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Haplo-block structure of Southern African village chicken populations inferred using genome-wide SNP data

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ABSTRACT. This study investigated the haplo-block structure, haplotype sharing, and diversity in extensively raised chicken populations of Southern Africa. Two hundred ninety village chickens from Malawi (N = 30), South Africa (N = 132), and Zimbabwe (N = 128) were included in the study, from which 649, 2104, and 2442 haplo-blocks were observed, respectively. The majority of haplo-blocks were smaller than 25 kb in size and only five blocks were more than 2000 kb in size. The low chromosomal coverage of haplo-blocks observed across the genome suggests that multiple recombination events fragmented the ancestral haplo-blocks into smaller sizes. Haplo-block sharing was observed between populations with 2325 haplo-blocks common between Zimbabwe and Malawi and 2689 between South Africa and Zimbabwe. Haplotype sharing allows transferability of genomic tools between these extensively raised chicken populations of Southern Africa. The unique haplo-blocks could have originated from isolated evolution taking place in specific agro-ecological zones. Quantitative trait loci analysis revealed that genes related to body composition were spanned by these haplo-blocks. Body composition traits are important for village

chicken populations, which have to harness poor quality feed obtained from the environment to meet their maintenance and production needs.

Key words: Haplo-block structure; Genetic diversity; SNPs; Village chickens

