

Application of genomic approaches in egg quality research

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Poor egg quality causes economic losses at all production stages. The two economically most important hereditary quality characteristics are the strength and integrity of the eggshell and the quality of the egg white. Broken eggshells are the cause of approximately 10 % of production losses and also provide a route for pathogen contamination. Yolk and albumen quality are important for processed egg products. Thinning of the egg white indicates quality loss and exposes the egg to microbial infections due to altered structure and composition. Other important quality factors for the consumers, such as olfactory characteristics or shell colour, also have genetic components. Improving the quality traits by traditional selection has been difficult, as the phenotypic measurements are difficult or time-consuming and in some cases unfavourable genetic correlations exist with other important production traits. Direct selection based on genetic markers might greatly enhance the breeding of egg quality traits.

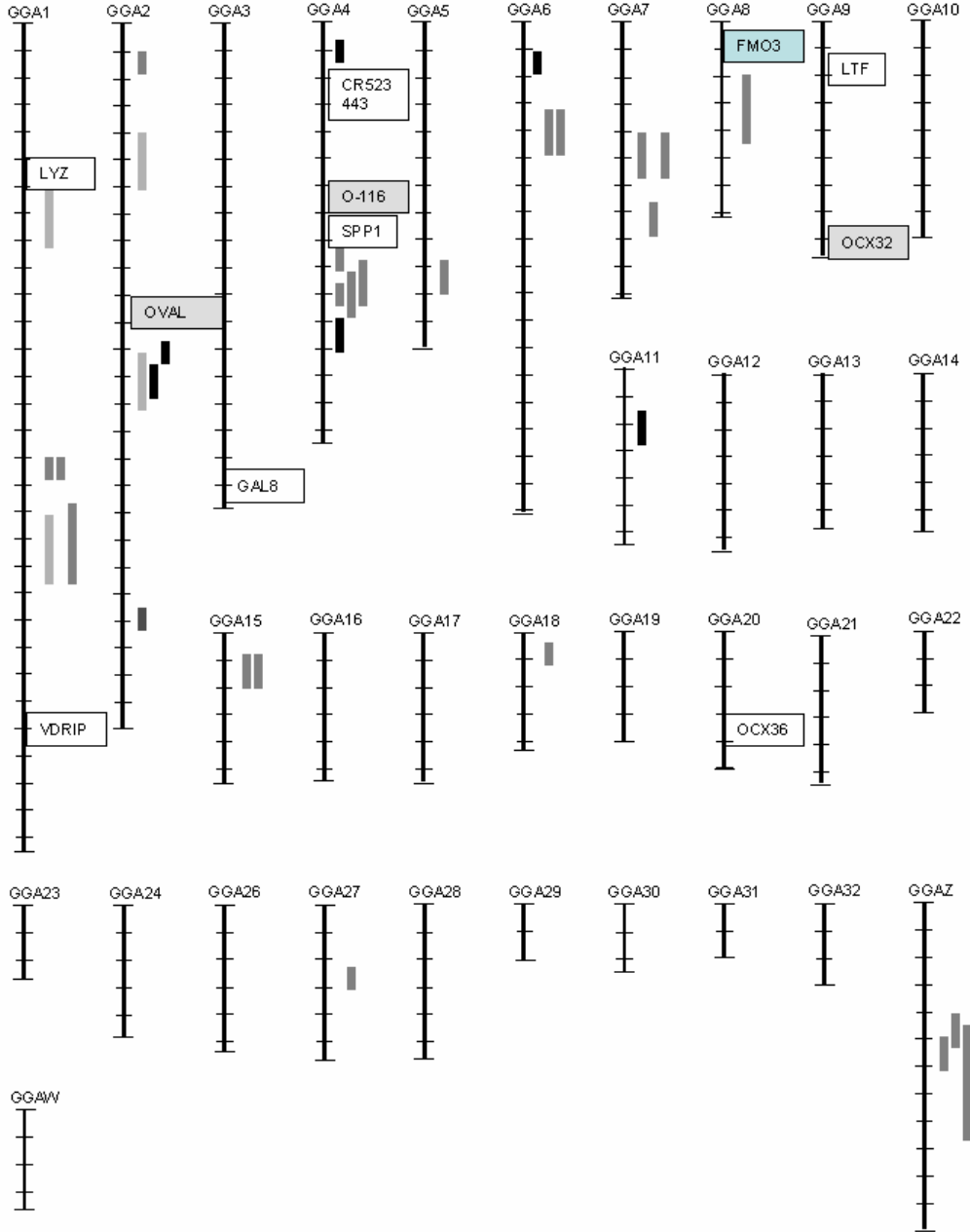
Recent advances in the availability of genomic information have made the dissection of the hereditary variation behind these traits possible. The first genome scans to identify loci affecting egg quality traits have been based on the availability of medium-density microsatellite maps. Quantitative trait loci (QTL) have been reported for various eggshell characteristics and for putatively correlated bone traits, such as bone density and mineral content. Less emphasis has been put on egg white quality, olfactory characteristics, or eggshell colour. At some of the locations, similar QTL are supported by several studies. However, their locations have not yet been refined with an accuracy useful for marker-assisted selection (MAS).

