Genetic architecture of body weight and carcass traits in Ghanaian local chickens

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Abstract
Little information on the genetic architecture of production traits of indigenous African chicken exists. We estimated genetic parameters and performed a genome-wide association study using imputed 600K SNP genotypes on three Ghanaian chicken ecotypes (n=1,113). Variance components and heritabilities for body weight at 22 weeks (BW22), average daily gain (ADG), and carcass traits were estimated, as well as genetic and phenotypic correlations among them. Heritabilities for all traits were high (0.51 - 0.69), while those for carcass traits corrected for BW22 were moderate (0.21 - 0.38). Seven 1-Mb windows from six chromosomes each explained up to 25% of the genetic variance in these traits. These windows contained genes such as *FOXO1*, *NCARP*, *LCORL*, *LAP3*, *LDB2*, *TGFBR2*, and *TAPT1*, previously reported to have effects on growth and carcass traits. The moderate to high heritabilities and highly positive genetic correlations between them indicate that these traits can be improved through selective breeding.

Introduction
Indigenous African chickens have over the years adapted very well to harsh climatic and environmental conditions (Birteeb *et al.,* 2016). They have several desirable characteristics, including natural resistance against diseases like Newcastle disease (Mpenda *et al.,* 2018). They, however, tend to have lower growth rates and body sizes compared to exotic chicken breeds (Osei Amponsah *et.al*., 2011; Birteeb *et.al*., 2016). Therefore, in the quest to increase local chicken's body size and growth rate, many farmers introduce birds of unknown genetic composition into their flocks, potentially leading to the loss of important traits. Some studies on genetic production trait parameters of local chicken in Africa have been carried out (Osei-Amponsah *et al*., 2013; Dekkers *et al*., 2017), but very limited comprehensive genome-wide association studies (GWAS) to explore the genetic basis of these traits are available. Therefore, it is important to explore the genetic architecture of production traits in local chicken populations to identify their potential for genetic improvement, whilst preserving their genetic diversity and retaining their ability to withstand the harsh environmental conditions of their habitats. The objective of this study was, therefore, to estimate genetic parameters and explore the genetic architecture of body weight and carcass traits of three local chicken ecotypes in Ghana using a genome-wide association study.

Materials and Methods
The chickens used in this study were offspring of those described in Walugembe *et al*. (2020). This study was conducted in four replicates, with a total of 1,113 chickens made up of the Forest, Interior Savanna and Coastal Savanna chicken ecotypes. Chickens were housed in deep litter pens and fed on a standard chick starter mash from day 1 to week 8 and on a standard

chick grower mash from week 9 to week 22. Water was provided *ad-libitum.* Vaccination, feeding, and general husbandry practices were the same for all the birds.
Body weights were taken bi-weekly from hatch until 22 weeks of age. Average daily gain (ADG) was calculated as the linear regression of body weight on age. At week 23, birds were humanely sacrificed, and several carcass traits were measured, including weights of breast, drumstick, thigh, wings, overall dressed weight and dressed percentage.
Blood samples were collected from chicks at 5 weeks of age and DNA was isolated for genotyping by sequencing. The resulting genome sequences were run through a customised in-house SNP-pipeline which resulted in 5K SNP genotypes for each bird. These were then imputed to 382,240 SNPs using post-quality control high-density genotype data of relatives, as described by Walugembe *et al*. (2020). Imputation was performed using Fimpute (Sargolzaei *et al.,* 2014). The three local ecotypes studied here were derived from three ancestral populations (Walugembe et al., 2020). Therefore, to infer the proportions of ancestral subpopulations for all chickens, we performed admixture analyses on the imputed genotypes using the Admixture software (Alexander *et al.,* 2009). The resulting ancestral subpopulation proportions were used as covariates in the downstream genetic analyses.
Variance components and heritabilities were estimated using a univariate model with the fixed effects of replicate, sex, and pen by replicate, ancestral subpopulation proportions as covariates, and random effects of animal genetics and a residual. The model (Model 1) is given by:
$\boldsymbol{y} = \mathbf{Xb} + \mathbf{Z_a a} + \mathbf{e}$, where $\mathbf{y}$ is the vector of phenotypes; $\mathbf{X}$ is the incidence matrix relating fixed effects and covariates to vector $\mathbf{y}$; $\mathbf{b}$ is the vector of fixed effects and covariates; $\mathbf{Z}_a$ is the incidence matrix relating the phenotypes to the vector of random bird genetic effects, $\boldsymbol{a}$, with a genomic relationship matrix computed using method 1 of Van Raden (2008); and $\boldsymbol{e}$ is the vector of random residuals. Some carcass traits were also analyzed by including body weight at week 22 as a fixed covariate (referred to as Model 2). To estimate genetic and phenotypic correlations, we fit pairwise bivariate models with the same effects as in the univariate models. All models were implemented in ASReml 4 (Gilmour *et al*., 2015).
We performed a GWAS using Bayes-B (Meuwissen *et al*., 2001), as implemented in the JWAS package (Cheng *et al*., 2018) to estimate the genetic variance explained by 1-Mb windows of SNPs across the genome. Both Models 1 and 2 were used. One-Mb windows that explained more than 1% of the genetic variance for a trait were considered significant. We used the Genome Data Viewer in NCBI with the *Gallus gallus* 6 genome build to identify candidate genes within the significant 1-Mb windows.

