

Evaluation of Pfizer Animal Genetics HD 50K MVP Calibration

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1) Genotypic Data

Pfizer Animal Genetics (PAG) provided trait MVPs computed for 1031 animals using prediction equations derived using Angus BREEDPLAN EBVs and converted US EPDs and genotypes from the 50K SNP chip. The majority of the animals (740) were from the Angus Progeny test program at Trangie with the remainder being sires from Australia and New Zealand. Summary statistics for the 9 MVPs which have BREEDPLAN equivalent EBVs are presented in Table 1. For the other 4 MVPs for feedlot traits and tenderness there is currently no BREEDPLAN equivalent EBV, and for NFI only trial EBVs exist. Results for those traits in Table 1 are based on MVPs from 975 animals only.

Table 1: Summary statistics for PAG MVPs from Angus 50K

Trait	MVP	N	mean	std	min	max
Birth weight	BW(kg)	1031	2.46	0.81	-0.92	5.78
200 day weight direct	WW (kg)	1031	16.44	4.39	2.44	42.4
200 day weight maternal	MA (kg)	1031	5.27	2.58	-7.40	14.86
Carcase weight	CW (kg)	1031	10.95	6.03	-18.93	36.25
Carcase rib fat	FAT (mm)	1031	0.11	0.57	-2.93	3.01
Carcase eye muscle area	REA (cm ²)	1031	1.67	1.26	-3.32	7.22
Intramuscular fat	MS (IMF%)	1031	0.44	0.39	-0.92	2.16
Calving ease direct	CED (% unass)	1031	0.21	1.03	-4.49	4.62
Calving ease daughters	CEM (% unass)	1031	0.67	1.37	-6.12	6.02
Net feed Intake	NFI (kg/d)	975	-0.09	0.08	-0.41	0.21
Dry mater intake	DMI (kg/d)	975	-0.11	0.23	-1.05	0.60
Average daily gain	ADG (kg/d)	975	0.13	0.05	-0.03	0.46
Shear force	TND (kg)	975	-0.25	0.05	-0.45	-0.13

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2) Phenotypic data

Phenotypic records were extracted from Angus NBRIS files and processed through the BREEDPLAN driver to pre-adjust the records (i.e. age and age of dam; Graser *et al.* 2005). All records were adjusted to a standard 5 year old age of a dam and ultrasound scan records were adjusted to 500 days of age, and abattoir carcass traits are adjusted to a 300kg carcass weight basis.

Due to MVPs being computed using prediction equations derived from Angus BREEDPLAN EBVs (and US EPD converted EBVs) the availability of a totally independent calibration dataset was not possible. Therefore all MVPs were used but data sets of phenotypes were restricted to **only grand progeny** of these animals. This was done in an attempt to remove the direct influence of own records and progeny records used in the computation of the EBVs (i.e. used in development of MVP predictions). While this may not be considered ideal in terms of independence it was thought to be the only option available to allow some kind of calibration of the new MVP predictions. However this restriction on the data meant that very few records were available for the direct abattoir recorded carcass traits. Therefore analyses were conducted using all abattoir carcass records and various sub-sets of that data. Heifer and bull ultrasound scan traits were also analysed as correlated carcass traits, but it should be recognized these are not the BREEDPLAN published EBV for carcass traits (i.e. those used to derive the prediction equations). Also, for the analyses of BWT and 200d WT, due to the large number of phenotypic records the datasets were each divided into 3 subsets based on random assignment of whole herds to a dataset.

Phenotypic records for the 3 feed intake/feedlot traits were extracted for all available Angus cattle and included all the Trangie Angus progeny test data. As per BREEDPLAN, the feed intake records were classified into those recorded under a post-weaning feed intake test (**P**) and alternatively under feedlot finishing test (**F**). All analyses were performed using the full dataset but also with removal of training animal phenotypes and MVPs.

