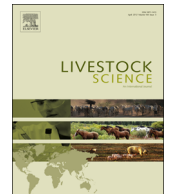




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Prior genetic architecture impacting genomic regions under selection: An example using genomic selection in two poultry breeds



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ABSTRACT

Background: The objective of this study is to investigate if selection on similar traits in different populations progress from selection on similar genes. With the aid of high-density genome wide single-nucleotide polymorphism (SNP) genotyping, it is possible to directly assess changes in allelic frequencies and regions under selection and address the question. We compared the allele frequencies before and after two generations of selection on an index containing body weight at 6 wk, ultrasound measurement of breast meat, and leg score in two commercial chicken breeds with different selection histories: M breed was primarily selected for rapid growth and commonly used as a broiler breeder sire line; F breed was primarily used as dual-purposed dam line selected for both egg production and growth. Selection was performed on both lines with the same selection intensity and method (Genomic Best Linear Unbiased Prediction, GBLUP, using the single-step approach, ssGBLUP).

Results: After quality control, 52,742 and 52,639 SNPs in M breed and F breed were kept in 4922 and 4904 animals, respectively. The average allele frequency change for both breeds on the autosomes was 0.049. Threshold value for detecting selected regions, where allele frequency changes exceeded expectations under drift were 0.140 and 0.136 for breeds M and F, respectively. According to the criterion used in this study, there were 25 and 17 selection regions detected on breeds M and F, respectively, without any overlap of regions between the breeds. Average heterozygosity change in F breed was greater compared to M breed (0.008 vs. 0.002, $P < 0.01$). Also, there was no overlapping of selected regions with high heterozygosity change between breeds M and F.

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Conclusions: The results indicate that in newly selected populations, even using the same criteria and selection methods, the historical selection goals and breed development determine the loci that most impact selection progress. These results are consistent with quantitative genetic theory that contribution of loci to selection progress depends on initial allele frequency. Therefore it should not be assumed that the same loci will be under selection in different populations even if similar selection goals and methods are used.

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1. Introduction

An interesting academic question with practical implications is, “does selection on similar traits in different populations progress from selection on similar genes?”. In practice the question is “will genes found to be important in one F breed or a given trait also be important for the same trait in another?”. Because selection on traits changes the allelic frequency of the underlying causative genes (Nielsen, 2005), the interspecific to intraspecific variability between populations or between generations increases (Lewontin and Krakauer, 1973). Directional selection is different from other evolutionary factors that either reduce the ratio of within and between population genetic variability, or have no effect on the genetic variability. Selective sweeps, which are genomic region that have recently become fixed due to the selection of advantageous alleles, reduces the variability in the causative genes and flanking sites. To detect incomplete selective sweeps, it should be possible to utilize genome-wide changes in the allele frequency spectrum over time in populations under selection.

For domestic animals, there were already several studies on the allele frequency spectrum of signature of selection by investigating heterozygosity (Elferink et al., 2012), Wright's fixation index (F_{st} test) (Moradi et al., 2012), and relative extended haplotype homozygosity (REHH test) (Sabeti et al. 2002). However, those studies used cross-generation data during selection, therefore, their results were impacted by both recent and historical selections. Furthermore, most previous studies only have allele frequency data after completion of selection, leaving the initial and change in allele frequencies unknown.

In order to separate the results caused by historical and new selection, our study used two methods: the straightforward allele frequency change from initial to last generation was used to detected genomic change in a recent selection experiment in broiler (meat-type) chickens; and heterozygosity change in above time cession was used to detect selective sweep. Two selection breeds from different origins, a sire breed (M) historically selected for rapid growth, and a dam breed (F) historically selected for both egg production and growth, were used. These breeds were selected for body weight at 6 wk (BW), ultrasound measurement of breast meat (BM), and leg score (LS) using the same index in both. Genotypes on animals in these breeds were collected for genomic selection. From this data, we attempted to identify the changes in allele frequency spectrum across chromosomes for each generation that

should provide insights into how the genome responds to selection.

2. Results

2.1. Effect of selection traits on the change of genetic variation

Changes in allele frequency between G_0 and G_2 (d_{02}) in M breed and F breed were calculated to compare the response to selection. Whole-genome patterns of allele frequency change in M breed and F breed were different with respect to the positions, the ranges of putative select regions, and values of the most extreme d_{02} (Figs. 1 and 2). Thresholds for significant d_{02} determined by gene dropping method were 0.140 for M breed and 0.136 for F breed (Fig. S1). None of the selected regions were overlapping between the two breeds. The average changes in allele frequency ($\overline{d_{02}}$) on autosomes were the same, 0.049, in both breeds (Table 3). As expected for the sex chromosome, and aggravated by the smaller number of male vs. female parents, chromosome Z had a larger average allele frequency change compared to the autosomes. This change was greater in M breed than that found for F breed (0.070 vs. 0.061, respectively, $P < 0.01$). The $\overline{d_{02}}$ of all chromosomes for M breed and F breed are 0.051 and 0.049. Also, the average minor allele frequency (MAF) of G_2 is higher than the MAF of G_0 in both breeds, again in both the Z chromosome and in autosomes (average MAF difference, autosomes: 0.002 for both breeds; chromosome Z: 0.016 and 0.008 for M breed and F, respectively, $P < 0.01$). In selected regions, the average allele frequency changes were 0.177 for M breed, and slightly smaller, 0.176 for F breed, but not significantly different between the breeds ($P = 0.7$). The distribution of d_{02} values showed a longer tail in M breed than F breed, indicating that SNPs in M breed have more extreme allele frequency changes after two generations of selection (Fig. 3).

2.2. Selected regions

With both GBLUP selected breeds, less than half of the chromosomes contained extreme regions where the running average of d_{02} exceeded the threshold (Figs. 1 and 2, Tables S2–S6). The threshold was exceeded on 12 and 9 chromosomes, and in 25 and 17 regions, in M breed and F breed, respectively. The total length of selected regions was 11,531 kb and 8396 kb; and the average length was 494 kb and 461 kb for M breed and F breed, respectively. No

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