

Genetic diversity of a large range of domestic chicken breeds and its use in genome-wide association studies

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P-19. Domestic chickens show massive phenotypic variation reflecting their genetic make-up. This can be used to detect relationships between breeds and genomic regions influencing trait divergence. This study aims at (1) evaluating the relationships of chickens from an extensive spectrum of breeds mainly according to the fancy chicken breed standard of Germany, and (2) applying a novel genome wide association approach to detect chromosomal regions causing trait differentiation. 2000 chicken blood samples from 111 breeds and colour variants were genotyped with the 600k Axiom-Genome-Wide Chicken Genotyping Array, and phenotypic trait information was collected for each bird within the framework of the SYNBREED project. Filtering excluded SNPs with call-rate <99% and animals with call-rate <95%. A principal component analysis visualized a strong association of individuals with their respective breed. Groups of breeds differing in trait variants were contrasted genotypically in a comprehensive genome-wide association study, establishing different test-statistics and sliding window strategies. As a proof of concept, this approach mapped known mutations for yellow skin colour and rose-comb mutation to the correct position. Methods established will be used to search for selection signatures and so far unknown genomic regions associated with phenotypic trait variations.