Results and Discussion
Means and estimates of heritabilities, genetic and phenotypic correlations of the studied traits are in Table 1. The effects of ancestral subpopulation proportions were not significant for any of the traits. Replicate and sex were significant for all traits except for breast weight adjusted for BW22. When BW22 was included as a covariate (Model 2), it was significant for all traits. Estimates of heritabilities based on Model 1 were high for all traits, ranging from 0.51 for thigh weight to 0.69 for ADG (Table 1), in line with the findings of Rance *et al.* (2002). Estimates of carcass trait heritabilities adjusted for BW22 were moderate and ranged from 0.21 for thigh weight to 0.38 for wing weight, and were similar to those reported by Gaya *et al.* (2012). All heritability estimates reduced when BW22 was included as a covariate, but the magnitude and direction of the phenotypic and genetic correlations did not change. Estimates of genetic and phenotypic correlations were all positive with moderate to high heritabilities. These findings agree with those previously reported by Zarehdaran *et al*. (2004) but not with the findings of Osei-Amponsah (2010), who reported weak to moderate negative correlations of live weight with most carcass traits at 24 weeks of age, except for carcass weight, for which the correlation

was high and positive. The positive genetic correlations of body weight with carcass traits suggest that the carcass traits will improve with selection on body weight.

Table 1. Means and estimates of heritabilities (along diagonal) and of genetic (above diagonal) and phenotypic (below diagonal) correlations. In each cell, an estimate without BW22 covariate is on top and an estimate with covariate is beneath it.

