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413. Phenotypic characterisation of African chickens raised in semi-scavenging conditions

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Abstract

In sub-Saharan Africa, most poultry production is traditional with birds being raised by smallholders in free-range semi-scavenging conditions. The aim of our project is to extensively characterise phenotypes of chickens raised in typical African farming conditions, by measuring production, immunity and survival characteristics. In total, 2,573 chickens were raised in five batches in the poultry facility at ILRI in Ethiopia. These chickens were phenotypically characterised and sampled across an eight-week period. Traits measured included weekly body weight, growth rate, breast muscle weight in carcass, mortality/survival, and immunological titres. The population of chickens had extensive variance at these phenotypes. For body weight, 65% of the total phenotypic variance was attributed to the individual birds providing an excellent source of variation for identifying potential selection markers. This data will subsequently be used along with whole genome sequencing data of these birds to identify selection targets to underpin future breeding programs.

Introduction

In recent years much progress has been made in identifying selection signatures in the genomes of poultry to improve poultry production. This has been primarily focussed on commercial species used in large farming enterprises in developed nations (Wolc *et al.* 2016), with huge gains made in growth rate and feed efficiency in the past few decades (Zuidhof *et al.* 2014). In Africa, 80% of poultry production is in the form of smallholder farms, where chickens are typically raised in free-ranging semi-scavenging conditions (Sonaiya 2008), but there is limited knowledge of the phenotypic characteristics and genetics of these chickens. Phenotypic characterisation and identification of genomic selection targets is necessary for the genetic improvement of chickens adapted to extensive semi-scavenging conditions.

In this study we aimed to comprehensively characterise the phenotypes of typical African dual-purpose village chickens, raised in simulated semi-scavenging conditions in Ethiopia, focusing on meat production, immunity and survival.

Materials & methods

Bird trials, phenotyping and sampling. A total of 2,573 T4451 Sasso birds, a dual-purpose chicken, were raised in five batches of approximately 500 birds across the span of a year at the poultry facility of the International Livestock Research Institute in Ethiopia. The birds were raised in outdoor, semi-scavenging conditions (feed mainly from scavenging with some supplementation from day 56 of age, for approximately 8 weeks until they reached an average market weight of approximately 1,500 g (except batch 1 which was raised until 1000 g was achieved). Body weight was recorded weekly. At the beginning of the experiment, blood (from wing vein) and cloacal swabs were collected for genotyping and immune phenotyping, and the

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sex of the birds was recorded. Across the trial period the health of the birds was monitored, disease episodes (including coccidiosis) were recorded, and the day and cause of death were recorded, when applicable. At the last day of the experiment (day of slaughter), blood, cloacal and buccal samples were collected for additional immune phenotyping. Breast muscle was excised and weighed, and liver, heart, spleen and ileum samples were collected and stored in RNA-later and frozen at -80 °C for future transcriptomic studies.

Immune phenotyping. Blood from 2,573 birds from day 56 and 2,097 birds from the day prior to slaughter, was allowed to coagulate overnight at room temperature prior to removal of serum. Serum samples were stored at -20 °C. The cloacal samples from the same birds were retrieved using floxed swabs that were subsequently placed in 500 µl of PBS and stored at -20 °C. Serum anti-NDV titres were analysed using commercial IDEXX NDV ELISA kits (serum dilution 1:100). Cloacal samples were analysed for total IgA levels using direct in house developed sandwich ELISA.

Statistical analysis. A mixed model was used to assess the impact of the batch, age and sex on body weight and estimate the proportion of variance attributed to individual birds. A fixed effect model was used to examine the impact of the same effects on the other traits. Model analysis was conducted in ASReml-W 4.2.

Results

Data are summarised in Table 1. The data demonstrated that the chickens were phenotypically diverse with extensive variance in body weight, growth rate and breast muscle weight.

The key quantitative traits measured all significantly differed by batch and age, likely due to variation in season across the batches (Table 2). In addition, sex differed significantly for weight-related traits, as

Table 1. Data summary of key traits from chicken trials.

