Genetic Parameters and Genome-Wide Association Study of Newcastle Disease Response Traits in Tanzania and Ghana Local Chicken Ecotypes

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Summary and Implications

Local chicken production is of great importance to African households but faces major threats due to devastating Newcastle disease (ND) outbreaks that can cause significant economic losses. Newcastle disease also remains a threat in the US, as illustrated by recent outbreaks in domestic poultry in California. This study was conducted in two countries, Ghana and Tanzania, where three ecotypes in each country were challenged with a lentogenic (vaccine) strain of the ND virus and various response traits, including growth, anti-ND virus antibody levels, and viral load were recorded. We estimated variance components and performed a genome-wide association study (GWAS) using 2839 birds. Moderate heritability estimates (0.15-0.55) for the above traits indicated that selection to improve these breeds/ecotypes for resistance to NDV could be feasible. GWAS results revealed several genomic regions that explained ≥0.5% of the genetic variance in response to ND virus. Ongoing research is establishing relationships of ND vaccine response with response to velogenic ND virus challenge.

Introduction

Local chicken ecotypes play an important role in household livelihoods in both rural and urban areas of African communities. They are a great source of high-quality protein in the form of eggs and meat, and an important asset to in, particular women and children. In Ghana, local ecotypes account for about 70% of the national poultry population and are the predominant source of chicken and eggs consumed in rural areas of most African rural communities.

Poultry diseases, such as Newcastle disease ND, are a major threat to the poultry industry globally and severe outbreaks of the velogenic strains of ND virus (NDV) in African local chicken populations often leave no survivors in unvaccinated flocks, which causes significant economic losses to households. Vaccination is not an adequate control means in these situations because of high costs, instability of vaccines, lack of a "cool chain", difficulty in correctly administering vaccines, and poor husbandry practices. Selective breeding would be an effective complement to vaccination, if genetic variation in 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 three Tanzanian local ecotypes (Ching'wekwe, Kuchi and Morogoro medium), were challenged with a high-titered LaSota lentogenic NDV strain, with the aim of estimating genetic parameters and identifying genomic regions associated with productivity and response to NDV challenge.

Materials and Methods

Challenge experiments (four and five replicates for Ghana and Tanzania, respectively, for a total of 1440 and 1399 birds, respectively) 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 doa via the 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 the anti-NDV 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 body weight on doa.

DNA was extracted from all birds and birds were genotyped using a 650K Affymetrix SNP panel. Various statistical methods were used to determine how much of the

observed variation in growth rate (pre- and post-infection), antibody production, and viral load was determined by the genetics of the birds rather than the environment. genome-wide association study (GWAS) was performed to identify genomic regions associated with the different response traits to NDV infection.

Results and Discussion

Viral load was higher at 2 than 6 dpi for all breeds or ecotypes, indicating that birds started to clear the virus by 6 dpi. Estimates of heritability and of proportion of phenotypic variance contributed by the dam are given in Table 1. Heritabilities for all traits were moderate to high, indicating that selection to improve these breeds or ecotypes for resistance to ND could be feasible. For the Ghanaian population, viral load had a higher heritability at 2 dpi than at 6 dpi.

For Tanzania, a 1-Mb window on chromosome 24 explained 12.4 and 11.5% of genetic variance for viral load at 6 dpi and viral clearance, respectively. This region contained markers that are in proximity of genes that are associated with immune response and has been reported as a candidate region for viral load to ND at 6 dpi in other studies. For other response traits, based on regions that explained >0.5% of genetic variance, there were 9 regions on 8 chromosomes that together explained 6% of genetic variance for pre-infection growth rate, 2 regions on 2 chromosomes that explained 2% of genetic variance for post-infection growth rate, 7 regions on 6 chromosomes explaining 4.7% of genetic variance for antibody titer, and 4 on 3 chromosomes explaining 3.8 % for viral load at 2 dpi. For Ghana, there were 11 regions on 9 chromosomes that together explained 10.4% of the genetic variance for pre-infection growth rate, 6 regions on 4 chromosomes explaining 17.4% of genetic variance for post-infection growth rate, 8 regions on 7 chromosomes explaining 6.3% of the genetic variance for antibody titer, 5 regions on 3 chromosomes explaining 8.2% of genetic variance for viral load at 2 dpi, and 6 regions on 5 chromosomes explaining 4.1% of the genetic variance. Although GWAS revealed several genomic regions that explained ≥ 0.5% of the genetic variance, we should note that all traits investigated in this study appear to be highly polygenic in nature.

Conclusion

Host response to infection with a lentogenic strain of NDV in local African chickens was found to be heritable and association studies revealed several genomic regions that explained ≥0.5% of the genetic variance, including candidate gene regions for different response traits. Understanding the genetic basis of ND will provide a discovery platform to develop strategies to aid in genetic selection of chickens for better NDV resistance and vaccine response. Enhanced genetic resistance to Newcastle disease will also improve global food security, as well as protecting the US poultry industry.

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Table 1. Estimates (± standard error) of heritability and proportion of phenotypic variance associated with maternal effects.

Trait	Ghana			Tanzania		
	N	Heritability	Maternal	N	Heritability	Maternal
Pre-infection growth rate	1436	0.55 ± 0.05	0.02	1392	0.34 ± 0.07	0.02
Post-infection growth rate	1400	0.43 ± 0.05	0.01	1359	0.21 ± 0.06	0.00
Log_{10}Antibody titer	1425	0.29 ± 0.05	0.02	1394	0.22 ± 0.05	0.00
Log_{10}Viral load, 2 dpi	1377	0.40 ± 0.06	0.03	1375	0.18 ± 0.07	0.06
Log_{10}Viral load, 6 dpi	1324	0.22 ± 0.00	0.01	1365	0.29 ± 0.15	0.00
Viral Clearance	1270	0.004 ± 0.03	0.003	1342	0.15 ± 0.06	0.04

N: number of records. dpi: days post-infection.