25	0.29	0.04	1.98	4.14	0.94	0.43	49	-0.035	0.80	0.20	0.73	-0.57	-0.10	16.59	10.15	9.12
30	284	149	143	14112	73	119	0.4	53	92	11	-0.06	0.6	47	0.40	0.17	9	24	0.26	0.03	1.88	3.93	0.87	0.44	47	-0.028	0.74	0.23	0.67	-0.36	-0.07	15.15	9.53	8.56
40	271	141	134	11960	60	98	1.0	50	86	24	-0.01	0.5	40	0.30	0.14	8	23	0.21	0.01	1.70	3.55	0.73	0.46	43	-0.016	0.64	0.28	0.58	0.00	-0.02	12.44	8.35	7.47
50	259	134	126	9993	47	79	1.5	47	82	37	0.04	0.4	33	0.20	0.12	7	22	0.17	-0.01	1.53	3.20	0.61	0.47	39	-0.005	0.55	0.32	0.49	0.34	0.02	9.82	7.18	6.40
60	247	126	117	7972	33	59	2.1	44	77	49	0.09	0.3	26	0.20	0.09	6	21	0.12	-0.02	1.36	2.87	0.48	0.49	35	0.006	0.46	0.37	0.40	0.66	0.06	7.19	5.93	5.27
70	234	119	108	5820	18	37	2.6	41	72	63	0.14	0.2	19	0.10	0.06	4	20	0.08	-0.04	1.19	2.51	0.34	0.50	31	0.017	0.37	0.41	0.31	1.00	0.11	4.41	4.53	3.98
75	227	114	103	4589	9	24	3.0	39	69	71	0.17	0.1	16	0.00	0.04	4	19	0.05	-0.05	1.09	2.31	0.27	0.51	28	0.023	0.32	0.44	0.25	1.18	0.14	2.89	3.75	3.26
80	219	110	97	3205	-2	10	3.3	38	66	79	0.20	0.1	11	-0.10	0.03	3	18	0.02	-0.06	0.98	2.09	0.18	0.52	26	0.030	0.26	0.46	0.19	1.38	0.16	1.22	2.88	2.48
90	197	97	80	-781	-32	-31	4.4	33	57	102	0.28	-0.1	0	-0.20	-0.03	1	16	-0.06	-0.09	0.70	1.52	-0.06	0.55	19	0.047	0.12	0.53	0.01	1.90	0.24	-2.89	0.69	0.52
95	176	86	64	-4700	-60	-71	5.3	29	50	122	0.34	-0.3	-9	-0.40	-0.07	0	14	-0.13	-0.11	0.46	1.04	-0.29	0.57	13	0.061	0.00	0.59	-0.16	2.32	0.30	-6.05	-0.92	-0.93
99	107	57	33	-15426	-126	-177	7.3	22	38	161	0.47	-0.5	-26	-0.60	-0.18	-3	11	-0.25	-0.16	-0.05	0.08	-0.77	0.61	2	0.087	-0.23	0.69	-0.49	3.07	0.42	-10.96	-3.46	-3.47
Min	-52	-45	-58	-61725	-471	-367	-8.6	-6	-17	-183	-0.82	-1.4	-73	-1.40	-0.42	-11	2	-0.65	-0.33	-1.85	-3.40	-2.17	0.18	-47	-0.208	-0.83	-0.57	-1.16	-4.72	-0.81	-15.15	-8.36	-7.68
Mean	258	134	124	9557	40	74	1.6	47	82	38	0.04	0.4	33	0.24	0.11	7	22	0.17	0.00	1.54	3.24	0.60	0.47	39	-0.007	0.57	0.32	0.48	0.31	0.02	9.61	6.87	6.11
Max	506	284	269	25000	120	388	12.7	100	171	278	0.88	2.1	152	1.80	0.64	23	41	1.02	0.32	5.20	10.66	3.19	0.77	105	0.178	2.28	1.01	2.12	5.34	0.89	33.26	21.53	18.96
StdDev	52	30	34	8532	56	85	2.2	11	19	50	0.19	0.4	26	0.36	0.11	4	4	0.18	0.07	0.68	1.38	0.52	0.06	15	0.044	0.36	0.18	0.37	1.24	0.18	9.27	4.47	4.06

in the average adjusted 365-day yearling weight of future progeny, as compared to other animals in the evaluation. Higher YW GEPD values – and lower percentile ranks – equate to genetic merit for heavier and generally more desirable progeny yearling weights.

Dry Matter Intake (DMI) GEPD are in units of pounds and predict genetic differences in average dry matter intake (feed) during the post-weaning to yearling phase of production (standardized to 112 days) for future progeny, as compared to other animals in the evaluation. Lower DMI GEPD values – and lower percentile rankings – mean less dry matter intake (appetite) for progeny. The desirability of lower dry matter intake (input, or cost) depends upon the relative associated genetic merit across traits that describe quantity, quality, and composition of output (revenue).

