GENOMICS OF CARCASS AND MEAT QUALITY TRAITS IN HEREFORD – PRELIMINARY RESULTS

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Abstract – Preliminary genome-wide association studies based on the incipient training population of 239 Hereford steers were performed for hot carcass weights (HCW), rib eye muscle at 11/12 rib by ultrasound (REA) and Warner-Bratzler shear force (WBSF) after one week of ageing. Genotyping information on 80k SNPs was available. Approaches used for data analysis were; a) BayesC, which considers the SNP population as a mixture of a small number of SNPs involved in this variability and a large number of neutral markers; b) GBLUP (genomic BLUP) that assumes that all SNPs may contribute to trait variability. Important proportions of the total variance were explained by the SNPs, suggesting an important contribution of genomic information at the time of predicting the genetic merits. Evidences of SNPs linked to genes of major effects on REA and WBSF were also found. Methodologies differed on the proportion of variance explained by markers WBSF, but were similar for REA and HCW, in agreement with the literature. The most significant SNPs tended to agree between methods. Although increasing training population is essential for more accurate QTL findings and genomic value predictions, this first study on carcass and meat quality traits using high density of SNPs shows that genomic information provides useful insight on the underlying genetics of carcass and meat quality traits.

I. INTRODUCTION

There are traits that are economically important for the beef industry, but inherently difficult or expensive to measure. This is the case of carcass and meat quality traits which have not been routinely included in beef cattle genetic evaluations systems [1].

Genomics provide new alternatives for the genetic improvement of traits which are not cost effective to measure on an industry-wide basis. Recent developments in DNA technology and genome sequencing led to the detection of thousands of single nucleotide polymorphisms (SNPs) making possible a very dense coverage of the genome, at affordable genotyping costs [2]. Dense arrays of SNP are commercially available for cattle, as well as other relevant species [3].

These data made feasible the implementation of genomic selection, which is a form of marker-assisted selection in which all quantitative trait loci (QTL) are in linkage disequilibrium (LD) with at least one marker [4]. Genomic selection increases genetic progress by higher accuracies of genetic merit at younger ages, and facilitate selection of economically relevant traits that are difficult or expensive to measure.

Information provided by the high density SNP chips enables not only the implementation of genomic selection but also genome-wide association studies (GWAS) that provide valuable information for the identification of QTLs with favorable effects on carcass and meat quality. Different methodologies for GWAS have been developed. For instances, GBLUP (genomic BLUP) method assumed that all SNPs may contribute to trait variability, while all other methods considered the SNP population as a mixture of a small number of SNPs involved in this variability and a large number of neutral SNPs [5].

Implementation of animal genomics faces challenges such us developing training population, as well as capabilities and expertise on database design and data analysis and interpretation. A training population for carcass and meat quality in Hereford is being built based on past and ongoing experiments with several traits recorded and DNA samples available. This study presents preliminary results on genome-wide association studies of carcass and beef quality.

II. MATERIALS AND METHODS

Animals and phenotypic data**.** Animals used in this study were of two experiments that are described in Table 1. In both experiments steers were slaughter when they reached in average 500 kg of live weights. Data recorded included

ultrasound measurements, and carcass and meat quality traits. Three variables were analyzed here: (1) rib eye area by ultrasound (REA), which was measured the day before slaughter at the 11/12 rib; hot carcass weights (HCW) recorded automatically in the slaughter line, and Warner-Bratzler shear force (WBSF) of the *longissimus dorsi et lumborum* muscle samples at the 10th rib after 5 or 7 days of ageing. Descriptive statistics are shown in Table 2.

