# Genetic Parameters For Ultrasound Live Traits In Pasture Fed Angus Cattle

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## Introduction

The use of ultrasound traits such as rib eye area (uREA), fat depth (uFAT) and intramuscular fat (uIMF) as a selection tool for improvement of carcass traits is widely accepted and implemented by most of the selection plans worldwide (Bertrand et al., 2001; Wilson 1992).

The Uruguayan Aberdeen Angus breed association has been recording real time ultrasound rib eye area and fat depth since 2003 and counts today with these traits in the national genetic evaluation. In 2005, the National Agricultural Research Institute of Uruguay (INIA) started to record ultrasound intramuscular fat together with the routinely collected uREA and uFAT. This was done on a trial basis since it was believed that the cattle might be too lean to be able to capture any genetic variation in intramuscular fat since most animals are fed range forage. The objective of this study was to obtain an heritability estimate of uIMF fat to determine feasibility of a future genetic evaluation for uIMF in Aberdeen Angus cattle in Uruguay. The second objective of this study was to estimate genetic parameters for the three ultrasound measurements in 18-months old Angus cattle.

## Material and methods

**Data:** RTU measurements of subcutaneous fat thickness, *longissimus dorsi* muscle area and intramuscular fat percentage at 18 months of age were obtained from INIA national performance database. Images were collected using an Aloka SSD 500 unit, equipped with a 3.5 MHz, 17.2-cm linear array transducer and a superflab (Aloka Co. Ltd., Tokyo, Japan). between the 12th and 13th ribs. From 2002 through 2004 images were interpreted through the CVC software and from 2005 onwards, images where interpreted through the Biosoft Toolbox® offline interpretation software (Biotrinics Inc. version 2.1). which enabled uIMF to be obtained. All images within herd were taken by the same person and all interpretations where made by the same experienced technician. Data came from 65 breeders during a time span of 6 years, with a total of 640 sires for uREA and uFAT. For uIMF, the time span was of 3 years and included progeny of 349 sires. Data was evenly distributed between males and females (i.e. 5013 females and 5583 for uFAT). See table 1 for a description of data.

Contemporary groups where formed using the national genetic evaluation criteria (same herd, season, sex and management group). Pedigree information was provided by ARU (*Asociación Rural del Uruguay*). Several quality controls on performance records were

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carried out in order to exclude logical inconsistencies and biological incompatibilities. Animal with unknown sires, contemporary groups with less than five observations or with less than two sires, and trait values beyond three standard deviations of the contemporary group mean were ignored for analysis.

**Model and analysis:** The following univariate analyses were performed for each of the three ultrasound traits to obtain reference values.

$y_{ijk} = CG_i + AOA + AOA^2 + a_j + e_{ijk}$

where:

$y_{ijk}$ … is the uREA, uFAT or uIMF for animal j,

$CG_i$ … is the effect of contemporary group i (1 to 483, 492 and 245 respectively),

AOA … is the effect of age of the animal at measurement as a linear covariable,

$AOA^2$ … is the effect of age of the animal at measurement as a quadratic covariable,

$a_j$ … is the random animal effect,

$e_{ijk}$ … is the random residual effect.

A multiple trait animal model with same effects including the traits uREA, uFAT and uIMF was used to estimate heritabilities and genetic correlations between traits. Maternal effects were not included in the model since preliminary analysis (not shown) resulted in very low estimates for maternal variances and covariances.

Analysis where made using GIBBS2F90 (Misztal *et al.* 2002) via the Bayesian approach usign Gibbs sampling. For each trait, a single chain of 200,000 samples was run, with the first 20,000 samples discarded as burn-in. Posterior mean and standard deviation, high posterior density interval (HPD) and effective sample size were calculate for each parameter. Convergence was determined by graphical inspection of the chain and by the effective sample size of the parameter of interest. Same criteria were used for the multivariate model.

## Results and discussion

A description of dataset utilized for the estimation is presented in table 1. As can be observed, trait means are significantly lower than observed in literature (Crews *et al.*, 2002; Hassan *et al.*, 2003; Reverter *et al.*, 2000) for Angus, but similar to the ones reported by Touruco (2006) for Braford and Hereford animals in Brasil.

**Table 1. Descriptive statistics for weaning weight and ultrasound traits**

| Traits | N° | Mean | Std.Dev. | Min | Max |
|---|---|---|---|---|---|
| uREA ($cm^2$) | 10709 | 46.39 | 11.57 | 15.68 | 99.74 |
| uFAT (mm) | 10636 | 2.70 | 0.93 | 0.80 | 12.70 |
| uIMF (%) | 5070 | 1.99 | 0.72 | 0.10 | 5.70 |
| Age (days) | 10709 | 545.97 | 30.10 | 447 | 656 |
| Weight (kg.) | 10709 | 333.16 | 79.54 | 150 | 680 |

The results of the main statistics of the marginal posterior distributions of genetic parameters for the univariate models are presented in table 2 and from the multivariate model in table 3.