Feed to Gain (F:G) GEPD are in units of pounds and predict genetic differences in the average pounds of feed (dry matter) per pound of live, post-weaning weight gain (during the same period as when DMI was collected) of future progeny, as compared to other animals in the evaluation. Lower F:G GEPD values - and lower percentile rankings – translate to genetic merit for more desirable feed efficiency and lower costs of feedlot gain for progeny.

Yearling Height (YH) GEPD are expressed in inches and predict genetic differences in the average height of future progeny at 365-days of age, as compared to other animals in the evaluation. Higher YH GEPD values – and lower percentile rankings – mean genetic merit for taller progeny. In typical production systems, intermediate optimums for YH GEPD are desirable. Excessively tall, late maturing animals are often maternally undesirable due to compromised adaptability and higher feed requirements, while extremely short, early maturing animals often possess undesirable combinations of lower growth rate, lighter carcass weight and less favorable yield grade.

Mature Cow Height (MH) GEPD are expressed in inches and predict genetic differences in the average height of daughters at maturity, as compared to other animals in the evaluation. Higher MH GEPD values – and lower percentile rankings – mean genetic merit for taller progeny. In typical production systems, intermediate optimums for MH GEPD are desirable. Genetic merit for excessively tall, late maturity is typically maternally undesirable due to compromised adaptability and higher feed requirements. Conversely, genetics for particularly short MH are often undesirable because of too early maturity and related fatness, yield grade and carcass weight in feedlot progeny. Tested females' express differences in GEBV - two times their EPD - for MW. The heritability estimate for MH was .59 (highest of all traits included in the ZMBE), and the correlation between GEPD for MH and YH was .67.

Mature Weight (MW) GEPD are in units of pounds and predict genetic differences in the average mature cow weight (adjusted for age, parity and body condition score) of future daughters, as compared to other animals in the evaluation. Higher MW GEPD values – and lower percentile rankings – equate to genetic merit for heavier mature cow weight. In typical production systems, intermediate optimums for MW GEPD are desirable, due to associated feed requirements and costs for heavier cows, but usually lower transmitted growth rate to progeny and less salvage value for lighter weight cows. It should be noted that when comparing INHERIT tested females, differences in their Breeding Value for MW – two times the difference in MW GEPD – are indicative of expressed differences in MW. The correlation between MW GEPD and MH GEPD was .60.

Cow Body Condition Score (BCS) GEPD are expressed in units of score (1 to 9 visual scoring system) and predict genetic differences in condition scores collected from daughters around the time progeny are weaned. Higher BCS GEPD and lower rank values indicate more desirable fleshing ability. INHERIT Select tested females express differences in EBV – two times their EPD – for BCS. Genetic merit for greater fleshing ability is especially advantageous for cow adaptability to harsh environments, including operations with limited feed resources, during periods of droughts, and/or extreme cold weather, and serves as a buffer to related stress. The heritability estimate for BCS was .18, and the correlation between GEPD for BCS and cow MW was .71.

Calving Ease Maternal (CEM) GEPD are expressed in units of probability (%) and predict genetic differences in the likelihood of unassisted birth as first-calf heifers. CEM GEPD include both the maternal and one-half of the direct effects (Calving Ease Direct) transmitted to calves, for calving ease. The genetic evaluation uses BIF calving ease scores (1 to 5)2 and birth weight records, the genetic correlations for which are moderately negative – many of the same genes for higher birth weight have an unfavorable impact on direct and maternal calving ease. Higher CEM GEPD and lower percentile rankings are more favorable. INHERIT tested females express their Breeding Value for CEM.

MILK GEPD are in pounds and predict genetic differences in the average adjusted 205-day weaning weight of future calves from daughters due to milk, as compared to other animals in the evaluation. Higher MILK GEPD values – and lower percentile rankings – mean genetic merit for more milk as expressed through difference in progeny weaning weight. In typical production systems, intermediate optimums for MILK GEPD are usually desirable, because of tradeoffs between input costs to support higher genetic potentials for milk production versus the value of added progeny weaning weight from milk. It should be noted that when comparing INHERIT tested females, differences in their Breeding Value for MILK – two times the difference in MILK GEPD – are indicative of expressed differences in progeny weaning weight due to dam's milk.

Teat and Udder Composite (TUC) GEPD are expressed in units of score and predict genetic differences in the average combined teat and udder scores of future daughters, as compared to other animals in the evaluation. Teat and udder scores are assigned to cows at time of calving and range from one to five (repeat measure). Higher TUC GEPD values – and lower percentile rankings – translate to more desirable combinations of smaller teat size and stronger udder suspension. The weighting of teat size and udder suspension in the TUC GEPD is 50:50, and the genetic correlation between the two measures is high. It should be noted that when comparing INHERIT tested females, differences in their Breeding Value for TUC – two times the difference in TUC GEPD – are indicative of expressed differences in teat size and udder suspension among tested females.

