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Mapping genomic regions associated with resistance to infectious diseases in Ethiopian indigenous chickens

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Background

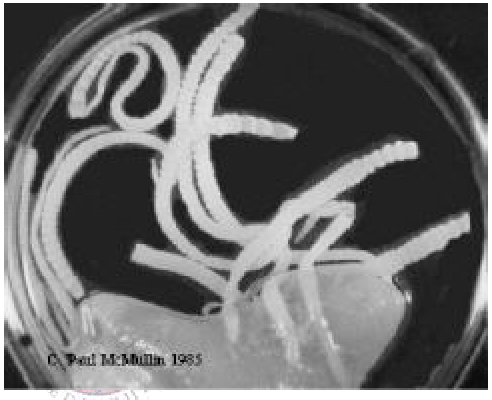
- **Poultry in Ethiopia:**
  - **Smallholder productive systems– backyard chickens**
- **Indigenous chickens:**
  - **well adapted**
  - **low productivity**
  - **infectious diseases**
- **Breeding programmes** to improve **productivity**
- **Is it also possible to select for enhanced resistance to infectious diseases?**

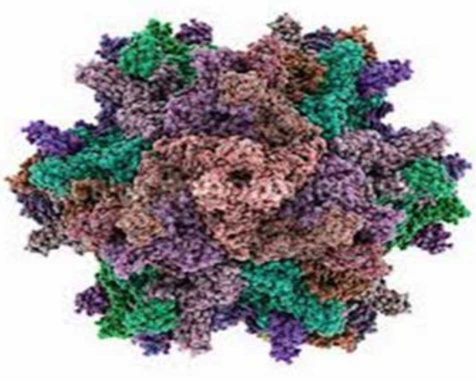
More background -Objectives

The **major infectious diseases** in Ethiopia:

- Fowl typhoid (*Salmonella gallinarum,* SG)
- Fowl cholera (*Pasteurella multocida,* PM)
- Infectious Bursal Disease (IBDV)
- Marek's Disease (MDV)
- Coccidiosis (*Eimeria* spp)
- Cestodes

To identify **SNP markers** associated with:
enhanced immune response to SG, PM, IBDV, MDV and resistance to *Eimeria* and cestodes parasitism





Populations

Two populations of indigenous Ethiopian village chickens

384 chickens from **Horro region**

376 chickens from **Jarso region**

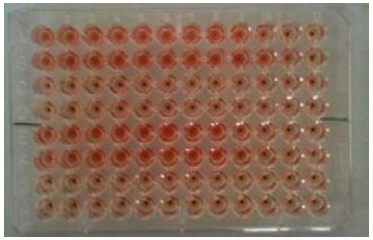
>800 km

Random sampling :

- **4 villages**
- **50 farms**
- **2 chickens**

Psifidi et al., *2016*

Phenotypes/Genotypes



For immune responses: **serological data (ELISA**)

