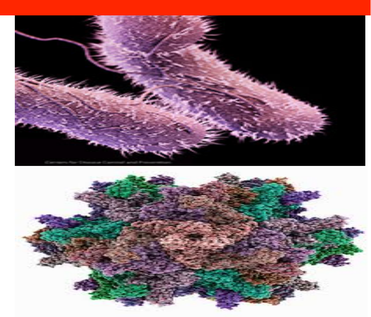
Identification of SNP markers for resistance to *Salmonella* and IBDV in Indigenous Ethiopian Chickens

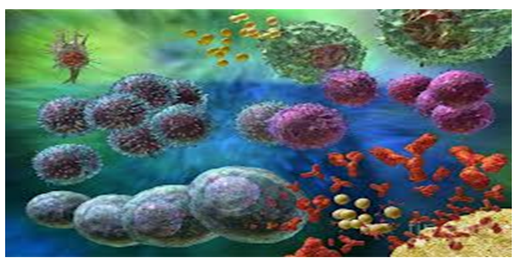
A. Psifidi[1], G. Banos[1], O. Matika[1], T. Dessie[2], R. Christley[3], P. Wigley[3], J.M. Bettridge[3], O. Hanotte[4], T. Desta[4], P. Kaiser[1]

[1]The Roslin Institute & R(D)SVS, University of Edinburgh, UK; [2]International Livestock Research Institute, Addis Ababa, Ethiopia; [3]Institute of Infection & Global Health, University of Liverpool, UK; [4]School of Life Sciences, University of Nottingham, UK.

Introduction

- **Poultry** play an important role in the agriculture of Ethiopia. Indigenous chickens tend to be well adapted to their local environment.
- **Infectious diseases** have a major impact on productivity since there is limited use of **prophylactic medication** and **vaccination.**
- **Salmonellosis,** a zoonosis caused by a gram-negative enteric bacterium, and **Infectious Bursal Disease** (IBD), a highly contagious immunosuppressive viral infection (caused by Infectious Bursal Disease virus (IBDV) have been identified as two of the most important infectious diseases in Ethiopian poultry.
- There is evidence of **genetic variation** associated with **resistance** to ***Salmonella*** in different chicken lines, but **nothing** is known for **IBDV resistance**.
- **Breeding chickens resistant to *Salmonella* and IBDV** provide an under-exploited, cost-effective and permanent **approach to control these diseases**.



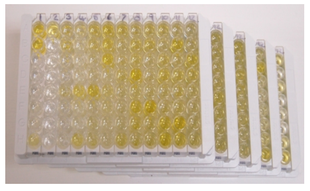


Hypotheses and Objectives:

- Previous studies in inbred and outbred exotic chicken lines using whole genome microsatellite markers have identified QTLs (Quantitative Trait Locus) for *Salmonella* resistance.
- Our **hypothesis** is that there are **QTLs for *Salmonella* and IBDV resistance** circulating among **indigenous Ethiopian chickens**.
- **Using two important indigenous chicken populations and high density whole-genome SNP (Single Nucleotide Polymorphism) arrays we will try to identify SNP markers for increased resistance to *Salmonella* and IBDV infection.**

Materials and Methods

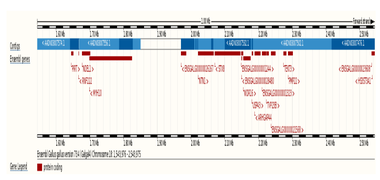
- Blood samples from **760** birds, 384 from **Horro** and 376 from **Jarso**, two geographical regions about 800 km from each other, were collected over two years.
- **Phenotypes** (serological data) were based on single tests of individual's sera using an **in-house ELISA for *Salmonella*** and a **commercially available ELISA kit for IBDV**.
- A high density whole genome SNP array (**620K, Affymetrix**) was used.
- A multidimensional scaling analysis (**MDS**) was performed using GenABEL software to identify if there are any genetic differences between the two chicken populations.
- A Genome-Wide Association Study (**GWAS**) was performed using PLINK and GEMMA software. **Bonferroni correction** for multiple testing was applied.
- Searching for **genes of interest** located close to the identified markers was performed using **Ensembl** database**.**



