

MHC-B variability in the Finnish Landrace chicken conservation program

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The Finnish Landrace chicken is adapted to free range and modest living conditions in the northern European climate. The native breed was almost completely replaced by the large-scale egg production hybrids in the 1950s. Only remnants of the native chicken survived and several unknown breeds were likely introduced into the ancestral population in the last century. Conservation efforts to protect this endangered breed were initiated by a hobby breeder in the 1960s. However, the official conservation programme was established in 1998. The conservation program aims to insure breed purity of 12 landrace lineages originally obtained from isolated villages in Finland. The program relies on a network of over 400 non-professional breeders. The chicken Major Histocompatibility Complex B region (MHC-B), located on chromosome 16, contains over 45 highly polymorphic immune response genes. Variation within the MHC has been shown to enhance resistance to multiple viral, bacterial and parasitic pathogens. To assess variability in the chicken MHC-B region in the Finnish Landrace breed, a panel of 90 SNPs encompassing 210 kb was utilized. A total of 195 samples from 12 distinct lineages (average of 15 individuals sampled per population) were genotyped. Variation in the MHC-B region in these populations was examined using the MHC SNP panel. A total of 36 haplotypes were found, 16 of them had been previously identified in other breeds and 20 haplotypes were novel. The average number of MHC-B haplotypes within each lineages was 5.9, ranging from 1 to 13. Some of the haplotypes were lineage-specific. This study shows that substantial MHC-B region diversity exists within the Finnish Landrace breed. Abundant variability within the MHC region indicates overall health and robustness of Finnish Landrace chicken lineages. Finally, the results exemplified successful implementation of the conservation program.

Effect of peri-implantational undernutrition on interferon stimulated gene expression in beef cattle

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For pregnancy to occur, the maintenance of a functional corpus luteum requires a complex embryo-maternal crosstalk. Reduced nutrient intake during early pregnancy could impair the pregnancy recognition mechanisms in cattle. The aim of this study was to analyse the effects of peri-implantational undernutrition on the expression of Interferon tau Stimulated Genes (ISG) during early pregnancy in two beef cattle breeds. Thirty-five Parda de Montaña (PA) and 19 Pirenaica (PI) multiparous cows were synchronized to estrus and artificially inseminated (AI). Pregnancy was confirmed by transrectal ultrasonography on day 37 post-AI. Dams were randomly allocated to a control (CONTROL, n=30) or nutrient-restricted (SUBNUT, n=24) group, which were fed at 100 or 65% of their estimated energy requirements during the first 82 days of pregnancy. Blood samples were drawn on day 18 after AI. Gene expression of ISG15, OAS1, MX1 and MX2 in peripheral blood mononuclear cells was analyzed by real time PCR. The effects of pregnancy, breed of dams and undernutrition and possible interactions of paired factors on ISG expression were assessed by proc MIXED with SAS and JMPro statistical software (SAS Institute Inc., Cary, NC). Pregnant dams had a higher gene expression of ISG15, MX1 and MX2 compared to those non-pregnant ($P < 0.001$). Breed and undernutrition did not affect ISG gene expression. However, interaction between pregnancy, breed and undernutrition showed that mRNA OAS1 expression was significantly downregulated in SUBNUT PI pregnant dams ($P = 0.0325$), suggesting different immune responses to dietary deficiency in these two cattle breeds during the pregnancy. To sum up, undernutrition during the peri-implantation period down-regulated ISG expression in pregnant PI dams but not in PA dams. This study received financial support from the Spanish INIA RTA2013-059-C02.