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Genomic studies of growth resilience to weather change in indigenous free-ranging chickens in Ethiopia

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Introduction

Poultry is a significant part of the farming systems and household economies in the Ethiopian rural communities. Chickens reared in smallholder village farms yield 98.5% and 99.2% of the national egg and meat output, respectively (Sime, 2022). The indigenous Tilili chicken ecotype is an example of smallholder poultry reared mainly in the West Gojam, Awi Zone, Tilili, Sekela, and Fagita Lekoma districts, exhibiting high phenotypic and genetic diversity (Kassa *et al.*, 2025). Significant genetic variation has been reported for body weight and egg production of Tilili chickens and a selective breeding programme to enhance performance is now in place (Kassa *et al.*, 2025). At the same time, climate change, manifested in recurrent droughts and floods in sub-Saharan Africa (Simane *et al.*, 2016), challenges the stability of production. However, there is evidence that village chickens vary in their ability to perform against increasing weather volatility emanating from climate change (Banos *et al.*, 2025). The present study aims to derive novel phenotypes on the response of growing Tilili chickens to weather variation and investigate the genetic profile of these phenotypes.

Materials & Methods

Animals and data. A total of 3,115 Tilili chickens, reared under smallholder village conditions at the poultry facility of the International Livestock Research Institute (ILRI) in Addis Ababa, Ethiopia, were monitored in 13 batches during 2024-2025. Body weight was recorded weekly on each chicken between weeks 9 and 19 of age. Weather data for the same time-period, including daily maximum, minimum and average air temperature, relative humidity, and amount of precipitation, were extracted from the weather station at the facility. A temperature-humidity index (THI) was developed (Finocchiaro *et al.*, 2005). The study period spanned all local weather seasons (Bega: October-January; Belg: February-May; Kiremt: June-September).

Chicken phenotyping and genotyping. Average daily growth rate was estimated for each chicken based on successive body weight records. Animal growth resilience phenotypes, reflecting changes in chicken growth in response to weather volatility, were then developed using the following random regression models:

$$\mathbf{y}_{ij} = \mathbf{X} + \mathbf{f}(\boldsymbol{\beta}, \mathbf{X}_j) + \boldsymbol{\alpha}_i + \mathbf{e}_{ij} \quad (1)$$

$$\mathbf{y}_{ij} = \mathbf{X} + \mathbf{f}(\boldsymbol{\beta}, \mathbf{X}_j) + \mathbf{f}_i(\boldsymbol{\beta}_i, \mathbf{X}_j) + \mathbf{e}_{ij} \quad (2)$$

Model (1) describes the population level response to weather change: $\mathbf{y}_{ij}$ is the average daily growth rate of chicken *i* in relation to weather variable *j*; **X** denotes the fixed effects (sex and combined batch and local season); $\mathbf{f}(\boldsymbol{\beta}, \mathbf{X}_j)$ is the population norm function describing the relationship between overall performance and weather; $\boldsymbol{\alpha}_i$ is the deviation of chicken *i* from the

population mean; $\mathbf{e}_{ij}$ is the random residual. Model (2) describes the individual animal response: $\mathbf{f}_i(\boldsymbol{\beta}_i, \mathbf{X}_j)$ is the second-degree Legendre polynomial function of the relationship between the daily growth of chicken i and weather variable j, expressed as a deviation from the population norm $\mathbf{f}(\boldsymbol{\beta}, \mathbf{X}_j)$; all other effects are as in model (1).

The slopes at the tangent on each point of the individual reaction norm represent animal phenotypes of growth resilience to weather change at specific points. Specifically, we derived two resilience phenotypes for each chicken and individual reaction norm by calculating the derivatives at two points of the quadratic curve, each on either side of the absolute maximum value. The latter, for example, was 14ºC for minimum air temperature and the two chosen derivative points were at 7ºC and 12ºC. Thus, for the six weather variables of study, 12 growth resilience phenotypes were derived per chicken. These calculations considered chickens with at least seven weekly body weight measurements (n=2,406).

All chickens were sequenced at low coverage (0.5X). Single-nucleotide polymorphisms (SNPs) were imputed using the *Gallus gallus* 6 assembly (GRCg6a) and a reference panel of approximately 21 million variants. Quality control removed samples and markers with call rates <0.90, loci with minor allele frequency <0.01, deviation from Hardy-Weinberg equilibrium ($P<10^{-8}$) and identity-by-state >0.98. Following Linkage Disequilibrium pruning ($r^2=0.8$), 2,305 chickens and 2,681,680 autosomal SNPs remained for the genomic analyses.

Genomic analyses. Univariate single-step genome-wide association analyses were conducted to estimate variance components and identify genomic markers and regions associated with the growth resilience traits. Models included the fixed effects of batch and the first Principal Component (PC) from the PC analysis of genotypes and the random animal additive genetic effect linked to both pedigree (n= 4,469) and genomic relationship matrices (Legarra *et al.,* 2009).

