zoetis

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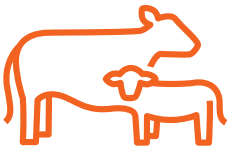


INHERIT OPTIMIZE FOR BEEF TECHNICAL REPORT

INHERIT Optimize Product Features for North America

Kent Andersen and Lane Giess – Global Genetics Technical Services;
Tom Short – Outcomes Research

Zoetis Genetics
333 Portage Street
Kalamazoo, MI 49007-4931

TECHNICAL SUMMARY

- INHERIT Optimize for Beef is a genomic test and genetic evaluation primarily for commercial feeder cattle that provides Genomic Expected Progeny Differences (GEPD) and Percentile Ranks for ten traits, an economic selection index, two carcass production indexes, as well as sire and dam parentage discovery, genomic predictions of breed composition, genotypes for color and polled, to better inform breeding and feeding decisions.
- INHERIT Optimize trait predictions and indexes are updated weekly through the Zoetis Multi-Breed Genetic Evaluation (ZMBE) that currently includes over 1.6 million animals – as well as an expanding database of traditional and unique phenotypes intended to comprehensively inform profit functions for commercial cow-calf producers, backgrounders, and cattle feeders.
- Notably during the 2025 calendar year, nearly 120,000 terminally identified genotyped crossbred beef and beef-dairy cross animals with carcass records from various industry collaborators were added to the INHERIT carcass trait evaluation.
- INHERIT Optimize for Beef results are easy to use with well-designed, balanced economic selection and production indexes. Zoetis Feedlot | Carcass (ZFC) is an economic selection index specific to U.S. production and economic assumptions and enables users to identify animals with improved genetic merit for feedlot value. Zoetis Grid Price (ZGP) and Zoetis Carcass Value (ZCV) are economic production indexes which enables users to identify animals with genetic merit for improved carcass value.
- INHERIT Connect is a companion test to INHERIT Optimize that enables genomic testing of bull batteries and A.I. sires to support parentage discovery for progeny. Connect also reports genomic breed composition, black/red/wild type, and dilution color, and horned/polled.
- INHERIT Optimize for Beef reports genomic breed composition and is intended for use in crossbred Bos Taurus males and females comprised of the following breeds: Angus, Red Angus, South Devon, Hereford, Simmental, Gelbvieh, Limousin, Charolais, and up to 50% Brahman. Breed composition is also reported for Shorthorn, Wagyu, Akaushi, Nelore and dairy breeds.
- INHERIT Optimize delivers genotypes for Polled (based on Celtic and Friesian variants), Color as determined by the Extension locus (black, red, and wild type variants) and Silver Color Dilution, the variant present in Hereford and Simmental (different from dilution in Charolais).
- INHERIT Optimize can be used to better inform feeder cattle price discovery; retained ownership; selection and breeding decisions for feeding, carcass, and simple recessive traits; growing and finishing management; fed cattle marketing; and to authenticate breed claims associated with branded programs.
- An optional add-on to INHERIT Optimize is Bovine Viral Diarrhea Virus (BVDV).

INHERIT OPTIMIZE PRODUCT FEATURES

ZOETIS MULTI-BREED EVALUATION

The Zoetis Multi-Breed Evaluation (ZMBE) is a proprietary engine that generates INHERIT Optimize results using software and ssGBLUP[1] 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 Optimize possible – namely, GEPDs derived using genomic information, effectively informed through large pedigree, breed composition and phenotypic performance databases from genetically related, connected seedstock populations.

The data resources that fuel the ZMBE and INHERIT predictions are from more than 1.6 million animals and are continuously expanding. 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 global partners, along with Zoetis strategic collaborators and company-owned resources. Just under 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, the Limousin, Charolais, and fractions of the Brahman breed are also represented in the evaluated population. It follows that the target spectrum of breed composition to qualify for INHERIT Optimize testing is currently confined to crosses of these nine breeds.

At this time, INHERIT Optimize is not recommended for animals with fractions of composition made up of breeds other than those listed above. Trait predictions and indexes are not reported for animals predicted to possess more than 25% genomic breed composition from any combination of Nelore, Wagyu, and Akaushi. An alternative version of INHERIT Optimize for Beef-Dairy crosses as determined by genomic breed composition is available for crosses including the Bos Taurus breeds listed above and the Holstein, Jersey, Brown Swiss and Guernsey dairy breeds[2].

