High resolution genomic analysis of four local Vietnamese chicken breeds

F A R A H

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Introduction

Local chicken breeds in VN:

- 70% of the national poultry population

- Well adapted to survive under village condition

- Source of protein

- An essential part of cultural and socio-economic activities in the villages

    BUT

- Low productivity

- Threatened by the massive importation of foreign productive breeds

➔ Conservation programs targeting several emblematic breeds

Introduction

Goals of conservation programs:

- Characterize the endangered breeds

- Keep a pool of characteristic animals

- Preserve genetic heritage

Introduction

Main goal of this study:

- Characterize 4 local chicken breeds at genomic level

Dong Tao   **Ho**   **Mia**   **Mong**

- Use of (high-density) **SNP** genotyping

- Identification of **population structure**

- Evaluation of **global and individual inbreeding**

METHOD

Material

- ## Sample
  - 94 individuals from 4 breeds:
    - 32 Dong Tao (DT), 26 Ho (HO), 18 Mia (MA), 18 Mong (MN)

- ## Genotyping
  - Use of 600K Affymetrix® Axiom® genotyping array (Kranis et al., 2013)
  - QC1, across breeds (% call (SNP) > 0.9; MAF > 0.01)
    - 454,297 SNPs (28 autosomes) used for population structure analyses
  - QC2, within breeds (MAF > 0.05; p(HWE) < 0.0001)
    - 308,307 SNPs used for genetic diversity analyses

Methods

- ## Method to evaluate inbreeding

  - ### Runs of homozygosity

    - $F_{ROH} = \sum L_{ROH} / L_{AUTOSOME}$

      (Mc Quillan et al. (2008))

  - ### History of inbreeding: based on # and lengths of ROH

    (e.g., Kirin et al., 2010; Pemberton et al., 2012)

  - ### Softwares:

    - Plink (Purcell et al., 2007), Germline (Gusev et al., 2008), Beagle (Browning and Browning, 2010), SVS (Golden Helix SNP & Vaiation Suite v7.6.8), ...

      - Based on empirical rules (min # of SNP in a ROH, max # of heterozygous & missing calls, minimal density)
      - No consensual view hampers studies comparisons
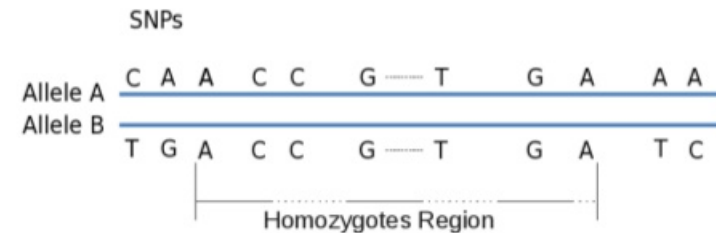
Methods

- ## Method to evaluate inbreeding

  - – Softwares:

    - ZooROH (Druet & Gautier, 2017)

      - – use of hidden Markov model

      - – allows to partition autozygosity into different classes based on the length (~their age) of HBD segment
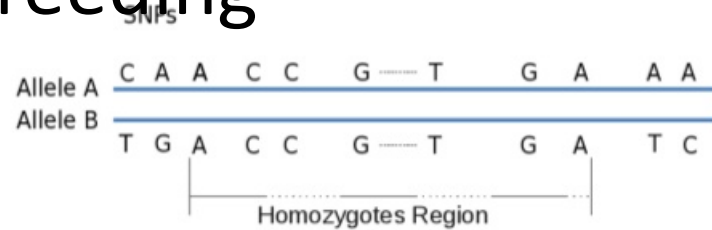
- ## Method to evaluate effective population size

  – Using a very rough estimate of Ne based on F

  (Kempthorne, 1957)

