

SABRE Placement Report for visit to Roslin Institute

My two visits to The Roslin Institute, University of Edinburgh were funded by a SABRE integrating award. I worked at the Roslin Institute in the Genetics and Genomics division led by Dr. DJ de Koning.

The aim of my first visit (1.11.2009-12.11.2009) was to analyse the chicken fine mapping data from a F₂ cross for egg shell quality traits in WP7 (Product Safety) of the SABRE project.

The data originates from a chicken inter cross between two different chicken lines. For the whole genome scan we have used an F₂ population of 668 females to map quantitative trait loci (QTL) affecting egg shell traits (egg shell deformation, egg shell breaking force, egg shell weight). By using 160 microsatellite markers on 27 chromosomes we found 12 genome-wide and 13 suggestive QTL for the shell traits measured at different times during production. From these results the best 5 areas with several QTL affecting egg shell quality traits in different chromosomes were chosen for fine mapping with SNP markers in the whole F₂ population 1599 female chickens. On chromosome 2 the area was between markers ADL236 – MCW0056, included 289 SNP markers from which 128 were informative. On chromosome 3 the area was between ADL0024 – MCW0016, 10 cM, with 69 SNP markers, chromosome 6 between HUI0012-ADL0142 with 85 SNP markers, chromosome 14 with 151 SNP markers and the area between ADL117-MCW0258 on sex chromosome Z with 212 SNP markers were analysed with IlluminaBeadXpress reader. Chromosomes 2, 3, 6 were analysed at the Roslin Institute and chromosome 14 and Z in MTT Jokioinen.

During my first visit to the Roslin Institute I analysed the SNP and microsatellite data with the GridQTL program with kind assistance from Dr Ian Dunn. I learned a lot about calculating and necessity of making maps for the SNP markers. The fine mapping results with SNP markers together with microsatellites for the bigger population shows that part of the results from earlier findings are still significant.

During my second visit (14.2.2010-20.2.2010) I started to analyze the association between the SNP markers and the egg shell quality traits for all significant traits found in the previous analyses. I started my work with exporting the data from resSpecies database. The second step was learning GenABEL: an R package for Genome Wide Association Analysis. In this program each SNP undergoes several types of analysis: characterization of frequency distribution, testing of Hardy-Weinberg equilibrium, analysis of association between single SNPs and haplotypes for different traits. The best SNP markers from these analyses are going to be tested in commercial breeding lines. The association program “sliding 5-window genotype model” from Dave Waddington was also used. I am very grateful to Dr Ian Dunn, Dr Dirk-Jan de Koning and Dr Dave Waddington for introducing me to the methodology of association study.

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