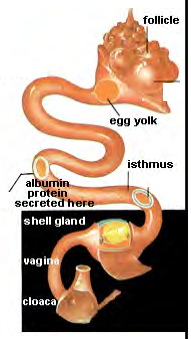
Application of genomic approaches in egg quality research

Johanna Vilkki

Biotechnology and Food Research
MTT Agrifood Research Finland

Application of genomic approaches in egg quality research – outline

1. Egg quality
2. Chicken genomic resources
3. Gene mapping
   - eggshell quality
   - egg white quality
   - olfactory characteristics
4. Candidate genes
5. Marker assisted selection
6. Future possibilities



Egg quality

Egg shell strength:

- poor quality -> cracked or broken eggs -> a route for pathogen contamination
- losses may be up to 10 % of total production
- measured by breaking strength (quasi-static compression) or resonance (dynamic stiffness)
- indirectly by e.g. specific gravity, egg shell thickness and weight

Egg quality

Egg white thinning:

- causes problems in processing, consumer sense perception
- evaluated as the height of the egg white relative to egg weight (Haugh-value, HU)

Egg quality

Other hereditary characteristics

- off-flavours in the freshly laid egg, fishy taint
- shell colour
- blood and meat spots

Chicken genomic tools

- linkage maps -> consensus linkage map (2000) www.thearkdb.org -> RH panel (2002) –> BAC contig maps
- first livestock genome to be sequenced (2004) www.ensembl.org
- SNP map with > 2.8 million single nucleotide polymorphisms
- various cDNA arrays for expression analyses available

Presented at: XVIII European Symposium on the Quality of Poultry Meat and XII European Symposium on the Quality of Eggs and Egg products, September 2 - 5, 2007, Prague, Czech Republic.

Chicken genomic tools

- transcriptional analyses underway (EU FP6: www.sabre-eu.eu and www.rescape-project.eu)
-> to identify differentially expressed genes in the relevant tissues
e.g. 230 genes overexpressed in the shell gland may be involved in biomineralisation process (Gautron)

- proteomic analyses conducted
-> identify the proteins present in the tissues
e.g. >500 proteins identified in the eggshell (Mann et al. 2006)

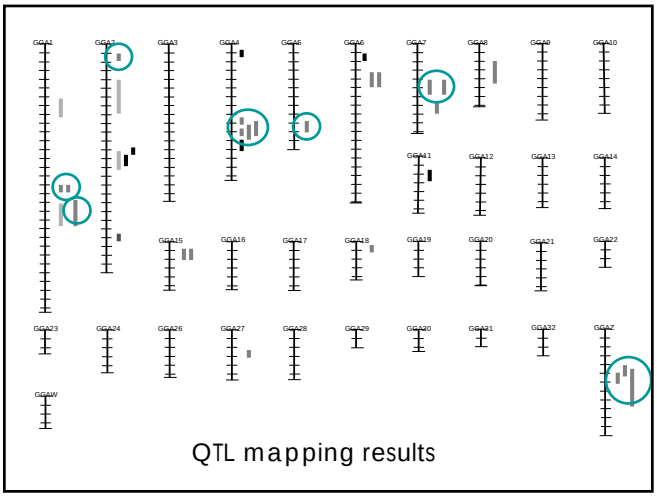
Chicken genome scans

- first genome scans based on medium-density linkage maps (microsatellites)

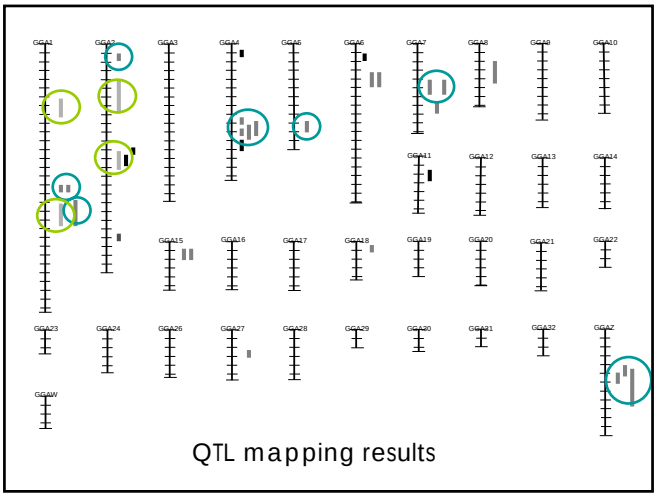
- significant QTL findings can be found in the Chicken Quantitative Trait Loci database http://www.animalgenome.org/QTLdb/chicken.html

- includes tools to link the QTL information to genomic tools (RH maps, FPC maps, linkage maps and SNP information)

