

ity was measured as albumen height in Haugh units at ages of 40 and 60 weeks, HU40 and HU60, respectively. Because the confidence intervals for the detected QTL were over 50 cM wide, a method to improve the QTL locations after initial detection was needed. We chose the most significant QTL on chromosome 2 for further analyses. For fine-mapping a backcross design with multiple marker regression was used together with denser microsatellite marker intervals. Both poor and superior F₂ hens in egg white quality were selected for the female parents of backcross generation. Adding three microsatellite markers on the QTL area narrowed its position from 55 to 31 cM. Moreover, a grid search fitting two QTL was performed on the chromosome to test whether there could be more than one QTL on the chromosome affecting egg white thinning. It was tested with a standard F-test whether the best two QTL model explained significantly more variance than the best single QTL. The result suggested that instead of one QTL there are two distinct QTL areas affecting egg white thinning. In addition, the results from the backcross generation indicated that one of the QTL areas predominantly affects HU40 and the other HU60.

E022

Mapping of Quantitative Trait Loci for growth and fatness in chickens

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Two chicken lines divergently selected for growth have been used to create an F₂ intercross mapping population. The parental lines show a 9-fold difference in body weight at 8 weeks of age and differ markedly in traits related to appetite and deposition of fat. These two extreme chicken lines have been established by selecting for high and low body weight at 8 weeks of age for over 40 generations by P. B. Siegel. The mapping population was generated by crossing 30 individuals from each parental line reciprocally to generate 8 F₁ males and 76 F₁ females. A total of 974 F₂ individuals were phenotyped for growth and body composition traits including body weight

from 0 to 10 weeks, abdominal fat, and plasma concentrations of insulin and glucagon. A genome scan using 100 markers on 25 linkage groups in the chicken genome has been completed. The scan covers 85% of the chicken genome and an additional 50 markers are being typed to reach a coverage of 90%. Results of QTL analyses will be reported.

E023

Chicken fatness QTL mapping using an Advanced Intercross Line

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We have performed a total genome scan in chicken resulting in the localisation of QTLs for several economically important traits including fat deposition. Briefly, 480 F₂ animals were individually genotyped for 284 microsatellite markers, and 3 different batches of 2000 F₃ animals each were phenotyped for fatness traits. Deposited abdominal fat was measured in 2000 F₃ animals at 7, 9 and 10 weeks of age. QTL analysis, using a regression interval mapping approach, were performed for total fat and fat percentage for the three groups of animals. Six different regions, located on six different chromosomes, were identified that showed highly significant F-statistics for several of the fatness traits, indicating the presence of (a) gene(s) at these locations that control the amount of fat deposition in chicken. For the fine mapping of the regions containing the fatness QTLs an Advanced Intercross Line (AIL) has been produced. Over 3000 F₉ animals were produced and measured for the fatness traits and typed with markers from the six identified QTL locations.

E024

Frequency of *ER* and *RYR1* alleles and their association with reproductive performance in primiparous sows of synthetic line 990

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