Phenotypes: ELISA data for Salmonella *and IBD*

Genotyping with 620K Affymetrix array

GWAS using PLINK and GEMMA software

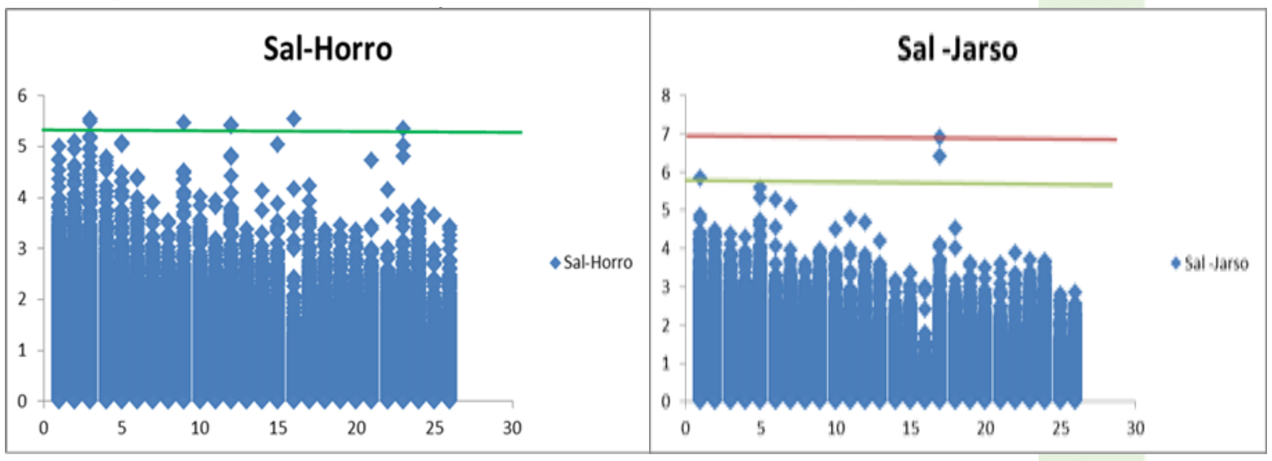


Searching for genes of interest using Ensembl

Results

GWAS results:

- The multidimensional scaling analysis showed that **Horro** and **Jarso** populations were **genetically distinct**.
- In **Horro** chickens, the genome-wide scan revealed **9 SNP with chromosome-wide** significant association with ***Salmonella*** **resistance** and **7 SNP with genome-wide** significant association with **IBD resistance**.
- In **Jarso** chickens, the genome-wide scan revealed **1 SNP with genome-wide** and **2 SNP with chromosome-wide** significant association with ***Salmonella*** **resistance** and **1 SNP with genome-wide and 3 SNP with chromosome-wide** significant association with **IBDV resistance**.



Manhattan plot: x-axis shows the chicken chromosomes, y-axis the P values of the markers associated with Salmonella *(Sal-Horro and Sal-Jarso) and IBDV resistance (IBDV-Horro and IBDV-Jarso), the red line is the genome-wide threshold, the green line is the chromosome-wide threshold.*

Conclusion

Different QTLs for ***Salmonella*** **and IBDV resistance** were **identified in the two indigenous Ethiopian chicken populations**; this is consistent with the **MDS analysis** which showed that the two populations are different genetically.

Almost all the **markers** identified for resistance were **located close** to **candidate genes** involved in the **immune response**.

Results of this study are encouraging for breeding for *Salmonella* and IBDV resistance in indigenous Ethiopian chickens. However, a different genomic selection programme should be developed for each of the two populations.