- 113 QTL reported for egg quality traits



QTL mapping results



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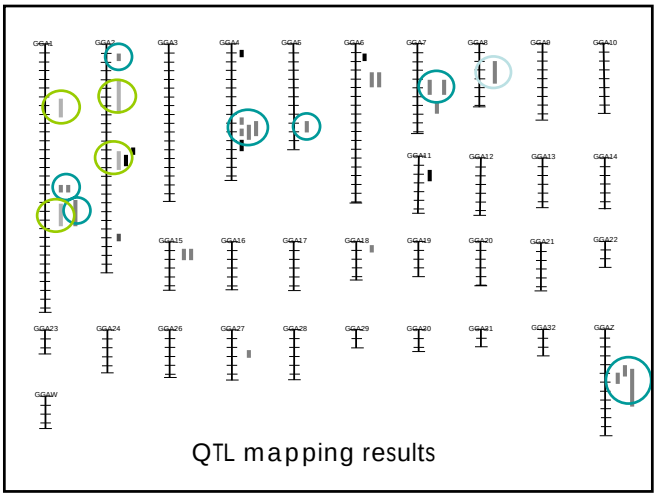

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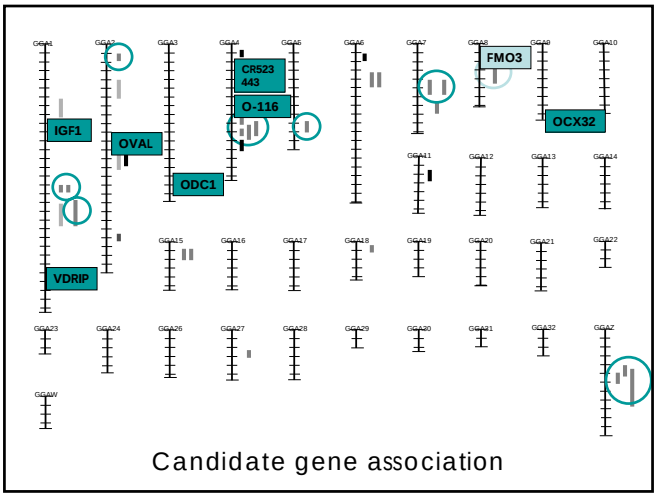

Candidate gene association

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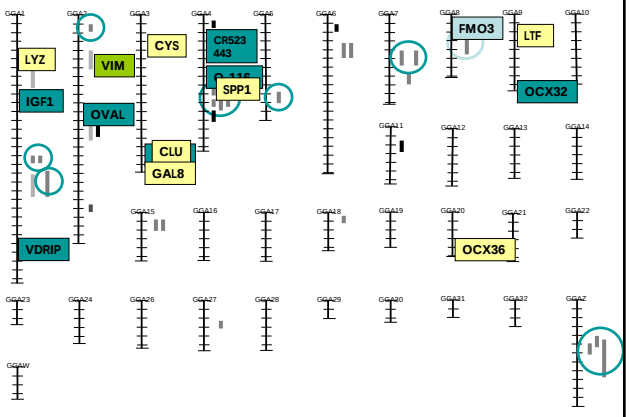
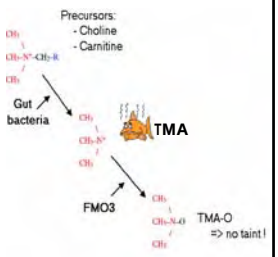


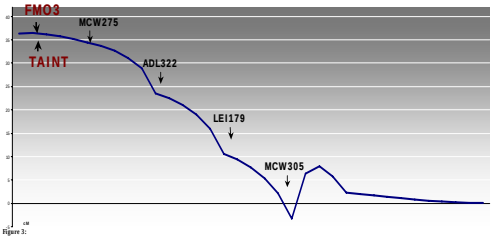
Candidate genes, proteomics

Single gene defect: Fishy taint in eggs

- fishy taint of fresh eggs revealed when rapeseed was added to the feed
- cause: elevated level of TMA in egg yolk
- selection by olfactory testing after feeding challenge with TMA or its precursors
- hypothesis: fishy taint in chicken may be caused by a defective *FMO3* gene

