

WHOLE GENOME SCAN FOR QUANTITATIVE TRAIT LOCI AFFECTING GROWTH AND FEED EFFICIENCY TRAITS IN CHICKENS USING A THREE GENERATION DESIGN

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SUMMARY

Growth and feed efficiency traits in broilers were analysed to detect QTLs. Data was from 10 families of a cross between two broiler lines in a three generation design. The first two generations consisted of full sib animals, which were genotyped. The third generation consisted of half sibs, which were used to obtain observations. These observations were used to calculate trait values for animals in the second generation. Difference in variance of observations on both sexes was taken into account by standardising. A whole genome scan was performed using a linkage map consisting of 368 microsatellite markers on 24 autosomal linkage groups. QTL detection was done with an across family weighted regression interval mapping approach. The most likely position for a QTL affecting feed consumption and body weight at 48 days was found on chromosome 1 at 234-240 cM. A permutation test indicated a genomewide significance level of this QTL for feed consumption of 4 %.

Keywords: Chicken, Quantitative Trait Loci, Body weight, Three generation design, Regression

INTRODUCTION

The availability of a considerable number of DNA markers and a genetic linkage map (Groenen et al. 1997) for chickens facilitates genome wide scans for genes affecting quantitative traits (QTLs). Van der Beek et al. (1995) suggested the use of a three generation full sib-half sib design. In this design, genotypes are determined for first and second generation full sib animals while phenotypic information is collected on third generation half sib grandoffspring.

The aim of this study was to detect and localise QTLs in a three generation design. For this purpose a regression approach was developed that takes the full sib structure of the design into account. This regression approach was based on the method of Knott et al. (1994) for half sib designs. The method was applied to body weight at 23 and 48 days, feed consumption and feed efficiency.

MATERIAL AND METHODS

Data. The design was based on what Van der Beek et al. (1995) termed a three generation full sib half sib design: parents (G_1), full sib offspring (G_2) and half sib grandoffspring (G_3). The G_1 parents were produced by crossing two genetically different outcross broiler dam lines originating from the White Plymouth Rock breed. The G_1 animals were mated to produce full sib G_2 families. Each G_2 animal was repeatedly mated with other G_2 animals to generate sufficiently large half sib families. On average, each of the 10 G_1 full sib families consisted of 45.1 genotyped G_2 animals and on average, each G_2 animal had 8.9 progeny. In the three generation design, G_1 and G_2 animals were typed for genetic markers and phenotypic information was collected for G_3 animals on several traits in a feed efficiency experiment. In total 20 G_1 animals were genotyped and 451 G_2 animals were genotyped and had progeny with observations in this experiment. Genotyping was for 368 informative microsatellite markers. The markers were mapped to 24 autosomal linkage groups covering 3128 cM. In total 240 markers were genotyped on all 10 families, 128 additional markers were genotyped on 4 families only. The average marker distance was 8.5 cM. This population had on average 4.3 different marker alleles resulting in an average heterozygosity of 60.4 %. The average information content (Kruglyak and Lander, 1995) was 0.71 for both males and females. In this paper besides body weight at 23 and 48 days, feed consumption and feed efficiency between 23 and 48 days were analysed. Phenotypic observations for body weight at 23 days were available for 2146 G_3 animals. For all other traits observations were available for 2081 G_3 animals, since not all animals reached the age of 48 days. In total about 1.5 % of the records was regarded as outliers and was excluded from the analysis.

Analysis of phenotypic data. The data was analysed in a two step procedure: first phenotypic data was analysed and combined and secondly QTL analysis was performed using the results of the previous analysis. Phenotypic observations on G_3 animals were used to calculate the mean progeny performance of G_2 animals. Observations were adjusted for systematic environmental effects and for the maternal genetic effect of the G_2 dam. Males and females differed with respect to mean and variance of the traits. To account for this, observations on males and females were treated as separate traits and a bivariate variance component and breeding value estimation was performed using an animal model. For each of the grandoffspring, two adjusted trait values were calculated: one for each parent. Adjusted trait values were calculated by correcting the phenotypic observations for the fixed effects and for the contribution of the parental mate. Correction for the mate was done by subtracting half the estimated breeding value of the mate. The differences between the sexes in mean and variance was taken into account by standardising the adjusted trait values before combining them to an average adjusted progeny trait value for each G_2 animal. The average adjusted progeny trait values from the G_2 animals were used as the dependent variable in the QTL analysis.

