



MINISTRY OF AGRICULTURE



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 (N_{eLD})
 - 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 (Extremadura)
- 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**



- ROH detection and inbreeding levels estimate – Ferenčaković et al., 2013

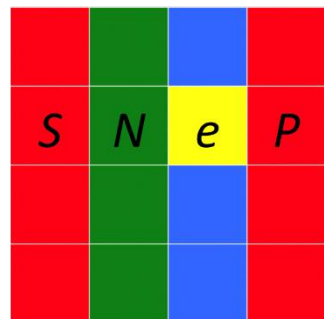
- Min. 15 homozygous SNP in row
- Min. density 1 SNP every 120kb
- Max. gap between 2 SNPs $\leq 1000\text{kb}$



- ROH $> 2\text{Mb}$ $\rightarrow F_{\text{ROH} > 2\text{Mb}} \approx 25$ gen ago
- ROH $> 4\text{Mb}$ $\rightarrow F_{\text{ROH} > 4\text{Mb}} \approx 12.5$ gen ago
- ROH $> 8\text{Mb}$ $\rightarrow F_{\text{ROH} > 8\text{Mb}} \approx 6$ gen ago

Method (cont)

- Principal Component Analysis
- Effective population size



- $MAF < 0.05$
- Barbato et al., 2015

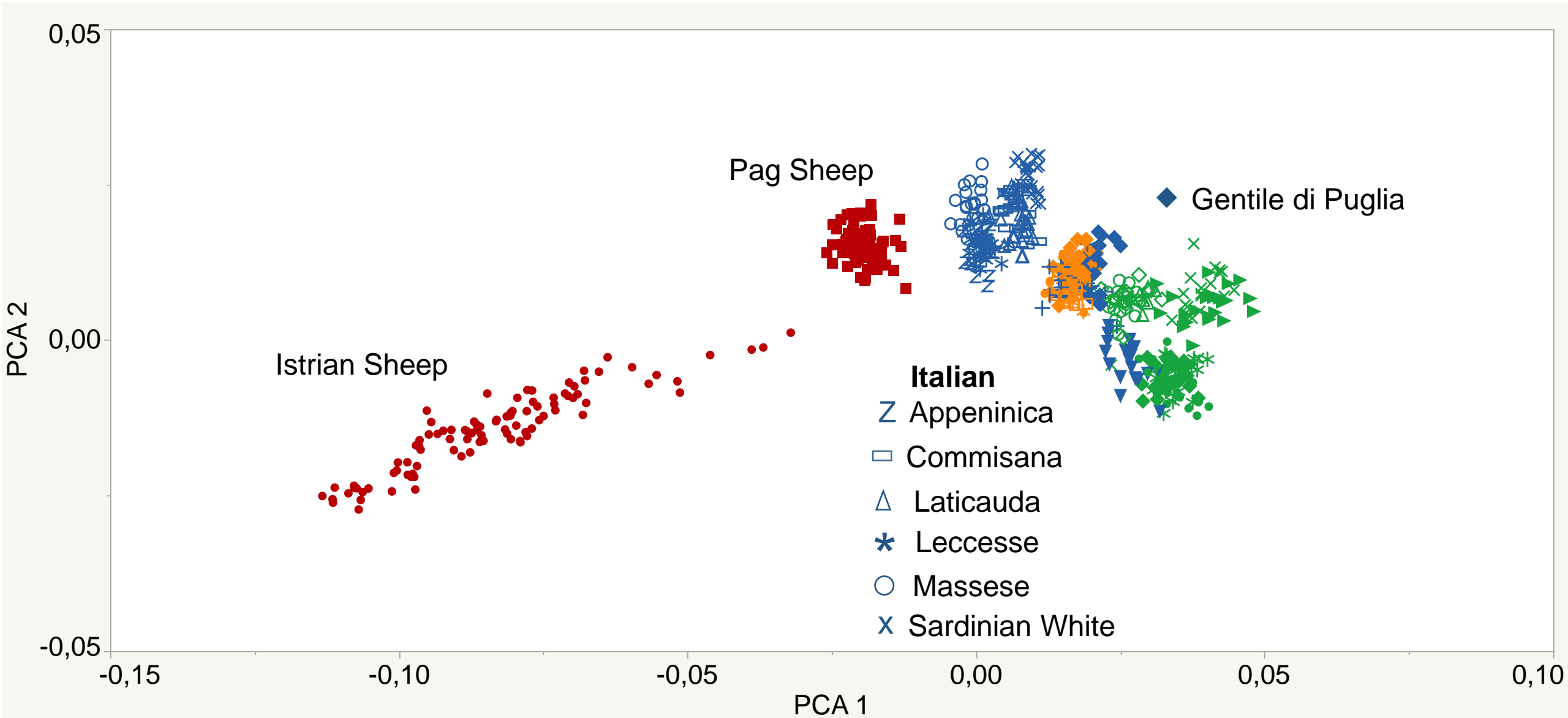
NeEstimator (v2)

