Genome-wide structure of non-pedigree chicken populations allows fine mapping of Mendelian traits

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Traditional chicken breeds exhibit a wide range of phenotypic diversity, having been selected by man for fanciful traits over hundreds of years. Wide-ranging phenotypic variation is also present in village chicken populations found throughout much of the developing world. We present here an assessment in non-pedigree traditional and village chicken populations, using the Illumina 60k SNP chip, of their genome-wide diversity for mapping purposes. Analysis of admixture reveals a genetic background in traditional breeds influenced by European and Asian ancestry, whilst Kenyan and Ethiopian village chickens show distinct genetic ancestries. Association mapping across traditional breeds successfully remapped the yellow skin phenotype and yielded refined mapping intervals for oocyan. Analysis of linkage disequilibrium (LD) indicate that at least a 90-110k SNP chip would be required for genome-wide analysis of haplotype block ancestry and association mapping. Our results underline the importance and uniqueness of the phenotypic diversity of traditional and village chicken breeds for genetic mapping of Mendelian traits.

Funding was from the BBSRBC and the Rare Breeds Survival Trust.