Docility (DOC) GEPD are expressed in units of score and predict genetic differences in the average docility score of future offspring, as compared to other animals in the evaluation. Higher DOC GEPD values - and lower percentile rankings – mean genetic merit for calmer progeny. The data resource that informs this GEPD are Docility Scores assigned during weaning and/or yearling processing. While the docility scoring system used in this evaluation mirrors what's recommended by the Beef Improvement Federation (BIF)2, the scores are inverted, where one is wild and aggressive, two is wild, three is nervous, four is restless and five is calm. As well, DOC GEPD published by many breed associations are expressed as differences in probability of acceptable temperament, not score units as used in the INHERIT evaluation.

Fertility (FRT) GEPD are in units of number of calves and predict genetic differences in the average number of progeny produced by daughters from the second through the eighth parity at nine years-of-age. Differences in INHERIT Select tested females' FRT **EBV**, along with predicted Heterosis for number of calves, collectively predict additive and nonadditive genetic differences in the number of **Predicted Parities** (benchmark Percent Ranks reported in Table 1), which are incorporated in ZCC and ZTR indexes. Fertility Heterosis is the product of percent heterozygosity from genomic approximations of breed composition and maximum F1 heterosis (.65 calves) derived from calving records in the evaluation database. For consistency and simplicity across traits, FRT GEPD are reported, not FRT Heterosis or number of PP.

Scrotal Circumference (SC) GEPD are in units of centimeters and predict genetic differences in the average 365-day adjusted yearling scrotal circumference of future sons, as compared to other animals in the evaluation. The trait Scrotal Circumference in bulls is an indicator of age at puberty in females, and cyclicity in advance of the start of the breeding season is favorably related to earlier first conception. Higher SC GEPD values – and lower percentile rankings – correspond to larger scrotal circumference of sons and earlier age at puberty in daughters as well as INHERIT tested females.

Foot Score Composite (FSC) GEPD are expressed in units of score and predict genetic differences in the average combined CLAW set and Foot ANGLE scores of future progeny as compared to other animals in the evaluation. CLAW and ANGLE scores are assigned to bulls and cows as repeat measures at various ages and range from one to nine. The ideal CLAW set includes symmetrical shaped toes that are even and soundly spaced, while ideal foot ANGLE is 45-degrees at the pastern joint with appropriate toe length and associated depth of heel.

Lower FSC GEPD values – and lower percentile rankings – translate to genetic merit for foot soundness from desirable combinations of genetic merit for CLAW and ANGLE. The weighting of CLAW and ANGLE in the FSC GEPD is 50:50. In most production situations, FSC is a threshold trait where outlier, undesirably high GEPD and especially high percent rank females are candidates for culling or corrective mating. Because thresholds and economic impact of different levels of genetic merit for FSC GEPD are unknown, currently it is not directly integrated into the Zoetis economic indexes.

Hair Shed (HS) GEPD are expressed in units of hair shed score – typically collected in the Spring (northern hemisphere) – and predict genetic differences in progeny for earlier and more complete hair shedding. Lower HS GEPD and associated ranks are more favorable and indicate genetics for earlier shedding and favorable adaptability to climates that cause heat stress, and related tolerance to grazing endophyte-infected fescue. INHERIT Select tested females' express differences in EBV – two times their EPD – for HS. The heritability estimate for HS was .43. Although low, correlations between GEPD for HS and traits related to fleshing ability, fertility, and marbling were favorable: BCS (-.14), FRT (-.13), MARB (-.07).

Bovine Respiratory Disease Health (BRDH) GEPD predict genetic differences in the probability of healthy progeny defined as not requiring pull and treatment for BRD during the post-weaning growing and finishing phases of production to harvest, where higher BRDH GEPD values and lower related percent ranks are desirable. The estimated heritability for BRDH as defined above in the resource population of mostly Bos taurus crossbred feedlot cattle was .13.

Bovine Respiratory Disease Survival (BRDS) GEPD predict genetic differences in the probability of progeny survival from weaning to harvest – not dying from BRD regardless of treatment – where higher BRDS GEPD values and lower related percent ranks are desirable. The estimated heritability for BRDS as defined above in the resource population of mostly Bos taurus crossbred feedlot cattle was .16. The correlation between GEPD for BRDS and BRDH was .74.

Carcass Weight (CW) GEPD are in pounds and predict genetic differences in the average carcass weight of future progeny, as compared to other animals in the evaluation. Higher CW GEPD values – and lower percentile rankings – equate to heavier and generally more valuable progeny carcass weights. Behind the scenes, the genetic evaluation uses carcass weight records adjusted to a fat constant endpoint of .50 inches, from both beef and beef-dairy crosses, along with correlated post-weaning gain records. It is important to note that during 2025, upwards to 70,000 carcass weight and other carcass records, mostly from genotyped beef and beef-dairy cross animals, were added to the ZMBE (now total over 100,000 head). Generally, this further enhanced efficacy and resulted in increased standard deviations of carcass trait predictions.