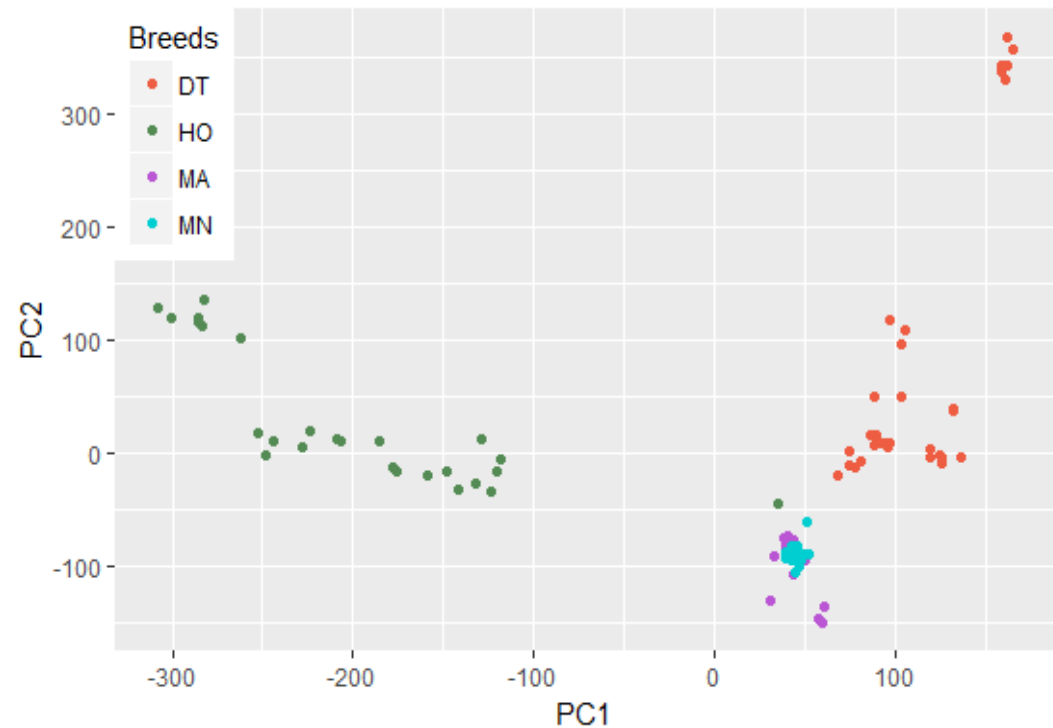$$N_e^{(F)} = \frac{1}{2\left(1 - \dfrac{1 - F_{t+1}}{1 + F_t}\right)}$$

t is the generation

Results

- ## Identification of 4 distinct breeds ?

FastSTRUCTURE

PCA

Results

- ## Identification of 4 distinct breeds ?
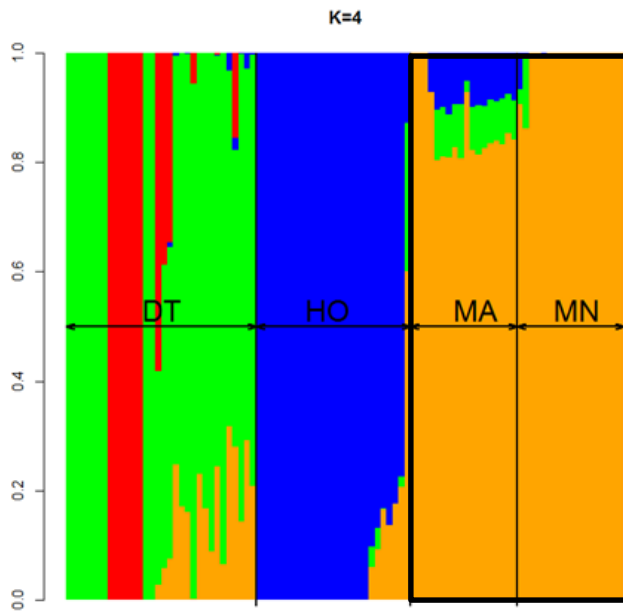
Not totally

