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Whole genome resequencing reveals loci under selection during chicken domestication

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Abstract

Domestic animals are prime models for the genetic dissection of phenotypic diversity. Here we have used massively parallel sequencing to identify selective sweeps of favorable alleles and candidate mutations that have played a prominent role during chicken domestication and subsequent specialization into broiler (meat-producing) and layer (egg-producing) chickens. We have generated 44.5x coverage of the chicken genome using pools of genomic DNA representing eight different populations of domestic chickens as well as red junglefowl, the wild ancestor. We have identified a number of the loci that have made it possible to transform the red junglefowl to an extremely efficient production animal. This study has direct application to animal breeding and enhances the importance of the domestic chicken as a model organism for biomedical research.