Trait definitions:

BWT: birth weight (kg)

CE: calving ease score

WWT: weaning weight adjusted 200d weight (kg)

CWT: carcass weight at 650 d (kg)

HIMF: ultrasound scan IMF% in heifers adjusted to 500 days of age

BIMF: ultrasound scan IMF% in bulls adjusted to 500 days of age

CIMF: carcass IMF % at a 300 kg carcass weight adjusted basis

HEMA: ultrasound scan eye muscle area (cm²) in heifers adjusted to 500 days of age

BEMA: ultrasound scan eye muscle area (cm²) in bulls adjusted to 500 days of age

CEMA: carcass eye muscle area (cm²) at a 300 kg carcass weight adjusted basis

HP8: ultrasound P8 fat depth (mm) in heifers adjusted to 500 days of age

BP8: ultrasound P8 fat depth (mm) in bulls adjusted to 500 days of age

CP8: carcass P8 fat depth (mm) at a 300 kg carcass weight adjusted basis

HRIB: ultrasound rib fat depth (mm) in heifers adjusted to 500 days of age

BRIB: ultrasound rib fat depth (mm) in bulls adjusted to 500 days of age

CRIB: carcass rib fat depth (mm) at a 300 kg carcass weight adjusted basis

NFI-P: net feed intake (kg/d) computed from individual daily feed intake records of animals tested post-weaning.

DFI-P: daily feed intake (kg/d) for animals tested for NFI-P.

TADG-P: average daily weight gain (kg/day) during the feed test for animals tested for NFI-P.

NFI-F: net feed intake (kg/d) computed from individual daily feed intake records of animals tested during feedlot finishing.

DFI-F: daily feed intake (kg/d) for animals tested for NFI-F.

TADG-F: average daily weight gain (kg/day) during the feed test for animals tested for NFI-F

3) Analytical methods

Each MVP was assessed against a target trait using a bivariate animal model (using WOMBAT, Meyer, 2010) with the MVP treated as a second trait. The residual covariance was fixed at 0. Target traits were pre-adjusted and therefore the only fixed effect was the BREEDPLAN formed contemporary group.

To estimate genetic correlations between MVPs and direct and maternal effects of BWT and 200d WT additional models and datasets were used. For BWT the analysis partitioning maternal effects (maternal genetic and permanent environment) and the genetic correlation was estimated between the BW MVP and the birth weight direct effect. For 200d WT, two MVPs were available (WWD and MA), and several analyses were run partitioning maternal effects and estimating covariances using different models outlined below.

Model	Direct	Maternal	PE	Cov(d,m)	Cov(mvp,d)	Cov(mvp,mat)
1	X				X	
2	X	X	X		X	
3	X	X	X	X	X	X

To further assist in the partitioning of maternal effects for BWT and 200d WT additional phenotypes were extracted that were the progeny of cows present in the dataset but were not grand progeny of the MVP animals (i.e. were not previously present). This helped increase the average number of progeny per cow and thus assisting in partitioning of effects. An additional analysis of the birth weight data was performed using only the MVPs from the progeny of Angus Progeny Test program. The 721 MVPs for BWT on these animals were analysed in a bivariate model with all available birth weight records from the Trangie herd. The birth weight records on those animals with an MVP were deleted.

Estimates of the genetic correlation between the 2 calving ease MVPs and calving difficulty scores were computed using a linear model and partitioning maternal effects as per model 3 in the above table. An important clarification is that the MVP called MVP_CEM that was analysed was derived using the EBV for CE-daughters (i.e. $\frac{1}{2}d + m$). Finally, estimated correlations have had their signs reversed to equate the MVPs (on a % unassisted birth observed scale) to calving ease (instead of difficulty).

4) Results

Genetic parameters for the MVPs studied are presented in Tables 2a and 2b. For all MVPs the REML estimates of their additive genetic variance are presented (σ^2_p). Estimates of their residual variances were very small ($< 0.1E-4$) with resultant heritabilities all one (or very close to one). For the target traits the phenotypic variance estimate (σ^2_p) and direct heritability (h^2) are presented or maternal heritability for 200d MA. Also included in the table are estimates of the regression of the phenotype on the MVP (b) and the genetic correlation between the target trait and the MVP (r_g) which is equal to the accuracy of the BREEDPLAN EBVs if only derived from MVP information.