Fat Thickness (FAT) GEPD are in units of fractional inches (in) and predict genetic differences in the average fat thickness of carcasses from progeny, as compared to other animals in the evaluation. Lower FAT GEPD values – and lower percentile rankings – translate to leaner progeny carcass composition and generally favorable impact on USDA Yield Grade9. In many production systems, intermediate optimums in FAT GEPD values are likely desired because of tradeoffs between carcass composition in harvested progeny versus related fleshing ability for maternal adaptability. The data resources for FAT GEPD are carcass fat thickness measures typically collected through instrument grading of beef and beef-dairy cross carcasses and yearling ultrasound scan measures mostly from breeding cattle, taken at the 12th - 13th rib, as described by BIF[2] guidelines.

Ribeye Area (REA) GEPD are in units of square inches (in^2) and predict genetic differences in the average ribeye size of carcasses from progeny, as compared to other animals in the evaluation. Higher REA GEPD values – and lower percentile rankings – mean larger and generally more favorable ribeye size and impact on USDA Yield Grade9. The data resources for REA GEPD are carcass ribeye area measures typically collected through instrument grading of beef and beef-dairy cross carcasses and yearling ultrasound scan measures, taken at the 12th – 13th rib, as described by BIF[2] guidelines.

Yield Grade (YG) GEPD are expressed in units of USDA Yield Grade Score, adjusted to a 900-pound carcass weight, and predict genetic differences in the average yield grade of future progeny, as compared to other animals in the evaluation. Lower YG GEPD values - and lower percentile rankings - generally mean more favorable USDA Yield Grade and higher percentage of closely trimmed retail cuts. The data resource for YG GEPD are USDA Yield Grades from beef and beef-dairy cross carcasses, typically collected through instrument grading.

Marbling Score (MARB) GEPD are expressed in units of BIF Score[2] and predict genetic differences in the average magnitude of marbling in carcasses of progeny, as compared to other animals in the evaluation. Higher MARB GEPD – and lower percentile rankings – equate to more desirable marbling scores, USDA Quality Grades, and associated carcass value in harvested progeny. The data resources for MARB GEPD are carcass marbling scores typically collected through instrument grading of beef and beef-dairy cross carcasses and yearling ultrasound scan measurements, taken at the 12th – 13th rib, as described by BIF[2] guidelines. Higher marbling contributes to the juiciness and flavor components of eating satisfaction.

Tenderness (TND) MVP are expressed in units of pounds and predict differences in genetic merit for the average magnitude of force required to shear through cooked steak samples, as compared to other animals in the evaluation. Lower TND MVP are desired and indicate less shear force required and more desirable tenderness, another important component of eating satisfaction. The marker effects used to calculate TND MVP were derived from the Carcass Merit Project conducted by the National Cattlemen's Beef Assocation.[4]

ACCURACY

In addition to GEPD, the ZMBE computes associated accuracy values. Accuracy ranges from 0 to 1, with higher values indicating greater dependability and less potential for the GEPD to change as additional information accumulates, especially from progeny. In the context of INHERIT Select, baseline accuracy is driven by genomic information and the strength of connectedness between tested females and other genotyped animals with performance information in the evaluation.

More specifically, the accuracy of GEPDs reported varies across evaluated traits, and is highest for more heritable traits with larger quantities of phenotypic information contributing to the evaluation (i.e. Birth Weight). In general, for commercial females that are genomically connected to the evaluation – and from HD50K tested sires represented in the evaluation – underlying accuracy values typically fall somewhere in the .2 to upper .4 range and are usually quite similar for any given trait across most tested females. An exception is the accuracy for BRD traits, which with lower heritability are often lower than .2. Since accuracy for non-parents is similar for most traits and to simplify reporting, individual accuracy values for specific animals and traits are not reported.

INHERIT SELECT ECONOMIC INDEXES

Economic selection indexes rank animals for combined genetic merit across evaluated traits, weighted according to associated impacts on costs and revenues from production. Most importantly, indexes are intended to help simplify proper, economically grounded, multiple trait selection and breeding decisions for long-term economic returns. For these reasons, signature features of INHERIT Select are the Zoetis Cow | Calf (ZCC), Zoetis Feedlot | Carcass (ZFC) and especially the Zoetis Total Return (ZTR) economic indexes.

The economic assumptions used for the INHERIT Select indexes were derived from a variety of beef industry sources and are consistent with assumptions used by major breed associations to formulate indexes[7,8]. Compared to previous economic assumptions (2023), adjustments for higher calf and carcass prices were made for the latest 2026 versions of the indexes. Production assumptions for the ZTR index includes within-herd retention of replacement heifers and either retained ownership and marketing of fed cattle/carcasses on value-based grids, or marketing of feeder cattle with price discovery that recognizes these genetic differences. Importantly, index development accounts for the genetic correlations among contributing traits, to not over or under emphasize associated economic contributions.

