Detection of QTL for beef fatty acid composition on bovine chromosome 22

Gutiérrez-Gil B[1]; Williams JL[2]; Richardson RI[3]; Wood JD[3] and Wiener P[4].

[1]University of León, Department of Animal Production , Campus de Vegazana, 24071, León, Spain; [2]Parco Tecnologico Padano, Polo Universitário, 26900, Lodi, Italy; [3]University of Bristol, Langford, BS40 5DU, Bristol, UK; [4]The Roslin Institute and Royal (Dick) School of Veterinary Studies, Roslin, EH25 9PS, UK

INTRODUCTION

The fatty acid (FA) composition of meat is important because of the impact of diet on human health.

Based on the average western diet, medical authorities recommend
- a reduction in the consumption of saturated FA (SFA)
- an increase in the consumption of n-3 polyunsaturated FA (PUFA)
- and an decrease of n-6 FA to n-3 FA ratio

Marker-assisted selection (MAS) could help to improve beef FA profiles, which show low heritabilities and are difficult to measure routinely.

OBJECTIVE

Search for QTL influencing beef fatty acid composition using a a Charolais X Holstein experimental cattle population.

We present here the results obtained for chromosome 22 (BTA22)

MATERIAL & METHODS

1-Resource Population and Experimental Design

- Combined F2-reciprocal backcross design (Fig 1).
- Founders: **Charolais** sires (beef) and **Holstein** dams (dairy). Second generation animals: **CB1**, **F2** and **HB1** (raised in four annual cohorts).

3-Phenotypes: Beef fatty acid composition

- **The 235 bull calves** from the **second generation** were reared on the same diet and slaughtered at ~12 monts of age (~ 550 Kg).
- Fatty acid composition was determined from the *longissimus dorsi* muscle of meat samples, using a chlorofom:methanol (2:1) extraction method and gas-liquid.
- **Phenotypic measurements analysed:**
  - Content measurements for 18 individual FA based on total FA (mg/100g muscle)
  - 3 FA indexes: saturated FA (SFA), polyunsaturated FA (PUFA) n-3 polyunsaturated FA (n-3 PUFA);
  - Sum of total fatty acids (SUMWFA)
  - 2 FA ratios: n-6/n-3 and polyunsaturated-saturated (P:S) ratios
- Raw data were **log transformed** before further analyses to achieve a normal distribution.

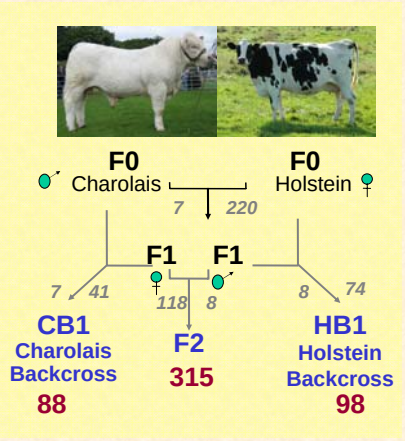

Fig 1. Resource experimental population

2-Genotypes

- **8 microsatellite markers evenly** distributed on BTA22 were genotyped for the whole population.
- The linkage map was built with the **CRIMAP v2.4 software.**

4-QTL analysis

- The web-based **QTL Express software** was used to
  - -estimate the information content (IC) across the linkage map
  - -perform the QTL analysis
- Significance thresholds were obtained by **permutation testing**

RESULTS

- For the 24 analysed traits → 9 overlapping QTL mapped in the first half of chromosome 22 (chromosome-wise p-values < 0.01-0.05).
  - All the significant associations showed an additive mode of inheritance.
  - The Charolais allele increased the levels of myristic, palmitic, stearic, palmitoleic, oleic and conjugated linoleic fatty acids compared to the Holstein allele.
  - The Holstein allele was associated with decreased levels of the two FA indexes and an increased P:S ratio.

Trait	Name	cM	F-value	p-value	Additive Effect	%Variance due to QTL
lnW14:0	Myristic acid	29	6.29	0.014	-0.17 ± 0.05	5.57
lnW16:0	Palmitic acid	31	7.12	0.005	-0.14 ± 0.04	6.30
lnW16:1	Palmitoleic acid	33	8.14	0.004	-0.18 ± 0.05	7.20
lnW18:0	Stearic acid	29	5.74	0.024	-0.11 ± 0.03	5.08
lnW9C18:1	Oleic acid	35	8.02	0.003	-0.16 ± 0.04	7.10
lnWCLA	Conjugated linoleic acid	29	6.97	0.008	-0.19 ± 0.05	6.17
lnSUMWFA	Weight of total FA (mg/100 g)	32	6.77	0.009	-0.11 ± 0.03	5.99
lnSFA	Saturated FA	30	6.84	0.011	-0.13 ± 0.04	6.05
lnP:S	Polyunsaturated:Saturated FA ratio	32	6.56	0.012	0.10 ± 0.03	5.80

Table 1: Characterization of the QTL identified in BTA22 at the 5% chromosome-wise level.

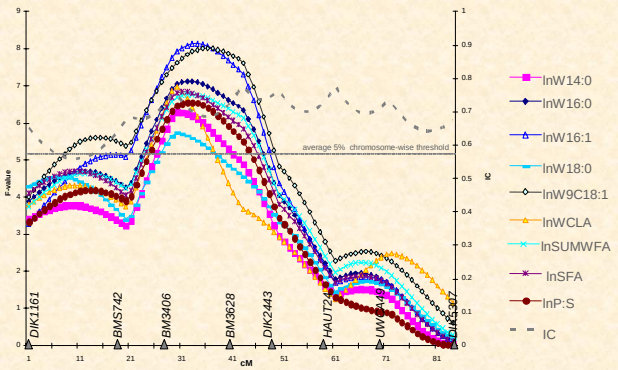

Fig 2. Statistical profile obtained for significant FA traits on BTA22

DISCUSSION

- The QTL reported here overlap with a QTL for intramuscular fat content previously reported in this population, which showed the same mode of inheritance.
- Our results suggest that the same gene or genes mapping in the marker interval [BM3406-BM3628] may control the level and composition of fat deposition in cattle. Genes related to fatty acid pathways such as *SCD, ACACA, SREBF1, DGAT1* and *FABP4* map to different genomic regions.
- An increase of marker density in the QTL region is required to redefine the QTL position and identify positional candidate genes.

ACKNOWLEDGMENTS

Financial support from the UK Department of Environment, Food and rural Affairs (Defra), the UK Biotechnology and Biological Sciences Research Council (BBSRC) and the UK Meat & Livestock Commission (MLC). B. Gutiérrez-Gil was funded by Marie Curie IntraEuropean fellowship during her stay at The Roslin Institute. She is now funded by the *Juan de la Cierva* Spanish Program from the Spanish Ministry of Science and a Marie Curie Reintegration Grant (Ref: Nº QL K5 CT2000 0656).