Detection of selective sweeps in two divergently selected chicken lines using a combination of SNP and sequence data

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To study the effect of selection on body weight a long-term selection experiment started in 1957 and is still ongoing. Starting from a single population of White Plymouth Rock, two lines have been selected for high and low body weight, respectively, at 8-weeks of age (Dunnington and Siegel, 1996). This selection has resulted in a nine-fold difference in 8-week body weight. Analysing genomic data from these lines is a promising approach for finding regions in the genome that are associated with body weight in chickens. Several QTLs, including a network of interacting QTLs, have previously been identified from an intercross between the high and low line (Jacobsson et al., 2005; Carlborg et al., 2006). We analysed individuals after 40, 50 and 53 generations of selection (generations S40, S50 and S53) with a 60k SNP chip. Genome re-sequencing was done on pools of samples from generation S40 from the high and low line, respectively. A first sequencing round used SOLiD v2 and a genomic fragment library and 35 bases per read with ~5X depth coverage (Rubin et al, 2010; Marklund and Carlborg, 2010). A second sequencing round on new pools of samples was performed through SOLiD using paired-end library of 50 bases per read with ~7X depth coverage in each line. Combined use of both rounds makes ~12X depth coverage for SNP detection.

We show that the effect of selection is as dramatic on the genome as on the phenotype. Using the SNP chip data from generation S40 and S50, more than 50 regions were identified where alternative alleles have been fixed in the two lines (Johansson et al., 2010). New genotype data from generation S53 have allowed us to identify the regions with large change in allele frequency in the same direction both between generations S40 and S50 and between S50 and S53. Analyses of the pattern of LD show that the average size of haplotype blocks is larger in the high line than in the low line, both in terms of number of SNPs included in the blocks and in terms of physical length. This is in agreement with the larger phenotypic selection response in the high line. The average number of SNPs per block is similar in both lines for macrochromosomes, microchromosomes and intermediate chromosomes, whereas the average length is considerable larger for the blocks on macrochromosomes. There are several very large blocks that are larger than 4 Mb. There are three regions with overlapping haplotype blocks larger than 5 Mb in both lines. The regions with overlapping large haplotype blocks in both lines were studied in more detail. Ensembl and KEGG databases were used to extract genes from these regions, and the genes were mapped to KEGG biological pathways. Eight pathways with two or more genes in the 3 largest regions were identified. The sequence data was used to find the sub-regions with highest variation between the high and low chicken lines. The sequence data is currently being used to find the genes and functional mutations in the regions where selective sweeps have been identified.

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