Table 2a: Bivariate animal model results using all phenotypes and Pfizer GeneSTAR Angus MVPs from 50K chip. σ^2_p = phenotypic variance of the observed data after fitting the models or variance of the MVP, h^2 = heritability of the trait, r_g = genetic correlation between MVP and target trait, r_g^2 = portion of genetic variance explained by marker, b = regression coefficient of phenotype on MVP. Standard errors of estimates are in brackets, r_p correlation between MVP and phenotypes

Test	Trait	Data*	Phenotypic parameters				Genetic Parameters			
			N	σ^2_p	b (se)	r_p	h^2 (se)	r_g (se)	r_g^2	
Pfizer MVP BWT	BWT	Rep1	Phenot = 79,335 MVP = 1,031	17.30 0.401	1.61	0.25(0.04)	0.34 (0.01)	0.40 (0.06)	0.16 (0.05)	
		Trangie	Phenot = 7,660 MVP = 721	17.23 0.278	1.42	0.18 (0.04)	0.43 (0.03)	0.35 (0.08)	0.12 (0.06)	
Pfizer MVP WWD	WWT	Rep1	Phenot = 85,449 MVP = 1,031	536.87 13.09	1.08	0.17 (0.03)	0.21 (0.01)	0.37 (0.07)	0.14 (0.05)	
		Rep2	Phenot = 88,915 MVP = 1,1031	517.99 13.03	1.08	0.17(0.03)	0.23 (0.01)	0.35 (0.07)	0.12 (0.05)	
		Rep3	Phenot = 85,645 MVP = 1,031	518.96 13.09	1.37	0.22 (0.03)	0.24 (0.01)	0.44 (0.07)	0.19 (0.06)	
Pfizer MVP WW MA	WWT	Rep1	Phenot = 85,449 MVP = 1,031	543.90 4.67	1.60	0.07 (0.04)	0.16 (0.01)	0.37 (0.07)	0.14 (0.05)	
		Rep2	Phenot = 88,915 MVP = 1,031	524.70 4.66	1.62	0.05 (0.03)	0.16 (0.01)	0.38 (0.07)	0.14 (0.05)	
		Rep3	Phenot = 85,645 MVP = 1,031	526.7 4.68	1.32	0.05 (0.04)	0.16 (0.01)	0.31 (0.07)	0.10 (0.04)	

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Pfizer MVP CED	CE	Full	Phenot = MVP =	138,813 1028	0.052 0.66	-	-	0.09(0.01)	0.24(0.07)	0.06 (0.03)
Pfizer MVP CEM	CE	Full	Phenot = MVP =	138,813 1028	0.052 1.00	-	-	0.04(0.01)	0.21(0.07)	0.04 (0.03)
Pfizer MVP FAT	HRIB	Full	Phenot = MVP =	51,478 1,031	1.94 0.233	0.75	0.26 (0.04)	0.39 (0.02)	0.42 (0.06)	0.18 (0.05)
	BRIB	Full	Phenot = MVP =	45,844 1,031	0.85 0.233	0.37	0.19 (0.03)	0.26 (0.02)	0.38 (0.06)	0.14 (0.05)
	CRIB	ALL	Phenot = MVP =	1,603 1,031	7.22 0.233	1.68	0.30 (0.18)	0.47 (0.12)	0.44 (0.26)	0.19 (0.23)
	CP8	ALL	Phenot = MVP =	3,194 1,031	11.45 0.233	1.36	0.20 (0.07)	0.26 (0.07)	0.39 (0.14)	0.15 (0.11)
Pfizer MVP REA	HEMA	Full	Phenot = MVP =	51,322 1,031	26.74 0.939	0.87	0.16 (0.04)	0.29 (0.01)	0.31 (0.07)	0.10 (0.04)
	BEMA	Full	Phenot = MVP =	45,908 1,031	37.66 0.933	1.30	0.20 (0.03)	0.23 (0.02)	0.43 (0.07)	0.18 (0.06)
	CEMA	ALL	Phenot = MVP =	2,137 1,031	27.59 0.928	1.29	0.22 (0.05)	0.25 (0.07)	0.45 (0.12)	0.20 (0.11)
Pfizer MVP MS	HIMF	Full	Phenot = MVP =	46,578 1,031	1.52 0.074	0.78	0.17 (0.03)	0.28 (0.01)	0.33 (0.06)	0.11 (0.04)
	BIMF	Full	Phenot = MVP =	39,959 1,031	0.89 0.074	0.50	0.15 (0.03)	0.19 (0.02)	0.34 (0.07)	0.12 (0.05)
	CIMF	ALL	Phenot = MVP =	3,557 1,031	2.51 0.066	0.75	0.12 (0.05)	0.36 (0.06)	0.20 (0.08)	0.04 (0.03)
Pfizer MVP CW	CWT	ALL	Phenot = MVP =	4,732 1,031	547.1 22.77	1.03	0.21 (0.05)	0.34 (0.06)	0.36 (0.10)	0.13 (0.07)
	600-W	Full	Phenot = MVP =	82,398 1,031	1259.2 22.73	1.09	0.15 (0.04)	0.35 (0.01)	0.25 (0.06)	0.06 (0.03)