	BW22	ADG	Dressed wt	Dressing %	Breast	Thigh	Wing	Drumstick
Trait mean	**1179.2**	**7.9**	**798.2**	**70.3**	**194.1**	**128.4**	**97.3**	**116.3**
BW22	**0.58 (0.07)**	0.96 (0.01) 0.96 (0.01)	0.95 (0.02) 0.95 (0.02)	0.24 (0.17) 0.24 (0.17)	0.86 (0.04) 0.78 (0.06)	0.92 (0.03) 0.90 (0.04)	0.88 (0.03) 0.85 (0.04)	0.88 (0.03) 0.84 (0.05)
ADG	0.90 (0.006) 0.91 (0.06)	**0.69 (0.07)**	0.91 (0.02) 0.81 (0.05)	0.22 (0.16) 0.28 (0.16)	0.79 (0.04) 0.60 (0.09)	0.86 (0.04) 0.77 (0.06)	0.83 (0.04) 0.70 (0.07)	0.82 (0.04) 0.69 (0.07)
Dressed wt	0.87 (0.0008) 0.87 (0.008)	0.82 (0.01) 0.65 (0.02)	**0.60 (0.07)** **0.30 (0.07)**	0.53 (0.13) 0.82 (0.09)	0.94 (0.02) 0.77 (0.08)	0.95 (0.02) 0.75 (0.1)	0.93 (0.02) 0.71 (0.09)	0.91 (0.02) 0.61 (0.11)
Dressing %	0.004 (0.03) 0.004 (0.03)	0.06 (0.03) 0.09 (0.04)	0.41 (0.03) 0.69 (0.02)	**0.15 (0.06)**	0.61 (0.13) 0.75 (0.11)	0.47 (0.16) 0.51 (0.2)	0.44 (0.15) 0.45 (0.17)	0.38 (0.16) 0.28 (0.2)
Breast	0.72 (0.02) 0.60 (0.03)	0.67 (0.02) 0.41 (0.03)	0.87 (0.00) 0.74 (0.01)	0.43 (0.03) 0.56 (0.02)	**0.52 (0.07)** **0.29 (0.07)**	0.84 (0.0.5) 0.39 (0.17)	0.86 (0.04) 0.48 (0.13)	0.79 (0.05) 0.22 (0.18)
Thigh	0.78 (0.01) 0.71 (0.02)	0.73 (0.02) 0.59 (0.03)	0.82 (0.01) 0.58 (0.02)	0.27 (0.03) 0.34 (0.02)	0.65 (0.02) 0.30 (0.03)	**0.51 (0.07)** **0.21 (0.07)**	0.89 (0.04) 0.58 (0.14)	0.94 (0.03) 0.76 (0.12)
Wing	0.78 (0.01) 0.72 (0.02)	0.73 (0.02) 0.53 (0.03)	0.87 (0.01) 0.67 (0.02)	0.30 (0.03) 0.40 (0.03)	0.73 (0.02) 0.45 (0.03)	0.73 (0.02) 0.43 (0.03)	**0.62 (0.07)** **0.38 (0.08)**	0.94 (0.03) 0.75 (0.09)
Drumstick	0.82 (0.01) 0.65 (0.02)	0.71 (0.02) 0.53 (0.03)	0.85 (0.01) 0.67 (0.02)	0.35 (0.03) 0.46 (0.03)	0.68 (0.02) 0.35 (0.03)	0.72 (0.02) 0.42 (0.03)	0.80 (0.01) 0.57 (0.02)	**0.55 (0.07)** **0.29 (0.07)**

wt: weight; All weights are given in grams.

After quality control, data on 1,113 birds and 382,240 SNPs were used for the GWAS analysis. When using Model 1, a 75 Mb region on chromosome 4 was significant for all traits except dressing %. This region explained 19.7, 11.6, 12.2, 20.6, 25.2, 19.6, and 14.0% of the genetic variance of BW22, ADG, breast weight, drumstick weight, wing weight, thigh weight and dressed weight, respectively. This region contains the *NCARP, LCORL, LAP 3, LDB2* and *TAPT1* candidate genes. The *NCAPG* gene has been reported to be associated with body size, ADG, carcass traits, and muscle development in beef cattle (Lindholm-Perry *et al*., 2013). Polymorphisms in *LCORL* have been reported to be associated with growth traits in cattle (Lindholm-Perry *et al*., 2013), while *LDB2* has been associated with body weight and ADG in chicken (Gu *et al*., 2011). A 170-172 region on chromosome 1 explained 12.49, 10.6, 6.18, 3.11, 11.91, 11.12, and 14.04% of the genetic variance of BW22, ADG, dressed weight, breast weight, drumstick weight, thigh weight, and wing weight, respectively. This region includes the F*oxO1* gene, a transcription factor that plays a critical role in muscle growth, metabolism, and cell differentiation, and has been shown to be involved in regulating muscle fibre type specification (Yuan *et.al*., 2011). A 19 Mb window on chromosome 2 was found to explain 1.3% of the genetic variance of BW22. This region contains the *TGFBR2* gene, which, together with TGFB-2 proteins, seems to play a role in cell proliferation and differentiation, apoptosis, regulation of muscle tissues, body fat, and bone development. When BW22 was added to the model as a covariate (Model 2), there was a reduction in genetic variance for the carcass traits. Only 6.6% of the genetic variance of breast weight was now explained by three 1-Mb windows on three chromosomes. For drumstick weight, three 1-Mb windows on three chromosomes together explained only 4.4% of the genetic variance. One 1-Mb window explained 1% of the genetic variance of thigh weight, and four windows on four chromosomes together explained 10.2% of the genetic variance of wing weight.

Conclusion

The moderate to high heritabilities obtained for the studied traits and the positively high genetic correlations between them, coupled with the several 1-Mb windows that explained >1% of the genetic variance indicate that these traits can be improved in Ghanaian indigenous chicken populations through selective breeding.

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