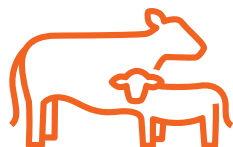


TECHNICAL BULLETIN

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INHERIT SELECT™ FOR COMMERCIAL FEMALES TECHNICAL SUMMARY

INHERIT Select Product Features

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KEY POINTS

- 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 nineteen traits and five economic indexes, as well as sire and dam parentage and genomic approximations of breed composition, to collectively enable more informed 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 1.3 million animals—as well as 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 five economic indexes—Zoetis Cow|Calf; Zoetis Feedlot|Carcass; and Zoetis Total Return and optional Leachman Cattle of Colorado \$Ranch™ & \$Profit™—that simplify proper multiple-trait selection for net return
- INHERIT Select is exclusively for females, with results only reported for genomic determined females
- INHERIT Connect™ is a companion test to INHERIT Select, that enables testing of bull batteries to determine daughter parentage - connect candidate sires to tested daughters—no other results are reported for INHERIT Connect
- INHERIT Select is intended for use in crossbred *Bos taurus* females comprised of the following breeds: Angus, Red Angus, South Devon, Hereford, Simmental, Gelbvieh, Limousin and Charolais
- 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. and Zoetis
- Optional add-ons to INHERIT Select include GeneSTAR® Polled, GeneSTAR® Black, Bovine Viral Diarrhea Virus (BVDV), GEPD for Pulmonary Arterial Pressure (PAP) and previously mentioned Leachman Cattle of Colorado \$Ranch™ and \$Profit™ indexes

INHERIT SELECT™ PRODUCT FEATURES

Zoetis Multi-Breed Evaluation

The Zoetis Multi-Breed Evaluation (ZMBE) is a proprietary evaluation that generates INHERIT Select results using methodology and software from the University of Georgia called ssGBLUP¹—single-step Genomic Best Linear Unbiased Prediction—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, GEPD from genomic information, effectively informed through large quantities of pedigree, breed composition and phenotypic performance data from genetically related, connected seedstock. These sources of information are ever expanding so, on a regular 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 more than 1.2 million animals was used for initial development.² These data originated from a variety of sources, but primarily included Leachman Cattle of Colorado (LCoC) and associated Cooperators as well as Profit Share partners and Zoetis company-owned resources. Just over half of the animals were relatively straight-bred, while the remainder were crossbred representing various combinations of breed composition. Initial ZMBE development encompassed just over 20,000 animals with high density genotypes, including influential A.I. sires from various populations. As of July 31, 2022, just over two years

following the launch of INHERIT Select, the population of genotyped animals expanded to nearly 145,000.³

The six most influential breeds, ranked in descending order of prevalence among both straight-bred and crossbred animals included in the ZMBE are: 1) Angus, 2) Red Angus, 3) Simmental, 4) South Devon, 5) Gelbvieh and 6) Hereford. Although less influential, the Limousin and Charolais breeds are also adequately 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 breeds. INHERIT Select is not recommended for females with fractions of composition made up of breeds others than those listed above. Trait predictions and indexes are not reported for animals predicted to possess more than 20% genomic breed composition from breeds other than the eight noted, namely of dairy (Holstein and Jersey) and/or indicus breeds (Brahman and Nelore). In addition to these breed composition requirements, heifers sired by HD50K™ for \$Profit tested bull batteries are ideal candidates for testing.

GENOMIC DETERMINED GENDER

INHERIT Select is for commercial females—replacement heifers and cows—and not designed or intended for use in bulls. In order to effectively manage such use, genomic information is utilized to determine the sex of animals tested with INHERIT Select. In cases where orders and samples are submitted, tested and identified as genomic males, the only result reported is a sex conflict (bull), and no other results are provided. INHERIT Select is exclusively for females because the essential pedigree,

performance and genomic resources used to inform 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 is only for commercial females recognizes the vast ongoing investments in pedigree, performance data collection and genotyping made by these seedstock partners. More importantly, as compared to untested heifers, results from INHERIT Select provide a better understanding of genetic strengths and weaknesses, as well as sire parentage and breed composition of commercial cow herds, to inform and complement bull-buying decisions based on information provided by seedstock producers⁴.

