




## QTL for eggshell quality



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## Eggshell quality

- 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



## 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, only a handful for eggshell quality

## WP7, aims for QTL analysis

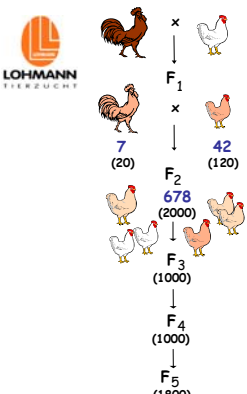
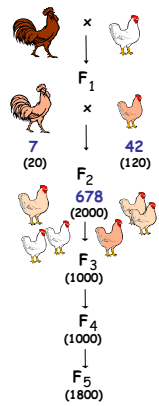
To understand the genetics of eqq quality:

- conduct comprehensive genome scan
- analysis of epistatic QTL -> knowledge of the effects of alleles in different genetic backgrounds
- combining the information from QTL mapping, transcriptomics and proteomics to identify candidate genes

To improve selection efficiency:

- fine-mapping to identify markers associated with eggshell quality to be included in evaluation

## Task 7.1: Fine mapping of QTL in a resource population

**Reciprocal line cross**  
 - RIR, White Rock

**Phenotypes**  
 - scored for 6000 animals

**Genome scan**  
 - 162 microsatellites, 27 chromosomes  
 - single chromosomes by QTLEXPRESS -> GridQTL (WP1): different models with different covariates & analysis of epistatic effects

## Phenotypes

	at age (weeks)
deformation (mm)	35, 40, 50, 70
breaking strength (kp)	35, 40, 50, 70
shell weight (g)	42
egg weight (g)	25, 30
body weight (g)	30
yolk weight	42
feed intake	35-45
feed conversion	35-45
Haugh unit	40
shell colour	40
egg production (%lay)	28-52

### Statistical approach

Single chromosomes with QTLEXPRESS + custom linear regression for additive effects on the Z chromosome

GridQTL (WP1):

- search models incl. fixed sire effects and biologically correlated traits as covariates

- nested search algorithm for epistasis:

1) Model (Q1+Q2+Q1Q2) to search for best pair with minimum residual sum squares

2) Residual sum squares of model (Q1+Q2) with QTL positions from 1) -> derive F

### Results

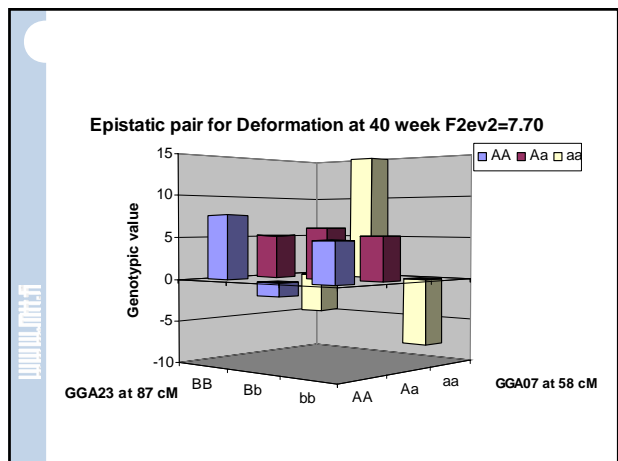
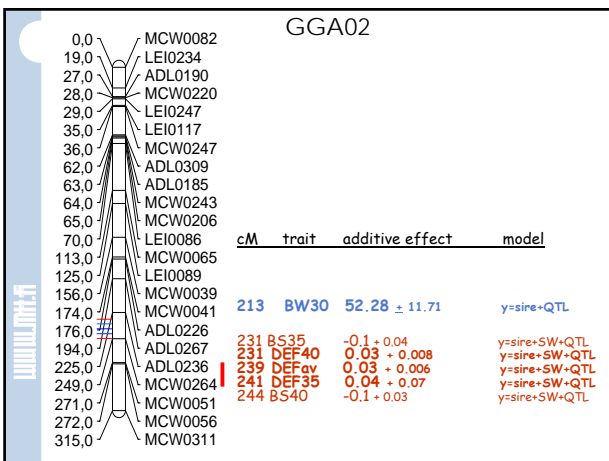
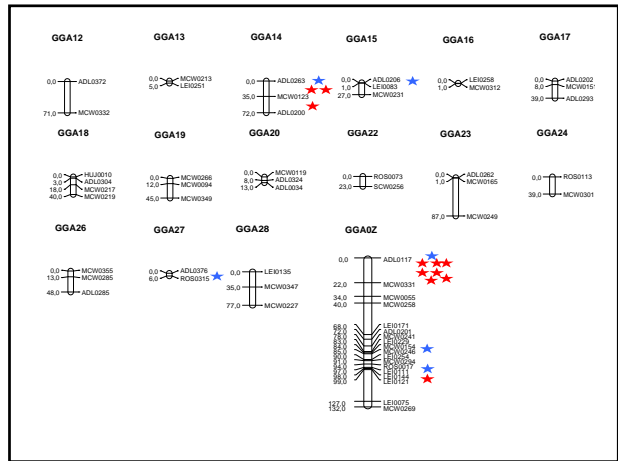
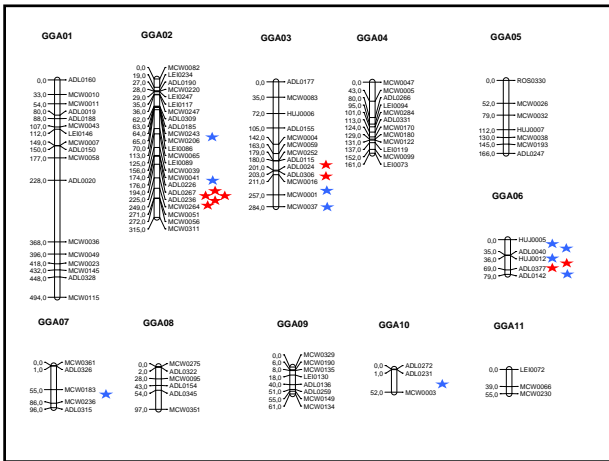
• Significant QTL findings for:

