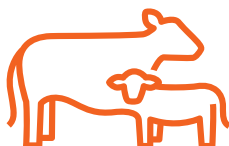


TECHNICAL BULLETIN

ZOETIS AND THE RED ANGUS ASSOCIATION OF AMERICA (RAAA)

November 2016



HIGH-DENSITY (HD) 50K AND I (IMPUTED) 50K FOR RED ANGUS VERSION 2 (V2)

Genomic Enhanced Expected Progeny Differences (GE-EPD), Index and Accuracy Values, Molecular Value Predictions (MVP®) and associated Percentile Rankings

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KEY POINTS

- The RAAA is the exclusive distributor of HD 50K/i50K for Red Angus seedstock
- HD 50K/i50K™ for Red Angus V2 provides GE-EPDs, Index and Accuracy values, as well as MVP Percentile Ranks, for the complete range of 14 traits routinely evaluated in the RAAA performance program, as well as parentage verification
- HD 50K/i50K for Red Angus V2 was developed using a resource population of over 8,500 seedstock animals (predominantly red and some black) representing the full range of high, medium and low accuracy EPDs across evaluated traits
- Genetic parameters – correlations (r) between MVP and true breeding values computed by the University of Nebraska – averaged .63 (range of .46 to .79), indicating 40% average explained genetic variation (r^2) across evaluated traits
- GE-EPD accuracy values (BIF) associated with verified parentage and integration of MVP powered by HD 50K and i50K marker information, equate to an average of 19 progeny equivalents across evaluated traits
- When available, HD 50K/i50K for Red Angus genotypes will contribute to International Genetic Solutions (IGS) BOLT one-step genetic evaluations
- Breeders and commercial users of Red Angus genetics can make notably more informed selection, mating and marketing decisions – especially for young animals – with GE-EPDs and verified parentage powered by HD 50K and i50K

INTRODUCTION

Zoetis, formerly Pfizer Animal Health, and the RAAA first introduced GE-EPDs powered by HD 50K for Red Angus in 2012. The initial training of marker effects and MVP for Red Angus seedstock was completed by Zoetis using company resources that included domestic and global Red and Black Angus animals. Genetic parameters for blending initial MVP into EPD were derived by Colorado State University in collaboration with the RAAA. Technical

cooperation between Zoetis and the RAAA from 2012 to 2016 enabled Red Angus breeders to test animals directly with Zoetis and have GE-EPDs computed and reported by the RAAA.

Adoption of HD 50K by Red Angus breeders created the expanded resource of tested animals with pedigree and performance information that enabled the V2 predictions described in this Technical Bulletin. As well, the technical cooperation between Zoetis and the RAAA has now evolved into a comprehensive distribution agreement, whereby the RAAA now directly receives samples, processes Zoetis orders, invoices members and distributes results. In turn, Zoetis provides genotyping, a variety of customer services and technical support, as well as research and development.

PRODUCT DESCRIPTION

The GE-EPDs and associated Accuracy values powered by HD 50K and i50K for Red Angus V2 span all 14 traits included in the RAAA performance program, and as such also comprehensively impact the HerdBuilder and GridMaster Indexes. For the purpose of helping breeders gauge the impact of MVP on EPDs, Percentile Ranks associated with underlying MVP are confidentially reported.

As with percentile rankings for EPDs, genomic rank values indicate the “top” position of the animal in the population, with lower values indicating higher and generally more desirable rank for most traits as benchmarked against the current population of tested animals (n=4,306). Since GE-EPDs are the most dependable prediction of genetic merit - because they include pedigree, performance, marker (MVP), and eventually progeny information - breeders are encouraged to exclusively use such for selection, mating and marketing decisions. However, transparent visibility to genomic percent ranks helps breeders know the source and general degree to which HD 50K/i50K derived MVP impact resultant GE-EPDs.

Another feature of HD 50K/i50K is parentage verification. USDA SNP parentage markers included on these genotyping platforms are used to verify the sire and dam of record for tested animals, to the maximum extent possible based on

the availability of such genotypes for parents. Reliable pedigree information is the fundamental building block for dependable non-parent EPDs, and is essential for managing inbreeding when making mating decisions.

Together, incorporation of MVP and authenticated pedigree information combine to help jumpstart the accuracy of GE-EPDs for young, unproven Red Angus animals. Beyond higher accuracy values, a useful way to quantify the impact of genomic enhancement is to compute the approximate number of equivalent progeny with performance records in conventional genetic evaluation that would be required in order to achieve similar accuracy to what’s immediately gained through HD 50K/i50K testing. The lower the heritability (h^2) of the trait and higher the genomic correlation, the greater the number of progeny equivalents (Table 1).

