

Evaluation of Pfizer Animal Genetics 56 Marker Panel

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Pfizer Genetics GeneSTAR MVP from four Australian beef cattle populations

Version 3 updates the regression coefficients for tenderness/shear force. The original Tenderness MVPs were expressed in pounds and not kilograms; this has now been changed by Pfizer and subsequently reanalysed by AGBU.

[Pfizer Animal Genetics](#) provided GeneSTAR MVPs for three traits, Marbling (AUSMEAT marble score), Tenderness (shear force kg) and Net Feed Intake (kg/day) based on their panel of 56 markers for animals from four CRC1 groups for analysis and calibration of MVPs for the inclusion into BREEDPLAN EBV^M. The animals genotyped here were selected on the basis that they had a NFI phenotypic record. The animals belonged to four distinct breed groups described in Table 1. Table 2 presents mean, standard deviation and minimum and maximum of phenotypes and MVP for each dataset. Table 3 contains the estimated genetic parameters and the regression coefficient of MVP on phenotype based on datasets including all phenotyped animals in each data using an animal model.

Table 1: Phenotypic Data used in the calibration of Pfizer Genetics GeneSTAR MVPs for use in BREEDPLAN

| Data set code | Description |
|---------------|--|
| 1 | CRC 1 Purebred Taurus breeds Phenotypic data includes: IMF, MSA marble score, LDSF, NFI Genotype data on animals with feed intake records only and DNA available, this is therefore a subset of total finished in feedlot with higher than average marble score. |
| 2 | CRC 1 Purebred Indicus breeds Phenotypic data includes: IMF, MSA marble score, LDSF, NFI Genotype data on animals with feed intake records only and DNA available, this is therefore a subset of total finished in feedlot with higher than average marble score. |
| 3 | CRC1 F1 crossbreds from Bos Taurus sire breeds over Brahman cows Phenotypic data includes: IMF, MSA marble score, LDSF, NFI Genotype data on animals with feed intake records only and DNA available, this is therefore a subset of total finished in feedlot with higher than average marble score. |
| 4 | CRC1 F1 crossbreds from Bos indicus sire breeds over Brahman cows Phenotypic data includes: IMF, MSA marble score, LDSF, NFI Genotype data on animals with feed intake records only and DNA available, this is therefore a subset of total finished in feedlot with higher than average marble score. |

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Statistical Analyses.

1) Data preparation

Experimental design of the CRC 1 straightbred (data 1&2) and CRC1 crossbred (data 3&4) are described by Upton et al (2001) and Newman et al (2002). Data edits, trait definitions and fixed effect classification for datasets 1 and 2 are presented in Johnston et al. (2001, 2003) and Reverter et al (2003) for IMF/marbling and shear force, and in Robinson and Oddy (2004) for NFI, respectively. For datasets 3&4 trait definitions and data edits were performed as part of this study and followed the same protocols as CRC1 straightbred. No editing was performed on the MVPs. More detailed description of the data can be found at the end of the document.

2) Phenotypic trait definitions

IMF: intramuscular fat % of LTL sample using ether extract or NIR

MSA marble score: chiller assessed marble score at 12/13 rib by trained MSA technician using 0.1 gradations

LDSF: shear force (kg) of the eye muscle [*M. longissimus thoracis et lumborum* (LTL)] from carcasses electrically stimulated and aged approximately 2 days

NFI: net feed intake (kg/day) computed from individual daily feed intake records (adjusted for metabolic mid-test weight and feedlot average daily gain).

3) Analytical methods

Analyses were run for each of the four datasets separately using a series of bivariate animal model. For each analysis the first trait was the target trait (using all phenotypic records) and the second trait was the relevant MVP. For trait 1 the models included fixed effects previously determined for D1 &2 including herd which accounted for breed. For trait 1 in D3&4 fixed effects models were developed using similar design variables as defined in d1&2, with sire breed also included as fixed effect. Animal was always fitted as a random effect. For trait 2 (i.e. the MVP) the model included the mean and breed for datasets 1&2 and breed of sire for data 3&4, respectively. To assist convergence the residual effects for the MBV was fixed at 0.001 and the residual correlation at 0.0. Variance components were used to compute target trait heritabilities, genetic correlations and genetic regressions along with approximate standard errors.