Batch[1]	F/M[2]	1	2	3	4	5	Total
No. birds		511	520	520	507	515	2,573
No. mortalities		152	21	75	85	175	511
Sex ratio (%F)		79.7	58.5	60.0	61.7	59.4	62.2
Body weight – start (g)	F	495(85)	516(53)	544(95)	525(113)	566(92)	527(93)
	M	548(89)	566(71)	638(88)	671(142)	662(87)	624(109)
Body weight – end (g)	F	1,092(176)	1,434(190)	1,474(259)	1,280(289)	1,269(233)	1,312(271)
	M	1,220(195)	1,572(257)	1,786(314)	1,528(322)	1,543(265)	1,572(319)
Growth rate (g/d)	F	21.1(4.4)	16.4(3.1)	13.8(3.3)	13.3(4.0)	12.5(3.6)	15.6(4.8)
	M	23.8(4.9)	18.0(4.1)	17.2(4.2)	15.3(4.5)	15.7(4.4)	17.3(5.0)
Breast muscle weight	F	173(38)	266(45)	236(54)	201(58)	217(53)	219(59)
	M	190(36)	289(56)	270(59)	226(61)	246(47)	253(63)
Start NDV titres		0.35(0.24)	0.29(0.23)	0.16(0.15)	0.61(0.44)	0.31(0.42)	0.34(0.30)
End NDV titres		0.12(0.13)	0.15(0.22)	0.13(0.12)	0.17(0.14)	0.97(0.28)	0.35(0.36)
Start IgA titres		0.27(0.42)	0.57(0.61)	1.09(0.81)	0.45(0.62)	0.86(0.76)	0.65(0.72)
End IgA titres		0.97(0.58)	0.86(0.93)	0.46(0.60)	1.21(0.81)	1.41(0.86)	0.87(0.83)

[1] Mean(sd).

[2] Female/male.

Table 2. Significance (F-stat) of fixed effects on key quantitative traits.[1]

	Sex	Age	Batch
Body weight	322.65**	242.28**	136.38**
Growth rate	160.58**	355.22**	234.74**
Breast muscle weight	109.88**	152.8**	176.61**
Start NDV titre	5.36*	93.25**	109.34**
End NDV titre	1.84	113.97**	1,351.61**
Start IgA titre	5.14*	152.61**	93.51**
End IgA titre	0.04	111.09**	83.67**

[1] * = P<0.05, ** = P<0.001.

expected, though had less impact on the NDV antibody and IgA titres. The proportion of phenotypic variance in body weight attributed to the individual bird was 65.3% (±0.8%).

Across the five batches, 511 mortalities were recorded for a range of reasons including predation, huddling and disease (primarily coccidiosis infection) (Figure 1), which are common causes of mortality in smallholder African farms. The cause and rate of mortality varied by batch, particularly in terms of predation and diseases.

NDV titres showed extensive variance across the samples, indicating a range in immune response to NDV vaccination (Figure 2). This varied both within and between batch, with titres falling across the test period in batches 1-4 but increasing in batch 5. IgA titres likewise showed strong variance across the dataset. Batch 5 also experienced a large outbreak of the parasitic disease coccidiosis, and NDV titres at the beginning of the experiment were found to be significantly associated with coccidiosis mortality ($P<0.01$).

Discussion

In this study we phenotypically characterised over 2,500 closely monitored chickens raised in simulated semi-scavenging smallholder village conditions in Ethiopia. This includes key production and health traits