Dollar Bovine Respiratory Disease Economic Index ($BRD) predicts differences in the direct and indirect impacts on revenue per progeny due to combined genetic merit for BRD Health (BRDH) and BRD Survival (BRDS), where higher $BRD values and lower ranks are desirable.

Importantly, $BRD includes four assumptions consistent with the moderate to high BRD risk reference populations from which the predictions were developed and that continue to contribute records to the ZMBE. Two of the assumptions were related to incidences, 1) of pull and related treatment (13.5%), and 2) of death due to BRD (3.8%). The other two assumptions were economic and included 3) the direct and indirect (reduced feedlot performance and carcass value) costs of treated versus untreated ($75), and 4) the average cost of dead based on means for standardized feeder cattle purchase price, purchase weight, days on feed to death, and related costs ($2,500).

At present, relationships between these post-weaning to harvest trait definitions and GEPD for BRD versus similar or alternative birth to weaning trait definitions for BRD are unknown. For this reason, and because $BRD is also quite sensitive to the four assumptions discussed above, BRDH and BRDS are not yet included in the INHERIT indexes discussed below.

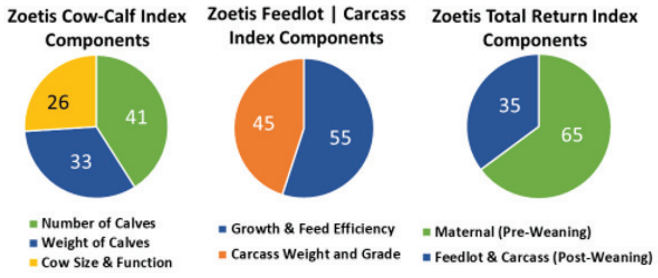
Zoetis Cow | Calf (ZCC) index is expressed in dollars (US) on a per calf basis and predicts differences in combined genetic merit across evaluated maternal traits, including GEPD for BW, WW, Milk, MW, CEM, TUC, FRT and DOC, as well as Heterosis for FRT. As the index name indicates, ZCC encompasses the cow-calf phase of production and assumes that calves are marketed shortly after weaning. The ZCC index places the most weighting on traits related to fertility, calving ease and the lifetime number of calves (41%), weaning weight of calves produced (33%), while seeking to keep mature cow size, milk and associated feed requirements relatively constant, and improve functional traits (26% - see figure 1).

Zoetis Feedlot | Carcass (ZFC) index is expressed in dollars (US) on a per calf basis and predicts differences in combined genetic merit across evaluated feedlot and carcass traits, including YW (post-weaning gain – PWG), DMI, CW, MARB, REA and FAT. The ZFC index assumes that fed cattle are marketed in-the-beef – on a carcass weight basis – with price determined by a value-based grid that rewards higher marbling (MARB) and conformance to acceptable USDA Yield Grades (influenced by FAT, REA and CW). Overall, based on costs, revenues, genetic variation and trait relationships, in the ZFC index the relative economic weighting on feedlot traits is 55%, as compared to 45% on carcass traits.

Zoetis Total Return (ZTR) index is expressed in dollars (US) on a per calf basis and predicts differences in combined genetic merit across most all traits included in the ZMBE, as well as the ZCC and ZFC indexes. For ZTR, nearly two-thirds of the emphasis is on pre-weaning maternal trait predictions, while just over one-third of the weighting is on predicted post-weaning terminal trait genetic merit. The ZCC and ZFC indexes are not additive as related to ZTR, because some traits included in both indexes are highly correlated – namely the growth traits WW and YW – and it would be inappropriate to double count growth in the ZTR index. Since ZTR encompasses nearly the full range of evaluated traits, it is the single most inclusive and informative Zoetis source of genetic information provided by INHERIT Select to use when making selection and breeding decisions (alternatively, see $Profit explanation below).

With over 16 traits directly or indirectly included in the ZTR index, there are many ways for animals to achieve favorably similar values. As such, cow-calf producers may also consider the component indexes and traits that are important to their individual goals and production environments. Figure 1 illustrates the magnitude of contribution that maternal, growth-efficiency and carcass trait groups have on applicable INHERIT Select indexes. The ZTR index helps simplify and ensure that the most economically valuable animals – sometimes from unexpected combinations of genetic merit – are not overlooked in the selection process.

Figure 1. Relative contributions (%) of trait groups to the Zoetis Cow-Calf (ZCC), Feedlot | Carcass (ZFC) and Total Return (ZTR) indexes.



SELECTION BASED ON ZTR – ANTICIPATED RESPONSE IN COMPONENT TRAITS

Replacement heifer selection decisions based on the ZTR index are expected to yield favorable genetic improvement across component traits. Using the global Zoetis database of tested animals, component trait means were computed and contrasted for animals that ranked in the top 25% versus bottom 75% for ZTR (Figure 2)[9]. Contrasts in mean GEPD were standardized so that the magnitude of deviated means were comparable across traits.