FastSTRUCTURE

PCA
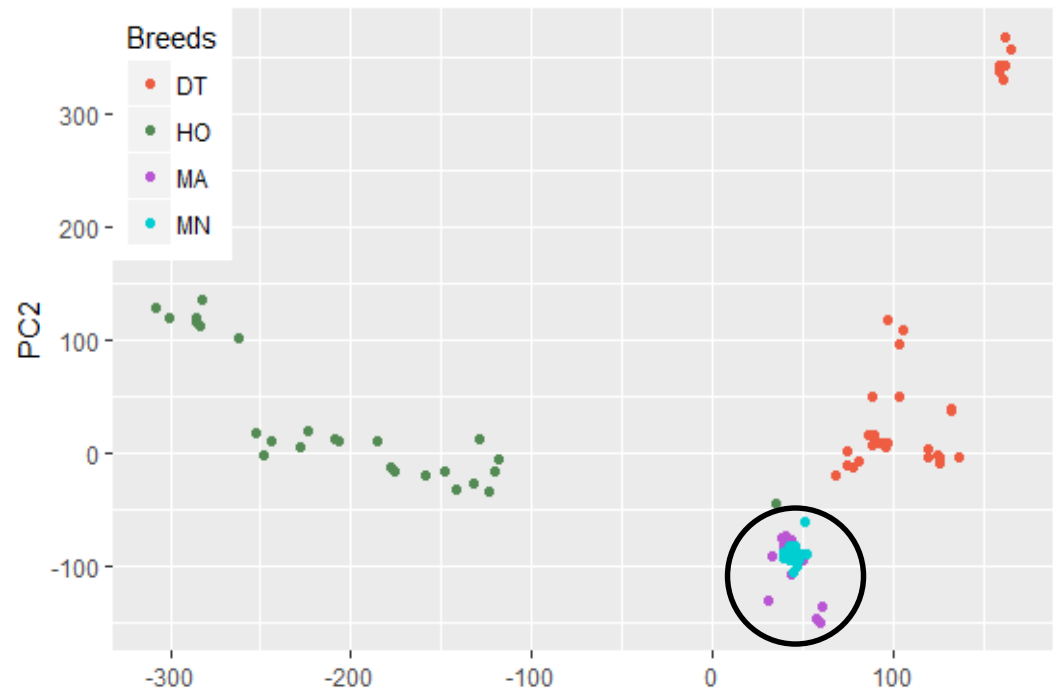
Difficult to distinguish Mia and Mong chickens

Results

- ## Identification of 4 distinct breeds ?

Not totally

PCA

FastSTRUCTURE

Results

- ## Identification of 4 distinct breeds ?