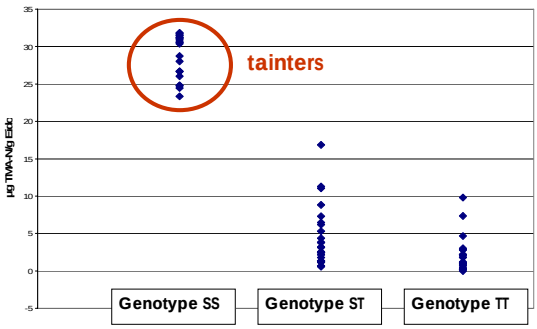


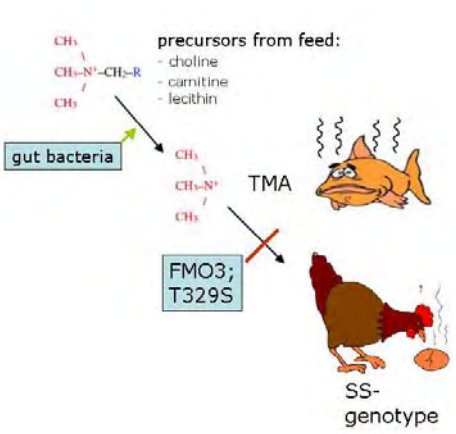
- Both *FMO3* gene and egg taint were found linked to chicken chromosome 8



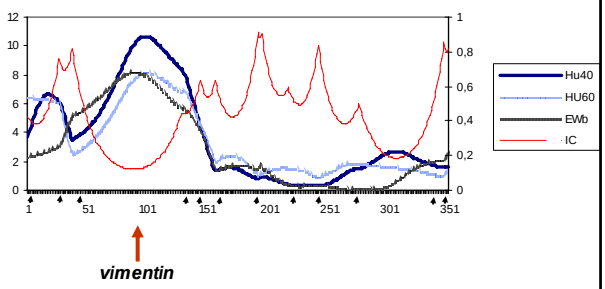
- Sequencing of the chicken FMO3 exons -> 17 SNPs, one aa substitution (T 329S)

TMA content in egg yolk is associated with FMO3 T329S genotype





QTL mapping: HU on GGA2



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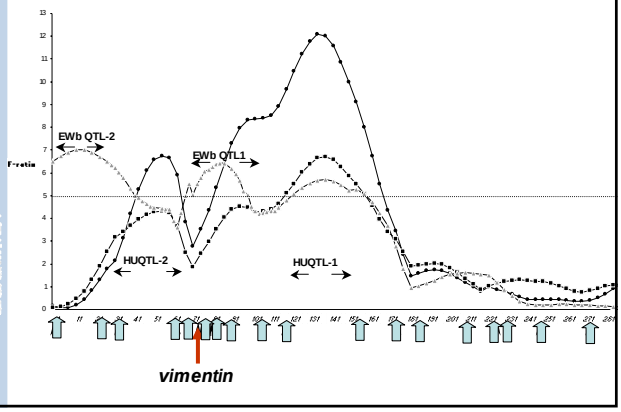
Fine-mapping: HU on GGA2



Marker-assisted selection (MAS)

To eliminate genetic defects

To increase selection intensity

- traits that are measured late in life or are difficult to measure
- selection within full-sib families for sex-limited traits

-> egg quality !

Marker-assisted selection (MAS)

Four levels

- GAS: known functional mutation
- LD-MAS: population-wide association
- LE-MAS: within-family associations
- GWS: genome-wide estimation of effects

- GAS and LD-MAS can be implemented in current evaluations
- LE-MAS and GWS require large-scale genotyping and specific statistics development

Marker assisted selection against taint

- Earlier selection method: identification of affected hens by organoleptical testing after challenge feeding
- FMO3 gene test from feathers allows direct detection of affected hens AND heterozygous carriers irrespective of age or sex

Marker assisted selection against taint

Commercial utilization by Lohmann Tierzucht GmbH

- lower frequency in brown female lines
- no association with production traits
- elimination of the mutation in female lines
- taint-free parent stock lines on the market in 2006
- advantages: use of local protein sources, no need for different feeds for brown and white stock

Future possibilities

To understand the biology of eqq quality:

- analysis of epistatic QTL -> knowledge of the effects of alleles in different genetic backgrounds

- combining the information from QTL mapping, transcriptomics and proteomics

To improve selection efficiency:

- to identify candidate gene markers associated with egg quality to be included in evaluation

- high-density marker sets for genome-wide breeding values (eEBV)

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Conclusions

- excellent genomic tools for chicken
- marker assisted selection possible for identified single gene trait(s)
- QTL affecting egg quality traits have been identified; but the regions remain large and do not well overlap with the few candidate gene associations found
- combining new QTL information with proteomics and transcriptomics is required to elucidate the major genetic variation affecting egg quality

Conclusions

- QTL affecting egg quality traits have been mapped both by linkage mapping and candidate gene association analyses
- the locations do not really overlap (or with locations for major known proteins) -> no effects confirmed
- future fine-mapping and transcriptomic analyses are both needed to elucidate the genetic background of egg quality

Thank you for your attention!