MINISTRY OF AGRICULTURE

1919 · 2019
100
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Conservation genomic analyses of two Croatian autochthonous sheep breeds

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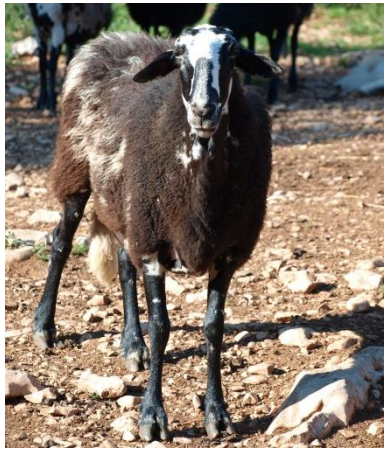
About breeds – Istrian sheep (IS)

- Breeding began in 1771
- Native ewes x Gentile di Puglia and Bergamo rams?
  - Southdown and Merinolandschaf rams
- Breeding population – 1082 ewes, 86 rams
- Dairy breed (lactation milk yield = 171 kg)

About breeds – Pag sheep (PS)

- Breeding began between 1805 and 1813
- Native ewes x merino Negretti, Southdown and Gentile di Puglia rams?
  - Sardinian White rams
- Breeding population – 4292 ewes, 123 rams
- Dairy breed (lactation milk yield = 137 kg)

Objective



- To define
  - Genomic position of **IS** and **PS** concerning Italian, Spanish, and some Merino and Merino-derived sheep breeds
- To estimate
  - Linkage disequilibrium effective population size (NeLD)
  - Genomic inbreeding levels (F_{ROH})

Material (animals)

- **660 animals** of 24 breeds
  - Italian, Spanish, and some Merino sheep breeds (15 – 20 animals per breed)
  - Available data from Dryad digital repository – Ciani et al., 2015
  - 96 Istrian and 75 Pag sheep

Italian
- **Appenninica**
- **Comisana**
- Gentile di Puglia
- **Laticauda**
- **Leccese**
- Merinizzata Italiana
- **Massese**
- **Sardinian White**
- Sopravissana

Spanish
- Castellana
- Churra
- Ojalada
- Rasa Aragonesa

Croatian
- Istrian sheep
- Pag sheep

Merino
- Arawapa
- Australian Merino
- Australian Poll Merino
- Australian Industry Merino
- Chinese Merino
- Merinolandschaf
- Rambouillet
- Spanish Merino (Estremadura)
- Spanish Merino (Cordoba)

Method

- Illumina OvineSNP50 BeadChip
- Quality control
  - Only autosomal SNPs with known position
  - GC score ≤ 0.7
  - GenTrain score ≤ 0.4
  - Gen Call > 0.9
  - Animals with < 5% missing SNPs
  - **43,937 SNPs**

SNP & VARIATION SUITE

- ROH detection and inbreeding levels estimate – Ferenčaković et al., 2013
  - Min. 15 homozygous SNP in row
  - Min. density 1 SNP every 120kb
  - Max. gap between 2 SNPs ≤ 1000kb

➡

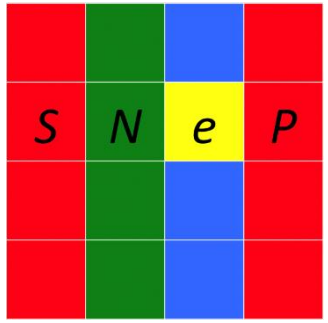
  - ROH > 2Mb → $F_{ROH > 2Mb}$ ≈ 25 gen ago
  - ROH > 4Mb → $F_{ROH > 4Mb}$ ≈ 12.5 gen ago
  - ROH > 8Mb → $F_{ROH > 8Mb}$ ≈ 6 gen ago

Method (cont)