Table 1 Experimental details

Description	Experiments	
	A	B
Nutrition after weaning	grazing and feedlot	grazing and feedlot
Nutrition at finishing	grazing and feedlot	feedlot
Sires	unknown	High & average REA EPD
Slaughter groups	3	4
Genotyped animals	137	102

Table 2 Descriptive statistics for REA, HCW and WBSF in Hereford steers

Trait	N	Mean	Sd	Max	Min
REA (cm^2)					
Exp A	132	63.39	5.72	75.8	51.5
Exp B	101	64.98	6.24	82.5	52.6
Total	233	64.08	5.99	82.5	51.5
HCW (kg)					
Exp A	137	250.35	19.21	302.0	201.6
Exp B	102	256.98	24.23	311.2	193.2
Total	239	253.18	21.70	311.2	193.2
WBSF (kg)					
Exp A	137	3.37	1.09	9.46	1.78
Exp B	102	4.46	1.18	9.19	1.79
Total	239	3.84	1.25	9.46	1.78

DNA samples and genotyping data**.** DNA was isolated from blood samples in the Biotechnology Unit of INIA. The SNP marker data were obtained from GeneSeek Genomic Profiler Bovine HD (GGP-HD; Geneseek, Lincoln, USA). Quality control criteria were call rate per sample of 90% and SNP call rate of 90%. Only autosomal markers were evaluated and Map BTAU4.6 was used in this study. Comparison of individual genomic information identified four repeated samples that were also excluded.

Data analysis**.** The potential of the genomic data to discriminate population structure explained by using high and average REA sires was evaluated using Principal Component Analysis (PCA) and the fixation index (Fst), which is a measure of the genetic differentiation between groups of progeny using the genomic information.

The subset of autosomal SNPs used in these analysis were in moderate linkage disequilibrium (r2<0.4) and MAF>0.01. These criteria were applied to identify informative molecular markers for population structure analysis.

The approaches followed in this preliminary genome-wide association study were GBLUP and BayesC methods. Data analysis were performed using BLUPF90 [6] modified for genomic analyses [7], and GenSel software [8], respectively. The GBLUP methodology is based on the infinitesimal model, which assumes equal variance for all SNP marker-QTL associated effect. On the other hand, BayesC assumes that many SNP have no effect on the trait because they are not in LD with any of the mutations that explain the variation in the traits. The parameter π is the proportion of SNP with no effect while the rest $(1 - \pi)$ have effects on the trait drawn from a normal distribution [9]. In this study, results with a π value of 1% are presented. QTL mapping and variances explained by markers were also estimated using both approaches.

III. RESULTS AND DISCUSSION

Only one sample had call rate <90% and was therefore excluded from the analysis. A total of 70,967 SNPs presented a call rate higher than 90%. A total of 43,268 autosomal SNPs achieved the criterion to study the population structure by PCA and Fst. The PCA analysis did not show a very clear patron of clusters for high and average REA sire progeny (Figure 1). This is in agreement with the Fst value which was 0.011, showing a low differentiation between the two groups.

Clearer clustering and higher values of Fst are expected after divergent selection lines as showed by Grasso *et al.* (2014). In our study the low differentiation may be explained by the fact that although "divergent" sires were used the

experiment did not imply divergent selection. In addition, data came only from the first year of experiment. Although the magnitude of the Fst was low, it is comparable to those reported by Bolorma *et al.* (2013) between composite breeds and pure breed used in those composites.

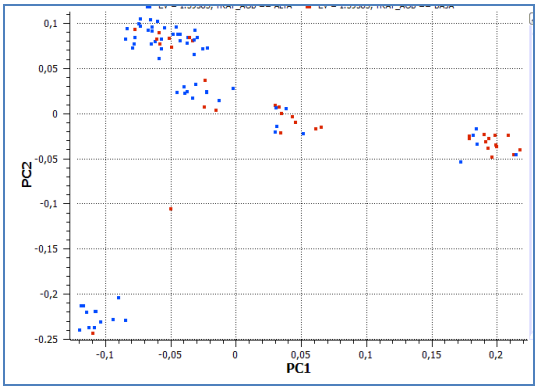


Figure 1. First and second principal components based on allele frequency. Each point represents one animal. The red dots represent the average REA group and the blue the high REA group