PARENTAGE

Sire and/or dam parentage determination are included features of INHERIT Select and are delivered as output from the ZMBE. An essential prerequisite for parentage determination, is that candidate parents must have INHERIT Select and Connect (see below), or HD50K for \$Profit or for JLC genotypes included in the ZMBE. Since the evaluation is executed regularly, it follows that genotypes for parents may enter the ZMBE at any time—prior to, at the same time, or after INHERIT females are tested—with updated parentage results reported via SearchPoint.® Successful sire parentage determination usually results in more dependable trait GEPD (higher accuracy) and index predictions, so having tested bull batteries to enable immediate identification of sires is advised.

INHERIT Select sire parentage determination is flexible, and both 1) verifies presumed sires of record, as well as 2) identifies the specific sire of females from tested bull batteries without necessarily having to nominate defined groups of candidate sires. If sires of record exist for specific females, based on A.I. breeding and calving records, single sire breeding pastures, or observed services, the presumed sire's registration number is requested on the order form for testing purposes. Alternatively, if there's no apparent sire of record due to multiple sire breeding schemes, the sire registration number and breed association fields of the order form 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 has a status of 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, 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 and there was no sire or dam found by the evaluation

INHERIT CONNECT™

Recognizing that those who test with INHERIT Select may have portions of their bull battery that do not have HD50K for \$Profit genotypes included in the ZMBE, INHERIT Connect is available as a companion product to enable such testing. As the name indicates, the purpose is to connect candidate sires to tested daughters as well as connect both sires and daughters to other genotyped animals in the evaluation. INHERIT Connect thus enables more complete sire determination 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, the only result delivered for bulls tested with INHERIT Connect is sire parentage determination for females tested with INHERIT Select.

TRAIT PREDICTIONS – GENOMIC EXPECTED PROGENY DIFFERENCES

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 merit transmitted to the animal's progeny. Regardless, the primary function of both EPD and EBV is to rank individual animals across defined populations from lowest to highest for predicted genetic merit of evaluated traits.

Beyond ranking, in the context of comparing animals as parents, EPDs predict the magnitude of difference in the average performance of progeny 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 EBV—two times the GEPD—are more indicative of differences in expected observed female productivity. For example, differences in expressed progeny weaning weights are a function of both the Breeding Value 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 EBV 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 primarily the U.S. beef industry (females from Australia, Canada and New Zealand are also included). 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 (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 July 6, 2022, the INHERIT Select reference population for computing percent ranks included 30,966 animals, which expands with each weekly ZMBE (Table 1).⁵