PARENTAGE

Sire and/or dam parentage determination are included features of INHERIT Optimize and are delivered as output from the weekly ZMBE. An essential prerequisite for parentage determination, is that candidate parents must have HD50K® or qualifying genotypes - INHERIT Connect - included in the ZMBE. Since the evaluation is executed weekly, genotypes for parents may enter the ZMBE at any time – that is prior to, at the same time (with these two options recommended), or after animals are tested, with updated parentage results reported via SearchPoint®. Over time, successful sire parentage determination usually results in slightly more dependable (higher accuracy) trait and index predictions. The details of INHERIT Connect are noted below.

INHERIT Optimize sire parentage discovery is flexible, and both 1) verifies presumed sires of record, as well as 2) finds specific sires of progeny from tested bull batteries without having to nominate defined groups of candidate sires. If records of the candidate sires exist, (based on A.I. breeding and calving records, or observed services), the presumed sire's registration number may be included on the order form. Alternatively, if there's no apparent sire mating records due to multiple sire breeding schemes, the sire registration number and breed association fields on the SearchPoint order upload form should be left blank.

There are five possible Parentage Status outcomes – detailed separately for sire and dam – reported by INHERIT Optimize. These outcomes apply to the reported 'Sire and Dam of Evaluation' (the Sire and Dam used in the ZMBE 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 Optimize customers may have portions of their bull battery or have used A.I. sires that have not been genotyped or their genotypes are not 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 sires to tested progeny as well as connect both sires and progeny to other genotyped animals in the evaluation. When ordering INHERIT Connect, 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 determination across groups of tested progeny, 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 other features of INHERIT Connect includes Polled (based on Celtic and Friesian variants), Color as determined by the Extension locus (black, red, and wild type variants) and Silver Color Dilution, the variant present in Hereford and Simmental (different from dilution in Charolais). The combination

of INHERIT Connect (sires) and INHERIT Optimize (progeny) enables genomic parentage discovery for progeny testing programs.

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 the animal's EPD, where the former (EBV) pertains to the animal itself and the latter (EPD) to average genetic merit 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 decisions.

INHERIT Optimize for Beef reports GEPD for feeding and carcass traits. Beyond ranking, in the context of comparing animals, EPDs predict the potential magnitude of difference in progeny performance due to additive genetic merit and are typically expressed in units of the given trait. **Feeder animals are expected to express differences in their Estimated Breeding Values (EBV = 2 X EPD) for evaluated traits.** 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. Traits evaluated in INHERIT Optimize range in heritability from .25 to .54, so it is important to remember that non-genetic, environmental factors also have notable impact on expressed performance.

PERCENTILE RANKINGS

Percentile rankings (%) associated with GEPD and indexes from INHERIT Optimize are reported for individual animals, for the purpose of easy benchmarking against representative commercial animals across the global beef industry (males and females from the U.S., Argentina, Canada, Australia, New Zealand 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 (top 95%, which means most animals are better). Depending upon the production scenario, intermediate optimums typically exist for traits such as fat thickness and dry matter intake.

Published percent rank tables are intended as a general guide and may differ from reported percent ranks for specific animals that are re-calculated weekly based on an ever-expanding reference population Table 1)[8].