Not totally

PCA

FastSTRUCTURE

Results
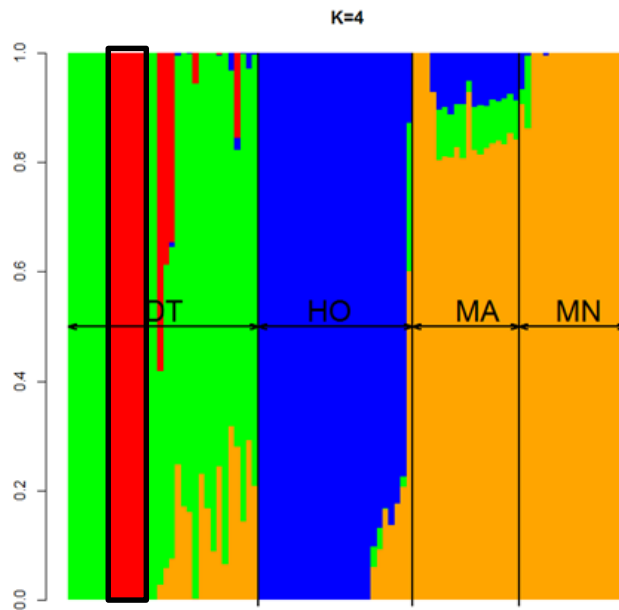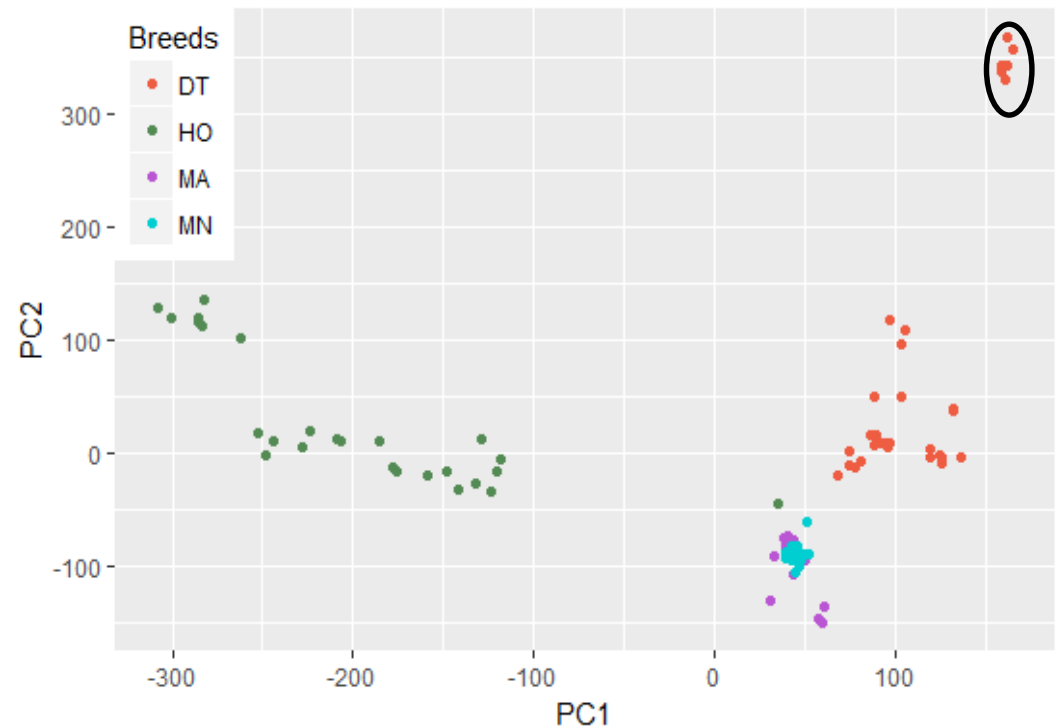
- ## Assignation of each individual to his breed?
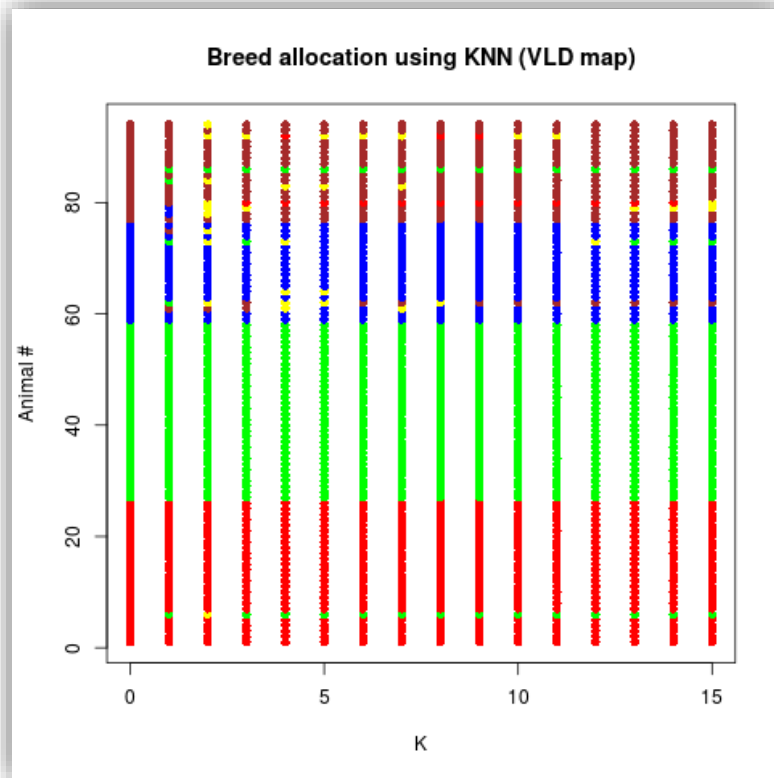
K-nearest neighbors