**Table 2. Estimated statistics of marginal posterior distributions of additive genetic effect ($\sigma_a^2$), residual ($\sigma_e^2$) and heritability ($h^2$) from the univariate analysis**

| Trait | Parameter | Mean | PSD | 95%HPD$_L$ | 95%HPD$_U$ | ESS |
|---|---|---|---|---|---|---|
| | $\sigma_a^2$ | 746.97 | 93.39 | 569.80 | 930.00 | 337.20 |
| uREA | $\sigma_e^2$ | 1981.67 | 76.47 | 1826.00 | 2123.00 | 393.91 |
| | $h^2$ | 0.27 | 0.03 | 0.21 | 0.34 | 336.70 |
| | $\sigma_a^2$ | 3.57 | 0.64 | 2.29 | 4.81 | 166.73 |
| uFAT | $\sigma_e^2$ | 28.83 | 0.68 | 27.47 | 30.13 | 298.10 |
| | $h^2$ | 0.11 | 0.02 | 0.07 | 0.15 | 165.60 |
| | $\sigma_a^2$ | 3.61 | 1.08 | 1.44 | 5.75 | 168.89 |
| uIMF | $\sigma_e^2$ | 27.87 | 1.09 | 25.67 | 29.88 | 284.16 |
| | $h^2$ | 0.11 | 0.03 | 0.05 | 0.18 | 166.80 |

PSD: posterior standard deviation; 95%HPD: 95% highest posterior density interval Lower (L) -Upper (U) bound. ESS: Effective Sample Size.

Posterior means for heritability estimates for uREA, uFAT and uIMF were smaller than average heritability estimates from diverse papers reviewed by Bertrand *et al*., (2001) (0.32, 0.28 and 0.41 respectively) but within the range of observed values (Arnold *et al.,* 1991, Shepard *et al.,* 1996, and Meyer 1999, all cited by Bertrand *et al*., 2001) for uREA and for uFAT but not so for uIMF. Reverter *et al.* (2000) presented higher estimates for the Angus breed for all three traits as did Hassan (2003). Results in this study though, are similar to those obtained by Tarouco *et al.* (2006) for uREA and uFAT in a study with Braford and Hereford cattle in Brasil.

**Table 3. Estimates of genetic parameters (± standard deviation) from the multivariate model.**

| | uREA | uFAT | uIMF |
|---|---|---|---|
| uREA | **0.273**[*] ± 0.029 | 0.212 ± 0.100 | -0.181 ± 0.129 |
| | *(0.213;0.331)* | *(0.0037 ; 0.389)* | *( -0.406 ; 0.095 )* |
| uFAT | 0.237 ± 0.0199 | **0.114** ± 0.0186 | 0.384 ±0.149 |
| | *(0.199;0.277)* | *(0.073;0.150)* | *(0.098 ; 0.663)* |
| uIMF | -0.316 ± 0.241 | 0.044 ± 0.025 | **0.120** ± 0.031 |
| | *(-0.780;0.163)* | *(-0.006;0.0936)* | *(0.063;0.181)* |

[*]Heritabilities on diagonal in bold, genetic correlations on upper diagonal and phenotypic correlations on lower diagonal. 95% highest posterior density interval Lower (L) ;Upper (U) bound in italics.

Heritability estimates for the traits in both univariate and multivariate models where similar. Genetic correlation between uREA and uFat was positive and smaller than most estimates presented by Bertrand (2001). Genetic correlation between uREA and uIMF coincided with the two papers mentioned by the same author, being negative and small. When analyzing the data considering these traits as different traits in heifers and bulls, Reverter et al, 2000 obtained a positive though small (0.19) genetic correlation between uREA and uIMF for

heifers and a negative larger correlation for bulls (-0.35) for the Angus breed. A positive genetic correlation of smaller magnitude between both fat traits was obtained compared to Reverter *et al.* (2000) estimates for both sexes.

## Conclusion

Parameter estimates for uREA and uFat coincided with the parameters used in the actual genetic evaluation for the breed in Uruguay (not published). Though the heritability estimate for uIMF is smaller than in literature, magnitude is high enough to merit the inclusion of the trait in the national genetic evaluation. Some genetic variation is captured even though mean phenotypic values are low. Further research needs to attend related issues like the economical impact of this indicator trait, given present and future payment system in Uruguay. Part of this is obtaining carcass data in order to be able to estimate genetic correlations between measured ultrasound traits and carcass traits in slaughtered steers.

## Acknowledgements

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