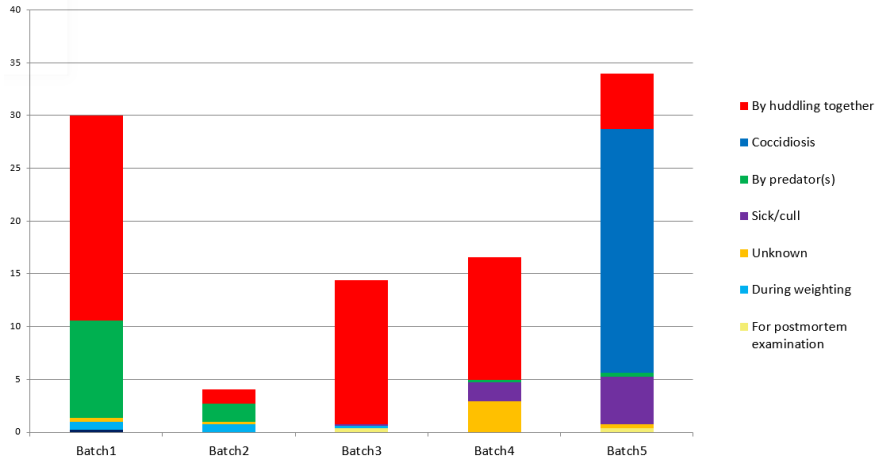

Figure 1. Percent mortalities by batch and cause.

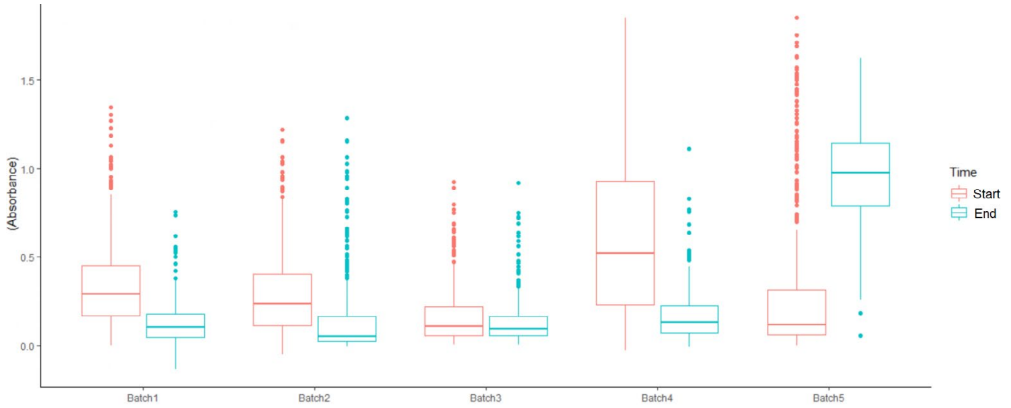

Figure 2. NDV titres of birds at the start and end of the experiment by batch.

including body weight, growth rate, carcass breast weight, disease, mortality, and antibody titres. The analysis of these traits, and selection of chickens adapted to smallholder farm conditions in developing and tropical nations has not achieved the same progress as in the developed world.

We observed extensive variation in the studied traits; we anticipate a proportion of this will reflect genetic variability which can be used for the identification of selection sites for use in breeding programs. Additionally, the substantial number of mortalities observed in this study due to predation and infection will be key for identifying genetic signatures important for survival. These will be critical for African farms as high mortality has been identified as the greatest constraint to poultry production (Sonaiya 2008).

We now aim to genotypically sequence and characterise all of the chickens used in this study. Using the combined phenotypic and genomic data we will identify genes and genomic regions associated with these traits that can be subsequently used as selection targets in breeding programs. In addition, we have identified 48 birds which have the highest and lowest growth and immune trait records, which will be studied using RNA-Seq to further understand the molecular mechanisms underlying these traits. This study will be key for the optimisation of breeding programs and the improvement of poultry in typical smallholder farms in Africa.

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References

Sonaiya F. (2008) Smallholder family poultry as a tool to initiate rural development. International Conference Poultry in the Twenty-first Century: avian influenza and beyond: 5–7 November 2007. Bangkok, Thailand: FAO.

Wolc A., Kranis A., Arango J., Settar P., Fulton J.E., *et al.* (2016) Anim. Front. 6 (1):23–31. https://doi.org/10.2527/af.2016-0004

Zuidhof M., Schneider B., Carney V., Korver D., Robinson F. (2014) Poult. Sci. 93:2970–2982. http://doi.org/10.3382/ps.2014-04291