MA

MN

DT

HO
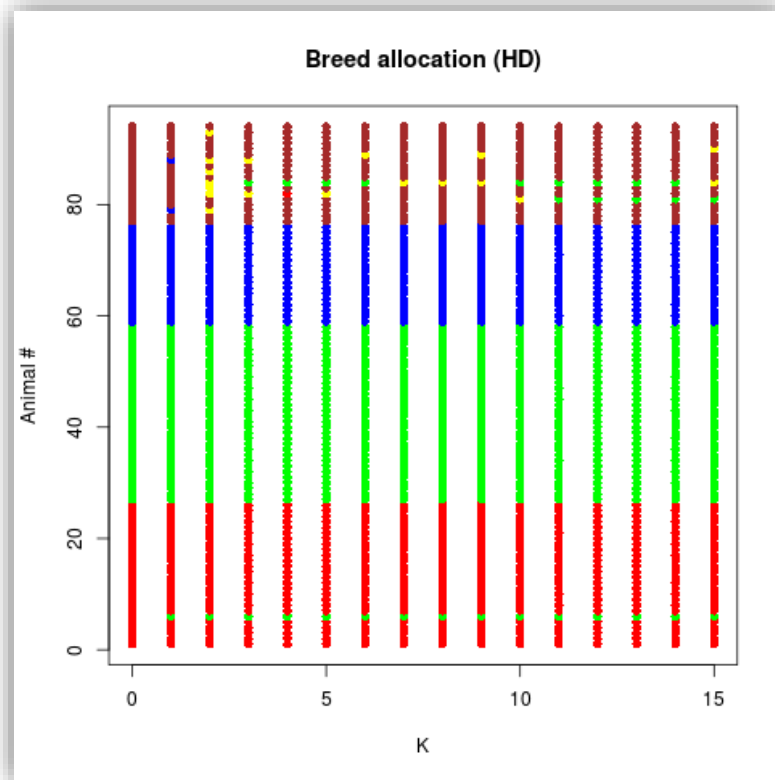
Works well with 400k map, except in Mia chickens

Results

- ## Assignation of each individual to his breed?
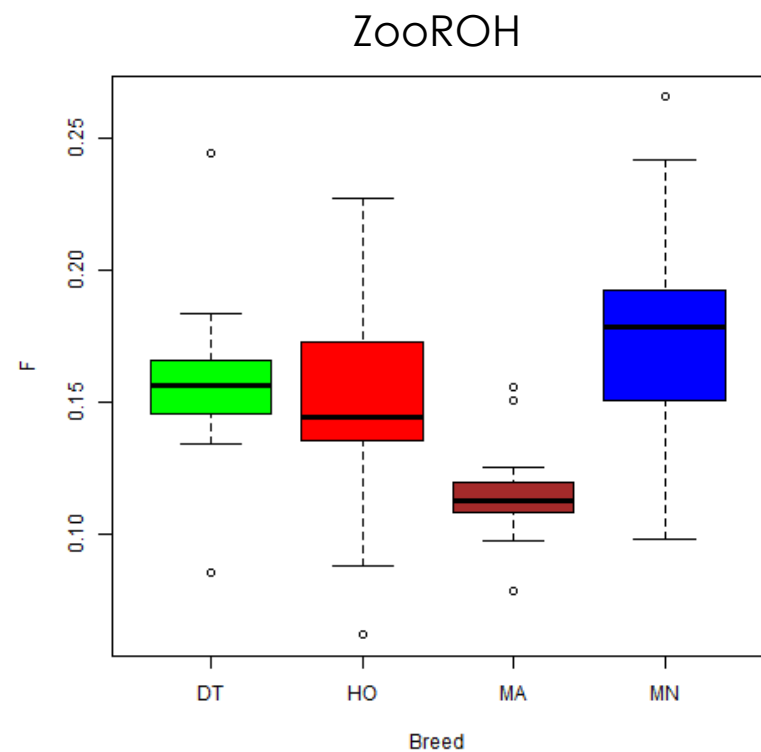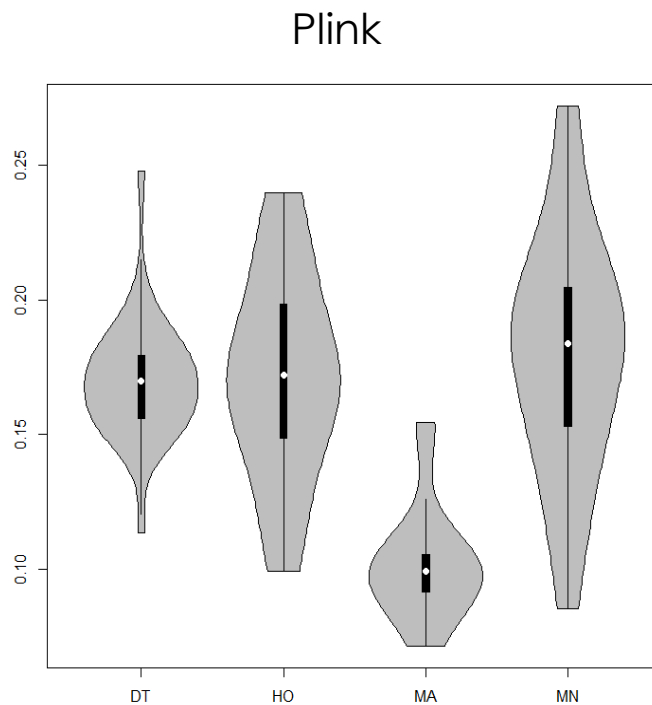
K-nearest neighbors