The quantitative trait loci identified and the experimental designs used in the chicken have been recently reviewed by Abasht et al (2006). All significant QTL have been collected in the Chicken Quantitative Trait Loci database (<http://www.animalgenome.org/QTLdb/chicken.html>). The database also includes tools to link the QTL data to other types of genomic information, such as radiation hybrid (RH) maps, finger printed contig (FPC) physical maps, linkage maps, comparative maps to the human genome and SNP information aligned against the chicken genome (Hu et al. 2007). These new tools will greatly facilitate further characterization of the QTL regions. The majority of the 698 chicken QTL in the database are affecting growth or carcass traits, and only 113 are reported for egg quality traits. Based on the information it is clear that there are several interesting chromosome regions with potential genetic variation for egg quality traits. The approximate locations of egg quality QTL (as presented in the database) and the locations of some putative positional or functional candidate genes are shown in Figure 1. The most interesting findings will be reviewed consequently by trait.

As a next step, the QTL regions need to be fine-mapped to identify tightly associated marker loci for MAS or positional candidate genes that could be searched for relevant sequence variation. Until now, only few fine-mapping studies have provided suitable markers for selection or information of genes underlying the quantitative variation. Not more than one gene mutation causing a quality defect is presently known (fishy taint in brown egg layers, Honkatukia et al. 2005). Before the results of the fine-mapping can be used for selection, it is necessary to estimate the pleiotropic effects of the QTL on other economically important traits. In addition, one should be aware of the possibility of epistatic effects between loci, i.e.

the different outcome of allelic effects with different genetic backgrounds. Including epistatic effects in QTL analyses may also help in uncovering novel QTL and their interactions.

Figure 1. Chicken egg quality QTL on different chromosomes. The QTL confidence intervals are presented as bars with different colour schemes for different traits. Light grey indicates egg white traits, dark grey eggshell and bone mineral traits, and black bars indicate eggshell colour. The linkage groups and QTL positions are as presented in the Chicken QTL database. Some positional or functional candidate genes have been added as boxes beside the linkage groups.



Eggshell quality

Regions affecting eggshell quality have been found on chromosomes 1, 2, 4, 5, 7 and Z (Sasaki et al. 2004, Schreiweis et al. 2006, Tuiskula-Haavisto et al. 2002, Wardecka et al. 2002). In addition, several QTL affecting bone strength, mineral density and mineral content are possibly related with the process of recruitment of calcium reserves for eggshell formation (see e.g. Dunn et al. 2007). The mapping populations as well as phenotypic measurements (eggshell thickness, eggshell strength, eggshell weight, eggshell percentage, egg shape, specific gravity and different bone measures) have varied among studies and it is not therefore clear which of the findings may reflect the action of same loci. No fine-mapping studies have been reported for these traits yet. However, some functional candidate genes have been tested for association with bone and eggshell quality (Bennett et al. 2006, I. Dunn, personal communication). Significant associations have been found between vitamin D receptor polymorphism and bone mineral content of the humerus (Bennett et al. 2006); as well as ovalbumin, ovocleidin-116 and ovocalyxin-32 with quasi-static compression measurements and mammillary layer thickness (I. Dunn, personal communication). 12 positional candidates for a QTL affecting eggshell thickness on chromosome 4 (ST53, Wardecka et al. 2002) have been tested for differences in expression, and some evidence has been found for a correlation in the Green-legged Partridge breed between cDNA CR523443 expression and egg shell thickness (Sazanov et al. 2007).

Egg white quality

Egg white quality QTL (Haugh units) have been mapped to chromosomes 1 and 2 (Hansen et al. 2005, Tuiskula-Haavisto et al. 2002). The attempt to fine-map the major QTL affecting HU in the White Leghorn X Rhode Island Red mapping population (explaining 7% of the phenotypic variation) (Tuiskula-Haavisto et al. 2002) resulted in the splitting of the QTL region to two distinct QTL regions and excluding one potential candidate gene, vimentin, within the original QTL region (Honkatukia et al. 2005).

Olfactory characteristics

Honkatukia et al. (2005) have shown that fishy odour in brown eggs is caused by a missense mutation in the chicken FMO3 gene, located on chromosome 8. The mutation is associated with elevated trimethylamine (TMA) levels (after feed containing TMA precursors) in several brown egg layer lines. The mutation causes an amino acid substitution in an evolutionary highly conserved motif of the mono-oxidase enzyme, leading to improper oxidation of the odorous TMA. A QTL for egg "after taste" has also been mapped to a distinct location in the middle of chromosome 8 and a QTL for egg odour to the linkage group E22C19W28 (Wright et al. 2006).

No transcriptomic analyses related to egg quality traits have been yet published. Within the SABRE project (FOOD-CT-2006-016250; Cutting edge genomics for sustainable animal breeding), WP5 Product Safety, aims at fine-mapping of QTL affecting egg shell quality, genome-wide association of candidate gene SNPs and transcriptomic profiling of genes and gene pathways involved in shell formation. Proteomics provides an alternative approach for identifying important genes related to egg quality traits. The first proteomic analysis of the acid-soluble organic matrix of the calcified eggshell layer identified over 500 proteins in the matrix (Mann et al. 2006). The classification of these proteins according to their function and their analysis will give some insights into the genes responsible for the important characteristics of the eggshell.

MAS by using linked markers is not necessarily directly applicable across lines as the linkage phase between QTL alleles and marker alleles may vary among populations. Gene assisted selection (GAS), based on the identified causative mutations can be used directly in breeding programmes to increase the frequency of favourable alleles or to eliminate unfavourable

ones. The first example of GAS used for improving egg quality is the use of FMO3 markers by Lohmann Tierzucht GmbH for eliminating fishy egg taint from brown layer lines.

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