- Principal Component Analysis

SNP & VARIATION SUITE

- Effective population size

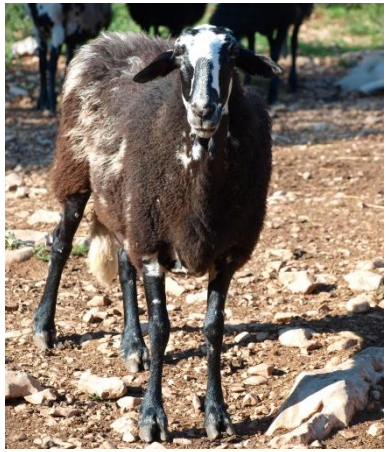


- MAF < 0.05
- Barbato et al., 2015

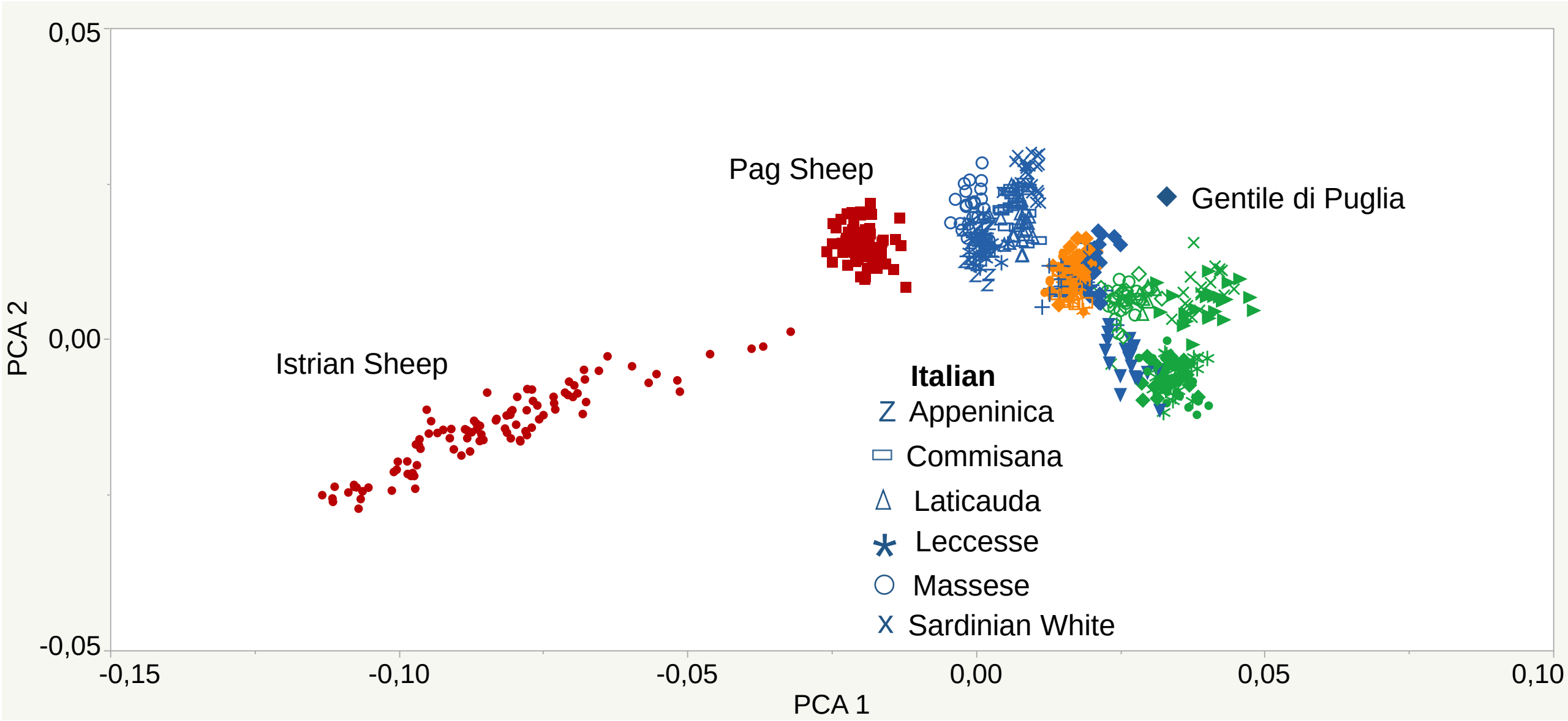
NeEstimator (v2)