MA

MN

DT

HO

Still stable in HO and DT with LD map (450 markers)
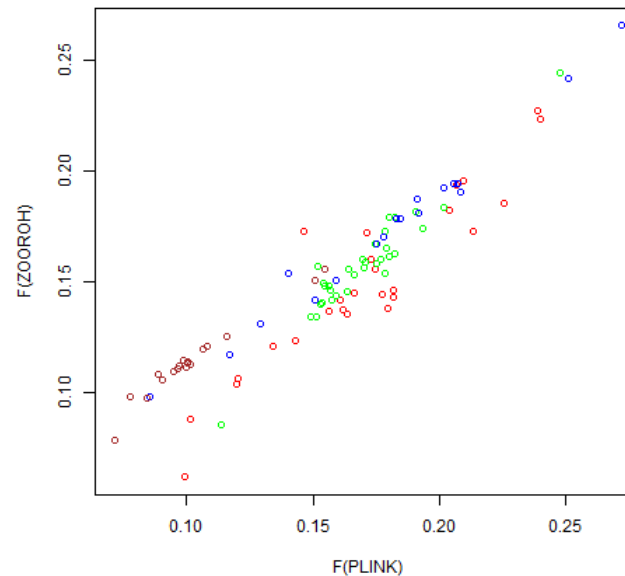**More classification errors for MN and MA**

Results

- ## Global inbreeding

- High levels of inbreeding in all breeds

- More variability among Ho and Mong chickens

- Lower levels of inbreeding in Mia chickens

Plink

ZooROH

Results

- # Global inbreeding
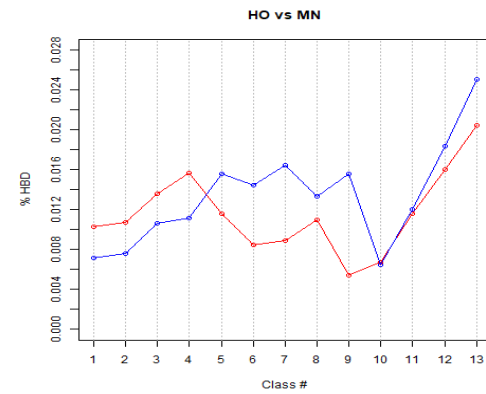 - Correlation between inbreeding coefficients calculated with the two methods
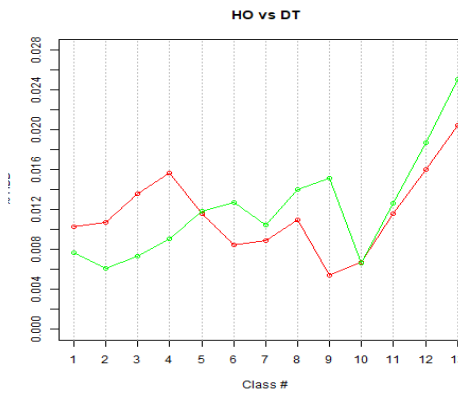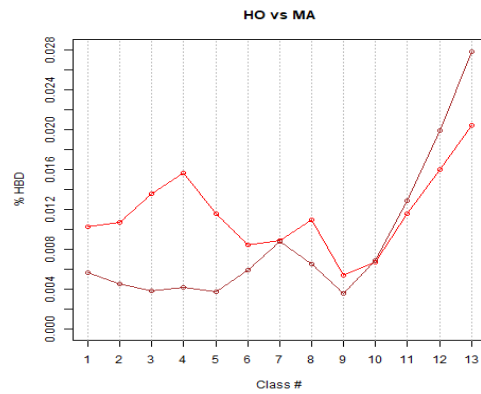