Animals that ranked in the top 25% as compared to the bottom 75% for ZTR, had standardized GEPD that were notably higher for the key drivers of the index, namely cow fertility (FRT), BW, CEM, WW, and YW, slightly lower DMI, F:G, YH and MW (favorable impact on cow costs); slightly positive response for Milk, TUC, DOC, and FAT, as well as beneficial response in CW, REA and MARB. This illustrates how selection based on ZTR helps simplify proper multiple-trait selection. Selection for ZTR is also expected to result in favorable response in the ZCC and ZTR indexes.

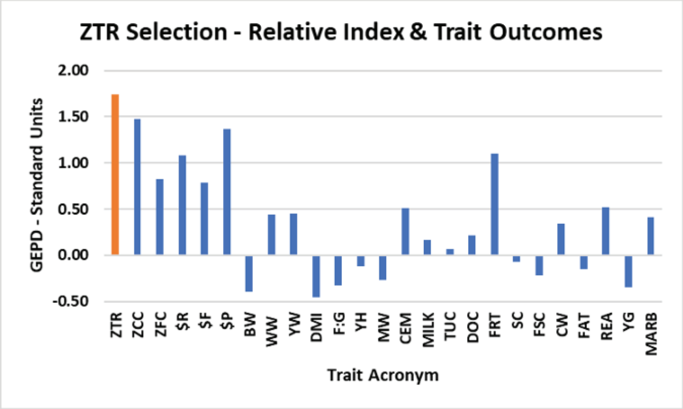
SIMPLE RECESSIVE FEATURES

The Polled Test determines whether phenotypically polled animals are heterozygous or homozygous polled. This positively supports animal well-being by helping to identify animals that are genetically dehorned. Possible outcomes of the test include:

- PP = Homozygous polled
- Ph = Heterozygous polled
- I = Indeterminate: The polled status of the animal was horned or not definitive
- N/R = No result: Sample failed testing

The Black Test is primarilyused to identify if black animals are homozygous or heterozygous for black coat color at the Extension locus. Homozygous Black seedstock animals are often more valuable because they always transmit the black allele. More specifically, the test identifies the black (ED), red (e) and wild-type (E+) alleles present at the Extension (E) locus. The order of dominance for these alleles as related to expression of color translates into black as dominant to red, and both black and red as dominant to wild-type. Heterozygous black animals only transmit the black allele to one-half

Figure 2. Standardized differences in component trait GEPD means for animals ranking in the top 25% versus bottom 75% for ZTR.



of their progeny. Importantly, additional genes exist that also affect color. Possible outcome of this test include:.

Specifically, the test identifies the black (ED), red (e) and wild-type (E+) alleles present at the Extension (E) locus. The order of dominance for these alleles as related to expression of color translates into black as dominant to red, and both black and red as dominant to wild-type. Heterozygous black animals only transmit the black allele to one-half of their progeny but are black in appearance. Importantly, additional genes exist that also affect color. Possible outcome of this test include:

- EDED: Homozygous Black
- ee: Red (Homozygous)
- EDe: Heterozygous Black
- E+E+: Homozygous Wild Type
- E+ED: Black - Wild Type Carrier
- E+e: Red - Wild Type carrier
- NR: No Result: Sample failed testing

Silver Color Dilution (CD) Test results involve the variant most frequently found in Hereford and Simmental breeds, that results in grey or light red expression of color when combined with black (ED) or red color (e) at the Extension locus, respectively. This dilution variant is different than the variant most prevalent in Charolais. The allele for this variant of dilution is dominant to the corresponding allele for non-dilution, hence either one or two copies – heterozygous (CDC) or homozygous (CDA) for dilution - result in diluted expression of color. Reported results for SCD are as follows:

- CDF – Silver Color Dilution Free – homozygous free of CD
- CDC – Silver Color Dilution Carrier - heterozygous for CD
- CDA – Silver Color Dilution Affected – homozygous for CD

OPTIONAL ADD-ONS

Customers may optionally request different add-ons to the normally included features of INHERIT Select –1) Bovine Viral Diarrhea Virus (BVDV) test, 2) GEPD for Pulmonary Arterial Pressure and 3) Leachman Cattle of Colorado dollar Ranch and Profit indexes. There are added fees for each of these optional add-ons, ideally requested at time of ordering, for individuals or all animals in test groups.

Bovine Viral Diarrhea Virus (BVDV) Test uses a licensed Erns Antigen Capture ELISA kit that detects BVDV Types 1 and 2 antigens from ear tissue (TSU) samples to help identify persistent infection (PI) status. Tissue samples – using either Allflex or Caisley – are required for BVDV testing, and the same sample can be used for INHERIT testing.

