

QTL for egg shell quality

Maria Tuiskula-Haavisto¹, Mervi Honkatukia¹, Wenhua Wei², Ian Dunn³,
Rudolf Preisinger⁴, Johanna Vilkki¹

1 Animal Genomics, Biotechnology and Food Research, MTT Agrifood Research Finland, 31600 Jokioinen, Finland

2 Human Genetics Unit, Medical Research Council, Western General Hospital, Crewe Road, Edinburg EH4 2XU, Scotland UK

3 The Roslin Institute and Royal (Dick) School of Veterinary Studies, Roslin Midlothian EH25 9PS Scotland UK

4 Lohmann Tierzucht GmbH, P.O.Box 460 D- 27454 Cuxhaven

Summary

The overall objective of SABRE (Cutting Edge Genomics for Sustainable animal Breeding) Work Package 7, "Product Safety", is to develop genomic tools to improve egg shell quality by selection to enhance resistance to structural failure and bacterial penetration. One aim is to scan the chicken genome for egg shell quality QTL. The mapping population consisted of 668 hens from a F2 population. A scan of 27 autosomes and the Z chromosomes has been analyzed using 162 microsatellite markers. Autosomal chromosomes were analyzed with QTL Express and the epistatic effects using a new module for GridQTL. In all, 23 QTL affecting eggshell quality were found on the autosomes. Each QTL explains 2-5 % of the phenotypic variance of the trait. Genome wide QTL were found on chromosome 2, 6 and 14 and suggestive QTL on chromosome 3. On the Z chromosome, a cluster of 5 QTL affecting both eggshell breaking strength and deformation was found within one marker interval. One genome-wide epistatic pair was detected for egg quality traits. For fine mapping with additional 17 microsatellites and 348 SNP markers were selected from chromosome 14 and Z. For fine mapping all 1800 F2 animals are going to be analyzed.