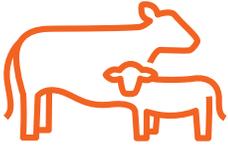# TECHNICAL BULLETIN

INHERIT SELECT™ FOR COMMERCIAL FEMALES TECHNICAL SUMMARY

INHERIT Select Product Features

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KEY POINTS

- INHERIT Select™ is a genomic test for commercial replacement females (heifers and cows) that provides Genomic Expected Progeny Differences (GEPD) and Percentile Rankings for sixteen traits and three economic indexes, as well as sire parentage and genomic approximations of breed composition, to collectively enable more informed selection, breeding and marketing decisions
- INHERIT Select trait predictions are generated and updated regularly through the Zoetis Multi-Breed Genetic Evaluation (ZMBE) that currently includes over 1.2 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 three economic indexes— Zoetis Cow|Calf; Zoetis Feedlot|Carcass; and Zoetis Total Return—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 parentage testing of bull batteries to connect candidate sires to tested daughters—no 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[1]
- Optional add-ons to INHERIT Select include GeneSTAR® Polled test, GeneSTAR® Black test, Bovine Viral Diarrhea Virus (BVDV) test, GEPD for Pulmonary Arterial Pressure and access to Leachman Cattle of Colorado Dollar Ranch and Dollar 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 ssGBLUP[2]—single-step Genomic Best Linear Unbiased Prediction—as well as proprietary Zoetis procedures. This joint 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. These data originated from a variety of sources, but primarily included Leachman Cattle of Colorado (LCoC) and associated Cooperators as well as Dollar ($) Profit Share partners along with 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.

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. Secondarily, Limousin and Charolais are also reasonably well represented in the ZMBE. 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. 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 potentially 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. INHERIT Select is only for commercial females and recognizes the vast ongoing investments in pedigree,

performance data collection and genotyping made by these seedstock partners. More importantly, results from INHERIT Select provide greater understanding of genetic strengths and weaknesses, as well as parentage and breed composition of commercial cow herds to inform and complement bull-buying decisions based on all the information provided by seedstock producers.

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 HD50K for $Profit genotypes included in the ZMBE. Since the evaluation is executed regularly, it follows that HD50K for $Profit 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.® However, 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 provided for testing purposes.

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.

PERCENTILE RANKINGS

Percentile rankings (%) associated with GEPD from INHERIT Select are reported for individual animals and traits for the purpose of easy benchmarking of tested females against what's believed to be representative of commercial crossbred heifers across the U.S. beef industry. 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 directly comparable to GEPD for seedstock animals included in the ZMBE, the reference populations for percent rank benchmarking are different to enable more appropriate comparisons.

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.

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 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 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. 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 compare 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)[3], 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.

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 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.

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.

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 Grade. 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 BIF[3] guidelines.

Ribeye Area (REA) GEPD are in units of square inches (in^2) 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 Grade. The data resource for REA GEPD are ultrasound scan measurements, taken at the 12th – 13th rib, as described by BIF[3] 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 progeny. The data resource for IMF GEPD are ultrasound scan measurements, taken at the 12th – 13th rib, as described by BIF[3] guidelines. Higher IMF and marbling contribute 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 and delivers 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™ for $Profit-tested sires represented in the evaluation—underlying accuracy is comparable to that of non-parent animals with pedigree and own-performance information in conventional