Table 2: Mean, Standard deviation (SD) Minimum and Maximum on the data available for analysis

| Test | Trait | Data | N | Mean | SD | Min | Max | |
|-------------------------------|----------------------|-------------|----------|-------------|-----------|------------|------------|-------|
| Pfizer MVP Marbling | IMF (%) | 1 | Phenot = | 3,594 | 4.64 | 2.23 | 1.23 | 18.94 |
| | | | MVP = | 703 | -0.09 | 0.21 | -0.68 | 0.66 |
| | | 2 | Phenot = | 3,524 | 2.88 | 1.42 | 0.08 | 13.19 |
| | | | MVP = | 668 | -0.26 | 0.17 | -0.93 | 0.49 |
| | | 3 | Phenot = | 876 | 3.01 | 1.30 | 0.36 | 9.57 |
| | | | MVP = | 253 | -0.21 | 0.17 | -0.62 | 0.16 |
| | | 4 | Phenot = | 878 | 2.67 | 1.20 | 0.42 | 8.22 |
| | | | MVP = | 225 | -0.24 | 0.14 | -0.60 | 0.13 |
| Pfizer MVP Marbling | MSA MS (score) | 1 | Phenot = | 1,454 | 1.17 | 0.75 | 0.00 | 4.30 |
| | | | MVP = | 703 | -0.09 | 0.21 | -0.68 | 0.66 |
| | | 2 | Phenot = | 1,808 | 0.76 | 0.62 | 0.00 | 3.80 |
| | | | MVP = | 668 | -0.26 | 0.17 | -0.93 | 0.49 |
| | | 3 | Phenot = | 594 | 0.85 | 0.56 | 0.00 | 3.00 |
| | | | MVP = | 253 | -0.21 | 0.17 | -0.62 | 0.16 |
| | | 4 | Phenot = | 636 | 0.73 | 0.58 | 0.00 | 3.00 |
| | | | MVP = | 225 | -0.24 | 0.14 | -0.60 | 0.13 |
| Pfizer MVP Tenderness | LDSF (kg) | 1 | Phenot = | 3,322 | 4.12 | 0.82 | 2.01 | 8.75 |
| | | | MVP = | 659 | -0.01 | 0.15 | -0.37 | 0.55 |
| | | 2 | Phenot = | 3,254 | 4.55 | 0.94 | 2.34 | 8.92 |
| | | | MVP = | 585 | 0.24 | 0.23 | -0.38 | 0.79 |
| | | 3 | Phenot = | 785 | 4.83 | 0.99 | 2.56 | 8.53 |
| | | | MVP = | 253 | 0.22 | 0.17 | -0.20 | 0.77 |
| | | 4 | Phenot = | 762 | 5.17 | 1.10 | 2.85 | 8.98 |
| | | | MVP = | 225 | 0.38 | 0.18 | -0.05 | 0.76 |
| Pfizer MVP Feed Efficiency | NFI (kg/d) | 1 | Phenot = | 785 | 0.01 | 1.19 | -4.03 | 4.52 |
| | | | MVP = | 706 | -0.11 | 0.32 | -1.04 | 1.06 |
| | | 2 | Phenot = | 687 | 0.00 | 1.01 | -3.92 | 3.10 |
| | | | MVP = | 671 | -0.19 | 0.25 | -1.10 | 0.62 |
| | | 3 | Phenot = | 254 | -0.00 | 1.25 | -3.82 | 3.48 |
| | | | MVP = | 253 | -0.11 | 0.29 | -0.76 | 0.74 |
| | | 4 | Phenot = | 215 | -0.00 | 1.07 | -3.16 | 2.80 |
| | | | MVP = | 225 | -0.10 | 0.24 | -0.88 | 0.69 |