Table 1. Percentile ranking table for INHERIT Select as of July 6, 2022

Top %	Genomic Expected Progeny Differences (GEPD)																				Selection Indexes (USD)				
Rank	BW	WW	YW ¹	DMI	F:G	YH	MW	MILK	TUC	DOC	FRT	PP ²	SC	FSC	CW	FAT	REA	IMF ¹	TND	PAP	ZCC	ZFC	ZTR	\$R ¹	\$P ¹
1	-3.7	65	113	-71	-0.37	1.3	81	34	0.49	0.10	2.70	5.66	1.75	0.32	856	-0.056	0.94	0.91	-0.65	-2.37	174	175	325	79	19999
5	-2.1	59	102	-40	-0.25	1.1	65	31	0.38	0.06	2.34	4.91	1.41	0.37	843	-0.040	0.79	0.74	-0.60	-1.70	158	158	300	70	17465
10	-1.3	55	96	-24	-0.19	0.9	57	29	0.31	0.04	2.15	4.52	1.23	0.39	836	-0.032	0.71	0.65	-0.58	-1.31	150	150	288	64	15747
20	-0.4	51	89	-4	-0.12	0.8	48	28	0.24	0.02	1.92	4.05	1.01	0.42	828	-0.023	0.61	0.55	-0.56	-0.80	140	140	271	56	13663
25	-0.1	50	86	4	-0.09	0.7	44	27	0.21	0.01	1.84	3.87	0.93	0.43	825	-0.019	0.58	0.52	-0.55	-0.61	137	136	265	53	12841
30	0.2	48	84	11	-0.06	0.6	41	26	0.18	0.00	1.77	3.72	0.86	0.44	822	-0.016	0.54	0.48	-0.49	-0.44	133	132	259	50	12100
40	0.7	46	80	23	-0.02	0.5	35	25	0.14	-0.01	1.63	3.43	0.74	0.46	817	-0.011	0.49	0.43	-0.37	-0.11	127	126	250	45	10750
50	1.2	43	76	35	0.03	0.5	30	24	0.09	-0.03	1.50	3.16	0.62	0.47	812	-0.006	0.43	0.37	-0.34	0.19	122	121	241	41	9483
60	1.7	41	72	46	0.07	0.4	24	23	0.05	-0.04	1.37	2.88	0.50	0.49	808	-0.001	0.38	0.33	-0.28	0.48	116	115	232	36	8247
70	2.3	38	68	58	0.11	0.3	19	22	0.00	-0.06	1.23	2.59	0.37	0.50	803	0.004	0.33	0.27	-0.25	0.79	110	109	222	31	6957
75	2.6	37	65	65	0.14	0.2	16	21	-0.03	-0.06	1.15	2.43	0.30	0.51	800	0.007	0.30	0.24	-0.14	0.96	106	106	217	29	6216
80	2.9	36	63	73	0.17	0.2	12	21	-0.06	-0.07	1.06	2.24	0.22	0.52	798	0.010	0.27	0.21	-0.09	1.14	103	102	211	26	5399
90	3.8	32	56	93	0.24	0.0	2	19	-0.14	-0.09	0.83	1.74	0.02	0.55	790	0.018	0.18	0.13	-0.04	1.62	92	93	196	18	3319
95	4.6	28	51	110	0.30	-0.1	-6	17	-0.20	-0.11	0.63	1.33	-0.15	0.57	784	0.025	0.11	0.07	0.16	2.00	83	85	183	11	1684
Min	-6.8	6	12	-165	-0.64	-0.8	-49	8	-0.86	-0.26	-0.98	-1.96	-1.32	0.19	752	-0.103	-0.34	-0.32	-0.89	-4.13	-16	24	91	-36	-10139
Avg	1.3	44	76	36	0.02	0.5	31	24	0.09	-0.03	1.49	3.17	0.63	0.47	813	-0.006	0.44	0.39	-0.34	0.20	121	121	241	40	9491
Max	10.1	91	115	236	0.66	2.0	125	44	0.77	0.20	3.70	7.76	2.76	0.70	885	0.063	1.29	1.00	0.41	4.50	212	219	377	80	20000
SD	2.0	9	15	46	0.17	0.4	21	4	0.17	0.05	0.52	1.09	0.47	0.06	18	0.020	0.20	0.21	0.22	1.10	23	22	35	18	4774

¹Predictions reported for YW, IMF, \$R and \$P truncated at 115, 1.0, \$80 and \$20,000, respectively.

²PP = Predicted Parities = Fertility Breeding Value = (2 X FRT GEPD) + Fertility Heterosis. Included in ZCC and ZTR, not published for individual animals.

Birth Weight (BW) GEPD are expressed in pounds and predict genetic differences in the average birth weight of future progeny, as compare 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 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. Per the data sharing agreement with seedstock partners, YW GEPD reporting is truncated at 115 (females with values greater than 115, are reported as 115).

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 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 full Breeding Value for MW—two times the difference in MW GEPD—are indicative of expressed differences in MW.

MILK GEPD are in pounds and predict genetic differences in the average adjusted 205-day weaning weight of future calves from daughters, 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 full

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 full 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),⁶ 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** (PP - 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 symmetrically 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, at this time it is not directly integrated into the Zoetis economic indexes.

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 desirable progeny carcass weights. Behind the scenes, CW GEPD are computed as an index from growth and carcass composition GEPDs, the efficacy of which was documented shortly after the initial release of INHERIT Select⁷. While the CW predictions have the appearance of carcass weight phenotypes, differences

are indicative of progeny carcass weights.

Fat Thickness (FAT) GEPD are in units of fractional inches and predict genetic differences in the average fat thickness of future progeny at a year of age, 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 Grade⁷. 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 resource for FAT GEPD are ultrasound scan measurements, taken at the 12th – 13th rib, as described by BIF⁶ guidelines.

Ribeye Area (REA) GEPD are in units of square inches (in²) and predict genetic differences in the average ribeye size of progeny at a year of age in future 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 Grade⁷. The data resource for REA GEPD are ultrasound scan measurements, taken at the 12th – 13th rib, as described by BIF⁶ guidelines.

