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Association of genes involved in carcass and meat quality traits in 15 European bovine breeds

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ABSTRACT

Variations in meat quality traits are under complex genetic control and improvement has been hampered by the difficulty in their measurement. Several QTL have been reported for different meat quality related traits, but few genes have been described which explain large amounts of the phenotypic variation. The use of single nucleotide polymorphism (SNP) marker panels with predictive value for carcass traits have been evaluated for cattle and SNP are commercially available even though their predictive accuracy may be low in different breeds. To identify new molecular markers for meat quality, an association study was performed in 15 breeds of cattle using 389 SNP belonging to 206 candidate genes known to be involved in muscle development, metabolism and structure. Fifty-four SNP belonging to 20 different genes were found associated with different growth, carcass and meat quality traits. Some of them were novel associations and other were replications of known associations. Among the former, the gene-network associated with the calpain/calpastatin system was shown to be associated with meat texture, although small effects are found for the examined polymorphisms. Novel associations also included SNP in *AANAT* which was associated with collagen ($P=0.006$), *CAST* with fatty acid muscle composition ($P=0.00003$), *CYP1A1* with juiciness ($P=0.0005$), *DGAT2* with physical traits ($P=0.0009$) and lipid content ($P=0.01$) in muscle, *MADH3* with the myofibrilar fragmentation index (MFI) ($P=0.01$), *NEB* with weight ($P=0.00009$), *PCSK1* with juiciness ($P=0.002$), *PLOD3* with carcass performance ($P=0.0009$) and fatty acids ($P=0.04$), and *PGAM2* and *VIM* with post-mortem maturation ($P=0.00008$ and 0.000005, respectively). These data provide a starting point to investigate the complex gene-networks underlying economically important traits which are of importance to the beef industry for the improvement of production efficiency and meat quality.

1. Introduction

Meat quality traits are very complex, involve many genes and are greatly influenced by a variety of environmental factors. Being difficult and expensive to measure, they are not usually included in selection programs based on phenotypic performance. However, the identification of genetic markers for quality traits could provide the industry with

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the possibility to select for improved quality, while minimising the cost of trait recording. Many studies have identified QTL involved in meat quality related traits in beef cattle (e.g. Casas et al., 2000, 2003); however, the dissection of these QTL has not identified genetic variants explaining a large portion of phenotypic variance (Van Eenennaam et al., 2007). More recently, SNP within candidate genes have been tested for predictive value for carcass traits (e.g. Barendse, 2002; Buchanan et al., 2002; Page et al., 2002), and some commercial tests based on SNP marker panels are being proposed to breeders to genotype animals. However, to date few mutations within specific genes have been associated with the complex traits describing carcass and meat quality in cattle (see the review in Ibeagha-Awemu et al., 2008), and most of these SNP have relatively small effect, which may differ between breeds. It is unlikely that the genomic selection (GS) currently used to estimate breeding values for quantitative traits in dairy cattle (Luan et al., 2009), will be used in beef cattle populations due to small population sizes and lack of high accuracy estimated breeding values (EBV). Therefore, at least in the short term, genomic selection can be improved by extending the panel of SNP in the candidate loci and better estimating SNP effects in different populations.

In the study reported here, 389 SNP identified in 206 candidate genes possibly involved in muscle development, metabolism and structure (described in Williams et al., 2009) were tested for association with meat quality traits in 15 European cattle breeds.

2. Materials and methods

2.1. Animals

A total of 436 unrelated pure bred bulls and 539 parents (either sire, dam or both when available) belonging to 15 breeds were used. The breeds included specialised beef breeds, dairy breeds, and unimproved "local" breeds. The whole sample included 31 bulls and 30 parents Jersey, 27 bulls and 20 parents South Devon, 30 bulls and 26 parents Aberdeen Angus, and 29 bulls and 26 parents Highland from United Kingdom; 29 bulls and 39 parents Holstein, 29 bulls and 37 parents Danish Red Cattle, and 20 bulls and 20 parents Simmental, from Denmark; 30 bulls and 45 parents Asturiana de los Valles, 31 bulls and 42 parents Asturiana de la Montaña, 30 bulls and 44 parents Avileña-Negra Ibérica, and 31 bulls and 50 parents Pirenaica from Spain; 30 bulls and 45 parents Piedmontese, and 28 bulls and 13 parents Marchigiana from Italy; and 31 bulls and 47 parents Limousin, and 30 bulls and 55 parents Charolais from France.

Bulls from beef and local breeds were purchased between 6 and 9 months of age. Bulls of the dairy breeds were purchased as young calves (average 7 days for Jersey or 1–1.5 month for Holstein and Danish Red), and raised until 6 months when they were transferred to the standardised management protocol used for all the breeds. A uniform beef management system representative of those used in the European Union (EU) countries was used for all breeds to homogenise as far as possible influence of management and rearing system on meat quality (Albertí et al., 2008). Efforts were made to standardise as much as possible rearing conditions (identical feeding, rearing in groups of individuals of the same breed, slaughter in same conditions or in the same day whenever possible and at same age, etc.).

Blood sampling and DNA extraction were performed in Williams et al. (2009).

2.2. Feed system

Bulls were fed a total mixed ration containing barley and soy bean with appropriate minerals and vitamins. All ingredients were mixed into a form that prevented selection using molasses up to 3–5% as a binding agent. Metabolisable energy of the ration was 12.5 kJ/kg and straw was available *ad libitum* to provide fibre. Bicarbonate was added to the ration to prevent acidosis. This diet was designed to achieve the slaughter weight of 75% of mature weight for each breed within a window of 13–17 months (Albertí et al., 2008).

2.3. Phenotypes measured

A comprehensive range of carcasses phenotypes were measured which fell into four categories: growth traits, measured on the live animal until slaughter, carcass measurements, both described in Albertí et al. (2008); physical variables; and sensory analysis previously described in Christensen et al. (2011). Phenotypes were used individually in the association tests or were integrated into trait groups e.g. 'Taste Panel' trait group, which included juiciness, flavour, and tenderness. All traits are listed in Table S1.

2.4. SNP in candidate genes

Selection of candidate genes and identification and genotyping of the SNP have been described in Williams et al. (2009). The association analysis was performed using 389 SNP with minor allele frequencies above 10% in the breeds investigated (Williams et al., 2009). These SNP were genotyped across the 436 bulls and their available parents.

2.5. Statistical analysis

Two association strategies were used: a population level analysis based on linear models accounting for the known population substructures, and a transmission–disequilibrium approach using parental information (TDT; Spielman et al., 1993). In the latter case the methodological and operational extensions included in the PBAT software (Lange et al., 2004) were applied.

The first association test was a linear model developed to take advantage of the known information on population structure. Population-based models can detect spurious associations due to population structure when this is unknown. In this study there is a clear partition of the whole sample, formed by the different breeds, and this information was taken into account to avoid false positives. Therefore, the linear model calculated $Y_{i,j}$ as the