Table 3: Bivariate animal model results using all phenotypes and GeneSTAR MVPs from the 56 marker panel Version January 2009. σ^2_P = phenotypic variance of the observed data after fitting the models, h^2 = heritability of the trait, note MVP have a heritability fixed close to 1.0, r_g = genetic correlation between MVP and target trait, r_g^2 = portion of genetic variance explained by marker, b = regression coefficient of MVP on phenotype. Standard errors of estimates are in brackets, P = significant level of regression coefficient (b) being greater than zero, r_p .correlation between MVP and phenotypes

| Test | Trait | Data | Phenotypic parameters | | | | | | Genetic Parameters | | |
|--------------------------|-----------|------|-----------------------------|----------------|---------------|--------|---------------|---------------|--------------------|---------------|---------------|
| | | | N | σ^2_P | b (se) | P | r_p | r_p^2 | h^2 (se) | r_g (se) | r_g^2 |
| Pfizer MVP Marbling | IMF | 1 | Phenot = 3,594 MVP = 703 | 2.035 0.035 | 0.255 (0.30) | 0.20 | 0.033 (0.04) | 0.001 (0.003) | 0.39 (0.06) | 0.054 (0.06) | 0.003 (0.007) |
| | | 2 | Phenot = 3,524 MVP = 668 | 0.978 0.027 | 0.231 (0.24) | 0.17 | 0.038 (0.04) | 0.001 (0.003) | 0.37 (0.06) | 0.064 (0.07) | 0.004 (0.009) |
| | | 3 | Phenot = 876 MVP = 253 | 0.767 0.026 | 0.028 (0.33) | 0.47 | 0.005 (0.06) | 0.000 (0.001) | 0.23 (0.10) | 0.011 (0.13) | 0.000 (0.003) |
| | | 4 | Phenot = 878 MVP = 225 | 0.717 0.022 | 0.415 (0.39) | 0.14 | 0.072 (0.07) | 0.005 (0.010) | 0.37 (0.11) | 0.121 (0.11) | 0.015 (0.027) |
| Pfizer MVP Marbling | MSA MS | 1 | Phenot = 1,454 MVP = 710 | 0.281 0.035 | 0.218 (0.20) | 0.14 | 0.077 (0.07) | 0.006 (0.011) | 0.35 (0.09) | 0.131 (0.12) | 0.017 (0.031) |
| | | 2 | Phenot = 1,808 MVP = 670 | 0.236 0.027 | 0.171 (0.15) | 0.13 | 0.057 (0.05) | 0.003 (0.006) | 0.37 (0.08) | 0.096 (0.08) | 0.009 (0.015) |
| | | 3 | Phenot = 594 MVP = 253 | 0.211 0.026 | 0.024 (0.22) | 0.46 | 0.009 (0.08) | 0.000 (0.001) | 0.31 (0.13) | 0.016 (0.14) | 0.000 (0.004) |
| | | 4 | Phenot = 636 MVP = 225 | 0.229 0.022 | 0.262 (0.23) | 0.13 | 0.080 (0.07) | 0.006 (0.011) | 0.19 (0.11) | 0.189 (0.17) | 0.036 (0.064) |
| Pfizer MVP Tenderness | LDSF | 1 | Phenot = 3,322 MVP = 659 | 0.433 0.088 | 0.240 (0.20) | 0.11 | 0.049 (0.04) | 0.002 (0.004) | 0.08 (0.04) | 0.170 (0.14) | 0.029 (0.048) |
| | | 2 | Phenot = 3,254 MVP = 585 | 0.612 0.160 | 0.662 (0.20) | <0.001 | 0.154 (0.04) | 0.024 (0.012) | 0.30 (0.06) | 0.283 (0.08) | 0.080 (0.045) |
| | | 3 | Phenot = 785 MVP = 253 | 0.658 0.142 | 0.304 (0.35) | 0.19 | 0.064 (0.07) | 0.004 (0.009) | 0.26 (0.10) | 0.126 (0.14) | 0.016 (0.035) |
| | | 4 | Phenot = 762 MVP = 225 | 0.871 0.142 | 1.658 (0.40) | <0.001 | 0.302 (0.07) | 0.091 (0.042) | 0.31 (0.10) | 0.547 (0.13) | 0.299 (0.142) |
| Pfizer MVP Feed Effi. | NFI | 1 | Phenot = 785 MVP = 706 | 0.840 0.079 | 0.300 (0.13) | 0.01 | 0.092 (0.04) | 0.008 (0.007) | 0.14 (0.11) | 0.248 (0.15) | 0.062 (0.074) |
| | | 2 | Phenot = 687 MVP = 671 | 0.687 0.056 | 0.366 (0.15) | 0.01 | 0.104 (0.04) | 0.011 (0.008) | 0.21 (0.13) | 0.232 (0.11) | 0.054 (0.051) |
| | | 3 | Phenot = 254 MVP = 253 | 1.110 0.082 | -0.074 (0.27) | 0.81 | -0.020 (0.07) | 0.000 (0.003) | 0.21 (0.25) | -0.044 (0.16) | 0.002 (0.014) |
| | | 4 | Phenot = 215 MVP = 225 | 0.958 0.056 | -0.131 (0.33) | 0.86 | -0.032 (0.07) | 0.001 (0.004) | 0.37 (0.26) | -0.053 (0.14) | 0.003 (0.015) |