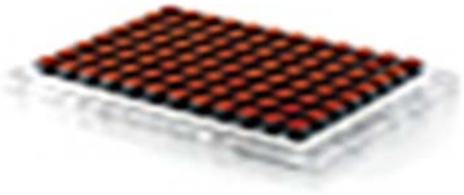
antibody titres: SG, PM,IBDV, MDV

Parasitic resistance: **oocysts counts (/gr of faeca)**

Blood samples were collected using **FTA cards**

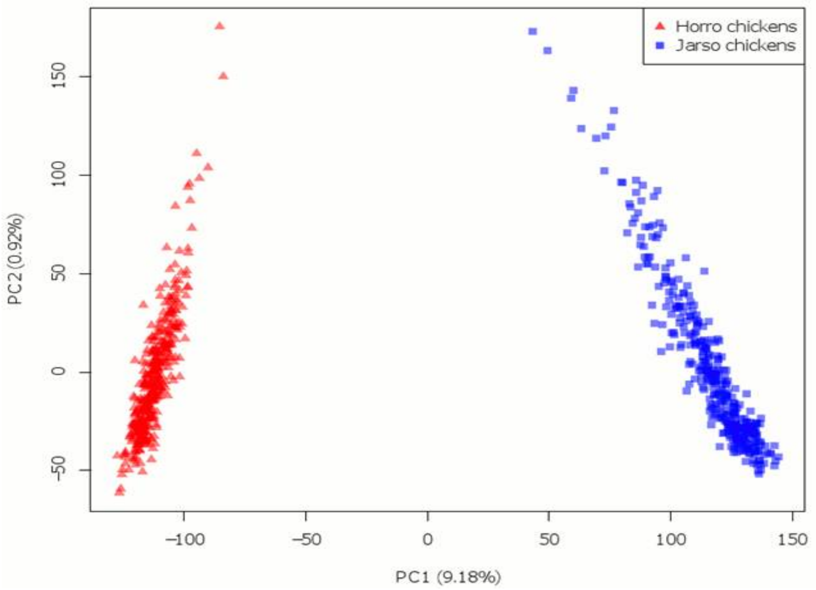
All (760) the birds were genotyped using the **620K array** (Affymetrix)

10 birds were **re-sequenced** (HiSeq, Illumina)



Analysis-GWAS

- **Quality control** (PLINK)
  - GENO 0.05, MAF 0.05, HWE 1x10^{-6}
  - 414,134 SNP markers remained
- **Principal component analysis** (GenABEL)
  - The two populations are **genetically distinct**



Analysis-GWAS

- **Association analysis** (GEMMA)
  - Mixed model accounted for:
    - **Genetic relationship matrix**
    - **population**
    - **village**
    - **collection date**
    - **sex**
    - **ELISA plate-to-plate variation**
    - **age**
    - **weight**
  - **Multi-testing**
    - **Bonferroni correction**
    - **$p < 0.05$,**
  - **Suggestive genome-wide, chromosome-wide significant**