- Do et al., 2014

Results

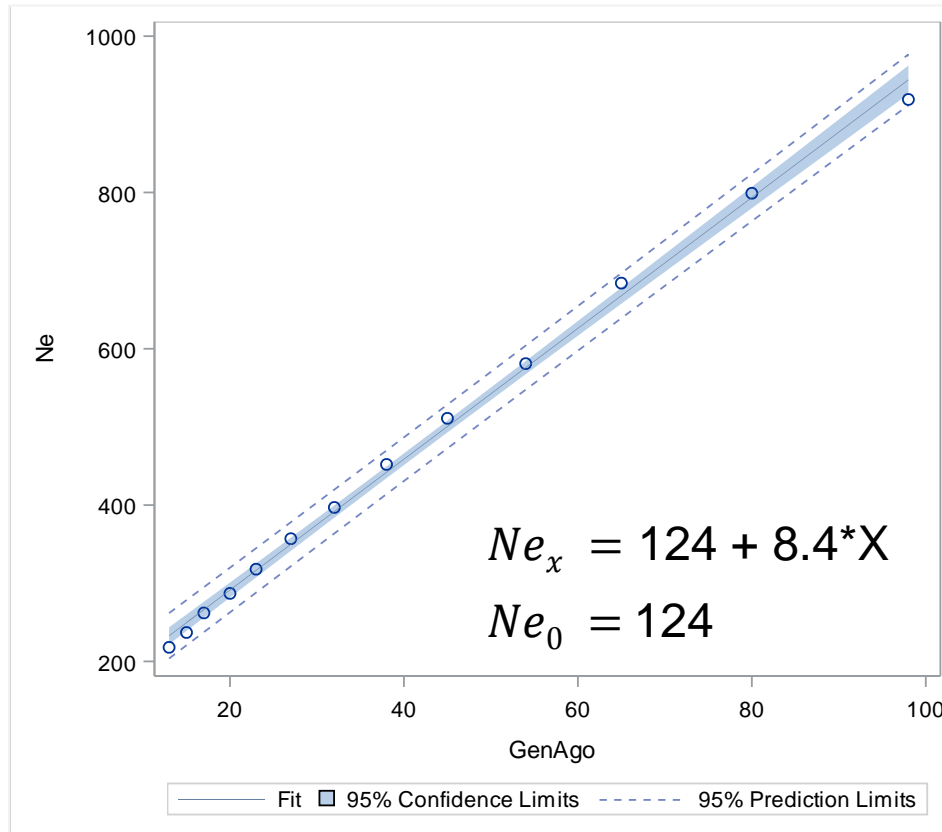
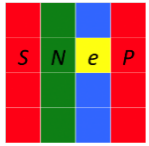


Principal component analysis

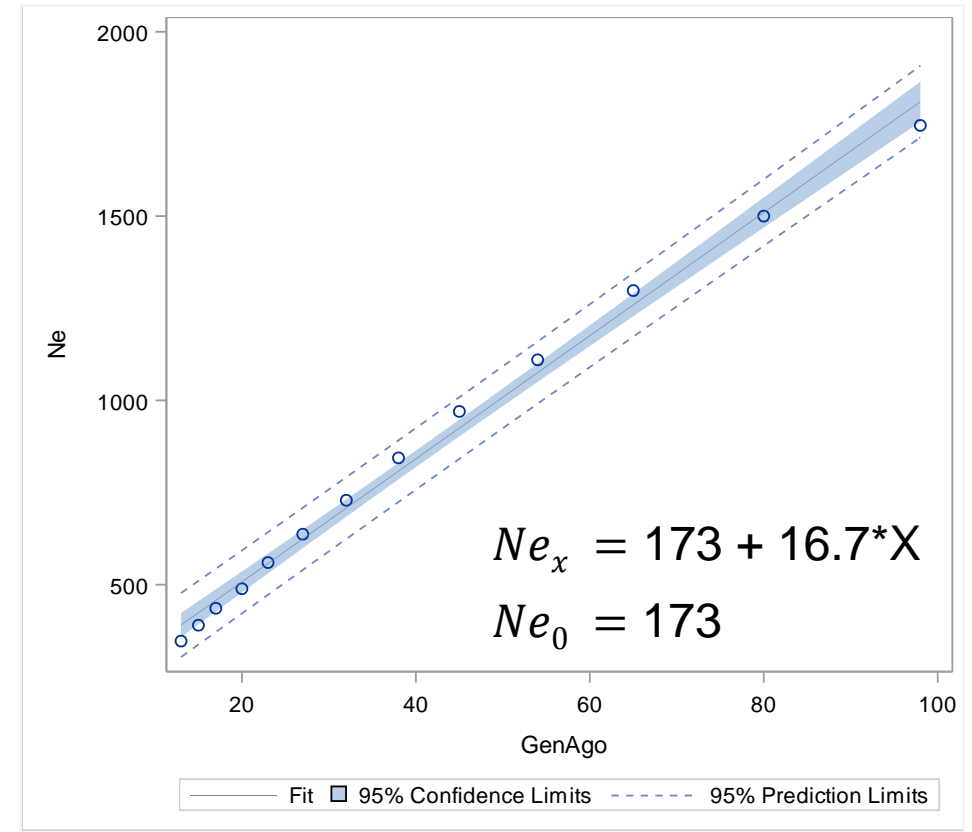


Effective population size

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

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Anagrams

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



Thank you for the attention!