Structural equation analysis and whole genome scan for growth, carcass quality and meat quality in beef

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INTRODUCTION

The goal of delivering a quantitative test of a theoretical hypothesized model by the scientist can be achieved applying structural equation models (SEM), provided that this kind of analysis uses various types of models to depict linear relationships among variables (Schumacker et al., 2010), in this case phenotypes underlying complex traits (Rosa et al., 2011).

The SEM analysis aims at determining whether a theoretical model is supported by sample data, or not. The SEM analysis relies on no rejecting the overall or structural model null hypotheses, while rejecting path-specific null hypotheses of no effect (Gefen and Straub, 2000).

The objectives of this study were:

1) To identify a model combining growth, carcass quality and taste quality in beef, able to most closely fit the variance-covariance structure present in the sample data. The theoretical model is based on predicting taste quality as a latent dependent variable using carcass quality as a latent dependent variable and growth as a latent independent variable.
2) To perform a whole genome scan for the latent variables growth, carcass quality and taste quality in order to identify QTLs with direct and indirect effect on these latent constructs.

MATERIALS AND METHODS

- Some 726 steers from the UF multibreed Angus-Brahman herd were used.
- A total of 21 phenotypes were used to construct the latent variables growth, carcass quality and taste quality.
- The R package lavaan (Rosseel, 2012) was used to model the latent variables growth, carcass quality and taste quality. The theoretical structural model was the following:

$$\eta 1 = \gamma 1\, \xi 1 + \zeta 1$$
$$\eta 2 = \beta 1\, \eta 1 + \zeta 2$$

ξ1 - exogenous latent construct growth
γ1 - model parameter representing the fixed effect of growth covariates on carcass quality
η1 - endogenous latent construct carcass quality
β1 - structural coefficient representing the magnitude of the casual effect among η1 and η2
η2 - endogenous latent construct taste quality
ζ's - residuals (Rosa et al., 2011).

- Genomic DNA was extracted from blood from 480 animals and genotyped with the commercial GGP Bovine F-250 SNP chip.
- A total number of 112,267 SNPs were included in the whole genome scan after pruning.
- The single-step genomic best linear unbiased prediction (ssGBLUP) was used for estimation of the amount of genetic variance explained by adjacent SNPs (Han & Peñagaricano, 2016) located inside a 1 Mb window across the genome.
- Gene functional classification analysis with DAVID server on 1656 genes located inside the associated windows was perform.

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RESULTS

The final structural model included carcass quality as an independent latent variable and taste quality as a dependent latent variable (**Figure 1**).

- Carcass quality included quality grade (QG), fat over ribeye (FOR) and marbling (MAR).
- Taste quality included juiciness (JC), tenderness (TD) and connective tissue (CT).

A total number of 49 windows were able to explain more than 0.5 percent of the additive variance present in the carcass quality, and taste quality latent phenotypes. BTA18 and BTA19 harbored sixteen of these windows.

Fifteen windows were associated with carcass quality, 16 windows have direct effect on taste quality. Thirteen windows were associated with carcass quality, taste quality and uncorrected taste quality, meaning that they harbor QLTs with effect on both traits, but also in taste quality through carcass quality; five windows were associated with carcass quality, having an indirect effect on taste quality (**Figure 2**).

The top three overrepresented gene functional groups from the associated windows were Intermediate filament cluster (enrichment Score: 23.31), Zinc finger cluster (enrichment Score: 3.46), and peptidase cluster (enrichment Score: 2.52). The functional annotation clustering identified 73, 134 and 60 genes for cluster 1, cluster 2 and cluster 3, respectively.

REFERENCES

- Rosa, G. J., Valente, B. D., de los Campos, G., Wu, X.-L., Gianola, D., and Silva, M. A. (2011). Inferring causal phenotype networks using structural equation models. *Genet. Sel. Evol.* 43, 6.
- Schumacker, R. E., Lomax, R. G., and Group, F. (2010). *Structural Equation Modeling Third Edition*.
- Gefen, D. and Straub, W. D. (2000). Structural Equation Modeling and Regression: Guidelines for Research Practice. 4, 2–79.
- Rosseel, Y. (2012). pkglavaan: An R Package for Structural Equation Modeling. *J. Stat. Softw.* 48.
- Han, Y., and Peñagaricano, F. (2016). Unravelling the genomic architecture of bull fertility in Holstein cattle. *BMC Genet.* 17, 1–11. doi:10.1186/s12863-016-0454-6.