Manhattan and QQ Plots- SG,PM

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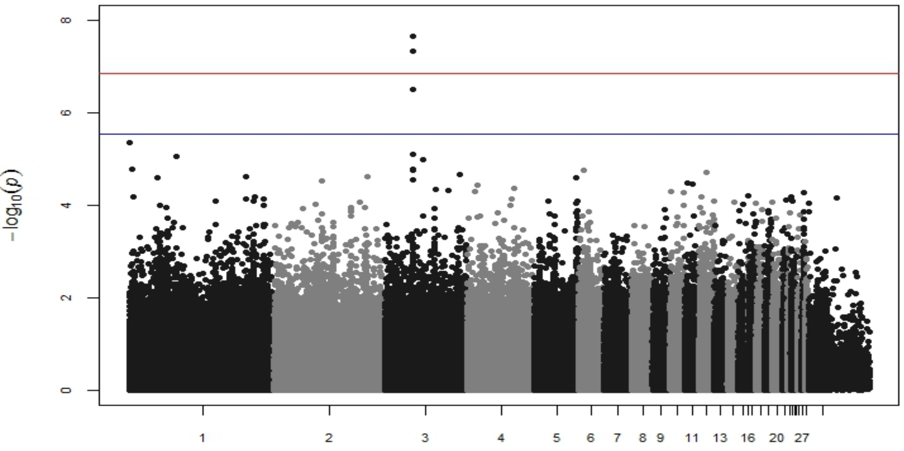
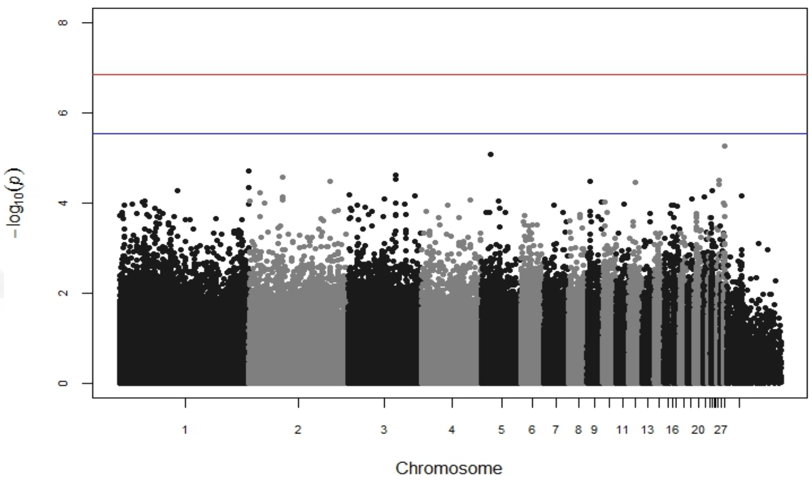
