

Extent and Consistency of Linkage Disequilibrium and Identification of DNA Markers for Production and Egg Quality Traits in Commercial Layer Chicken Populations

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Erin Beach, graduate research assistant;
Behnam Abasht, postdoctoral research associate;
Rohan Fernando, professor of animal science;
Jack C. M. Dekkers, professor of animal science;
Susan J. Lamont, distinguished professor of animal science;
Jesus Arango, geneticist, Hy-Line;
Petek Settar, geneticist, Hy-Line;
Janet Fulton, geneticist, Hy-Line
Neil. P. O'Sullivan, geneticist, Hy-Line

Summary and Implications

A 3,072 single nucleotide polymorphism (SNP) panel was used to identify genetic markers linked to quantitative trait loci (QTL). Two association methods were used to search for QTL, SNP-wise and genome-wise models. The QTL associated with SNPs, found using both of these methods, can be applied to breeding programs in marker assisted selection (MAS).

The extent and consistency of linkage disequilibrium (LD) was measured in two lines of commercial egg laying chickens by analysis of SNPs. Correlations were drawn between measurements of two consecutive years to determine consistency. At short distances, LD is retained which allows for markers at high LD with a trait to be effectively applied in MAS.

Introduction

Making advances in animal breeding is very important to the livestock industry so that they can continue to produce the best product. Recent advances in genetics have allowed breeders to make their breeding selections based on genotypic data rather than purely phenotypic data. MAS uses easily identifiable markers that are associated with a trait of interest in an animal. MAS is of great use for traits that have sex limited expression or difficult to measure phenotypes. For MAS to be effective the marker-trait association needs to be maintained over generations.

LD is a measurement from 0 to 1 that shows how often two alleles are inherited together or the strength of an association of a marker to a trait. An LD score of 0 implies no association whereas a score of 1 means a complete association. Correlation of linkage disequilibrium over years can measure how well the association is maintained.

Traits of interest must be identified before any breeding program can take place. Ideally for genetic selection the specific gene or place on the chromosome that affects the

trait is known. Quantitative traits may involve many different genes on many chromosomes and are important to identify so that breeders may make improvements in quantitative traits.

Many statistical models exist to locate QTL based on phenotypic data and genotypic data. SNP-wise models utilize single SNPs or SNP windows to look for association with a trait. Genome-wise models utilize all of the available markers and fit them simultaneously.

Materials and Methods

Data were provided from Hy-Line, International, for two egg-laying lines, one white and one brown. The data set contained progeny performance of sires for 12 traits, pedigree information and genotypes from the 3,072 SNP panel. The 12 traits, consisting of egg production and egg quality traits, were classified into two categories based on age of measurement; early and late traits. The SNP association analyses were performed on the white egg line. Two different association methods were used to identify markers, SNP-wise association and genome-wise Bayesian analysis. SNP-wise associations were performed using single SNPs and windows of 3 consecutive SNPs.

Genotype data over two consecutive generations was used. Chromosomes 1 and 4 were analyzed, with SNPs having a minor allele frequency of less than 0.05 removed. The programs Haploview and PowerMarker were used to measure LD by r^2 and r , respectively, for pairs of SNPs. The resulting LD score was plotted against distance between the markers to assess the extent of the LD (Figure 1). Correlations were drawn between matching marker pairs over the two years. Correlations were grouped based on the distance between the two markers in a pair (Figure 2,3).

Results and Discussion

The two methods of analysis, single SNP and three SNP models, yielded 159 and 76 significant tests, respectively, across 12 traits. With the Bayesian analysis, 33 SNPs were included in the model greater than 20% of the time. The two statistical analysis methods provided consistent results in the QTL scans. These egg production trait QTL will be useful in MAS for breeding programs.

The LD between markers pairs was high at short distances ($r^2 > 0.2$ at < 2 Mb) and remained high after one generation (0.80 to 0.92 at < 5000 kb) in both lines. This is a good indication that markers in close proximity to a QTL will retain high LD in consecutive generations and be effective in MAS.

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Figure 1. Plot of linkage disequilibrium measurement against distance in megabases. The blue dots represent a SNP pair, the red line the moving average of the points, and the yellow line the predicted LD curve.

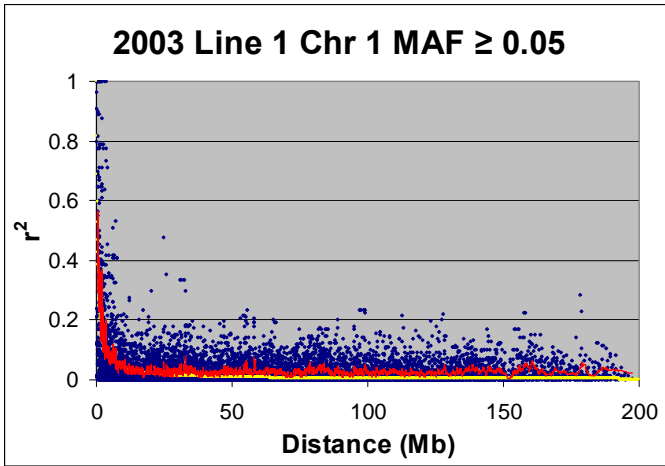


Figure 2. Graphs of the correlation between the two years for Line 1 and Line 2 as measured by r^2 for chromosomes 1 (left panel) and 4 (right panel).