- Do et al., 2014

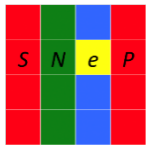
Results



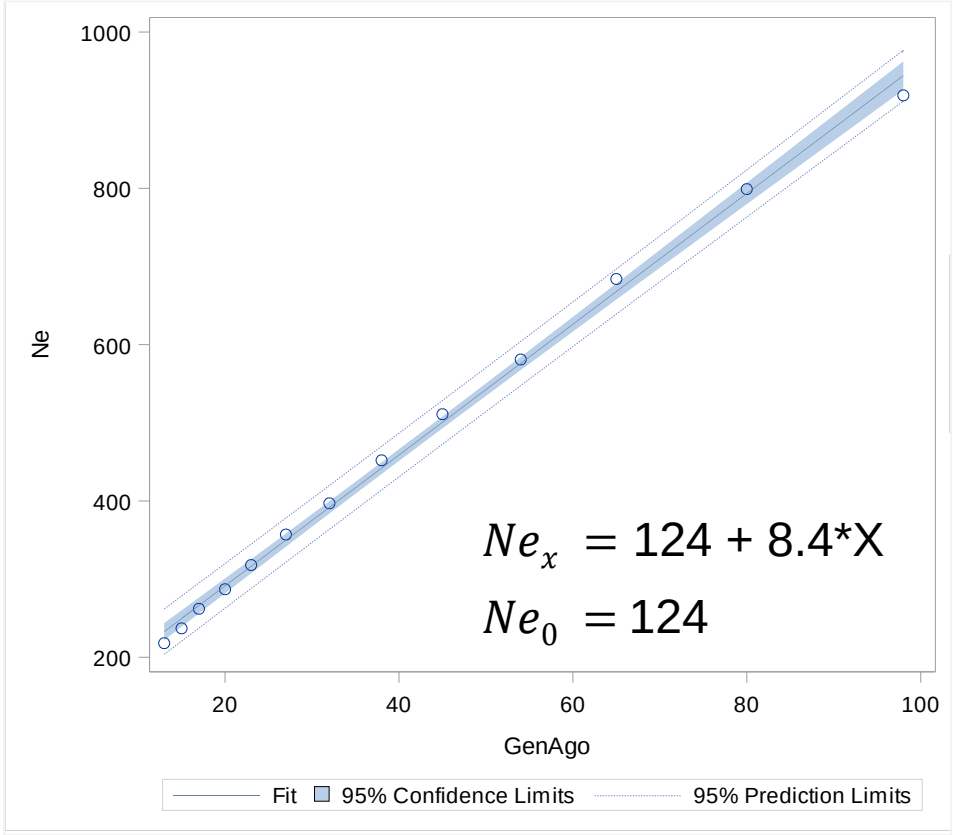
Principal component analysis



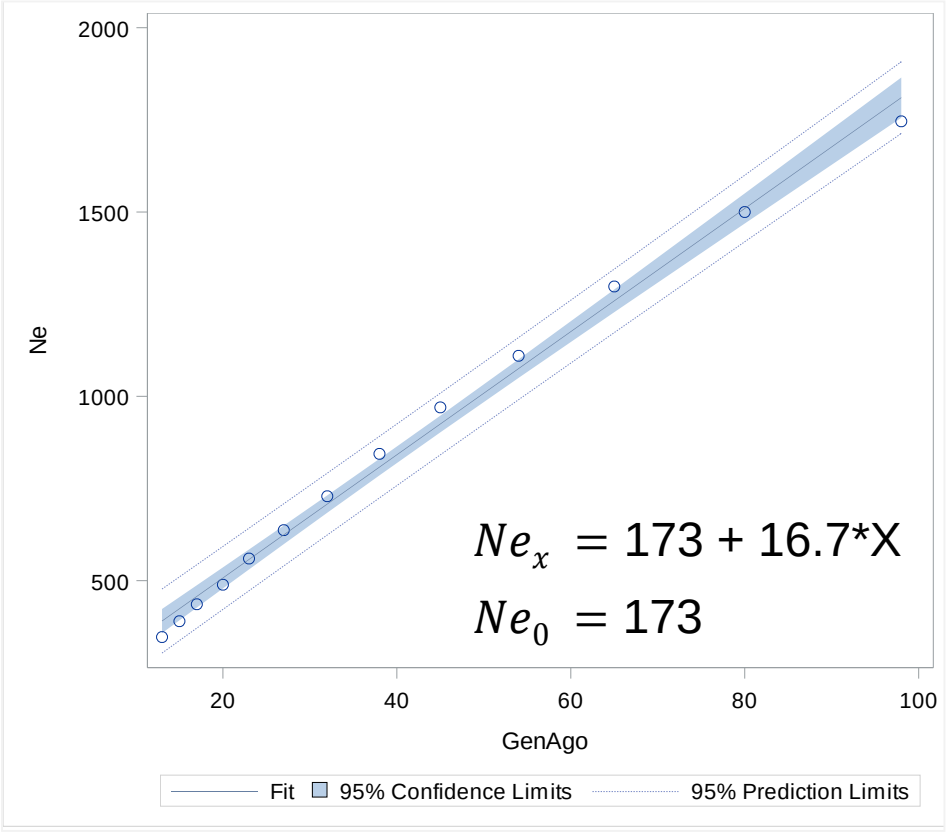
Effective population size



IS



PS

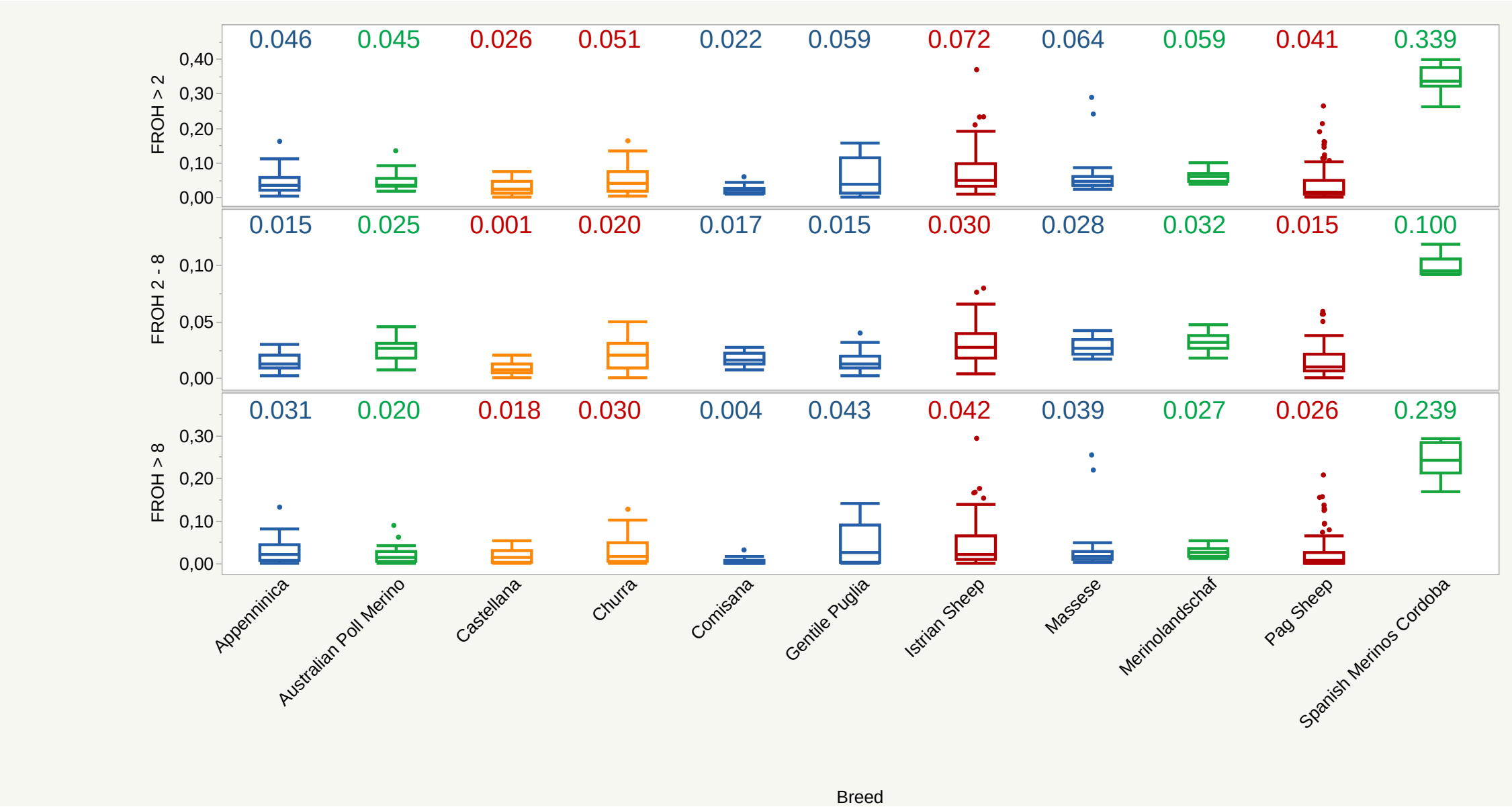


NeEstimator

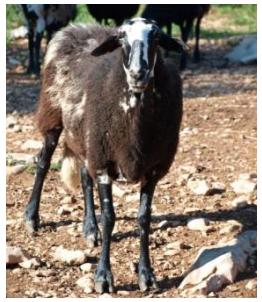
101 (95% CI = 81 - 130)

222 (95% CI = 161 - 343)

Inbreeding levels



Conclusions



- The first genomic analysis of IS and PS
- **IS**
  - Remote from the cluster of Mediterranean autochthonous breeds
  - Effective population size should be monitored
  - Higher inbreeding levels compared to PS and other breeds
- **PS**
  - Closer to some Italian breeds
  - Effective population size is satisfied
  - Inbreeding was small compared to other breeds
- Guidelines for the breeding program improvement

Acknowledgement

- Rural Development Programme of the Republic of Croatia for the Period 2014 - 2020
  - Measure 10.2. "Support for Conservation, Sustainable Use and Development of Genetic Resources in Agriculture"

- Support by the Croatian Science Foundation

Anagrams

01.12. 2018 – 30.11.2022 (HRZZ-IP-2018-01-8708)

“Application of NGS in assessment of genomic variability in ruminants”

Thank you for the attention!