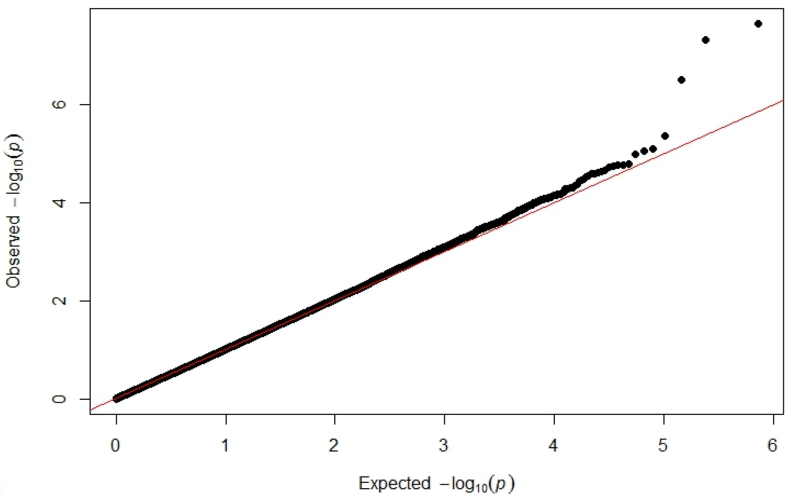
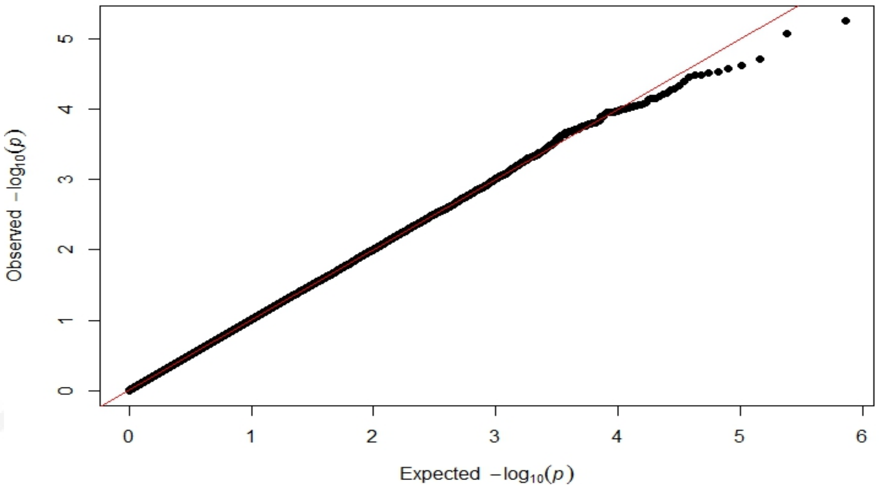
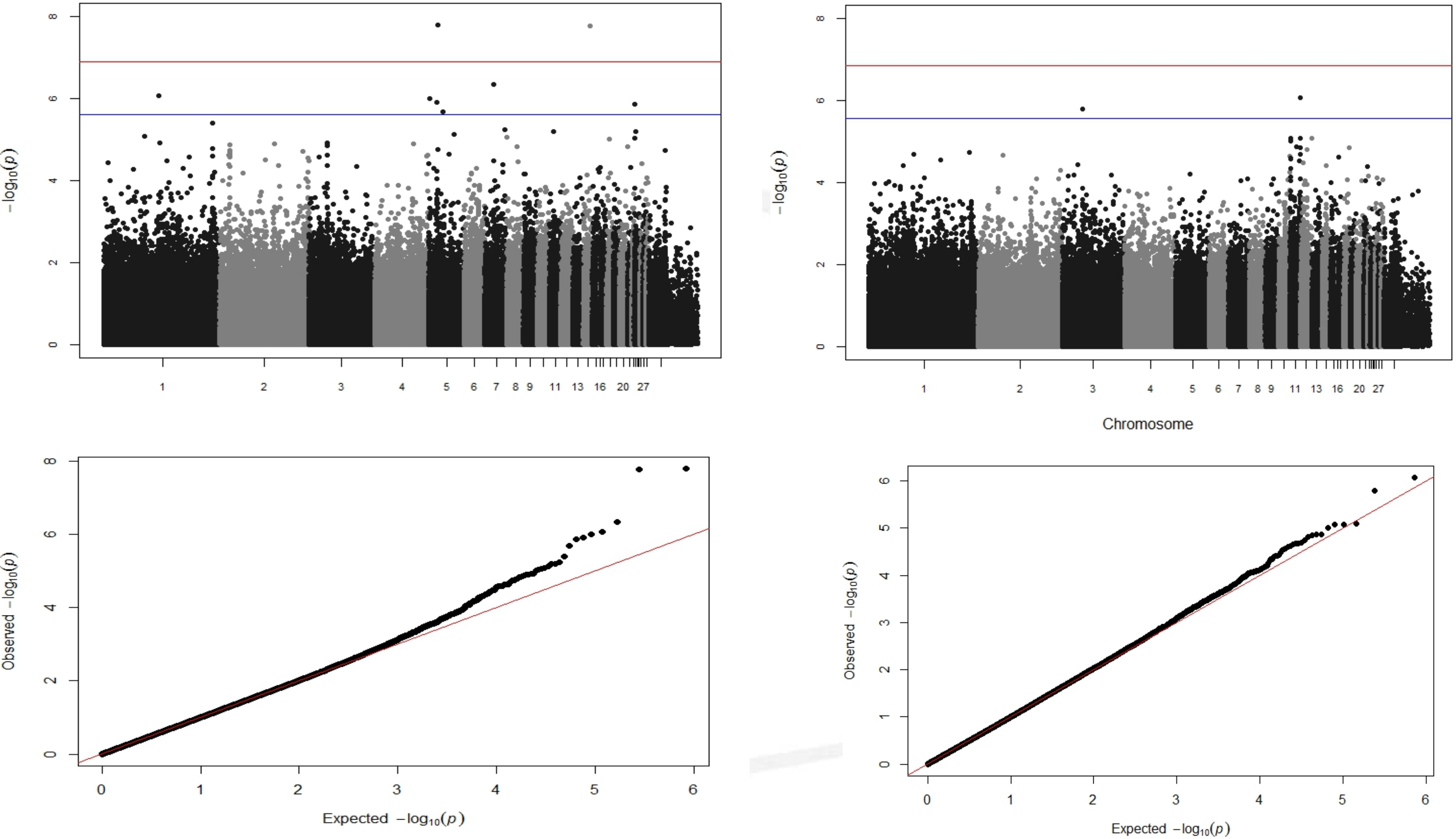