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

INHERIT descriptive statistics for beef males as of 12-13-2025 (n = 166,746 with trait and index predictions).															
Males	INDEX				EPD									MVP	EPD
Top % Rank	ZFC	ZCV	ZGP	$F	YW	DMI	F:G	YH	CW	FAT	REA	YG	MARB	TND	PAP
	$	$	$	$	lbs	lbs	ratio	in	lbs	in	in²	score	score	lbs	mm
1	199	360	13	236	129	-85	-0.39	1.4	75	-0.132	1.61	-0.20	1.23	-0.83	-2.43
5	174	258	9	180	113	-49	-0.26	1.1	64	-0.095	1.28	-0.03	0.96	-0.65	-1.82
10	161	204	8	151	105	-31	-0.19	1.0	58	-0.075	1.11	0.06	0.82	-0.60	-1.41
20	146	137	6	117	96	-9	-0.11	0.8	51	-0.051	0.91	0.16	0.67	-0.56	-0.86
25	140	112	5	104	92	-1	-0.07	0.7	48	-0.042	0.84	0.20	0.60	-0.50	-0.63
30	135	89	4	93	89	6	-0.05	0.6	46	-0.035	0.78	0.23	0.55	-0.43	-0.42
40	126	46	3	72	84	20	0.00	0.5	42	-0.021	0.67	0.28	0.45	-0.39	-0.06
50	117	7	2	52	79	32	0.05	0.4	37	-0.009	0.58	0.33	0.36	-0.34	0.28
60	109	-35	1	32	74	45	0.10	0.3	33	0.003	0.48	0.38	0.27	-0.32	0.61
70	99	-80	0	10	69	59	0.15	0.2	28	0.015	0.39	0.42	0.17	-0.25	0.96
75	94	-105	-1	-2	66	67	0.18	0.1	26	0.022	0.33	0.45	0.11	-0.14	1.14
80	88	-134	-2	-16	63	76	0.21	0.0	23	0.029	0.27	0.48	0.05	-0.09	1.35
90	72	-212	-3	-54	55	100	0.29	-0.2	15	0.047	0.13	0.55	-0.12	-0.04	1.87
95	58	-278	-5	-88	48	121	0.35	-0.3	8	0.062	0.00	0.61	-0.26	0.11	2.29
99	33	-400	-8	-169	36	163	0.47	-0.6	-4	0.090	-0.22	0.71	-0.52		3.06
Min	-47	-763	-19	-350	-6	-172	-0.75	-1.4	-47	-0.224	-0.82	-0.57	-1.09	-1.09	-4.47
Mean	117	1	2	50	80	34	0.05	0.4	37	-0.012	0.60	0.32	0.36	-0.34	0.26
Max	298	752	25	405	178	286	1.14	2.3	105	0.157	2.42	0.98	2.45	0.87	6.19
StdDev	35	163	4	83	20	52	0.18	0.4	17	0.048	0.39	0.19	0.37	0.23	1.25

INHERIT descriptive statistics for beef females as of 12-13-2025 (n = 198,909 with trait and index predictions).															
Females	INDEX				EPD									MVP	EPD
Top % Rank	ZFC	ZCV	ZGP	$F	YW	DMI	F:G	YH	CW	FAT	REA	YG	MARB	TND	PAP
	$	$	$	$	lbs	lbs	ratio	in	lbs	in	in²	score	score	lbs	mm
1	200	368	14	252	127	-75	-0.39	1.4	74	-0.119	1.47	-0.14	1.30	-0.83	-2.41
5	178	272	11	202	113	-42	-0.27	1.1	64	-0.084	1.19	0.01	1.06	-0.65	-1.76
10	167	221	9	175	106	-25	-0.20	0.9	58	-0.065	1.04	0.09	0.93	-0.60	-1.36
20	153	159	7	143	97	-4	-0.12	0.7	52	-0.043	0.86	0.17	0.78	-0.56	-0.79
25	147	134	7	130	94	4	-0.09	0.6	49	-0.035	0.80	0.20	0.73	-0.50	-0.57
30	143	113	6	119	92	11	-0.06	0.6	47	-0.028	0.74	0.23	0.67	-0.43	-0.36
40	134	74	5	98	86	24	-0.01	0.5	43	-0.016	0.64	0.28	0.58	-0.39	0.00
50	126	37	4	79	82	37	0.04	0.4	39	-0.005	0.55	0.32	0.49	-0.34	0.34
60	117	-1	3	59	77	49	0.09	0.3	35	0.006	0.46	0.37	0.40	-0.32	0.66
70	108	-43	1	37	72	63	0.14	0.2	31	0.017	0.37	0.41	0.31	-0.25	1.00
75	103	-67	1	24	69	71	0.17	0.1	28	0.023	0.32	0.44	0.25	-0.14	1.18
80	97	-94	0	10	66	79	0.20	0.1	26	0.030	0.26	0.46	0.19	-0.09	1.38
90	80	-167	-2	-31	57	102	0.28	-0.1	19	0.047	0.12	0.53	0.01	-0.04	1.90
95	64	-232	-4	-71	50	122	0.34	-0.3	13	0.061	0.00	0.59	-0.16	0.11	2.32
99	33	-367	-7	-177	38	161	0.47	-0.5	2	0.087	-0.23	0.69	-0.49		3.07
Min	-58	-750	-16	-367	-17	-183	-0.82	-1.4	-47	-0.208	-0.83	-0.57	-1.16	-1.09	-4.72
Mean	124	30	4	74	82	38	0.04	0.4	39	-0.007	0.57	0.32	0.48	-0.34	0.31
Max	269	651	25	388	171	278	0.88	2.1	105	0.178	2.28	1.01	2.12	0.87	5.34
StdDev	34	153	5	85	19	50	0.19	0.4	15	0.044	0.36	0.18	0.37	0.23	1.24

