Genetic Parameters and Genomic Regions Associated with Growth Rate and Response to Newcastle Disease in Local Chicken Ecotypes in Ghana and Tanzania

A.S. Leaflet R3260

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Summary and Implications

Local chicken enterprises in Africa are of great importance to household livelihoods but face major constraints with devastating disease outbreaks such as Newcastle disease (ND), which cause major economic losses. A study was conducted in two countries, Ghana and Tanzania, where three ecotypes in each country were challenged with a lentogenic (vaccine) strain of ND virus and various response phenotypes, including growth, anti-NDV antibody levels, and viral load from hatch to 38 days of age were taken. We estimated variance components and performed a genome-wide association study (GWAS) using ~2800 birds. Moderate heritabilities (0.14-0.55) of the above traits indicated that selection to improve these breeds/ecotypes for resistance to ND could be feasible. Genome-wide association analyses revealed several genomic regions that explained more than 0.5% of the genetic variance, including a candidate gene region for antibody response on chromosome 1. Future studies will characterize differences between the breeds/ecotypes, determine if large breed-specific quantitative trait loci can be identified, and evaluate the response of the same birds to endemic, velogenic ND virus strains.

Introduction

Local chicken ecotypes play an important role in household livelihoods in both rural and urban areas of Africa. They are mostly reared by small-holder farmers who depend on them for meat, eggs, and as source of income. In Ghana, they account for about 70% of the national poultry population, and they present a major supply of chicken and eggs consumed in rural and urban areas of Tanzania.

Diseases, particularly ND, are major challenges to local chicken production in sub-Saharan countries and often leave no survivors in unvaccinated flocks. Vaccination is not an adequate mean of controlling ND in rural Africa because of high costs, lack of a “cool chain”, poor husbandry practices, instability of vaccines, and difficulty in correctly administering vaccines. Selective breeding would be an effective complement or alternative to vaccination, if genetic variation for resistance, tolerance, and/or response to ND exits in the population.

In this study, local chickens from three Ghanaian ecological zones (Coastal Savannah, Forest, and Interior Savannah) and from three Tanzanian local ecotypes (Ching’wekwe, Kuchi, and Morogoro medium), were challenged with a high-titered LaSota lentogenic ND virus vaccine strain, with the aim of estimating genetic parameters and identifying genomic regions associated with productivity and response to ND challenge.

Materials and Methods

Challenge experiments (four and five replicates for Ghana and Tanzania, respectively, for a total of 1941 and 1904 birds) were conducted from hatch to 38 days of age (doa), with birds raised under similar conditions. Blood samples were collected at 27 doa and ELISA was used to quantify maternal antibody levels. Birds were challenged with a lentogenic NDV strain (LaSota) at 28 days of age via ocular-nasal route and tear samples were collected at 2 and 6 days post-infection (dpi) to measure viral load using RT-qPCR. At 10 dpi, blood samples were collected and ELISA was used to quantify ND virus antibody levels. Body weights were recorded at hatch, 7, 14, 21, 28, 34 and 38 doa. Pre- and post-infection growth rates were calculated from these by linear regression of weight on age.

DNA samples were extracted from all birds to determine genotypes for 346,067 markers using the 600K Affymetrix genotyping array. Various statistical methods were used to determine how much growth rate, antibody production, and viral load were determined by genetics vs the environment. GWAS was performed to identify genomic regions associated with these traits.

Results and Discussion

Numbers of records, heritabilities, and variances due to maternal effects (dam) are in Table 1. Heritabilities for all traits were moderate to high, indicating good potential for improving these traits with selective breeding. For the Ghanaian population, heritability for viral load was higher at 2 dpi than at 6 dpi.

For Ghana, there were 13 regions on 10 chromosomes that together explained 13.3% of genetic variance for pre-infection growth rate, 9 regions on 7 chromosomes explaining 8.4% of genetic variance for post-infection growth rate, 7 regions on 6 chromosomes explaining 8.3% of genetic variance for antibody titer at 10 dpi, and 9 regions on 6 chromosomes explaining 11.2% of genetic variance for viral load at 2 dpi. For Tanzania, there were 9 regions on 7 chromosomes that together explained 7.3% of genetic variance for pre-infection growth rate, 3 regions on 3 chromosomes explaining 2.6% of genetic variance for post-infection growth rate, and 4 regions on 3 chromosomes explaining 2.8% of genetic variance for antibody titer at 10 dpi, of which one, at around 100 Mb on chromosome 1, has been reported as a candidate region for antibody response. Although GWAS revealed several genomic regions that explained more than 0.5% of the genetic variance, we should note that all traits investigated in this study appear to be highly polygenic in nature.

Conclusion

These results provide novel insights that could be used to improve local chicken resistance to ND virus. Future studies will focus on identifying whether there are significant differences between the ecotypes and if any large ecotype-specific quantitative trait loci can be identified, such that genetic markers can be used for genomic selection and breeding for local chickens that are less susceptible to ND virus infection. We will also evaluate response of the same birds to endemic velogenic ND virus strains.

Acknowledgements

This study was funded by the USAID Feed the Future Innovation Lab for Genomics to Improve Poultry.

Table 1. Number of records, heritabilities and ratio of dam/phenotypic variance.

Trait	Ghana			Tanzania		
	N	h^2 (se)	σ_d^2/σ_p^2	N	h^2 (se)	σ_d^2/σ_p^2
Pre-infection GR	1436	0.55 (0.08)	0.07	1392	0.43 (0.05)	0
Post-infection GR	1401	0.41 (0.08)	0	1359	0.29 (0.05)	0
Log_{10}Antibody titer	1425	0.23 (0.07)	0.03	1394	0.14 (0.06)	0.03
Log_{10}Viral load, 2dpi	549	0.49 (0.15)	0.03	0	-	-
Log_{10}Viral load, 6dpi	333	0.26 (0.20)	0.01	529	0.22 (0.13)	0.006

N: number of records. se: standard error. σ_d^2: dam variance. σ_p^2: phenotypic variance. GR: growth rate. dpi: days post-infection.