

Review paper

# Review on quantitative trait locus (QTLs) for yield and quality of milk, meat, fibre, eggs and their application

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Multiple estimated QTL effects and multiple trait selection could help to make better decisions regarding the use of MAS in animal improvement. Markers have been identified for almost all farm animal species, including milk production in dairy cattle, buffalo, sheep and goats; growth and carcass traits of beef cattle, chicken and goat; fibre and egg quality. QTL affecting milk yield has been identified on 20 of the 29 bovine chromosomes. QTL for milk yield on chromosome 1, 3, 9 and 20 are with evidence of QTL at lower reported frequency on other chromosomes (5, 7, 10, 12, 14, 17, 18, 21, 23, 27 and 29). A number of gene detection projects have resulted in significant QTL for muscle, fat and other carcass traits as well as wool production efficiency is mainly determined by fleece weight and wool quality. Studies have been conducted in poultry that have focused on identifying QTL regulating body weight, carcass characteristics and egg traits; egg production and egg quality traits. Hence, this paper was aimed to review of quantitative trait locus (QTLs) for milk yield/quality, meat quality, fibre quality, eggs quality and their application.

**Keywords:** QTL, milk, meat, fibre, egg, quality.

## INTRODUCTION

Substantial advances have been made over the past decades through the application of molecular genetics in the identification of loci and chromosomal regions that contain loci that affect traits of importance in livestock production (Andersson, 2001, Dekkers, 2004). Since the 1970s, the identification and genotyping of large numbers of genetic markers, the use of this technology to identify genomic regions that control variation in quantitative traits and to show how the resulting quantitative trait loci (QTL) could be used to enhance selection, have raised high expectations for the application of marker-assisted selection (MAS) in livestock (Moniruzzaman *et al.*, 2014), markers linked to QTL have been identified, they can be used in selection programme (Wakchaure *et al.*, 2015). Dehnavi *et al.*, (2017) finding indicated cows in the reference population increased the accuracy of the genomic predictions across all scenarios and decreased bias of them as well, Guernsey breed Jenko *et al.* (2017) showed when only half of population was genotyped, genotyping cows with phenotypes in extremes was superior up to 8-10 folds in accuracy for yield traits than genotyping cows at random or genotyping cows with upper tail phenotypes, according to report of Cécile B., (2019) indicated the MSA model predicts an overall

quality score called MQ4 (for "Meat Quality 4") on a scale of 0 to 100.

Indeed, recently report of methodology for MAS (Hayes *et al.*, 2007, Kwame AD and Lawrence BS, 2012), genomic selection strategies (Thomasen *et al.*, 2013; Buch LH *et al.*, 2012a), use of molecular technologies for the advancement of animal breeding (Spelman *et al.*, 2013), the efficiency of MAS (Lande and Thompson, 1990) and genomic selection (Florian *et al.*, 2013; Roos *et al.*, 2011), QTLs and epistatic effects (Liu *et al.*, 2003), types of selection model (Luo *et al.*, 1997), genome-wide screening for markers (Meuwissen *et al.*, 2007), MAS in dairy breeding (Meuwissen and Van Arendonk, 1992), relationship between MAS and inbreeding (Pedersen *et al.*, 2009). ISAG-FAO recommended microsatellite markers for cattle, buffalo, sheep, goat, horse, donkey, camelid, pig, chicken (FAO, 2011), Predicting the Quality of Meat (Cécile B., 2019).

The potential benefits of using markers linked to genes of interest in breeding programmes, thus moving from phenotype based towards genotype-based selection, have been obvious for many decades (Dekkers, 2004). The advantage of using MAS is that the effect of genes on production that directly measured on the genetic

two selection methods which means traditional or conventional selection methods with molecular genetics methods are beneficial to the selection response. Multiple estimated QTL effects and multiple trait selection could help to make better decisions regarding the use of MAS in animal improvement (Wakchaure *et al.*, 2015).