r = 0.94

Results

- ## Age of inbreeding

  ZooROH

- High contribution of very ancient class

- Ho chickens have the highest recent inbreeding

- Mia chickens have the highest ancient inbreeding
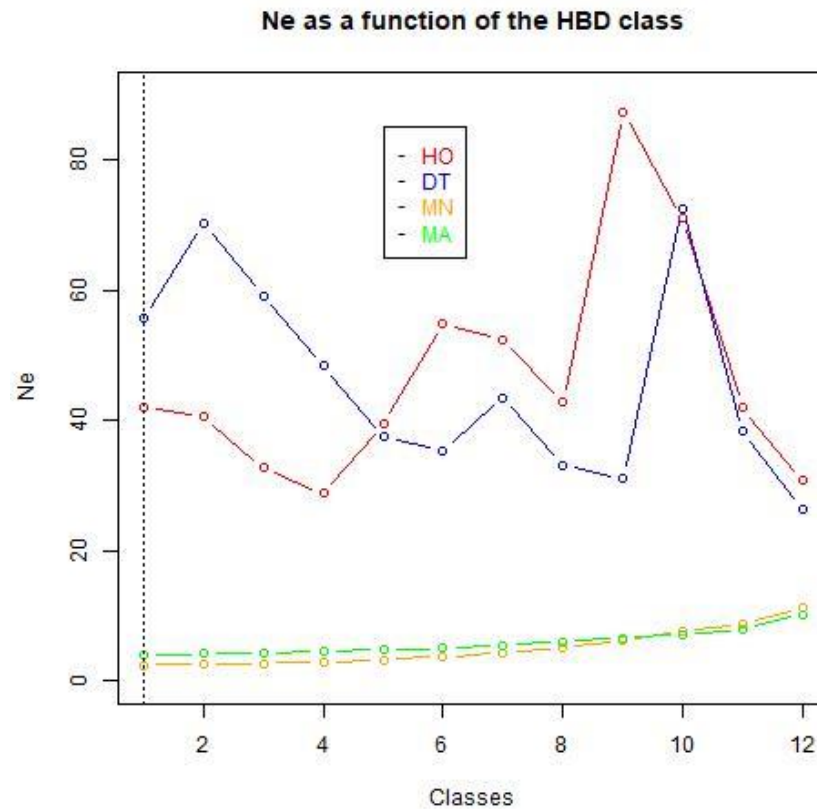
Results
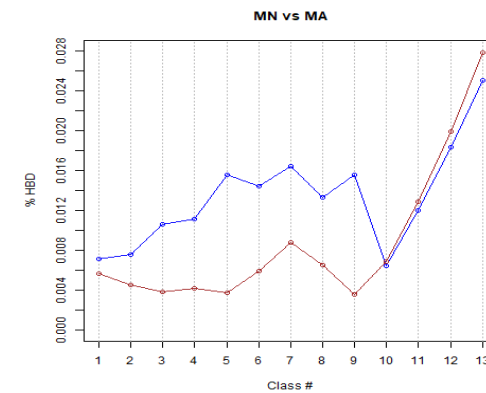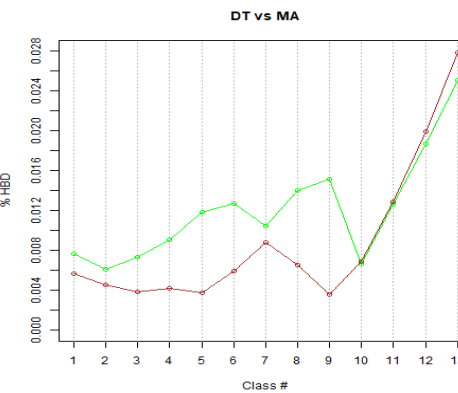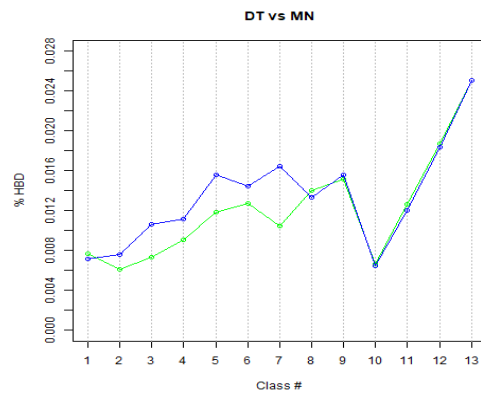
• Individual inbreeding