Pulmonary Arterial Pressure[5] (PAP) GEPD is expressed in units of millimeters of Mercury and predict genetic differences in the average blood pressure of future progeny, as compared to other animals in the evaluation. Lower PAP GEPD values – and lower percentile rankings – indicate lower, more desirable blood pressure and less susceptibility to brisket disease for high altitude production systems. It should be noted that when comparing INHERIT tested females, differences in their full Breeding Value for PAP – two times the difference in PAP GEPD – are indicative of genetic differences in tested females’ tolerance in higher altitude environments.

Dollar Ranch™ ($R), Dollar Feeder™ ($F), and Dollar Profit™ ($P) Indexes from Leachman Cattle of Colorado (LCoC), are collectively available as an add-on to INHERIT Select. These indexes are possible because the ZMBE engine primarily uses LCoC pedigree, performance, and genotype information as the fuel to power trait predictions and other features. As the names imply, $R focuses on maternal productivity during the conception to weaning phase of production on a per calf (progeny) basis, $F spans the post-weaning to carcass phase of production on a per calf (progeny) basis, while $P encompasses the complete range of traits related to revenues and costs, throughout the entire pre- and post-weaning (feedlot) as well as carcass phases of production. Per the data sharing agreement with seedstock partners, $R and $P index reporting is truncated at $120 and $25,000, respectively.

It should be noted that $P assumes that the average commercial bull has 100 lifetime progeny – which isn't applicable to commercial females. However, simple division by 100 transforms $P to a per calf basis, enabling more applicable scaling to female productivity. Further, $P assumes 30% of heifer progeny are retained as replacements and retained ownership on the remainder of calves through finishing and grid marketing. Another important distinction between $R, $R and $P versus indexes included in INHERIT (ZCC, ZFC and ZTR), is that $R, $R and $P include projected heterosis from assumed mating to opposite parents that are three-quarters (75%) Angus, one-quarter (25%) Simmental breed composition. Alternatively, INHERIT Select uses genomic breed composition to project maternal heterosis for Fertility of the tested female, which contributes to ZCC and ZTR.

In addition to differences in how these indexes incorporate heterosis that is described above, justifiable differences exist in modeled trait weightings. The $R and $P indexes place more downward emphasis on moderation of mature cow size and upward pressure on cow fertility and marbling, while ZCC, ZFC and ZTR place relatively more emphasis on growth, carcass weight, calving ease maternal, docility and teat/udder soundness.

GENOMIC BREED COMPOSITION

An informative feature of INHERIT Select are genomic estimates of breed composition. Using genotypes from tested animals that originated from defined "purebred" breeds represented in Zoetis reference populations, an algorithm was developed to predict genomic breed composition percentages. The current reference population supports approximations for 17 different breeds, reported individually and combined into breed categories defined as British, Continental, Indicus, and Dairy. Table 2 below provides the list of included breeds and associated codes, while Table 3 provides an example report.

At present, if derived genomic breed composition is 25% or more for any combination of Nelore and Wagyu, or more than 50% Brahman, animals are not eligible for INHERIT Select trait and index predictions. The reason is because currently these breed groups and related crosses are not adequately represented with performance data in the Zoetis Multi-Breed Genetic Evaluation (ZMBE), to yield predictions with documented accuracy.

INHERIT Select customers are advised against testing animals whose composition includes meaningful proportions of breeds other than those listed in Table 1. The algorithm used to predict genomic breed composition uses differences in allele frequencies among purebreds of included populations, with the sum of predictions across these breeds equaling 100%. If tested animals possess breed(s) that are not currently factored into the predictive algorithm – for example Salers or Senepol (composite) - it will erroneously allocate such to the closest match among one or more of the included breeds.

Table 2. INHERIT genomic predicted breed composition population groups and associated codes.

Breeds & Codes for Genomic Predicted Breed Composition				
British (B)	Continental (C)	Dairy (D)	Indicus (I)	Wagyu (W)
Angus (AN)	Simmental (SM)	Holstein (HO)	Brahman (BR)	Black Wagyu (KB)
Red Angus (RA)	Gelbvieh (GV)	Jersey (JE)	Nelore (NE)	Akaushi (AK)
South Devon (SD)	Limousin (LM)	Brown Swiss (BS)		
Hereford (HE)	Charolais (CH)	Guernsey (GU)		
Shorthorn (SH)				

Table 3. Example INHERIT Connect genomic predicted breed composition.