Another way for Red Angus breeders to think about the benefits of increased accuracy and progeny equivalents is to consider the impact on possible change, or the error associated with EPDs for young animals. While pedigree information indicates genes that animals have the opportunity to inherit, since every sperm and egg are different, additional information is needed to determine the genetic merit that animals truly inherited and will transmit to progeny.

Generally, depending upon the trait, for non-parent animals HD 50K/i50K serves to remove between 20% and 40% of the error associated with EPDs that are based on pedigree information. This is somewhat more than the increased accuracy and reduction in possible change that is achieved by what otherwise would require a first natural service calf crop and set of daughters’ production data in traditional genetic evaluation to achieve. Hence, GE-EPD technology helps breeders and commercial users of Red Angus Genetics reduce the frequency and magnitude of time-consuming and costly breeding (selection, mating, bull buying) mistakes.

DEVELOPMENT OF HD 50K/ I50K V2 FOR RED ANGUS

The core development tool used to calibrate marker effects was the GenSel software developed at Iowa State University (Fernando and Garrick, 2009). In addition, proprietary Zoetis grouping methodology helped eliminate over-prediction. Conventional EPDs were the response variable used for training. The analysis combined training and simultaneous cross validation resulting in marker effects referred to as calibrations. This procedure used two-thirds of available animals with highest accuracy EPDs in training processes, where training animals were subdivided into five cross-validation groups according to relationship. The remaining one-third of animals with lower accuracy

EPDs were used for Zoetis external validation. These processes included 8,553 HD 50K tested animals, including a comprehensive range of high accuracy Red Angus AI sires.

The third and ultimately most impactful form of validation involved calculation of genetic parameters – correlations between genomic predictions and “true” genetic merit - for weighting / integration of MVP information into GE-EPDs. The University of Nebraska conducted this independent analysis, using MVP provided by Zoetis and conventional EPD provided by the RAAA. The EPDs were deregressed following the methods of Garrick et al. (2009) to take into account variable levels of accuracy associated with the EPD. A four-generation pedigree was constructed for the genotyped animals used in the evaluation. A two-trait linear mixed model was fitted including the MBV and weighted deregressed EPD to enable the estimation of genetic correlations between these two variables. Results are included in table 1, in the column labeled HD 50K Genomic Correlation.

The average correlation (r) across traits was .63 (40% explained additive genetic variation – r^2), which is highly consistent with cross validation (.64) and external (.63) validation results.

IMPUTATION

The “i” in i50K stands for imputation. Imputation is a process that uses a strategically selected smaller subset of the HD 50K markers and pattern recognition to very accurately predict the full range of 50K marker genotypes. Fewer markers equate to lower costs for genotyping. The concordance between marker genotypes derived from i50K versus HD 50K is typically in excess of 98% agreement. Further, the correlation between MVP from i50K versus HD 50K is generally around .99. While diligence is required to maintain these levels of imputation accuracy over time, i50K notably enhances the value proposition for Red Angus breeders.

DESCRIPTIVE STATISTICS AND CORRELATIONS AMONG MVP FROM HD 50K/I50K

To help Red Angus breeders know the magnitude of genetic differences described across various traits by HD 50K/i50K, table 1 includes descriptive statistics for underlying MVPs that contribute to GE-EPDs and genomic percentile ranks. The reference population from which these were calculated included tested Red Angus animals recorded by the RAAA.

To help breeders know the degree to which the sum of marker effects (genes) for one trait relate to that of other traits, Table 3 provides correlations among MVP for traits included in HD 50K/i50K. Correlations may range from -1 to +1, with values close to zero indicating that relatively independent sets of marker effects (genes) impact genomic predictions. As expected, correlations were strongest among the growth traits (WW, YW, CW), between YG and component traits (REA, FAT), and between BW and CED (negative). Generally, the direction and magnitude of correlations among MVP align with documented genetic relationships derived from separate, more traditional analysis using pedigree and performance records.

TABLE 1. GE-EPD ACCURACY (BIF) AND APPROXIMATE PROGENY EQUIVALENTS POWERED BY HD 50K/I50K V2 FOR RED ANGUS

Trait	h ²	HD 50K Genomic Correlation	Pedigree (P) EPD Accuracy	Accuracy from 50K	GE-EPD Accuracy (P+50K)	Pedigree (P) EPD Progeny Equivalents	HD 50K Progeny Equivalents	Total Progeny Equivalents (P+50K)
CED	0.14	0.79	0.17	0.26	0.43	11	42	53
BW	0.37	0.71	0.24	0.16	0.40	7	10	17
WW	0.26	0.65	0.22	0.13	0.35	9	10	19
YW	0.22	0.72	0.22	0.17	0.39	11	17	28
Milk	0.13	0.46	0.16	0.07	0.23	11	7	18
ME	0.65	0.76	0.11	0.27	0.38	1	10	11
HPG	0.24	0.69	0.14	0.19	0.33	5	14	19
CEM	0.15	0.66	0.17	0.16	0.33	10	19	29
STAY	0.10	0.65	0.18	0.15	0.33	17	26	43
Marb	0.54	0.60	0.15	0.13	0.28	2	4	6
YG ¹	0.40	0.60	0.14	0.14	0.28	3	5	8
CW ²	0.38	0.78	0.19	0.24	0.43	4	15	19
REA	0.46	0.56	0.14	0.12	0.26	2	4	6
FAT	0.35	0.48	0.17	0.07	0.24	4	3	7