Plink

- • Individuals from the same breed tend to cluster

- • Individuals to the right of these clusters are the most inbred ones

- • More variability in total lengths in ROH in Ho and Mong chickens

- • Inbred individuals in all breed

• Effective population size

ZooROH

Ne as a function of the HBD class
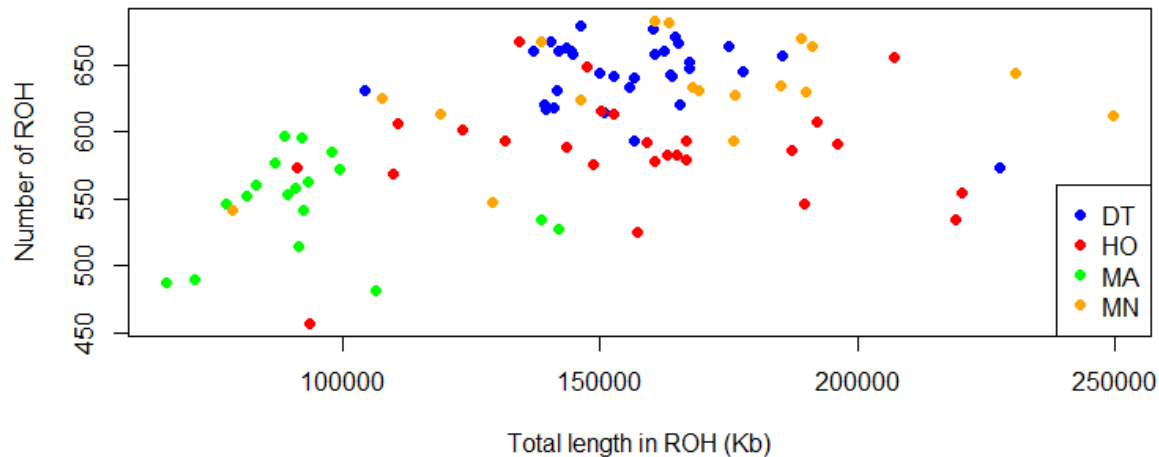
Results

- ## Effective population size

  ZooROH
  - Reasonable results for HO (42) and DT (56)

  - Underestimated for MN (3) and MA (4)

  - Could potentially provide a trend in Ne

Conclusions

- Overall clear genomic differences between breeds

  – Not so clear distinction between Mia and Mong chickens, but still sufficient in most cases to classify individuals

  – Genomic information allows to create nucleus of purebred animals
    - Identification of a crossbred animal in Ho chickens

- High levels of inbreeding in all breeds

  – Most inbred individuals have been identified

  – Must be taken into account in future nucleus mating strategies

Conclusions

- New methods (i.e. zooROH) allows distinction between ancient and more recent inbreeding

  – Might indicate recent population events leading to the reduction of the effective population size

- These approaches provide tools allowing the identification of pool of chickens to be included in a conservation program, along with tools to manage the nucleus in the future

THANKS !