Identification		British (%)				Continental (%)				Dairy (%)				Indicus (%)		Breed Summary (%)					
EID	TAG	AN	RA	HE	SD	SM	GV	LM	CH	HO	JE	BS	GU	BR	NL	B	C	D	I	KB	AK
982000426445318	H1658	75	0	0	0	25	0	0	0	0	0	0	0	0	0	75	25	0	0	0	0
982000426445475	H1326	50	25	0	0	0	25	0	0	0	0	0	0	0	0	75	25	0	0	0	0
982000425779448	H2490	25	0	0	0	25	0	0	0	50	0	0	0	0	0	25	25	50	0	0	0
982000427585450	H1166	0	0	0	0	0	0	50	0	0	50	0	0	0	0	0	50	50	0	0	0
982000426445394	H1021	50	0	0	0	0	0	0	0	0	0	0	0	0	0	50	0	0	0	50	0

[1] AN = Angus (black); RA = Red Angus; HE = Hereford; SD = South Devon; SM = Simmental; GV = Gelbvieh; LM = Limousin; CH = Charolais; HO = Holstein; JE = Jersey; BS = Brown Swiss; GU = Guernsey; BR = Brahman; NL = Nelore; B = sum of evaluated Bristish breeds; C = sum of evaluated Continental breeds; D = sum of evaulated Dairy breeds; I = sum of evaluated Indicus breeds; WG = Wagyu; AK = Akaushi.of Nelore, Wagyu and Akaushi breed makeup, animals are not eligible for INHERIT Optimize individual trait and index predictions. The reason is because currently these breed groups and related crosses are not adequately represented with performance data in the Zoetis Multi Breed Genetic Evaluation (ZMBE), to yield predictions with documented accuracy.

Genomic approximations of breed composition have several useful purposes. Breed composition is indicative of potential individual, maternal, and paternal heterosis, the increase in production of crossbreds above that of the average of parent breeds. Thus, knowledge of genomic breed composition helps inform selection and crossbreeding decisions for desired levels of heterosis expressed by tested animals and future calf-crops, often with more precision than theoretical breed composition based on available pedigree information.

As with all predictions, genomic breed composition is not perfect – possible error, or noise in the form of roughly 1% to 5% composition sometimes is allocated to sources other than what is thought to possibly be the true breed or breed-cross. At least partially, this may be due to "purebred and fullblood" resource populations - used to derive allele frequencies - that possess fractions of other breeds.

The algorithm used to predict genomic breed composition uses differences in allele frequencies among purebreds of included populations, with the sum of predictions across these breeds equaling 100%. If tested animals possess breed(s) that are not currently factored into the predictive algorithm – for example Salers - it will erroneously allocate such to the closest match among one or more of the included breeds.

As with all predictions, genomic breed composition is not perfect – possible error, or noise in the form of roughly 1% to 5% composition sometimes is allocated to sources other than what's thought possible. At least partially, this may also be due to "purebred and fullblood" resource populations - used to derive allele frequencies - that possess fractions of other breeds.

SIMULATED VALUE PROPOSITIONS

Value-returns from selection of replacement heifers based on the ZTR and ZCC indexes were simulated over a 10-year period, with and without reductions in replacement rate enabled by correlated responses in Fertility GEPD[10]. The various simulations included the following assumptions: 500 head cow herd; 92% weaned calf crop; an initial replacement rate of 20% and the testing of two heifers for every one selected (200 tested, 100 retained); testing cost per selected heifer of $50 ($25 per head); 25% annual replacement rate and continuous index advancement for purchased bulls. The simulations evaluated use of the above indexes versus traditional selection of replacement heifers and associated impacts on the cowherd and calf-crops over time. Genetic gain from traditional replacement heifer selection was defined as equivalent to parent-average index values for simulated calf crops.

PROPOSED INHERIT TESTING STRATEGY

INHERIT Select results inform more profitable female selection, breeding (including bull buying) and marketing decisions. While cows may be tested at any time, the bullet items below provide general guidance as to testing strategy - based on value proposition modeling[6] and practical experiences - for candidate replacement heifers and lifetime use of results:

- Collect DNA using Allflex® Tissue Sampling Units (TSU) or CaisleyTM Tissue Sampling Ear Tags at first processing (roughly two to three months of age), pre-conditioning, weaning or Brucellosis vaccination from at least the top three-quarters of the heifer crop that were earliest born and meet visual appraisal criteria (sound feet and legs, acceptable expressed growth, adequate body capacity, relatively calm temperament, etc.)

- Depending on the number or replacements needed, select roughly the top half of the heifers based primarily on ZTR or $P ranking, as well as desired thresholds for the other indexes (ZCC, ZFC and $R), individual traits, breed composition and INHERIT Connect sire parentage information.

- As replacements and throughout their lifetimes, use INHERIT Select results to inform breeding decisions to A.I. and natural service bull batteries, to accentuate genetic strengths, correct weaknesses and achieve desired levels of breed composition and retained heterosis according to ranch-specific objectives.

- Use INHERIT Insights[11] report information and updated (weekly) INHERIT results from cow and replacement heifer inventories to inform annual bull-buying decisions – to continuously advance additive genetic merit (GEPD) for maternal, feedlot and carcass performance, manage breed composition for desired levels of direct and maternal heterosis, as well as purchase/turnout of bulls that are relatively unrelated to groups of females for avoidance of inbreeding.
- When new bulls are added to the bull battery that have not been tested and have HD50K genotypes in the ZMBE, test those bulls with INHERIT Connect to enable future sire parentage determination to daughters.

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