

QUANTITATIVE TRAIT LOCI (QTL) WITH PARENT-OF-ORIGIN EFFECTS IN CHICKEN

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In poultry reciprocal effects in crosses have been detected for egg production traits, sexual maturity, egg quality traits and viability (Fairfull *et al.*, 1983). Reciprocal effects in poultry have been hypothesized to originate from sex-linked genes and/or maternal effects (Fairfull, 1990). An alternative explanation would be parent-of-origin expression, where the expression of alleles is dependent on the parent from which they are inherited. To understand the reasons for reciprocal effects we investigated potential effects of parent-of-origin specific QTL in chicken. Two divergent egg-layer lines differing in egg quality were reciprocally crossed to produce 305 F₂ hens (Tuiskula-Haavisto *et al.*, 2002). Searching the genome using models with uni-parental expression, we identified four new genome-wide significant QTL and three highly suggestive QTL affecting age at first egg, egg weight, number of eggs, body weight, feed intake, and egg white quality. Two genome-wide significant and one highly suggestive QTL show exclusive paternal expression while the others show exclusive maternal expression. The effects were found on chromosomes 1, 3, 9, and 11. Each of the parent-of-origin specific QTL explained 3–5 % of the total phenotypic variance, with the effects ranging from 0.18 to 0.4 phenotypic SD in the F₂. On chromosome 1 the parent-of-origin QTLs for age at first egg, body weight and feed intake are clustered between 200 and 350 cM. In the same area Mendelian QTL have been identified for different growth traits (Jennen *et al.*, 2004; Tatsuda and Fujinaka, 2001; van Kaam *et al.*, 1999). Using simulations and further detailed analyses, it was shown that neither departure from fixation in the founder lines, general maternal effects, nor Z-linked QTL, were unlikely to give rise to any spurious parent-of-origin effects (Tuiskula-Haavisto *et al.*, 2004). The present results suggest that QTL with parent-of-origin specific expression are a plausible explanation for reciprocal effects in poultry and deserve more attention. An intriguing hypothesis is whether these effects could be the results of genomic imprinting, which is often assumed unique to eutherian mammals. The new full genome sequence http://www.ensembl.org/Gallus_gallus/ and novel bioinformatics tools may give more information about candidate genes in the QTL regions, and provide possibilities to analyse imprinting effects.

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