

# Genetic Parameter Estimates for Age at Slaughter and Days to Finish in a Multibreed Population

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## Summary with Implications

*The objective of this study was to estimate genetic parameters for age at weaning, days to finish, and age at slaughter and their relationships with carcass traits. Heritability estimates using univariate models for days to finish and age at slaughter when adjusted to different endpoints ranged from 0.33 to 0.39 and 0.52 to 0.59, respectively. The genetic correlations between age at weaning and days to finish ranged from -0.26 to -0.43. Results indicate days to finish and age at slaughter are moderately heritable and would respond favorably to selection. Days to finish, even when adjusted to various endpoints, displays minimal phenotypic variation. Age at slaughter, although more variable than days to finish, is comprised of multiple identifiable sub-traits including age at weaning and days to finish. Consequently, a selection program for improved age at slaughter should consider the impact on the component traits.*

## Introduction

Considerable effort and expense have been spent on collecting individual animal feed intake on immature seedstock animals as a means of producing Expected Progeny Differences (EPD) for dry matter intake as indicators of feed consumption in commercial growing animals. Dry matter intake EPD represent the only predictions of genetic merit for costs associated with finishing cattle. However, the amount of feed consumed only represents a portion of the variable costs of finishing cattle, with other costs including yardage, morbidity, and mortality. The number of days cattle spend in a feedlot to reach a desired endpoint (e.g., weight, fatness, quality grade)

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Table 1. Summary statistics for data utilized within analyses.

Trait <sup>1</sup>	Mean (SD)			
	Steers		Heifers	
AAS	451	(18.4)	433	(20.4)
AAW	164	(18.9)	151	(17.0)
AFT	0.52	(0.19)	0.49	(0.17)
DtF	287	(11.0)	281	(15.2)
FW	1380	(134)	1208	(113)
HCW	871	(88.0)	767	(74.5)
MARB	506	(77.0)	501	(66.5)
REA	13.6	(1.58)	13.7	(1.48)

<sup>1</sup>AAS = age at slaughter, the number of days from birth until harvest (days), AAW = age at weaning, the number of days from birth until weaning (days), AFT = adjusted fat thickness (in), DtF = days to finish, the number of days from weaning until harvest (days), FW = final live weight (lbs), HCW = hot carcass weight (lbs), MARB = marbling (score), REA = ribeye area (in<sup>2</sup>).

is a function of the amount of feed they consume, rate of growth, and rate of tissue deposition. Reducing the amount of time on feed needed to reach a desired endpoint would be economically advantageous. However, the choice of the finish endpoint depends on the biological type of cattle being marketed and the marketing systems available to the owners. The objective of this study was to estimate genetic parameters for age at weaning (AAW), days to finish (DtF), age at slaughter (AAS), and their relationships with growth and carcass traits including; adjusted fat thickness (AFT), hot carcass weight (HCW), marbling score (MARB), ribeye area (REA), and final weight (FW).

## Procedure

All animal procedures followed U.S. Meat Animal Research Center (USMARC) standard operating procedure and cattle were treated according to Federation of Animal Science Societies guidelines. For the Germplasm Evaluation Program (GPE) generations, purebred AI sires were mated to purebred or crossbred dams to generate purebred and crossbred steers and heifers and purebred and F<sub>1</sub> bulls. The bulls were mated to the purebred and half-blood females to produce purebred, half-blood,

and F<sub>1</sub><sup>2</sup> steers and heifers. All germplasm introduced into the population entered through AI. Animals from the 8 cycles included only spring-born records whereas the advanced generations of GPE included spring and fall calving records. All heifers were bred via natural service during GPE cycles. Data were from steers and heifers (n=7,747) from the GPE at the USMARC (Table 1). The average age of the animals at feedlot entry was 162 days or equivalent to their AAW. All traits were analyzed with univariate and bivariate animal models using ASReml. Fixed effects fitted for all models included contemporary group (concatenation of birth year, birth season, sex, and experimental treatment group), breed covariates, and direct heterosis. Different endpoints for AAS and DtF were also investigated by fitting fixed linear covariates of AFT, HCW, MARB, REA, and FW.

## Results

Univariate heritability estimates for AAS and DtF ranged from 0.52 to 0.59 and 0.33 to 0.39, respectively (Table 2). Covariates of MARB and AFT led to the highest and lowest, respectively, heritability estimates for AAS and DtF. The genetic correlations between AAW and DtF ranged from -0.26 to -0.43, depending on the chosen endpoint

**Table 2. Genetic parameter estimates (SE) for univariate models for age at slaughter (AAS<sup>1</sup>) and days to finish (DtF<sup>2</sup>).**

Covariate <sup>3</sup>	Response Trait	
	AAS	DtF
	<i>h</i> <sup>2</sup>	<i>h</i> <sup>2</sup>
AFT	0.52 (0.04)	0.33 (0.03)
FW	0.57 (0.04)	0.38 (0.03)
HCW	0.56 (0.04)	0.38 (0.03)
MARB	0.59 (0.04)	0.39 (0.03)
REA	0.59 (0.04)	0.38 (0.03)
None	0.59 (0.04)	0.38 (0.03)

<sup>1</sup>AAS = age at slaughter, the number of days from birth until harvest.

<sup>2</sup>DtF = days to finish, the number of days from weaning until harvest.

<sup>3</sup>AFT = adjusted fat thickness (in), FW = final live weight (lbs), HCW = hot carcass weight (lbs), MARB = marbling (score), REA = ribeye area (in<sup>2</sup>).

**Table 3. Genetic correlations (SE) for multivariate models for age at weaning (AAW)<sup>1</sup> and carcass traits.**

Response Trait		Covariate <sup>3</sup> for 2	<i>r</i> <sub>r</sub>
1	2 <sup>2</sup>		
AAW	DtF	AFT	-0.26 (0.05)
		FW	-0.42 (0.04)
		HCW	-0.43 (0.04)
		MARB	-0.43 (0.04)
		REA	-0.41 (0.04)
		None	-0.41 (0.04)

<sup>1</sup>AAW = age at weaning, the number of days from birth until weaning.

<sup>2</sup>DtF = days to finish, the number of days from weaning until harvest.

<sup>3</sup>AFT = adjusted fat thickness (in), FW = final live weight (lbs), HCW = hot carcass weight (lbs),

MARB = marbling (score), REA = ribeye area (in<sup>2</sup>).

for DtF (Table 3). Selection to improve DtF could, in turn, lead to increases in AAW. The phenotypic variation in AAW is likely due to variation in calf birth date which is related to the date at which the dam conceived. Further research is required to investigate the addition of maternal additive genetic, heterosis, and breed effects for AAW and AAS.

### Implications

Results indicate that AAS and DtF are moderately heritable. The choice of the finish endpoint, and consequently the covariate included in the model for AAS and DtF, is dependent on the marketing scheme being targeted, although the most likely choices would be carcass weight or adjusted fat thickness. Both proposed traits, DtF and AAS, have issues that need to be considered before implementation in a genetic evaluation. The general lack of variation in DtF due to the reduced variation in the unadjusted number of days on feed potentially limits this trait's utility to make genetic progress for overall feedlot efficiency. Although AAS displays greater variation, the sources of variation need to be fully quantified to avoid unintended correlated responses to selection.

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