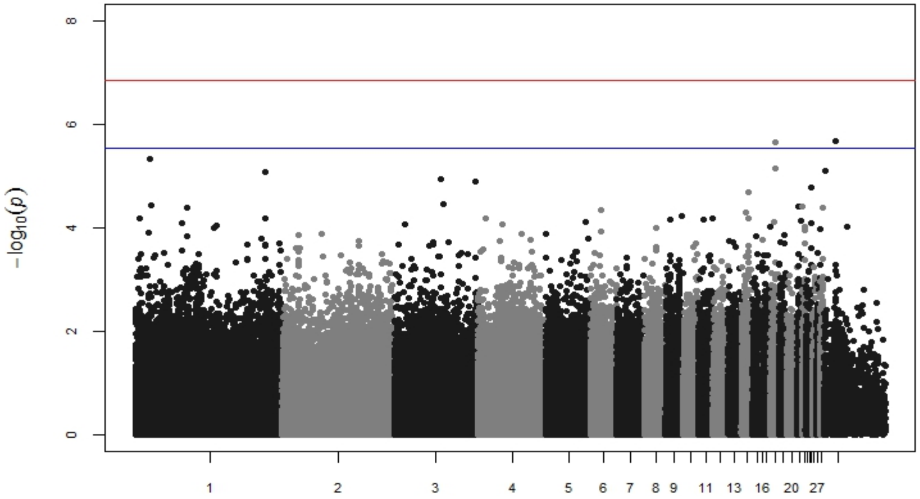


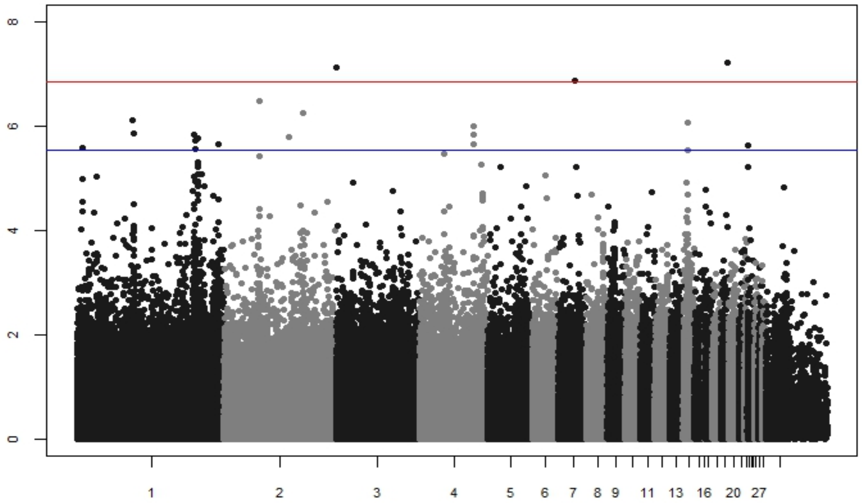


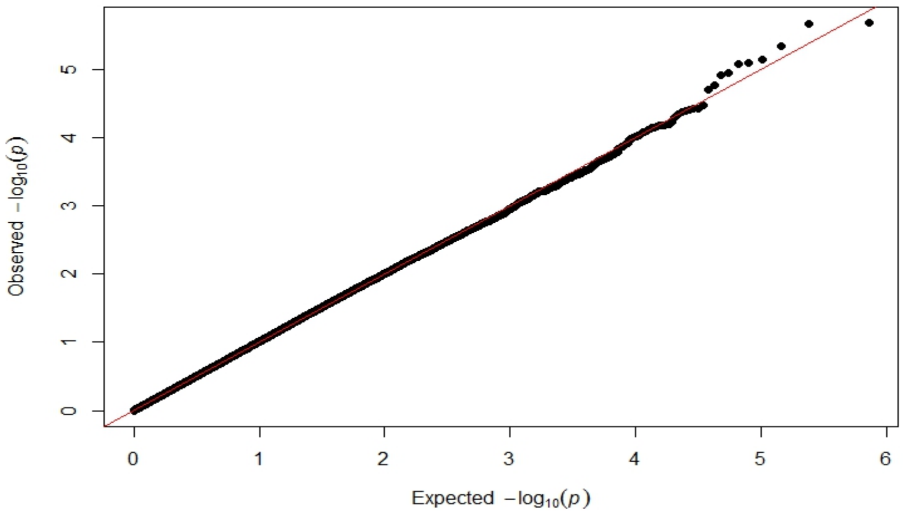
Manhattan and Q-Q Plots- IBDV,MDV

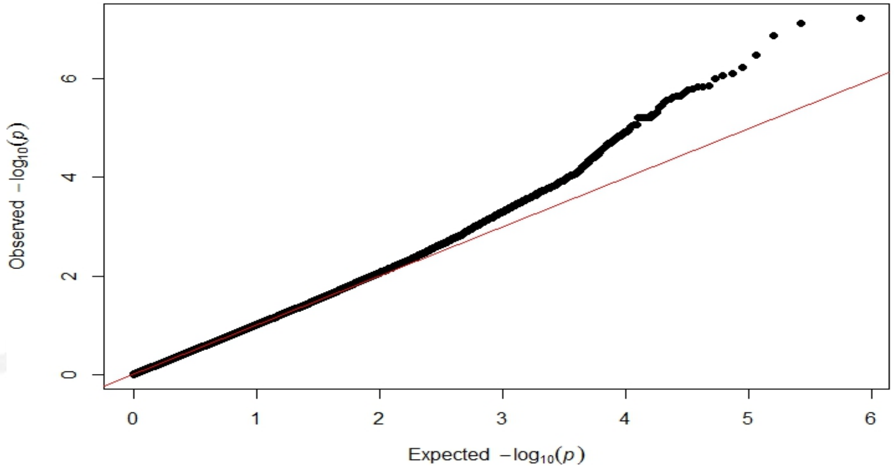


Manhattan and QQ Plots- *Eimeria*,cestodes









Heritability

- Mixed model analysis in ASReml
  - Validation of the significant markers
  - Most markers had a significant **additive effects**
  - Few had a significant **dominance effects**