However, in classical genetic improvement programmes, selection is carried out based on observable phenotypes of the candidates for selection and/or their relatives but without knowing which genes are actually being selected. The development of molecular markers was therefore greeted with great enthusiasm as it was seen as a major breakthrough promising to overcome this key limitation (Dekkers J, 2013). Markers have been identified for almost all farm animal species, including against milk production in dairy cattle (Ansari-Mahyari *et al.*, 2008; Lipkin *et al.*, 2008), buffalo (Sarika *et al.*, 2013), growth and carcass traits of beef cattle (Carr *et al.*, 2006), chicken (Lipkin *et al.*, 2002; Lahav *et al.*, 2006), and goat (Shen *et al.*, 2004). Therefore the objectives of this paper were to review QTLs for milk yield and quality, meat quality, fibre quality, eggs quality and their application.

#### **QTLs for milk yield/ quality and their application**

Adding genotypic and phenotypic information from cows to the reference population has the potential to increase the accuracy and decrease selection bias of genomic estimated breeding values (GEBV) in dairy cattle populations (Mc-Hugh *et al.* 2011; Thomasen *et al.* 2014; Wiggans *et al.* 2010). Milk yield and growth rate in animals or yield are typical examples of quantitative traits (Moniruzzaman *et al.* 2014). Indeed, several milk protein polymorphisms have been considered as potential tools for selection of dairy ruminants (F. Barillet *et al.*, 2004). Daughter design analyses (Mosig *et al.*, 2001; Ron *et al.*, 2004); Most studies have considered the five economic milk production traits: milk, fat and protein production, and fat and protein concentration, although a number of studies have also considered somatic cell score (SCS), female fertility, herd life, calving traits, health traits, temperament and conformation traits. Buch (2011) suggested that breeds other than Holsteins could differentiate themselves by selecting for traits that are closer to the breeding objective (novel traits, such as feed-conversion efficiency may be candidate traits). QTL affecting milk yield (MY) has been identified on 20 of the 29 bovine chromosomes. QTL for MY on chromosome 1, 3, 9 and 20 are with evidence of QTL at lower reported frequency on other chromosomes (5, 7, 10, 12, 14 17, 18, 21, 23, 27 and 29). Weller *et al.* (2002) estimated the frequency of the QTL allele that increases fat and protein concentration on BTA6. Regions with putative QTL affecting milk production or composition are located on BTA 3, 6, 7, 14, 19, 20 and 26; segments

phenotype (Wakchaure *et al.*, 2015). The integration of

affecting mastitis resistance are located on BTA 10, 15 and 21; and chromosomal segments affecting fertility are located on BTA 1, 7 and 21. Each region was found to affect one to four traits and on average three regions with segregating QTL was found for each trait. Whereas eleven chromosomes (BTA 2, 3, 4, 6, 7, 9, 12, 13, 26, 28, and 29) showed 2 QTLs, and the remaining ten chromosomes (BTA 5, 10, 11, 15, 17, 19, 20, 21, 23 and 24) showed only 1 QTL (Alessandro B., 2010).

The main limitation at this point to detecting and mapping more QTL is the sample sizes available, especially the number of progeny tested bulls per family. Of the two QTNs that have been detected, each has disadvantages with respect to application in MAS. The allele of DGAT1 that increases fat production and decreases water content in the milk, both desirable, also decreases protein yield, which is undesirable (Weller *et al.*, 2003). The allele of ABCG2 that decreases milk production and increases protein percent is clearly the favorable allele in nearly all current selection indices, but this allele is already at a very high frequency in all major dairy cattle populations (Ron *et al.*, 2006).

According to ALESSANDRO N., (2017) showed Genetic variants of milk proteins have been widely studied for their relationships with technological properties of cattle (k-casein-BB and  $\beta$ -casein-BB genotypes are deemed to determine shorter curd firming time, sheep and goat (k-CN-BB and  $\alpha$ s1-CN-AA have positive effects on cheese yield and cheese making properties. According to Guernsey breed Jenko *et al.* (2017) showed also genotyping cows with phenotypes in extremes was superior up to 8-10 folds in accuracy for yield traits. According to Dehnavi *et al.*, (2017) study that sampling cows from the most accurate EBVs on extremes seemed to be more informative on all SNPs, both favorite and unfavorite alleles in the population.

