Haplo-block Structure of Southern African Village Chicken Populations

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ABSTRACT: A total of 290 village chickens from Malawi (n=30), South Africa, (n=132) and Zimbabwe (n=128) were analysed for haploblock structure and diversity using the Illumina iselect chicken SNP60K bead chip data. Results showed 649, 2104, and 2442 haploblocks for the three populations, respectively. More haploblocks were observed in macro-chromosomes (range 118 to 402) compared to micro-chromosome (range from 13 to 125). The median block lengths were 13.6 Kb, 10.8 Kb and 9.7 Kb whilst genome coverage was 39 Mbp, 64.4 Mbp and 54.5 Mbp for Malawi, South Africa and Zimbabwe, respectively. Majority of the haploblocks were smaller than 25Kb and only five blocks were bigger than 2 Mbp. Significant haploblock sharing was observed between populations. Results imply transferability of genetic parameters between populations and suggest that unique haploblocks could be emanating from isolated evolutionary events specific to the agro-ecological zones of the sampled countries.

Keywords: chickens; haplotype; diversity.

INTRODUCTION

The evolution of village chicken populations of Southern Africa and other developing countries is not clearly understood. However, it is also hypothesized that the agro-ecological regions in which these chickens exist impose natural selection pressures that have shaped the gene pool of these extensively raised livestock species (Muchadeyi et al. (2007)) and generated sub-populations sharing, and diversity within and between village chicken populations. The Illumina chicken iSelect 60K SNP chip has been found useful in studying LD as well as haploblock partitioning in commercial (Qanbari et al. (2010)) as well as traditional free ranging chickens (Wragg et al. (2012)).

There is no information on haploblocks structure of extensively raised chicken population of Southern Africa. The influence of recombination and existence of haploblocks associated with the observed LD profile has not been investigated. An analysis of haploblocks structure in extensively raised chickens will shed more light into utility of the available SNP panel in studying village chicken populations.

The objective of the study was therefore to screen for haploblocks and investigate the haplotype structure, sharing, and diversity within and between village chicken populations of Southern Africa.

MATERIALS AND METHODS

Village chicken populations. A total of 312 village chickens were randomly sampled from different climatic regions in South Africa, Malawi, and Zimbabwe.

SNPs quality control and pruning. SNPs pruning was performed on those SNPs that had a minor allele frequency of 0.05, had over 5% missing genotypes, SNPs that deviated from Hardy-Weinberg equilibrium at P = 0.001 and individuals with over 5% missing genotypes. Using this quality control criteria analyzed using Plink (v1.07), a total of 290 individuals overall populations and 43175; 45676; 46905 and 44667 markers were used for further analysis for overall population, Malawi, Zimbabwe and South Africa, respectively.

Haploblocks partitioning. Haploblocks estimation was done in Plink 1.07 (Purcell et al. (2007)) which uses default procedures from Haplovie http://www.broad.mit.edu/mpg/haplovie/. Individuals within a population were considered similar and therefore treated as cases. Pairwise LD (r²) was calculated on a SNP distance of 10000 Kb for autosomal chromosomes except...
chromosome 16 since it had less than 20 markers. For blocks partitioning, the --blocks function was used in Plink using the default algorithm by Gabriel et al. (2002) as implemented in Haploview. Blocks were created if 95% confidence bounds on r². Haploblocks frequency was estimated in Plink using the --hap-freq function. Blocks of different frequencies were generated per chromosome from those blocks occurring at frequency of <0.1, 0.1-0.25, 0.25-0.5, 0.5-0.75 and 0.75-1.0.

**Haplotype diversity and QTL detection.**

Haploview version 4.2 (Barrett et al. (2005)) was used for LD plots and haplotype frequency within blocks per population. Haplotype diversity was considered as the number of haplotypes found within a haplotype block. Chromosome 8 and 22 where selected for further analysis because they had higher LD estimates than the other chromosomes (Kanyile et al. (2013)). The first and last position of SNP markers was used to search for possible QTLs spanned by these blocks. Majority of haploblocks were less than 10 kb with some falling between 10 and 25 kb across all populations (Table 2). Very few haploblocks were more than 500 kb. A large proportion of haploblocks occurred at a frequency greater than 20% in the respective populations. The moderately prevalent haploblocks can be used to assess haplotype diversity and genetic variation within and between populations. The number of observed haploblocks varied between populations. Malawi had lower number of haploblocks compared to South Africa and Zimbabwe. The number of haploblocks in Malawi is similar to those observed by Wragg et al. (2012) in traditional and village chicken populations. Number of haploblocks of South Africa and Zimbabwe are similar to those observed by Qanbari et al. (2010) in commercial (Broilers and layers) lines.