* Full = complete dataset of grandprogeny records; ALL= all available records; rep#= subset of data

Table 2b: Bivariate animal model results using all phenotypes and Pfizer GeneSTAR Angus MVPs from 50K chip. σ^2_P = phenotypic variance of the observed data after fitting the models or variance of the MVP, h^2 = heritability of the trait, r_g = genetic correlation between MVP and target trait, r_g^2 = portion of genetic variance explained by marker, b = regression coefficient of phenotype on MVP. Standard errors of estimates are in brackets, r_p correlation between MVP and phenotypes

Test	Trait	Data*	Phenotypic parameters				Genetic Parameters			
			N	σ^2_P	b (se)	r_p	h^2 (se)	r_g (se)	r_g^2	
MVP_NFI	NFI-F	CUT2	Phenot =	1,160	1.42	0.47 (1.24)	0.03 (0.07)	0.31 (0.09)	0.05 (0.12)	0.00 (0.01)
			MVP =	822	0.004			1.00		
	NFI-P	FULL	Phenot =	2,871	0.55	0.08 (0.75)	0.01 (0.07)	0.39 (0.04)	0.01 (0.11)	0.00 (0.00)
			MVP =	975	0.004			1.00		
MVP_DMI	DFI-F	CUT2	Phenot =	1,159	2.87	1.53 (0.67)	0.15 (0.06)	0.43 (0.11)	0.22 (0.10)	0.05 (0.04)
			MVP =	822	0.026			1.00		
	DFI-P	CUT1	Phenot =	2,871	1.31	1.00 (0.49)	0.14 (0.07)	0.50 (0.04)	0.20 (0.10)	0.04 (0.04)
			MVP =	822	0.026			1.00		
MVP_ADG	TADG-F	CUT2	Phenot =	1,159	0.059	1.16 (0.44)	0.17 (0.06)	0.32 (0.10)	0.31 (0.13)	0.10 (0.08)
			MVP =	822	0.001			1.00		
	TADG-P	CUT1	Phenot =	2,871	0.049	0.38 (0.47)	0.06 (0.08)	0.44 (0.05)	0.10 (0.05)	0.01 (0.01)
			MVP =	822	0.001			1.00		

*CUT1 = REMOVED MVP OF ANIMALS USED IN DERIVING OF MVPs; CUT2 = REMOVED MVP AND NFI PENOTYPE OF THOSE ANIMALS USED IN DERIVATION OF MVPs

5) Notes

- Partitioning of maternal variances does change the estimates of variances and correlations, particularly as the software requires a non-zero genetic correlation between the direct and maternal effects when estimating the correlations with the maternal MVP (MA) and the maternal genetic effect. As expected the genetic variances (and heritabilities) were inflated however MVP variances and genetic correlations don't appear to be greatly affected (possibly slightly inflated). The b values for milk MVP are considerably greater than one, reflecting the increased maternal genetic variance that would not be present in the training EBVs.
- For carcass traits the b values are all less than one and reflect the lower additive variance for scan traits compared to the abattoir carcass traits (i.e. the published EBVs).