#### **QTLs for meat quality and their application**

The control of meat quality, especially sensory traits, remains an important issue for any farm animal production (Cécile B., 2019). Performance recording for meat traits is well advanced, with not only weight traits measured, but also traits related to carcass quality such as body fat and muscle. Similarly growth and carcass traits of beef cattle were reported by the other researchers (Carr *et al.*, 2006). Most breeding programs for meat sheep focus on weight traits, and ultrasound scanning is commonly used for fat and muscle traits. Reproduction traits are recorded as numbers of lambs born and weaned ([www.journalofanimalscience.org](http://www.journalofanimalscience.org)). In cattle, the search for plasma biomarkers of the sensory qualities of meat was initiated by proteomic analysis (Cécile B., 2019). In addition, bioinformatics tools have identified secreted proteins that could be good potential candidates for quantification in plasma

**Table 1:** Examples of gene tests used in commercial breeding for different species (D = dairy cattle, B = beef cattle, C = poultry, P = pigs, S = sheep) by trait category and type of marker

Trait category	Direct marker	Linkage disequilibrium marker	Linkage equilibrium markers
<b>Milk quality</b>	$\kappa$ -Casein(Do), $\beta$ -lactoglobulin (Do), FMO3 (Dp)		
<b>Meat quality</b>	RYR (Pg), RN/PRKAG3 (Pq)	RYR (Ph), RN/PRKAG3 (Pr), A-FABP/FABP4 (Ps), H-FABP/FABP3 (Pt), Carwell (Srr), PRL (Dtt)	
<b>Milk yield and composition</b>	DGAT (Dss), GRH (Dvv), $\kappa$ -Casein (Do)		QTL (Bpp), QTL (Duu)

Dekkers J., 2004

applicable to other beef quality criteria (Cécile B, 2019). A number of gene detection projects have resulted in significant QTL for muscle, fat and other carcass traits, but not all of these have been published, confirmed or fine mapped. A number of studies have reported on QTL for meat traits in sheep (Broad *et al.*, 2000; Walling *et al.*, 2004; Johnson *et al.*, 2005; McRae *et al.*, 2005) and there are probably some unpublished QTL being further developed. Some of these sheep QTL are based on related cattle genes, e.g. the myostatin gene for double muscling (Grobet *et al.*, 1997) and the thyroglobulin gene affecting intramuscular fat (Barendse *et al.*, 2004).

A QTL for marbling as an indicator of the amount of intramuscular fat was identified by Casas *et al.* (1998) on bovine chromosome 2 as earlier. Also the QTL effects were initially attributed to myostatin as a candidate gene in the region. Fat associated QTL have been detected on chromosome 3 in three independent studies (Casas *et al.*, 2004; Stone *et al.*, 1999; Casas *et al.*, 2003) and on chromosome 27 in two separate studies (Casas *et al.*, 2000; Casas *et al.*, 2003). A QTL that is of particular interest was identified on pig chromosome 7 in a cross between the lean Large White and the fat Meishan pig breeds. This QTL had a particularly large effect, explaining about 30% of the difference in back fat thickness between the two breeds (de Koning *et al.*, 1999).

According to the Cécile B., (2019) a numerous technological innovations based on genomics or modeling approaches, or spectral or physical methods, have been described to predict the specific intrinsic qualities of meat such as sensory (tenderness, flavor), technological (defects related to tissue integrity, ultimate pH, processing yield), or nutritional (lipid content, fatty acid composition) traits.

### QTLs for fibre quality and their application

Wool production efficiency is mainly determined by fleece weight and wool quality. Wool quality traits are mainly fibre diameter and staple strength, and these are economically much more important for fine wools.

There is clear evidence of a strong association between the developmental activities that occur during follicle initiation in the foetus and the fibre and fleece quality attributes that subsequently grow in the animal over its life time (I.W. Purvis, I.R. Franklin, 2004). Staple strength is more expensive to measure, but has a high correlation with the coefficient of variation of fibre diameter, which is therefore a good predictor. Wool traits have generally high levels of heritability, especially fleece weight and fibre diameter. Crawford (2001) has characterized the features of nine flocks that have been set up to map chromosome regions.

According to Purvis and Franklin (2005) review a QTL for wool production traits and wool quality, wool traits can be measured easily and have high heritability.

