## State of the genetic diversity, structure and admixture of British chicken breeds

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The characterisation of livestock genetic diversity can inform breed conservation initiatives. The state of genetic diversity and genetic structure in 24 British chicken breeds was assessed. A total of 239 alleles in 685 individual genotypes were found across 30 microsatellite loci with a mean number of 7.97 alleles per locus. Genetic differentiation between the phenotypically diverse British chicken breeds was high with an average F<sub>ST</sub> value of 0.25. Genetic diversity was also high with an average expected heterozygosity of 0.49, ranging from 0.20 in Spanish to 0.62 in Araucana. However, the average observed heterozygote frequency was 0.39, ranging from 0.15 in Spanish to 0.49 in Cochin. A heterozygote deficit was observed in most breeds, with an average F<sub>IS</sub> value of 0.20. Individual-based clustering analyses revealed that most individuals clustered to breed origin. However, genetic subdivisions occurred in several breeds and this was predominantly associated with flock supplier and occasionally by morphological type. Overall, the levels of genetic diversity in British chicken breeds are comparable to those reported in mainland European chicken breeds, but the observed heterozygosity was considerably lower. It is likely that this was due to a Wahlund effect caused by sampling from subtly differentiated flocks, implying structure within breeds. It is proposed that gene flow amongst flocks within certain breeds should be enhanced to maintain the current levels of genetic diversity. Additionally, some breeds had low levels of both genetic diversity and uniqueness. Consideration is required for the conservation and preservation of these potentially vulnerable breeds.

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