- Moderate to high heritability estimates (ASReml):
  - Using Kinship matrix

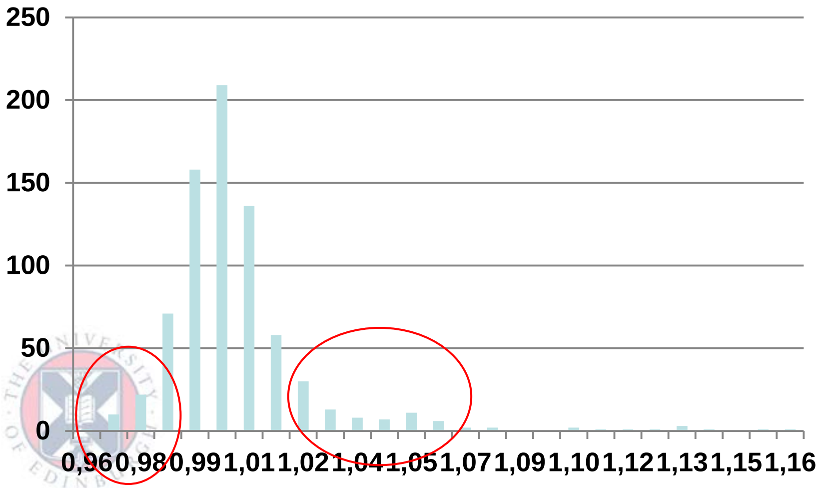
Heritability estimates

Trait	Heritability estimate(h^2)
Salmonella	0.08
Pasteurella	0.30
IBDV	0.46
MDV	0.42
Eimeria	0.22
Cestodes	0.31

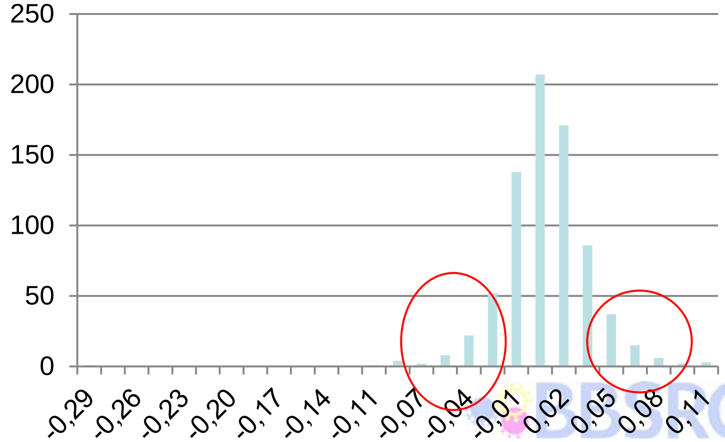
GEBVs

- Average reliability of GEBVs:
  - for IBDV and MDV ~0.40
  - for PM and cestodes ~0.30
  - for *Eimeria* = 0.20 while for SG=0.08