These authors suggested that research into certain wool production genes was still justified, for example, to break antagonistic correlations (between fleece weight and fibre diameter) or to target specific wool quality traits important for the processing of the product. However, the number of detected and confirmed QTL is low for sheep and goats and gene mapping is less advanced than in other livestock species. From an industry context perhaps the most important gene influencing fibre characteristics is the "N-type" gene, which has been re-named the "halo-hair 1" (HH1) gene according to the COGNOSAG nomenclature (Lauvergne J, 1996., I.W. Purvis, I.R. Franklin, 2004).

### QTLs for Egg yield and quality and their application

A number of QTL studies have been conducted in poultry that have focused on identifying QTL regulating body weight (Tatsuda *et al.* 2000; Tatsuda&Fujinaka 2001; Sewalem *et al.* 2002; Sasaki *et al.* 2004; Siwek *et al.* 2004), carcass characteristics (de Koning *et al.* 2003; Jennen *et al.* 2004); and egg traits (Schutz *et al.* 2002; Tuiskula-Haavisto *et al.* 2002); egg production and egg quality traits (Tuiskula-Haavisto *et al.* 2002; Wardecka *et al.* 2002; Kerje *et al.* 2003; Sasaki *et al.* 2004). Muir (2003) identified two cases where MAS could increase the selection intensity in poultry breeding: (i) traits that are measured later in life or are

full-sib families for sex-limited traits (e.g. male chicks for egg production).

According to M. A. Schreiweis *et al.*, (2005) a QTL regions influenced traits relating to egg size (chromosome 6), egg production (chromosome 7), body weight (chromosomes 8 and 13), and egg shell weight (chromosome 19). Tuiskula-Haavisto *et al.*, (2002) reported two divergent egg-layer lines differing in egg quality were reciprocally crossed to produce 305  $F_2$  hens and also show by searching the genome using models with uni-parental expression, they identified four new genome-wide significant QTL and three highly suggestive QTL affecting age at first egg, egg weight, number of eggs, body weight, feed intake, and egg white quality. Sasaki *et al.* (2004) reported QTL affecting egg quality traits (egg shell strength, shell colour, shape of egg); however, egg white quality was not included. Report indicates detected QTL regions affecting egg white thinning on chromosomes 2, 4 and 8. The QTL region on chromosome 2 harbouring genome-wide significant QTL effects on both egg white thinning and egg weight was chosen for further study. There are at least two QTL regions affecting egg white quality and/or egg weight on chicken chromosome 2.

In conclusion, several QTL regions affecting egg quality traits were successfully detected. Some of the QTL findings, such as albumen quality, remained at the level of wide chromosomal regions. For some QTL, a putative causative gene was indicated: miRNA gga-mir-1556 and/or its host gene ZO-2 might have a role in susceptibility to blood and meat spot defects across populations. Nonetheless, fishy taint in chicken eggs was found to be caused with a substitution within a conserved motif of the FMO3 gene. This variation has been used in a breeding program to eliminate fishy-taint defects from commercial egg layer lines (Honkatukia, M., 2010).

## CONCLUSION

MAS/GAS can potentially increase annual genetic gain by increasing the accuracy of evaluation, increasing the selection intensity and decreasing the generation interval. QTL mapping work is under way, focusing on production and functional traits. Adding genotypic and phenotypic information from livestock to the reference population has the potential to increase the accuracy and decrease selection bias of genomic estimated breeding values (GEBV) in dairy cattle populations.

Milk yields and quality identification in QTL have been considered as potential tools for selection of dairy ruminants. A number of gene detection projects have resulted in significant QTL for muscle, fat and other carcass traits. Wool production efficiency is mainly determined by fleece weight and wool quality. A number of QTL studies have been conducted in poultry that

have focused on identifying QTL regulating body weight, carcass characteristics and egg traits; egg production and egg quality traits.

The main limitation at this point to detecting and mapping more QTL is the sample sizes available, especially the number of progeny tested bulls per family. Complete phenotypic and pedigree information is often only available in intensive breeding units. However, in the developing country have low input production systems, some questions can be raised concerning the validity and practicality of the simulation studies MAS/GAS, and it would be more difficult to realize the value of marker information.

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