QTL analysis. To analyse the data of the full sib design a method was developed based on the multi-marker regression method of Knott et al. (1994) for outbred populations with a

half sib structure. The most likely haplotypes of all G_1 animals were reconstructed. For each G_2 animal, the probabilities of inheriting a putative QTL allele from one of the parents was calculated at fixed positions throughout all linkage groups. Probabilities were calculated conditional on the marker genotypes of the G_2 animals on the nearest informative marker or marker bracket per parent. QTL analysis was undertaken with a regression approach to fit a QTL across all families. Because marker-QTL linkage phase can differ between families, the QTL effects were estimated within each family. The average adjusted progeny trait values from the G_2 animals were regressed on the probabilities of inheriting the first parental allele of each parent. The family mean was included in the model to account for genetic differences between families. The regression coefficients represent the QTL allele substitution effects per parent (Falconer 1989). A weighting factor was applied to account for differences in number of G_3 animals contributing to G_2 average adjusted progeny trait values. In solving the equations, a generalised inverse was used to account for singularity. In order to test for the alternative hypothesis of the presence of QTL effects, versus the null hypothesis of the absence of QTL effects, a test statistic was calculated at every centimorgan for each linkage group. The test statistic is a ratio of the explained mean square of the QTL effects under study in the nominator and the residual mean square of the full model in the denominator. The position maximising the test statistic is the most likely location for the presence of a QTL. Genomewise significance thresholds were calculated by permutation (Churchill and Doerge 1994) over all linkage groups simultaneously. For each trait 10000 permutations were performed. A more detailed description is given by Van Kaam et al. (1997).

RESULTS AND DISCUSSION

The most significant result was obtained for feed consumption on chromosome 1. The most likely position was 234 cM with a test statistic of 2.80 and a 4 % genomewise significance level. In addition to that, a peak for body weight at 48 days was found at 240 cM on chromosome 1 with a test statistic of 2.32. The genomewise significance level was 41 %. Figure 1 gives the test statistics for feed consumption and body weight at 48 days on chromosome 1. The average information content was 0.81 at 234 cM and 0.91 at 240 cM. Results suggest the segregation of a QTL effect for both traits in the same three dams and furthermore in two sires for feed consumption only. Since the trait values for both traits were strongly correlated ($r=0.86$), it is most likely the same QTL which influenced both traits. All three dams, which seemed to segregate a QTL for body weight, also seemed to segregate a QTL for feed consumption, which supports the hypothesis that it was the same QTL affecting both traits. Although three dams had a Student's t-value above 2 for the QTL positioned at 240 cM, this is only an indication that it was probably segregating in these dams and no proof that was not segregating in any of the other parents. The average QTL effect (a) for feed consumption in the five parents was equal to $0.5 \sigma_a$ whereas the average QTL effect for body weight at 48 days in the three dams was equal to $0.6 \sigma_a$.

The most likely position for a QTL influencing body weight at 23 days was 165 cM at

chromosome 4. The test statistic at this location was 1.88, which was not significant. This area however also showed two peaks for body weight at 48 days at 138 cM and 167 cM and a peak for feed consumption at 137 cM. The trait values of body weight at 23 days had a correlation of 0.65 with the values of body weight at 48 days and 0.60 with the values of feed consumption.

For feed efficiency, the most likely QTL position was 419 cM at chromosome 2 with a test statistic of 2.25. This location also showed a peak for body weight at 48 days. Furthermore, there were peaks for feed efficiency at 161 cM on chromosome 1 and at 284 cM on chromosome 2.

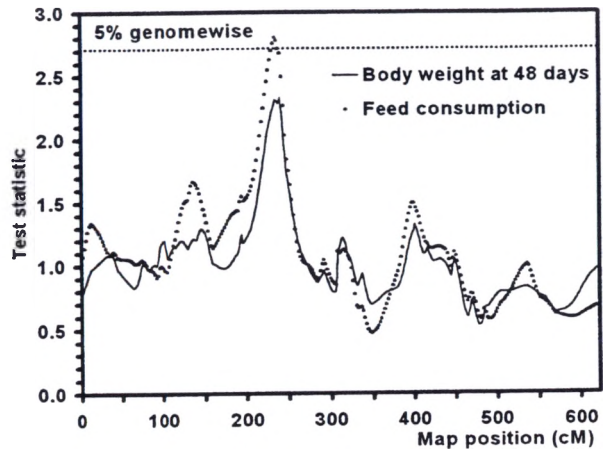


Figure 1. Test statistic values from the full sib QTL analysis of feed consumption and body weight at 48 days on chromosome 1 with the 5 % genomewide significance threshold of feed consumption.

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