IBDV



MDV



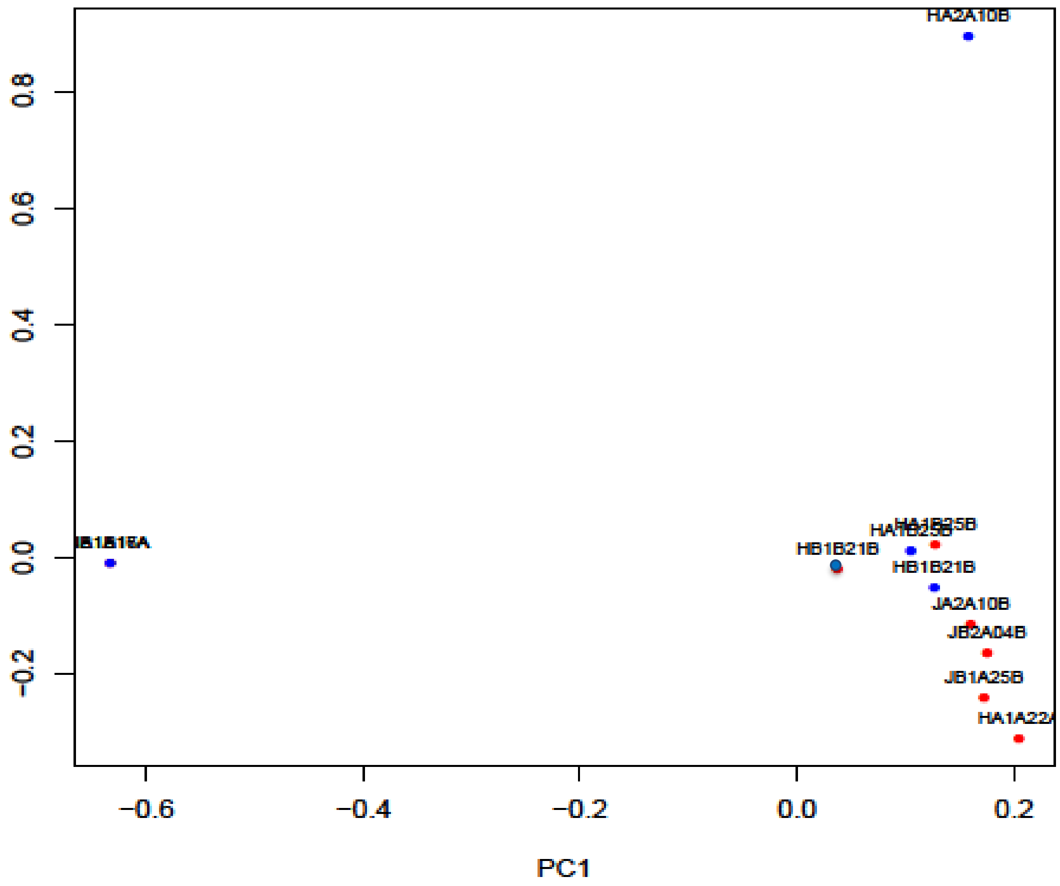
Accuracy of genomic predictions

- To estimate the accuracy of genomic predictions :
  - Cross-validation study-subdividing the data into 5 sets
  - Across ecotypes
  - Within ecotypes
  - GBLUP (ASReml)
- For IBDV accuracy ~0.40
- For MDV accuracy~0.42
- For *Eimeria* accuracy~0.30

Re-sequencing data-work in progress

PCA analysis for PM (R/Bioconductor package/SNP relate)

Red dots- low antibody
Blue dots-high antibody titres



Conclusions

- **Horro** and **Jarso** chickens are **two distinct populations** but they share **common genomic regions** of disease resistance
- **SNP markers** significantly associated with each of the studied infectious diseases were identified.
- The **heritability** of the traits were **moderate** with the exception of SG
- The **reliability** of the estimated GEBVs and the **accuracy** of the genomic predictions were **encouraging for breeding for enhanced resistance to infectious diseases** in indigenous Ethiopian chickens
- **Across indigenous ecotypes breeding programmes** may be plausible

Acknowledgements – CH4D

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