

Exploring the genomic basis of shank and eggshell coloration in Italian native chicken breeds

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Eggshell and shank colour play a role in poultry selection, breed recognition, and environmental adaptation. This study investigated the genomics of shank and eggshell pigmentation in Italian local chickens to uncover the mechanisms underpinning these phenotypes. To this purpose, 418 animals from 18 local breeds were evaluated for shank and eggshell pigmentation, and genotyped using the Affymetrix Axiom 600 K Chicken Genotyping Array. A genome-wide association study was performed to compare the case and control populations for shank and eggshell colour. The most interesting locus for shank pigmentation was detected on GGAZ, close to the *TYRPI* gene, which plays a key role in avian pigmentation. Also, novel loci and genes (e.g., *MTAP*, *CDKN2A*, *CDKN2B*) associated with shank and skin pigmentation, UV protection, and melanocyte regulation were identified. A new genomic region for shank pigmentation was detected on GGA1, in which *CHODL*, *TMPRSS15*, and *NCAM2* gene were mapped. Fewer significant loci were identified for eggshell pigmentation, including *SLC7A11* on GGA4 and *MITF* on GGA12, which are associated with melanocyte processes and pigment synthesis. This study shed light on the genomic architecture underlying shank and eggshell colour in Italian local chicken breeds. These phenotypes play an important role in breed identification and conservation. *This work was funded by MIPAAFT (project TuBAVI, PSRN 2014-2020, sottomisura 10.2).*