Intramuscular Fat (IMF) GEPD are expressed in units of percent and predict genetic differences in the average amount of intramuscular fat at a year of age in future progeny, as compared to other animals in the evaluation. Higher IMF GEPD—and lower percentile rankings—equate to more desirable, higher percentages of intramuscular

fat and corresponding marbling scores, USDA Quality Grades and associated carcass value in harvested progeny⁷. The data resource for IMF GEPD are ultrasound scan measurements, taken at the 12th – 13th rib, as described by BIF⁶ guidelines. Higher IMF and marbling contribute to the juiciness and flavor components of eating satisfaction. Per the data sharing agreement with seedstock partners, IMF GEPD reporting is truncated at 1.00 (females with values greater than 1.00, are reported as 1.00).

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 Association.⁸

ACCURACY

In addition to GEPD, the ZMBE computes associated accuracy values. Accuracy ranges from 0 to 1,⁶ 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.

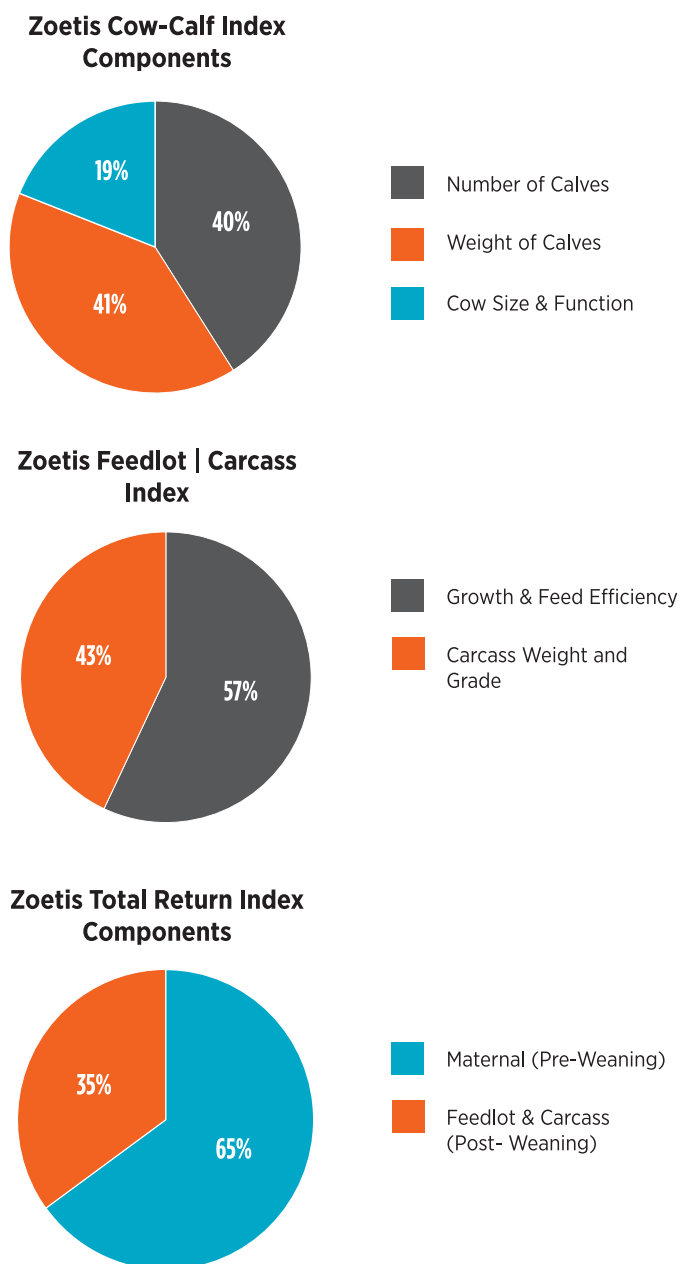
More specifically, the accuracy of GEPDs reported varies across evaluated traits, and is highest for more heritable traits with larger quantities of phenotypic information contributing to the evaluation (i.e., Birth Weight). In general, for commercial females that are genomically connected to the evaluation—and from HD50K™ for \$Profit-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. For this reason 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 economically grounded multiple trait selection and breeding decisions for maximum 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.^{9,10} Production assumptions for the ZTR index includes

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



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, in order to not over- or underemphasize associated economic contributions.