BLUPF90+ (Misztal *et al.*, 2014) was used to estimate genomic breeding values for each animal. SNP effects were then obtained by back-solving genomic breeding values using POSTGSF90 (Wang *et al.*, 2012). After Bonferroni correction, a SNP was considered as genome-wide significant if $P<1.864\times10^{-8}$ or suggestive if $P<3.729\times10^{-7}$. Additionally, 1 Mb sliding-window genomic analyses were conducted using POSTGSF90 and the proportion of genetic variance explained by each genomic window was calculated. Positional candidate genes were explored within the genomic window that accounted for the highest proportion of genetic variance for each trait using Ensembl BioMarts hub. All positional candidate genes were subjected to the g:Profiler web-based toolset for pathway analysis.

Results & Discussion

Trait variation and heritability. Substantial variation in all growth resilience phenotypes is reflected in the large coefficient of phenotypic variation estimates summarised in Table 1. All traits except for resilience to humidity exhibited significant ($P<0.05$) genetic variance with heritability estimates ranging from 0.05 to 0.19, which were slightly lower than a previous genomic study on the tropically adapted Sasso commercial cross reared in similar conditions (Banos *et al.*, 2025). Low heritability estimates are generally expected for animal fitness traits such as resilience to external stressors; nevertheless, presence of genetic variation supports the possibility of selective breeding to enhance growth resilience (Goddard, 2009).

Table 1. Coefficient of phenotypic variation (CV) and heritability (h^2) and genetic variance (σ^2_g) estimates for 12 phenotypes of growth resilience to weather change.

Growth resilience trait by weather variable		CV (%)	h^2 (se)	σ^2_g
Minimum air temperature	7°C	116.10	0.18 (0.03)	1.8×10^{-1}
	12°C	93.62	0.06 (0.02)	0.52×10^{-1}
Average air temperature	15°C	50.33	0.10 (0.03)	0.81×10^{-1}
	17°C	70.06	0.10 (0.03)	0.79×10^{-1}
Maximum air temperature	19°C	79.53	0.05 (0.02)	0.36×10^{-1}
	23°C	127.03	0.05 (0.02)	0.42×10^{-1}
Average humidity	45 %	293.96	0.01 (0.01)	0.83×10^{-2}
	75 %	342.65	0.00 (0.00)	0.66×10^{-4}
Average THI	14.5	79.03	0.10 (0.03)	0.83×10^{-1}
	16.5	85.26	0.11 (0.03)	0.92×10^{-1}
Average precipitation	4 mm	27.39	0.08 (0.02)	0.76×10^{-1}
	11 mm	29.04	0.19 (0.03)	1.8×10^{-1}

Genomic markers and regions and candidate genes. Twenty-five SNPs were detected across 10 of the studied traits. Two genome-wide significant SNPs were identified on chromosome 1 (170,489,776 bp, $P=6.68 \times 10^{-9}$) and 4 (75,891,838 bp, $P=1.43 \times 10^{-8}$) for minimum daily temperature (7°C) and average daily precipitation (11 mm), respectively. The *CAB39L (calcium binding protein 39 like)* and *NCAPG (non-SMC condensin I complex subunit G)* genes, which contained these SNPs, were previously associated with chicken growth (Wang *et al.*, 2022, Romanov *et al.*, 2023). The significance of the remaining 23 SNPs was suggestive.

Table 2 presents the 1 Mb sliding-windows explaining the highest proportion of the corresponding trait variance. A region on chromosome 18 (8,991,738-9,991,645 bp) was associated with five of the studied traits and included 68 annotated genes. In total, 96 genes were detected within these genomic windows, among which *MDM2* and *DYRK2* for average daily precipitation (11 mm) participate in the regulation of TP53 activity through the Phosphorylation pathway (FDR P=0.003). This pathway is related to genotoxic stress (Colman *et al.*, 2000). The small proportion of genetic variance accounted for by each window suggests a polygenic mode of inheritance of the studied growth resilience traits.

Conclusions

Random regression models enable the derivation of meaningful resilience phenotypes reflecting changes in chicken growth under varying weather conditions. The significant genetic variance reported in the present study may inform breeding programmes towards enhancing the Tilili chicken productivity under changing climate conditions. Correlations with other animal traits in the breeding goal should be considered.

Table 2. Genomic windows accounting for the highest proportion of variance for growth resilience traits.

Chromosome: genomic region (bp)	%of genetic variance explained	Growth resilience traits	Number of genes
1:34,945,607-35,945,352	0.98	Average daily precipitation (11 mm)	19
1:37,448,702-38,448,348	1.3	Average daily precipitation (4 mm)	9
1:37,676,456-38,676,150	1.88	Minimum daily temperature (12ºC)	9
18:8,991,738-9,991,645	1.41, 1.29, 1.29, 1.15, 1.15	Average daily temperature (15ºC), THI 14.5, Average daily temperature (17°C), THI 16.5, Minimum daily temperature (7ºC)	68
18:8,997,562-9,997,508	1.35, 1.21	Maximum daily temperature (19ºC), Maximum daily temperature (23ºC)	67

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