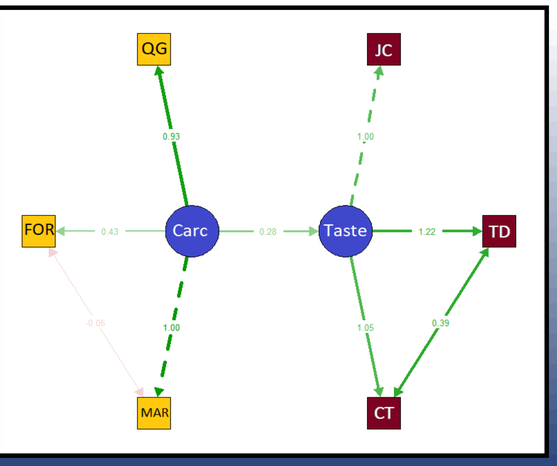
	Taste quality			Carcass quality		
	JC	TD	CT	MAR	FOR	QG
JC	1.00					
TD	0.45	1.00				
CT	0.39	0.87	1.00			
MAR	0.23	0.28	0.24	1.00		
FOR	0.10	0.12	0.10	0.30	1.00	
QG	0.21	0.26	0.23	0.78	0.33	1.00

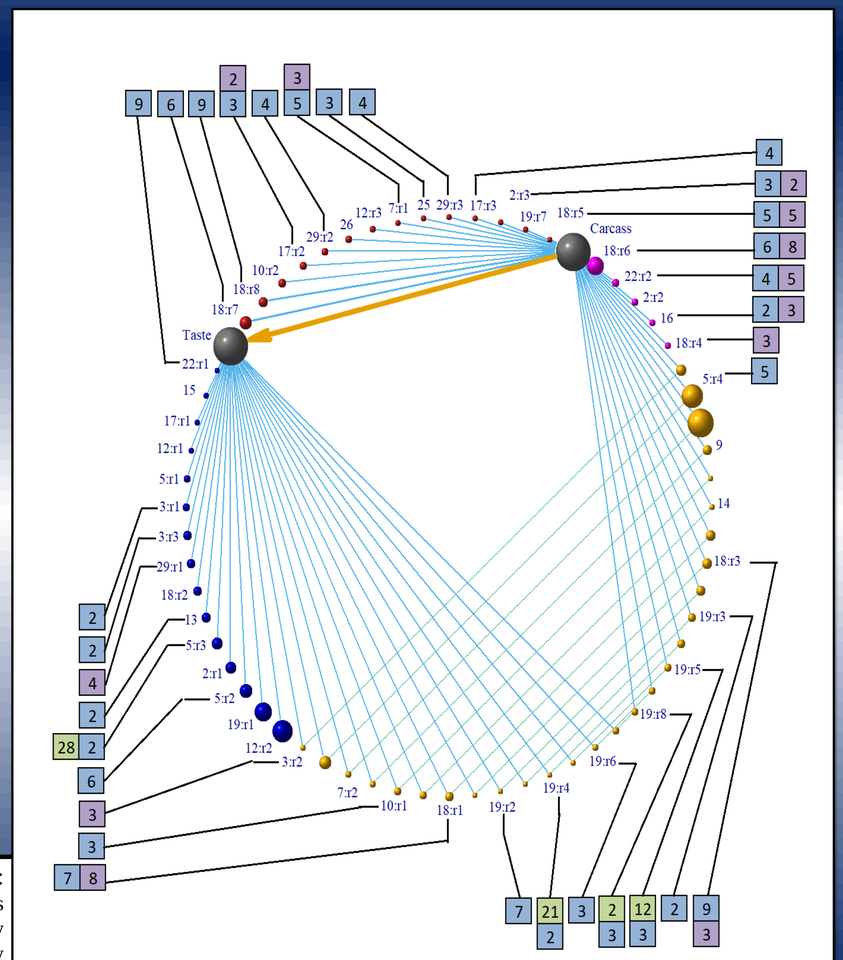
Table 1. Covariance matrix of the observed phenotypes utilized to measure the latent variables carcass quality and meat. Marbling (MAR); fat over ribeye (FOR); yield grade (YG); juiciness (JC); tenderness (TD); connective tissue (CT).

Figure 1.

Relationship between observed and latent variables (carcass and taste quality) in *longissimus dorsi* muscle in the final SEM model.

FOR = fat over ribeye
MAR = marbling
QG = quality grade
JC = juiciness
TD = tenderness
CT = connective tissue





Nodes:
- **Gray** = latent variables
- **Red** = genomic regions for carcass quality
- **Blue** = genomic regions for taste quality
- **Yellow** = genomic regions for carcass quality and taste quality
- **Magenta** = genomic regions for taste quality through carcass quality

Boxes:
- **Green**= Cluster 1; Intermediate filament related cluster
- **Blue**= Cluster 2; Zinc finger related cluster
- **Purple**= Cluster03; Immunoglobulin related cluster

Figure 2. Variability of the latent variables explained by 1 Mb windows (nodes) and number of genes in each window belonging to the top three overrepresented functional clusters (boxes) identified in *longissimus dorsi*. Orange arrow represents the causal relationship assumed between latent phenotypes.