- eggshell quality ★

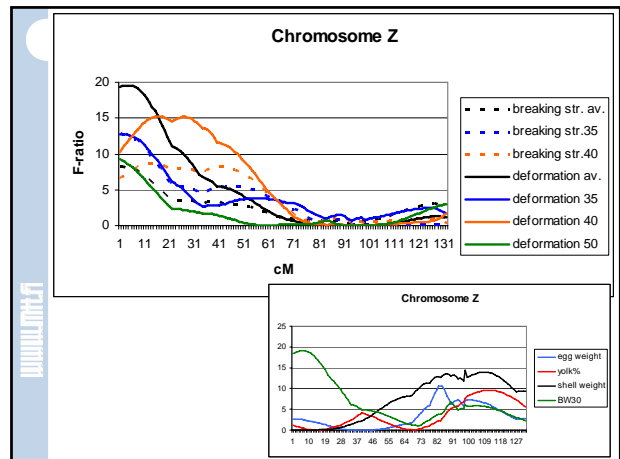
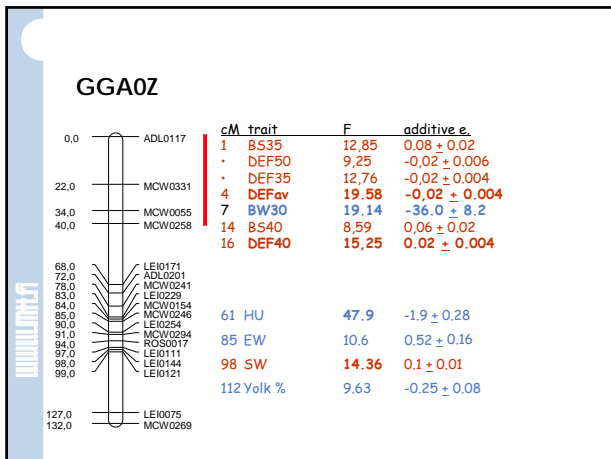
- other traits ★

• QTLs explain 2-5 % of the phenotypic variance

• Only a few epistatic effects identified



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- transcriptional analyses within SABRE WP7 are and will be done to identify differentially expressed genes in the relevant tissues; e.g. genes expressed in the shell gland may be involved in the biomineralisation process (Gautron)
- proteomic analyses have revealed >500 proteins in the shell calcified layer (Mann et al. 2006, 2007)

- from 230 genes specifically expressed in the shell gland (Gautron, INRA) 28 localise within the QTL regions (marker intervals) in the genome
- e.g. in chromosome 14: the homologue with mouse dentin matrix protein
- next analyses (INRA) will reveal differences in gene expression between shell glands with and without eggs (egg shell formation)

**Future work**

- fine mapping of QTL on the full F2 population (2000 individuals) in the QTL areas (chromosomes 2, 6, 3, 14, Z) – validated SNPs available via WP3
- testing of putative marker effects in the commercial population

**Collaboration**

MTT Agrifood Research Finland: Mervi Honkatukia, Maria Tuiskula-Haavisto, Jonna Tabell, Johanna Viikki

Lohmann Tierzucht GmbH, Germany: Ruedi Preisinger, Matthias Schmutz

Roslin Institute, Scotland: Dirk-Jan de Koning, Ian Dunn, Wenhua Wei

INRA, France: Joel Gautron