Detailed data and trait description

Beef CRC1 (datasets 1&2): The data from Beef CRC1 consisted of seven purebred breeds, four temperate breeds (Angus, Hereford, Murray Grey and Shorthorn) and three tropically adapted breeds (Brahman, Santa Gertrudis and Belmont Red). These cattle were born between 1993 and 1998. The basic design of the project and the phenotypic and genetic parameters extracted for these analyses have been described by Upton *et al.* (2001), Johnston *et al.* (2003) and Reverter *et al.* (2003). In brief, the progeny were generated over a number of years in various herds which had only one breed, so herd of origin and breed were confounded. Progeny (both steers and heifers) were purchased by the CRC at weaning and then backgrounded as cohorts in mixed breed groups, finished (either feedlot or pasture) and slaughtered together at the three target market endpoint weights. Individual feed intake was recorded on a sub-set of the feedlot finished groups and comprised 785 temperate animals (steers only) and 687 tropically adapted animals (steers and heifers). These animals were from all three markets where the mean age at the start of the feed test ranged from 459 days (temperate domestic steers) to 737 days (for tropically adapted Japanese market steers). The average number of days of recorded feed intake for domestic, Korean and Japanese market animals was 53, 57 and 74 days, respectively. For full details see Robinson and Oddy (2004).

At slaughter, all carcasses were electrically stimulated and marble score was assessed by Meat Standards Australia (MSA) technicians. At 24 h post-mortem a sample of the *M. longissimus thoracis et lumborum* (LTL) muscles were taken and frozen for later analyses (see Perry *et al.* 2001 for full details). Shear force measure of meat tenderness was taken on a cooked sample (equating to approximately two days ageing). Intramuscular fat percentage (IMF) was determined using either near infra-red (NIR) technology or ether extraction.

Beef CRC1 crossbreds (datasets 3&4): The data from Beef CRC1 crossbred project consisted of F1 progeny from nine purebred sire breeds out of straightbred Brahman cows, with straightbred Brahman calves as a control. The sire breeds included five temperate breeds (Angus, Charolais, Hereford, Limousin, and Shorthorn) and four tropically adapted breeds (Brahman, Charbray, Santa Gertrudis and Belmont Red). These cattle were born between 1996 and 1998 at two central Queensland herds. The basic design of the project has been described by Upton *et al.* (2001) and Newman *et al.* (2002) and design features and measures were the same as those in the CRC1 straightbred project.

Trait definitions

Marbling traits: Two traits were examined as dependent variables of marbling. Intramuscular fat percentage (IMF), determined by NIR or ether extract and MSA marble score (0-9 scores on 0.1 scale) (MSA MS). The CRC data was a combination of animals slaughtered for the domestic, Korean and Japanese markets. Age, carcass weight and IMF/marble scores increased from domestic to Korean to Japanese endpoints as described by Reverter *et al.* (2003). Models for analysing MSA marble score and IMF were described by Johnston (2001) and Reverter *et al.* (2003). The models included fixed effects for herd of origin, kill group and carcass weight as a linear covariate.

Meat tenderness: Shear force of LTL from normal hung sides (LTL_SF) was the trait used to assess tenderness. For CRC1 (datasets 1&2), the data edits and models were as described by Johnston *et al.* (2003) and included fixed effects for herd of origin, kill group and carcass weight as a linear covariate. Herd of origin accounted for the effect of breed. All carcasses were electrically stimulated and lab protocols equated to approximately two days ageing of the meat samples.

Feed efficiency. Net or residual feed intake (NFI) was the trait used as a measure of feed efficiency. The derivation of NFI and models were described by Robinson and Oddy (2004). Animals were recorded for feed intake for an average of 60 days and included animals fed for the three market endpoints. Individual daily feed intake records were adjusted for feedlot average daily gain and metabolic feed test weight to derive NFI.

References:

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