DESCRIPTION OF TRAIT PREDICTIONS

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 post-weaning growth rates.

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 larger framed progeny.

In typical integrated production systems, intermediate optimums for YH GEPD are usually desirable because of tradeoffs between cow size and feed requirements versus feedlot growth and carcass weight. While smaller framed animals usually express genetic potentials for marbling with fewer days on feed and lighter carcass weights, early maturing animals generally possess less desirable combinations of growth rate, carcass weight and yield grade. Even though larger framed animals typically grow more rapidly to heavier carcass weights with more desirable yield grades, later maturing animals usually require more days on feed to express genetic potential for marbling.

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 gain during the growing phase of production.

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.

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 Grade. In integrated production systems,

typically intermediate optimums in FAT GEPD values are desired because of tradeoffs between carcass composition in harvested progeny versus related cow 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[3] 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 Grade. 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[3] 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 grid price of 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[3] 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 estimating GEPDs, 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 Optimize, baseline accuracy is driven by trait heritability estimates, phenotypic performance data, pedigree and genomic information, and the strength of connectedness between tested animals 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. In general, for commercial animals genomically connected to the evaluation – and from INHERIT Connect tested sires represented in the evaluation – underlying accuracy values typically fall somewhere in the 0.2 to upper 0.4 range and are usually quite similar for any given trait across most tested animals. For this reason and to simplify reporting, individual accuracy values for specific animals and traits are not reported.

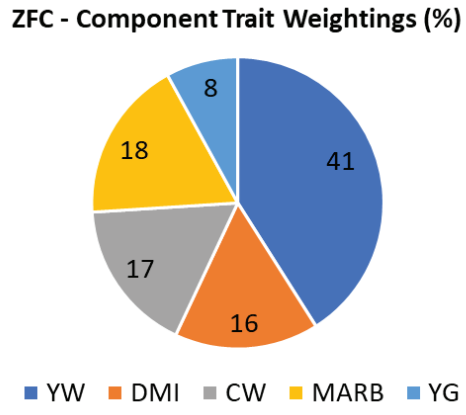
INHERIT OPTIMIZE FEEDLOT | CARCASS ECONOMIC SELECTION INDEX

Economic indexes are expressed in dollars and rank animals for combined genetic merit across evaluated traits, weighted according to associated impacts on costs and revenues from production. Importantly, indexes are intended to help simplify proper, economically grounded understanding of genetic differences among animals for predicted net return. For these reasons, a signature feature of INHERIT Optimize is the Zoetis Feedlot | Carcass (ZFC) economic index.

The economic assumptions used for the ZFC index 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 for the ZFC index includes ownership and marketing of fed progeny/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.

Zoetis Feedlot | Carcass (ZFC) index is expressed in dollars on a per calf (EPD) basis and predicts differences in combined genetic merit across evaluated feedlot and carcass traits, including YW, YH, DMI, CW, MARB and components of YG (FAT & REA). The ZFC index assumes that fed cattle are marketed on a carcass weight basis, with pricing that rewards higher marbling (MARB) and conforming YG. Based on costs, revenues, genetic variation, and trait relationships, in the ZFC index the relative economic weighting on feedlot traits (growth and feed intake) is 57%, as compared to 43% on carcass traits, driven primarily by carcass weight and marbling.[7]

Figure 1. Relative contributions (%) of trait groups to the Zoetis Feedlot | Carcass Index (ZFC).