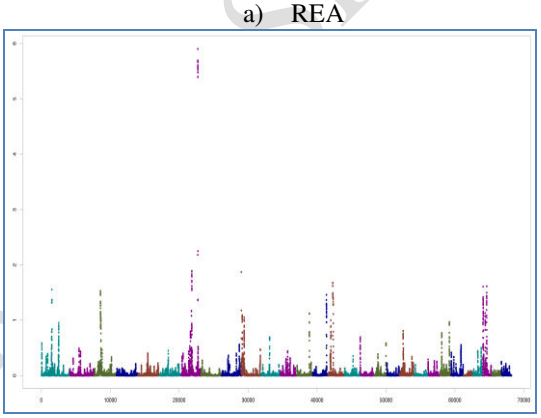
Results of GWAS for REA and WBSF are shown in Figure 2 (a and b). Two important peaks were found for REA and WBSF in BT07 at the position of the calpastatin gene. Schenkel *et al.* (2006) reported significant effects of this gene on both traits. Calpastatin acts as an inhibitor of calpain activity, which accelerate protein degradation, in the live animal and postmortem [12], which may explain its effect on both muscle development and tenderness.

Calpain gene which also influences WBSF has been mapped to BT29 in previous studies. Although a second high peak was found at BT29 (Figure 2b) in our study, the position did not overlap with the reported position of the gene. It is important to take into account that the size of the training population is still small which may reduce the precision of QTL mapping.

Variance component estimates for the three traits are presented in Table 3. Estimates of total, genetic (explained by markers) and residual variance are shown, as well as the proportion of variance explained by SNPs using BayesC and GBLUP. Markers explained important proportions of the variance of REA (0.30 and 0.32) and WBSF (0.25 and 0.43). However, SNPs capture very low proportion of the total variance in this data set for HCW.

Estimates of genomic variance for WBSF are in agreement with those reported by Snelling *et al.* (2013) for shear force measured 3 and 14 days after slaughter in several breeds. However, Bolormaa *et al.* (2013) estimated lower proportions for REA and WBSF with GBLUP and Bayesian methods. Their results also show differences between methods, with a similar trend to our results (Table 3). The lowest agreement between methods was found in the traits in which genes of larger effect are known such as tenderness (Bolormaa *et al.*, 2013).

a) REA



b) WBSF

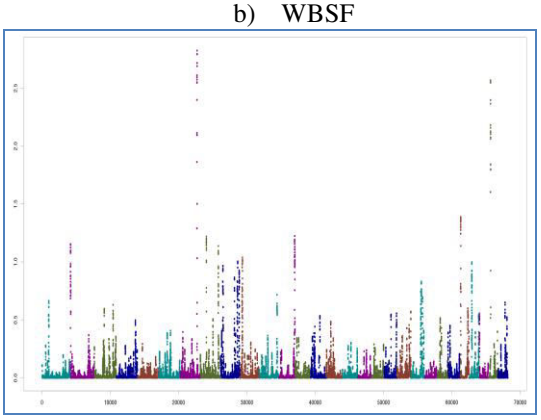


Figure 2. Proportion of SNP variance explained by 10Mb window of adjacent SNPs obtained by GBLUP analysis for (a) Rib eye area and (b) Warner-Bratzler shear force

IV. CONCLUSION

This first GWAS on carcass and meat quality traits using high density of SNPs shows that genomic information provides useful insight on the underlying genetics of carcass and meat quality traits. Important proportions of the total

variance were explained by the SNPs, suggesting an important contribution of genomic information at the time of predicting the genetic merits. Evidences of SNPs linked to genes of major effects on REA and WBSF were also found. Methodologies differed on the proportion of variance explained by markers WBSF, but were similar for REA and HCW, in agreement with the literature. The most significant SNPs tended to agree between methods. Increasing training population is essential for more accurate QTL findings and genomic value predictions.