Zoetis Cow|Calf (ZCC) index is expressed in U.S. dollars on a per calf basis and predicts differences in combined genetic merit across evaluated maternal traits, including GEPD for BW, WW, Milk, MW, 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 roughly equal weighting on traits related to fertility and the lifetime number of calves (40%) and weaning weight of calves produced (41%), while seeking to keep mature cow size and milk and associated feed requirements relatively constant (Figure 1)¹¹. Selection based on ZCC is designed to also yield favorable response in cow functional traits, namely docility and teat and udder quality.

Zoetis Feedlot|Carcass (ZFC) index is expressed in U.S. dollars 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, IMF, 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 (IMF) 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 57%, as compared to 43% on carcass traits. Based on the initial external evaluation of efficacy that included 671 animals, the top quartile ZFC genetic group produced the most valuable carcasses that earned the highest price per CWT, were the heaviest and of the highest marbling score as compared to the other groups ($P < .05$)⁷. In contrast, the bottom quartile ZFC genetic group produced the least valuable carcasses (\$100 less than the top quartile group), primarily due to significantly ($P < .05$) lighter carcass weight and slightly lower marbling score⁷.

Zoetis Total Return (ZTR) index is expressed in U.S. dollars on a per calf basis and predicts differences in combined genetic merit across most traits included in the ZMBE, as well as the ZCC and ZFC indexes. Because of the part-whole nature of the three Zoetis indexes, there are moderate to high correlations among the ZCC, ZFC and ZTR indexes. However, 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 source of genetic information provided by INHERIT Select to use when making selection and breeding decisions.

With 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 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 the INHERIT Select indexes. The ZTR index helps simplify and ensure that the most economically valuable animals—sometimes from unexpected combinations of genetic merit across various traits—are not overlooked in the selection process.

OPTIONAL ADD-ONS

Customers may optionally request different add-ons to the normally included features of INHERIT Select – 1) GeneSTAR® Polled test, 2) GeneSTAR® Black test, 3) Bovine Viral Diarrhea Virus (BVDV) test, 4) GEPA for Pulmonary Arterial Pressure (PAP) and 5) Leachman Cattle of Colorado \$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.

GeneSTAR Polled test accurately differentiates homozygous vs heterozygous polled genotypes for beef animals at an early age. This innovation from Zoetis positively supports the welfare of these animals as well as the beef industry overall, proliferating the number of polled animals in the marketplace. GeneSTAR Polled test is reported as:

- Tested homozygous polled: The genotype demonstrates that the animal is homozygous polled and will always produce a polled animal regardless of the horned status of the other parent (Coded PP)
- Polled carrier: The genotype reveals a

heterozygous polled animal capable of producing a horned progeny (Coded PC)

- Tested free of polled (i.e., horned): The genotype is consistent with an animal that is horned (Coded TP)
- Indeterminate: The polled status of the animal cannot be definitively determined (Coded I)

GeneSTAR Black test is coat color test primarily used to identify if a black animal is homozygous or heterozygous for black coat color. Homozygous Black animals often return greater profits in local markets. GeneSTAR Black test identifies the black (Ed), red (e) and wild-type (E+) alleles present at the Extension (E) locus. The order of dominance of these alleles for expression of color translates into black as dominant to red, and both black and red as dominant to wild-type. Homozygous black animals always transmit the black allele, while heterozygous black animals only transmit the black allele to one-half of their progeny. Importantly, additional genes that affect color exist that are not included in GSB.

- 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

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.

Pulmonary Arterial Pressure¹² (PAP)

GEPD is expressed in units of millimeters of Mercury and predicts 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 differences in tested females' tolerance in higher altitude environments.

\$Ranch™ (\$R) and \$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 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 \$80 and \$20,000, 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 sale on a grid. Another important distinction between \$R and \$P versus indexes included in INHERIT (ZCC, ZFC and ZTR), is that \$R and \$P include projected heterosis from assumed mating to opposite parents that are three-quarters (75%) Angus, one-quarter (25%) Simmental breed composition.

