Mapping and fine mapping of genes controlling differences in maternal behaviour

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Finding the genes that underlie variation in production and developmental traits has important economic applications. Incubation behaviour, also known as broodiness, results in lost production and can be a major problem in some breeds of chicken. Its expression is the consequence of sequential interaction of oestrogen, progesterone and prolactin acting centrally in the brain and peripherally(Sharp 2009). There are differences in the proclivity for maternal behaviour between chicken strains which is linked to their productivity (Vleck 2002). To study the genetics of the trait 280 F2 hens from 19 F1 families were created by crossing White leghorn (WL, 0 % incidence of incubation behaviour) and Silkie chickens (SLK, 100 % incidence of incubation behaviour). Broody phenotypes were recorded from hens placed in pens with nest boxes and were recorded each day for broodiness onset. Blood samples were collected for DNA genotyping. Phenotypes were regressed against 90 informative microsatellite markers genotypes in 23 autosomal linkage groups and the sex chromosome using the Grid QTL implementation of the Haley and Knott QTL mapping method(Haley and Knott 1992). Test statistics for broodiness showed that out of 276 birds studied for broodiness, 45% of birds showed full broodiness, 28% birds showed partial broodiness and 28 % birds showed no sign of broodiness. The evidence for a QTL affecting broody status on chromosome 5 at 79cM was significant at the genome-wide 1% level. The 95% Confidence Interval (C.I) for broody status however spanned a region around 95 cM. Standardized dominant effect represented 10.43 % of the trait standard deviation. TSHR is also found to be located at the same QTL position which is considered to be largest selective sweep associated with domestication of the chicken. Further fine mapping was done in this QTL region by adding 31 SNPs markers. Out of these, 15 SNPs markers were informative to fine map the loci which resulted in the CI reducing to 45cM and the most likely locus for the QTL remains at the TSHR. To further narrow down this loci, it is suggested to test this trait in other populations that segregate for the trait to increase the available recombinations.

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