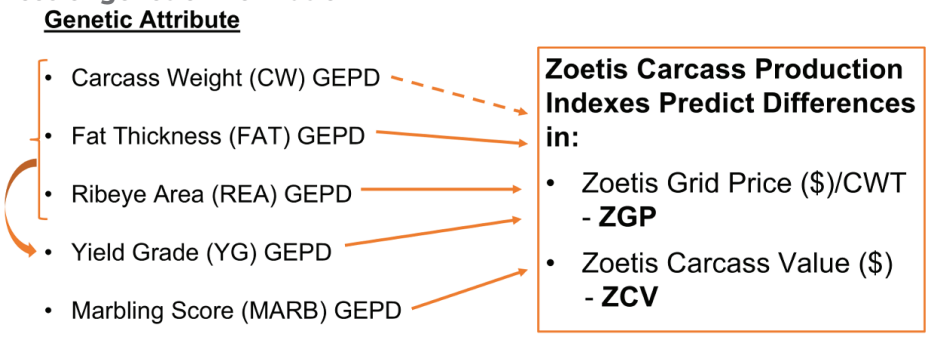
INHERIT OPTIMIZE ECONOMIC PRODUCTION INDEXES

INHERIT Optimize for Beef includes two economic carcass production indexes – Zoetis Grid Price (ZGP) and Zoetis Carcass Value (ZCV) – that are somewhat different than classic selection indexes. While selection indexes such as ZFC discussed above typically evaluate

and rank animals for differences in combined genetic merit **as parents (EPD)**, Zoetis production indexes rank feeders according to predicted genetic differences **as carcasses (EBV)**, and associated grid price and value. Genetic attributes of traits contributing to ZGP and ZCV are illustrated in Figure 2.

Recognizing difference in expressed carcass performance for steers versus heifers, ZGP and ZCV production indexes are intended for use in the comparison of individuals and groups of animals on a within sex basis, and not directly across sexes. As well, since behind the scenes different equations are used to predict

Figure 2. INHERIT Optimize for Beef Carcass Production Indexes and contributing sources of genetic information.



The ZFC, ZGP and ZCV indexes assume that finished cattle are marketed in-the-beef, on a carcass weight basis, with price determined by a value-based grid. As highlighted in Table 2, grid assumptions include a base price of $300 per hundredweight (CWT) of carcass, with a USDA Yield Grade of 3 and USDA Quality Grade of low Choice (Choice -). Premiums and discounts for Quality Grade and Yield Grade, as well as nonconforming carcass weight, are provided in Table 2.

Table 2. Assumed grid base price and premiums and discounts for the ZFC, ZGP and ZCV indexes.

		USDA Yield Grade				
		1	2	3	4	5
USDA Quality Grade	Prime	$25	$23	$20	$10	-$5
	CAB	$10	$8	$5	-$5	-$10
	Choice-	$5	$3	Base $300	-$10	-$15
	Select	-$10	-$12	($15)	-$25	-$30
	Standard	-$20	-$22	($25)	-$35	-$40

Carcass Weight	
<600	-$20
600 - 1100	$0
>1100	-$15

ZGP and ZCV in beef as compared to beef-dairy crosses – as determined by genomic breed composition - these indexes are only intended for comparison within each of these classes of animals.

Zoetis Grid Price (ZGP) index is expressed in dollars (US) and predicts differences in grid price ($ per carcass CWT) due to combined genetic merit for Quality Grade (MARB) and YG. In the reference population of beef steers used to derive prediction equations, the correlation between ZGP (predicted) and expressed grid price was .50, for an R^2 of 25%, while the relationship between ZGP and expressed carcass value (also driven by carcass weight) was .23 (Table 3).

Zoetis Carcass Value index is expressed in dollars (US) and predicts differences in carcass value due to combined genetic merit for CW and components of grid price (MARB, FAT and REA). In the reference population of beef steers used to derive prediction equations, the correlation between ZCV (predicted) and expressed carcass value was .60, for an R^2 of 36%. The correlation between

expressed grid price and expressed carcass value was .18, indirectly indicating the relative importance of predicted and expressed carcass weight (Table 3).