On the regions investigated, QTLs have been found that are associated with body composition related traits such as body weight, muscle weight, tibia, wings and thigh size. These traits are of importance in village chicken since they have to adjust to nutritional changes in their environment such as the scarcity or availability of feed under the management system there are kept under. The rate of growth and the body weight might be more dependent on these regions because village chickens are known to be slow growers (Muchadeyi et al. (2007b)) and this might enable them to reduce the risk of failing to cope during periods of feed scarcity or when there are no nutritional supplements.

Haplotype sharing varied between populations with a considerable number of haploblocks shared between populations. The sizes of haploblocks shared, their genomic content and their frequency between populations can give more insight into genomic regions spanning economically important traits that could be of use as genomic tools across village chicken populations. The variation in number of unique haploblocks within population indicates independent genomic sub-structuring and evolution of populations. There might be a need to understand what genomic regions are shared between populations with the aim of associating haplotypes with adaptive traits in these extensively raised populations. Despite the high number of haplotypes blocks

| Table 1. Characteristic of haploblock structure for each population |
|------------------|-------|-------|-------|
| Blocks           | Malawi| SA    | Zim   |
| Genome Coverage (Mbp) |       |       |       |
| Mean Block Length (kb)±SD | 60.7±239.6 | 26.4±132.9 | 25.9±140 |
| Median Block Length (kb)±SD | 13.6±239.6 | 10.8±132.9 | 9.7±140  |
| SNPs (%)         | 5.0   | 14.1  | 11.5  |
| Mean nSNPs       | 3.5±3.9 | 2.6±2.7 | 2.6±2.7 |
| Mode SNPs per Block | 2     | 2     | 2     |
| Max nSNPs        | 49    | 55    | 60    |

| Table 2. Number of haplo-blocks in relation to their sizes for each population |
|-----------------|------|------|------|
| Overall         | Malawi| SA   | Zim  |
| 10-25 Kb        | 214  | 1023 | 792  | 1115 |
| 50-100 Kb       | 56   | 81   | 63   | 83   |
| 100-250 Kb      | 63   | 87   | 70   | 71   |

The number of SNPs forming blocks was above 25 in some chromosomes such as chromosomes 1, 4, 5, 7, and 8. Such genomic regions that have long stretches of haploblocks should be further investigated for association with morphological or quantitative traits that could be spanned by these blocks. Majority of haploblocks were less than 10 kb with some falling between 10 and 25 kb across all populations (Table 2). Very few haploblocks were more than 500 kb. A large proportion of haploblocks occurred at a frequency greater than 20% in the respective populations. The moderately prevalent haploblocks can be used to assess haplotype diversity and genetic variation within and between populations. The number of observed haploblocks varied between populations. Malawi had lower number of haploblocks compared to South Africa and Zimbabwe. The number of haploblocks in Malawi is similar to those observed by Wragg et al. (2012) in traditional and village chicken populations. Number of haploblocks of South Africa and Zimbabwe are similar to those observed by Qanbari et al. (2010) in commercial (Broilers and layers) lines.

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on chromosome 8, there were few haplotype combination that were more frequent thereby compromising haplotype diversity (Figure 1).

CONCLUSION

Haplotype block structure varies between populations supporting different genetic background and the level of haplotype diversity is in support of population sub-structuring. The observed haplotypes on QTLs on chromosome 8 indicate possible selection for adaptation of these animals to the village chicken production systems. There is still need to investigate other genomic regions to get a genome-wide and broad perspective of QTLs spanned by long haplotype blocks across the genome of these animals. Further investigation may be required that associates the observed genetic variation on these haplotype blocks to key production traits relevant to smallholder village chicken systems.

Fig 1. Haplotype plots of chromosome 8 from three chromosomal sections.

LITERATURE CITED