Table 3. Variance components and proportion of variance explained by markers of REA, HCW and WBSF using BayesC and GBLUP method

Variance/Method	BayesC	GPLUP
	REA	
Residual	24	23
Genetic	10	11
Total	34	34
Var a/c markers	0.300	0.320
	HCW	
Residual	450	451
Genetic	1	9
Total	451	460
Var a/c markers	0.003	0.020
	WBSF	
Residual	0.94	0.66
Genetic	0.30	0.49
Total	1.2	1.1
Var a/c markers	0.245	0.425

ACKNOWLEDGEMENTS

Financial support was provided by the National Agency for Research and Innovation (grant FMV_1_2011_1_6671). The authors are very greatful with Alejandro LaManna, Georgget Banchero, Olga Ravagnolo, Fernando Baldi and María Paz Tieri for the contributions to the design and implementation of the experiments. We also thank Pablo Peraza, Sofía Ramirez, Carlos Monzalvo and Andrea Vergara (Biotechnology Unit) for their collaborations to the experimental work.

REFERENCES

1. Simm, G., Lambe, N.R., Bünger, L., E.A. Navajas & Roehe, R (2009). Use of meat quality information in breeding programmes. In J. Kerry & D. Ledward. Improving the sensory and nutritional quality of fresh meat (pp 265 – 291). Woodhead Publishing , Cambridge.
2. Garrick, D.J. (2011). The nature, scope and impact of genomic prediction in beef cattle in the United States. Genetics Selection Evolution 43: 17-28.
3. Snelling,W.M., Cushman, R.A., Keele, J.W, Maltecca, C. Thomas, M.G., Fortes, M.R.S *et al.* (2013). Networks and pathways to guide genomic selection. Journal of Animal Science 91:537–552.
4. Goddard, M.E. & Hayes, B.J. (2007) Genomic selection. Journal of Animal Breeding & Genetics 124:323-330.
5. Bolormaa, S., Pryce, J.E, Kemper,K, Savin, K., Hayes, B.J.; Barendse, W. *et al.* (2013). Accuracy of prediction of genomic breeding values for residual feed intake and carcass and meat quality traits in Bos taurus, Bos indicus, and composite beef cattle. Journal of Animal Science 91:3088–3104.
6. Misztal, I., Tsuruta, S., Strabel, T., Auvray, B., Druet, T. & Lee, D.H. (2002). BLUPF90 and related programs. Commun. No. 28–07 in 7th WCGLP, Montpellier, France.
7. Aguilar, I., Misztal, I., Legarra, A. & Tsuruta, S. (2011). Efficient computation of the genomic relationship matrix and other matrices used in single-step evaluation. Journal of Animal Breeding and Genetics 128: 422–42.
8. Fernando, R.L. & Garrick, D.J. (2009). GenSel: User manual for a portfolio of genomic selection related analyses. http://taurus.ansci.iastate.edu.
9. Habier, H., Fernando, R.L., Kizilkaya, K. & Garrick, D.J. (2011). Extension of the Bayesian alphabet for genomic selection. BMC Bioinformatics 12:186.
10. Grasso, A.N., Goldberg, V., Navajas, E.A., Iriarte, W., Gimeno, D., Aguilar, I., Medrano, J.F., Rincón, G. & Ciappesoni, C.G. (2014). Genomic variation and population structure detected by single nucleotide polymorphism arrays in Corriedale, Merino and Creole sheep. Genetics and molecular biology. In press.
11. Schenkel, F.S., Miller, S.P., Jiang, Z, Mandell, I. B., Ye, X., Li, H. & Wilton, J.W. (2006). Association of a single nucleotide polymorphism in the calpastatin gene with carcass and meat quality traits of beef cattle. Journal of Animal Science 84:291–299.
12. Koohmaraie, M., Kent, M.P., Shackelford, S.D., Veiseth, E. & Wheeler, T.L. (2002). Meat tenderness and muscle growth: is there any relationship? Meat Science 62: S345-S352.