Table 3. Correlations among predicted (ZCV & ZGP) and expresssed Carcass Value and Grid Price for harvested animals

		Predicted	Expressed[3]	
		ZGP[1]	Carcass Value	Grid Price
Predicted	ZCV[2]	0.40	**0.60**	0.05
	ZGP[1]		0.23	**0.50**
Expressed[3]	Carcass Value			0.18

[1]Zoetis Grid Price - phenotypes contributing to ZGP
[2]Zoetis Carcass Value - phenotypes contributing to ZCV
[3]Expressed performance is an animals own carcass value and grid price as determined from individual carcass weight, fat thickness, ribeye area, and marbling phenotypes and standardized.

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 primarily used 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, and phenotypic black, market animals sometimes qualify for branded beef premiums, such as Certified Angus Beef®.

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

GENOMIC BREED COMPOSITION

An informative feature of INHERIT Optimize are genomic estimates of breed composition. 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 4 below provides the list of included breeds and associated codes, while Table 5 provides an example report.

At the present time, if reported genomic breed composition is 25% or more for the combination 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 for feeder animals. Breed composition is indicative of potential individual heterosis, the increase in production of crossbreds above that of the average of

Table 4. INHERIT Optimize 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 5. Example INHERIT Optimize 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.

parent breeds, and there are meaningful breed differences in feeding and carcass performance. Since genomic breed composition usually has more precision than theoretical breed composition based on available pedigree information for commercial animals, it can be used to effectively authenticate possible breed composition claims for related branded beef products.

INHERIT Optimize customers are advised against testing animals whose composition includes meaningful proportions of breeds other than those listed in Table 4. 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.

OPTIONAL ADD-ON

Bovine Viral Diarrhea Virus (BVDV) Test uses an 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, Caisley, or Datamars Tissue Sampling Tags (TSTs) – are required for BVDV testing, and the same sample can be used for INHERIT testing.

INHERIT OPTIMIZE SAMPLE COLLECTION AND VALUE RETURN

INHERIT Optimize can be used to better inform various decisions, including retained ownership; feeder cattle price discovery; selection and breeding decisions for feeding, carcass, and simple recessive traits; backgrounding and finishing management; fed animal marketing; and authentication of breed claims associated with branded programs.

While animals may be tested at any time, the bullet items below provide general guidance about testing and ordering processes and use cases. The latter are based on value proposition modeling, efficacy evaluations, and practical experiences applicable to feeder and breeding animals, and use of results:

- Collect DNA using Allflex® Tissue Sampling Units (TSUs), CaisleyTM Tissue Sampling Ear Tags, or Datamars Tissue Sampling Tags (TSTs) as early in life as possible, or at least four weeks prior to when results are needed, and when sampling fits with your management schedule.
- INHERIT Optimize for Beef ordering and reporting is exclusively executed through SearchPoint, the secured Zoetis online genetics platform.
- INHERIT Optimize results provide genetic insights to cow-calf producers that can be used to inform feeder cattle retained ownership decisions; price discovery when marketing weaned calves and older feeder cattle; eligibility of feeder cattle for branded

programs that include breed claims; selection decisions for feedlot, carcass, color and polled traits; management of crossbreeding; as well as genomic discovered parentage for avoidance of inbreeding, and progeny testing programs.

- INHERIT Optimize results can be used by backgrounders and cattle feeders for many of the same purposes described for cow-calf producers but may also include grouping animals to help optimize days-on-feed for more uniform feeding and carcass performance to target endpoints and grids, with enhanced production efficiency.
- Beef processors and branded beef programs can use INHERIT Optimize results to reduce risk associated with end-product breed claims, to enable genomic traceability for auditing source and management practices, and perhaps eventually for price discovery when negotiating bids on fed cattle.
- While INHERIT Optimize testing of all individual animals enables the broadest range of more dependable uses, for group-based decisions related to calves, feeders and fed cattle, random testing of subsets of animals (i.e. 50%) can yield meaningful insights and compelling value propositions.
- Use INHERIT Optimize results from tested bulls to help inform annual bull-buying decisions – to continuously advance additive genetic merit (GEPD) for feedlot and carcass performance (ZFC), manage breed composition for desired levels of direct and maternal heterosis, as well as purchase/turnout of bulls with authenticated parentage that are relatively unrelated to groups of females for avoidance of inbreeding.
- When new bulls are used A.I. or added to the bull battery, test those bulls with INHERIT Connect to enable future sire parentage determination of progeny and inform progeny testing programs.

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