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Selective sweep mapping in the R+ R- chicken lines divergently selected for RFI (residual feed intake).

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Intense artificial selection of populations leads to the acceleration of evolutionary processes and often results in extreme phenotypes with associated changes across the genome. Selective-sweep mapping makes it possible to identify the genomic regions where allele-frequencies have moved after selection. In this project we performed a selective-sweep mapping in two experimental chicken lines, developed from a common Rhode Island Red base population, by long term divergent selection (40 years) for high (R+) and low (R-) residual food intake, an indicator of feed efficiency. High-density genotyping was performed using the 580K Affymetrix® Axiom® HD array on 96 animals per line sampled at three different generations: the 18th, the 25th and the 40th generation of selection. Such an interval was shown by simulation to be the optimal solution to infer the presence of selection allowing to characterize the dynamic of selection. From the 580 961 SNPs genotyped 326 004 were informative. A filtering was applied to keep only the SNPs with data missing <10 and a MAF > 0.05, leading to 255 103 SNPs suitable for analysis. We looked for genomic signatures of positive selection using the HapFLK method, which focuses on the differences of haplotype frequencies between populations, and retained those for which the differentiation was too large to result from a neutral evolution model. In total 5 regions were detected, at a FDR of 15%, on GGA1, GGA2, GGA6, GGA7 and GGA11 and their size varied between 60kb and 3Mb. When we looked at the haplotype frequency among generations for these 5 regions, we identify relatively similar selective scenarios suggesting, a divergent before the first generation (18th) analyzed in this study, and little evolution in the following generations (25th and 40th). The five selected regions contained in total 78 long non coding genes and 77 protein coding genes. These included candidate genes involved in important functions known to differ between lines, as the modulation of innate and adaptive immune responses (WWP1, RIPK2), the mitochondrial activity (ATP6VOD2, TFAM, CISD1) and physiological processes such as respiration, acid-base balance, bone resorption, calcification metabolism (CA2, CA13) and fatty acid uptake, transport, and metabolism (FABP4). Among all genes identified, the *Fatty Acids Binding Proteins 4* (FABP4) gene is particularly interesting because it is mainly expressed in adipocytes and macrophages and plays an important role in the development of insulin resistance and non-alcoholic fatty liver disease, conditions that were observed in the R- line. This study was supported by the CRB-Anim (SelMaR project) and the ANR (Chickstress project).