Quantitative trait loci for abdominal fat weight and feed conversion in chicken

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To reduce the body fat deposition is one of the current purposes of poultry breeding programs, because the fatness synthesis has a high energy cost, which depress the feed conversion. Molecular markers information can be very important for poultry breeding programs, due the expensive fatness evaluation. This study aimed to map QTL in 350 F2 chickens from the EMBRAPA resource population (broiler x layer cross). Abdominal fat weight was measured at 42 d of age and feed conversion between 35 and 41 d. Here we report results from analysing chromosomes 1, 2, 3, 4, 5, 6, 7, 8, 11, and 13 with 91 microsatellite markers, covering a total of 1659.5 cM. The data were adjusted after an analysis of the factors by stepwise regression. The fixed effects of sex and hatch and the random infinitesimal genetic value were adjusted for both traits, while the covariate body weight at 42 d of age was adjusted only for abdominal fat weight. Qxpak v.13 (Pérez-Enciso and Mizstal, 2004) was used for QTL mapping. Two QTLs for abdominal fat weight were found between MCW0297 and LEI0146 (86 cM) in GGA1 (Nominal P-value = 9x10⁻⁹), and between LEI0029 and ADL0371 (122 cM) in GGA3 (Nominal P-value = 1x10⁻⁵). For feed conversion a QTL was mapped between LEI106 and ADL183 (317 cM) in GGA1 (Nominal P-value = 5x10⁻⁶). The bivariate analysis of those traits did not indicate any pleiotropic QTL in those regions. The QTL for abdominal fat weight in GGA1 confirms that reported by Jennen et al (2005), although they found only suggestive linkage. Many QTLs mapped for abdominal fat weight by others authors, were not confirmed here, which probably due to age differences. Our population was evaluated with six weeks, therefore before the beginning of the largest adipocyte hypertrophy phase.