GENOMIC BREED COMPOSITION

An especially unique and informative feature of INHERIT Select is genomic approximations of breed composition. Essentially, these are estimates of the percentage of DNA possessed by tested females that originated from defined breeds and breed groups represented in the ZMBE.

Because of the prevalence, as well as genetic similarity, of black and red Angus (versus other breeds), the combined percent ANGUS across the two colors is one of four categories of breed composition reported. Other categories of differing biological types identified include: percent BRITISH (Angus, Red Angus, South Devon and Hereford); percent CONTINENTAL (Simmental, Gelbvieh, Limousin and Charolais); and percent OTHER (Dairy – Holstein and Jersey; Indicus – Brahman and Nelore).

As previously discussed, if females are believed to possess notable fractions of breeds not specifically identified in the first three categories (in other words, OTHER), they are not currently suitable candidates for the INHERIT Select test because the accuracy values of trait GEPD and indexes are anticipated to be non-representative of the specific cattle

being tested. It follows that if animals submitted for INHERIT testing are determined to possess OTHER genomic breed composition in excess of 20%, individual trait and index predictions are not reported. As additional populations of animals from other breeds are integrated into the ZMBE, identified breed and breed crosses that qualify for INHERIT Select testing are anticipated to increase, and the categories and specificity of breed composition reporting are expected to expand accordingly.

Genomic approximations of breed composition have several useful purposes. First, as it relates to the ZMBE, it helps determine how much emphasis an individual or group of breeds contributes to a crossbred female's GEPD. Second, breed composition is indicative of potential maternal heterosis, the increase in production of a crossbred cow above that of the average of her parent breeds. More specifically, Fertility Heterosis is the product of percent heterozygosity computed from genomic approximations of breed composition and maximum F1 heterosis (.65 calves) derived from calving records in the evaluation database. And finally, knowledge of genomic breed composition of females helps inform breeding decisions to bulls and bull batteries that yield desired levels of heterosis in future calf-crops.

SIMULATED VALUE PROPOSITIONS

Value-returns from selection of replacement heifers based on the ZTR and ZCC indexes were simulated over a 10-year time period, with and without reductions in replacement rate enabled by correlated responses in Fertility GEPD¹³. 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 \$56 (\$28 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.

Generally, depending upon the time horizon, the specific index used for selection and the assumed average number of calves produced from selected replacement heifers, projected returns on investment (ROI) in INHERIT Select as compared to traditional selection ranged from a high of over \$4 to a low of under \$2, per \$1 invested in testing. This doesn't include likely unquantified benefits related to smarter bull buying and mating decisions that more effectively accentuate genetic strengths and correct weaknesses of the cowherd, that were informed through adoption of INHERIT testing; or labor savings due to an anticipated reduction in problems associated with traits such as calving ease, docility, teat and udder quality, or susceptibility to brisket disease (PAP is not currently included in indexes).

Selection strategies with the highest simulated ROI were based on ZTR (retained ownership with efficiencies in the feedlot and carcass grid premiums), reduced replacement rates over time enabled through correlated gains in Fertility GEPD and Heterosis (resulting

in added revenue from more heifers to market and lower heifer development costs), and longer time horizons that tended to expand genetic gains over traditional heifer selection. The above generated \$4.50 return for every \$1.00 invested in INHERIT testing, assuming selected replacements produced an average of six calves during their lifetimes. While yielding favorable predicted productivity as compared to traditional selection and positive ROI, generally decisions based on combinations of ZCC (market weaned calves), static and higher replacement rates, shorter time horizons, and fewer assumed calves produced per selected replacement, generated lower projected ROI. More specifically, for these scenarios, ROI ranged from a low of somewhat over break-even to \pm \$3 return per \$1 invested.

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 modeling¹⁴ and practical experiences - for candidate replacement heifers and lifetime use of results:

- Collect DNA using Allflex® Tissue Sampling Units (TSU) at branding (roughly two to three months of age), pre-conditioning, weaning or Brucellosis vaccination from the top three-quarters or more of the heifer crop that were earliest born and meet visual appraisal criteria (sound feet and legs, acceptable expressed growth,

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- 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 ranking identified in the Zoetis Total Return (ZTR) index, as well as desired thresholds for the other indexes, 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 accumulated and routinely updated (weekly) INHERIT results from the active 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 verification to daughters.

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