¹Heritability and correlation estimated as the average of component traits

²Heritability estimate from black Angus

REPORTING RESULTS

The RAAA reports results of HD 50K/i50K testing to members in the form of GE-EPDs for 14 traits and two indexes with enhanced accuracy, as well as genomic (MVP) percent ranks as benchmarked against the current tested population of 4,306 animals. This reference population is periodically updated. Zoetis provides the trait MVP and ranks, which the RAAA internally uses to compute and report the GE-EPDs. Beyond predictions of genetic merit, Zoetis reports extracted USDA SNP parentage genotypes, which the RAAA uses to verify parentage

(when sire and/or dam genotypes are available). Normally, Red Angus breeders should submit samples at least 30 days in advance of when results are needed for decision-making.

SUMMARY

Zoetis HD 50K/i50K enables breeders and commercial users of Red Angus genetics to more dependably differentiate genetic merit among young, unproven animals for more dependable selection, mating and marketing decisions. On average, across all 14 traits included in the RAAA performance program – from MVP and verified parentage - HD 50K/i50K improve accuracy of EPDs to what otherwise would require a first calf crop with performance data in conventional genetic evaluation. Fewer selection and mating mistakes mean more rapid and competitive breed-wide multi-trait genetic improvement and benefits across the beef supply chain.

TABLE 2. DESCRIPTIVE STATISTICS FOR MVP FROM HD 50K/I50K FOR RED ANGUS

Trait	N	Mean MVP	Top 25%	Bottom 25%	MVP Standard Deviation	Minimum MVP	Maximum MVP
CED	4,306	2.7	4.9	0.7	3.2	-8.0	15.7
BW	4,306	-2.6	-3.6	-1.6	1.5	-8.8	2.6
WW	4,306	3.6	9.0	-1.2	7.6	-41.9	26.8
YW	4,306	12.8	22.3	4.9	13.6	-67.7	55.1
Milk	4,306	-3.7	-1.3	-6.0	3.7	-25.9	9.8
ME	4,306	2.3	-0.6	5.4	4.4	-19.9	21.3
HPG	4,306	2.6	3.9	1.1	2.8	-14.3	12.0
CEM	4,306	-0.1	1.8	-1.7	2.8	-17.3	14.4
STAY	4,306	7.1	9.0	5.4	2.7	-7.4	15.6
Marb	4,306	-0.04	0.08	-0.15	0.18	-0.77	0.83
YG	4,306	0.13	.08	.17	0.07	-0.14	0.38
CW	4,306	2.7	8.9	-2.9	9.1	-51.7	34.9
REA	4,306	-0.40	-0.28	-0.52	0.18	-1.16	0.20
FAT	4,306	0.01	0.002	0.024	0.02	-0.04	0.08

TABLE 3. CORRELATIONS AMONG MVP FOR TRAITS IN HD 50K/I50K FOR RED ANGUS

	CED	BW	WW	YW	Milk	ME	HPG	CEM	STAY	Marb	YG	CW	REA	FAT
CED	1	-0.69	-0.31	-0.29	0.19	-0.09	-0.10	0.23	0.17	0.17	-0.06	-0.44	-0.08	0.13
BW		1	0.29	0.23	-0.21	-0.02	0.05	-0.15	-0.33	-0.21	0.06	0.46	0.04	-0.16
WW			1	0.90	-0.11	0.30	0.18	-0.13	0.29	0.18	0.23	0.86	0.28	0.10
YW				1	-0.06	0.31	0.15	-0.08	0.26	0.18	0.28	0.95	0.29	0.13
Milk					1	-0.06	-0.02	-0.04	0.08	0.16	0.01	-0.11	0.12	0.22
ME						1	-0.08	0.03	0.01	0.00	0.00	0.28	-0.08	-0.29
HPG							1	0.05	0.16	0.19	0.08	0.13	0.11	0.16
CEM								1	-0.03	-0.06	0.27	-0.12	-0.33	0.10
STAY									1	0.24	0.17	0.14	0.05	0.21
Marb										1	0.19	0.11	0.13	0.36
YG											1	0.26	-0.56	0.64
CW												1	0.27	0.08
REA													1	0.07
FAT														1

References

1 Fernando R, Garrick D. GenSel – User manual for the portfolio of genomic selection related analyses. Iowa State University. Ames, Iowa. 2009.