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evaluation 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.[5,6] Production assumptions include 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 genetic differences in feedlot performance and grid-based carcass value. 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 BW, WW, Milk, MW, TUC and DOC. 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 is designed to keep mature cow size and milk (as well as YH) relatively constant, while improving other traits that are both directly included in the ZCC index as well genetically correlated. Case in point, selection based on ZCC is anticipated to also yield favorable correlated response in SC, post-weaning gain, as well as IMF and REA.
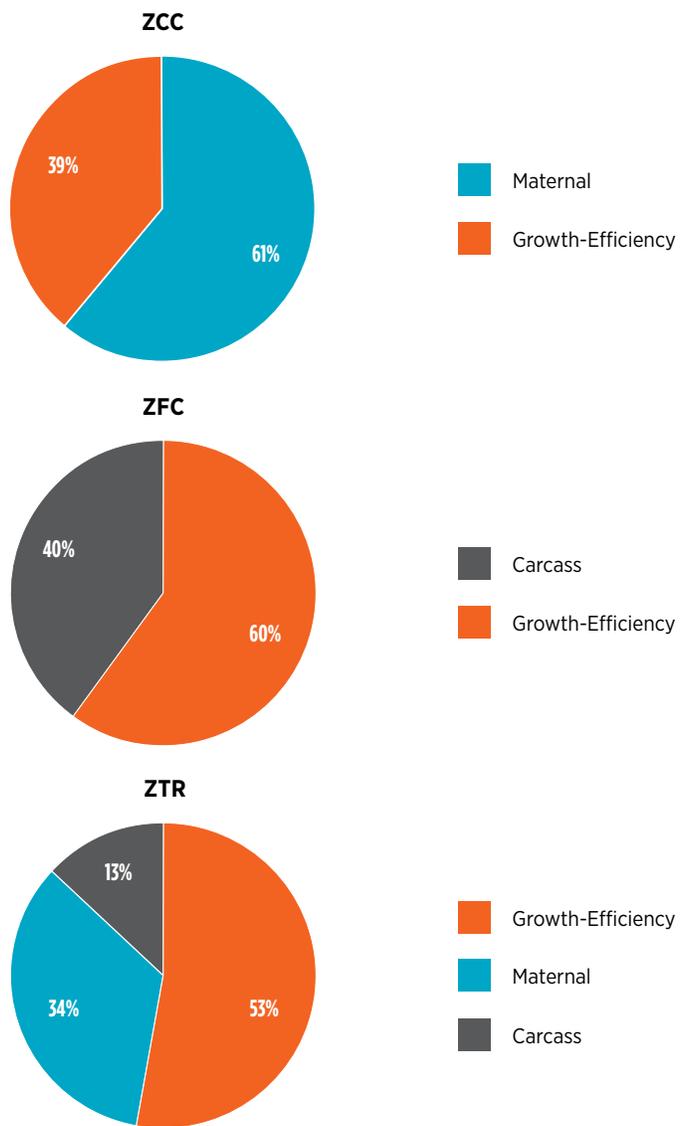
Zoetis Feedlot|Carcass (ZFC) index is expressed in U.S. dollars on a per calf basis and predicts differences in combined genetic merit across evaluated feedlot and carcass traits, including YW, DMI, CW, IMF, REA and FAT. The ZFC index assumes that fed cattle are marketed in-the-beef—on a carcass weight 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 60%, as compared to 40% on carcass traits.

Zoetis Total Return (ZTR) index is expressed in U.S. dollars on a per calf basis and predicts differences in combined genetic merit across all traits included in the ZMBE, as well as the ZCC and ZFC indexes. It follows that 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 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 15 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 each of the INHERIT Select indexes. Regardless, 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.

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

ZCC

- 61% Maternal
- 39% Growth-Efficiency

ZFC

- 40% Carcass
- 60% Growth-Efficiency

ZTR

- 53% Growth-Efficiency
- 34% Maternal
- 13% Carcass

OPTIONAL ADD-ONS

In addition to the features included with INHERIT Select,™ the following add-ons are available: 1) GeneSTAR® Polled test, 2) GeneSTAR® Black test, 3) Bovine Viral Diarrhea Virus (BVDV) test, 4) GEPD for Pulmonary Arterial Pressure and 5) Leachman Cattle of Colorado Dollar Ranch and Dollar Profit indexes.

GeneSTAR Polled test accurately identifies and differentiates homozygous vs heterozygous polled genotypes for beef animals at an early age. This innovation from Zoetis has the opportunity to positively support 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 breeding stock often sell for higher prices 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 Pressure[7] (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.

Dollar Ranch ($R) and Dollar Profit ($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 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.

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. The ZCC, ZFC and ZTR indexes only encompass differences in additive genetic merit across included traits.

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 (Indicus, Dairy, Wagyu, beef breeds not included above).

As previously discussed, if females are believed to possess notable fractions of breeds not specifically identified in the first three categories (i.e., 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. 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. And finally, knowledge of genomic breed composition of females can help inform breeding decisions to bulls and bull batteries that yield desired levels of heterosis in future calf-crops.

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