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Assessing of Runs of Homozygosity in indigenous poultry breeds of Veneto region

Filippo Cendron¹, Francesco Perini², Salvatore Mastrangelo³, Emiliano Lasagna², Martino Cassandro¹

¹Department of Agronomy, Food, Natural resources, Animals and Environment, University of Padova, Viale dell'Università 16, 35020 Legnaro, PD, Italy.

²Department of Agricultural, Food and Environmental Sciences, University of Perugia, Borgo XX Giugno, 74, 06121 Perugia, PG, Italy.

³Department of Agricultural, Food and Forest sciences, University of Palermo, Viale delle Scienze, Ed. 4, 90128 Palermo, PA, Italy.

Dott. Cendron Filippo

Department of Agronomy, Food, Natural resources, Animals and Environment; University of Padova. Mail: filippo.cendron@unipd.it

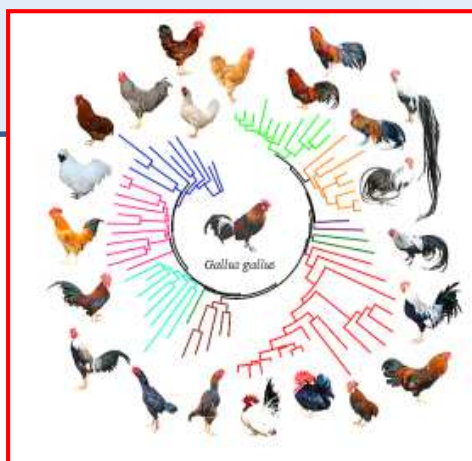




Italy

Veneto

**Veneto region
established a
poultry
biodiversity
action in
agreement with
FAO guidelines.**



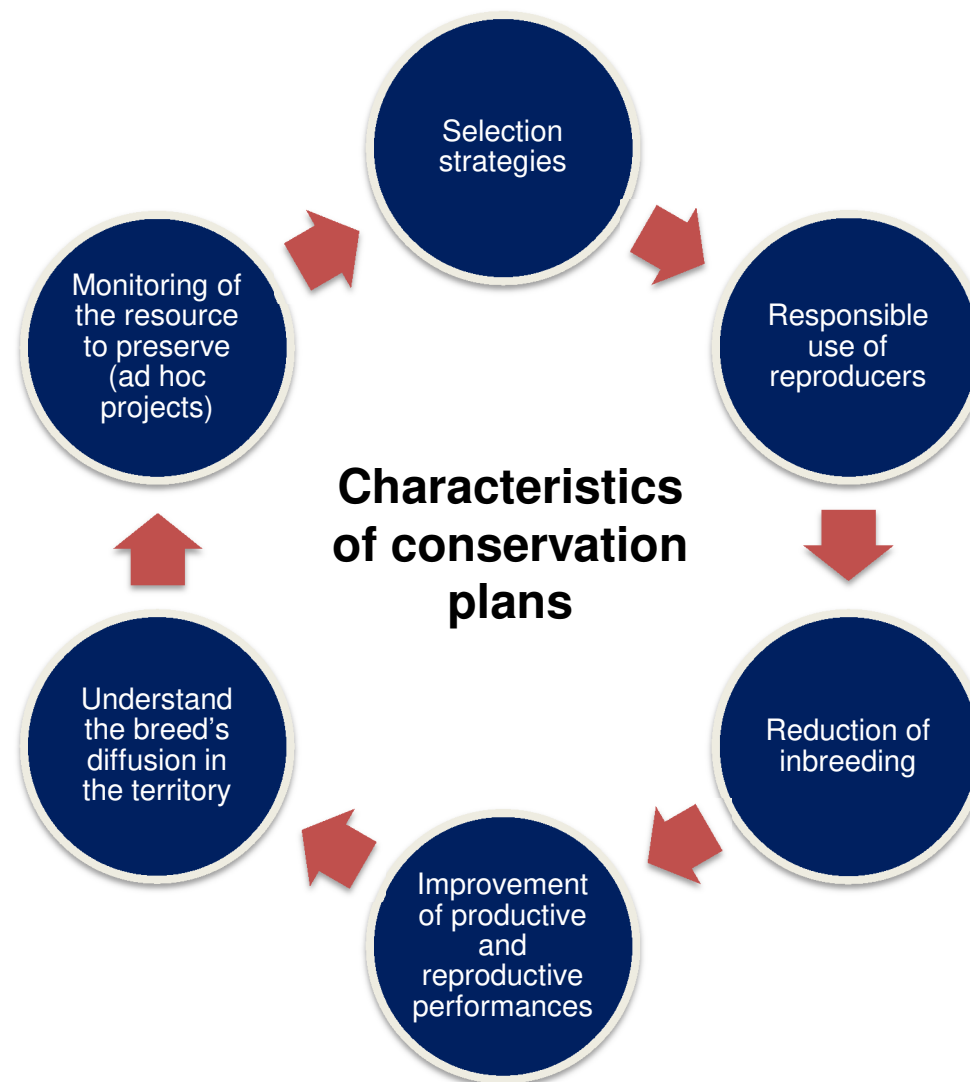
Aims

- To preserve local poultry breeds;
- To know productive and reproductive performances;
- Try to use crossbreeding and genotyping to promote local breeds.

How to counteract the global genetic erosion of poultry breeds?

1. Specific strategies for future breeding;
2. Researches and population studies;
3. Development of local and niche markets;
4. Conservation plans (Institutions, University, Public funds).

CONSERVATION : to maintain the genetic purity of breeds by implementing procedures that have proved a successful reproduction and traceability of lineages at different stages of the reproductive cycle, and the selection of the comeback of juveniles obtained.

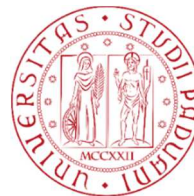


TUBAVI project

<https://www.pollitaliani.it/>

Aim

1. Aim of the project is targeted conservation to maintain and analyze the genetic purity of local poultry breeds in their location;
2. Financed by Italian ministry of agriculture (MIPAAFT – National Rural Development Programme 2014/2020);
3. Cooperation between different institutions :
 - **University of Padova;**
 - **University of Milano;**
 - **University of Molise**
 - **University of Perugia;**
 - **University of Torino**
 - **University of Firenze;**
 - **University of Pisa;**
 - Conservation centers;



UNIPD



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UNITO



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UNIFI



FONDO EUROPEO AGRICOLO
PER LO SVILUPPO RURALE:
l'Europa investe nelle zone rurali



UNIMOL



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Materials and methods

Materials and
methods

192 samples represents 8 Breeds under conservation schemes

Genotyping

- Axiom Wide Chicken Genotyping Array - Affymetrix 600K SNP chip.
- Reference genome *Gallus gallus* version 5.0.
- 580 961 SNP targets
- 33 set of Chromosomes.

Conservation centers:

- I.I.S. "Duca degli Abruzzi" di Padova;
- I.S.I.S.S. "D. Sartor" di Castelfranco Veneto (Treviso);
- I.I.S. "A. Della Lucia" di Feltre (Belluno);
- Azienda Sperimentale "Sasse Rami" di Ceregnano (Rovigo).

In collaboration with
University of Palermo

Plink

580 961 initial SNP targets

Only 28 Autosomes were considered.

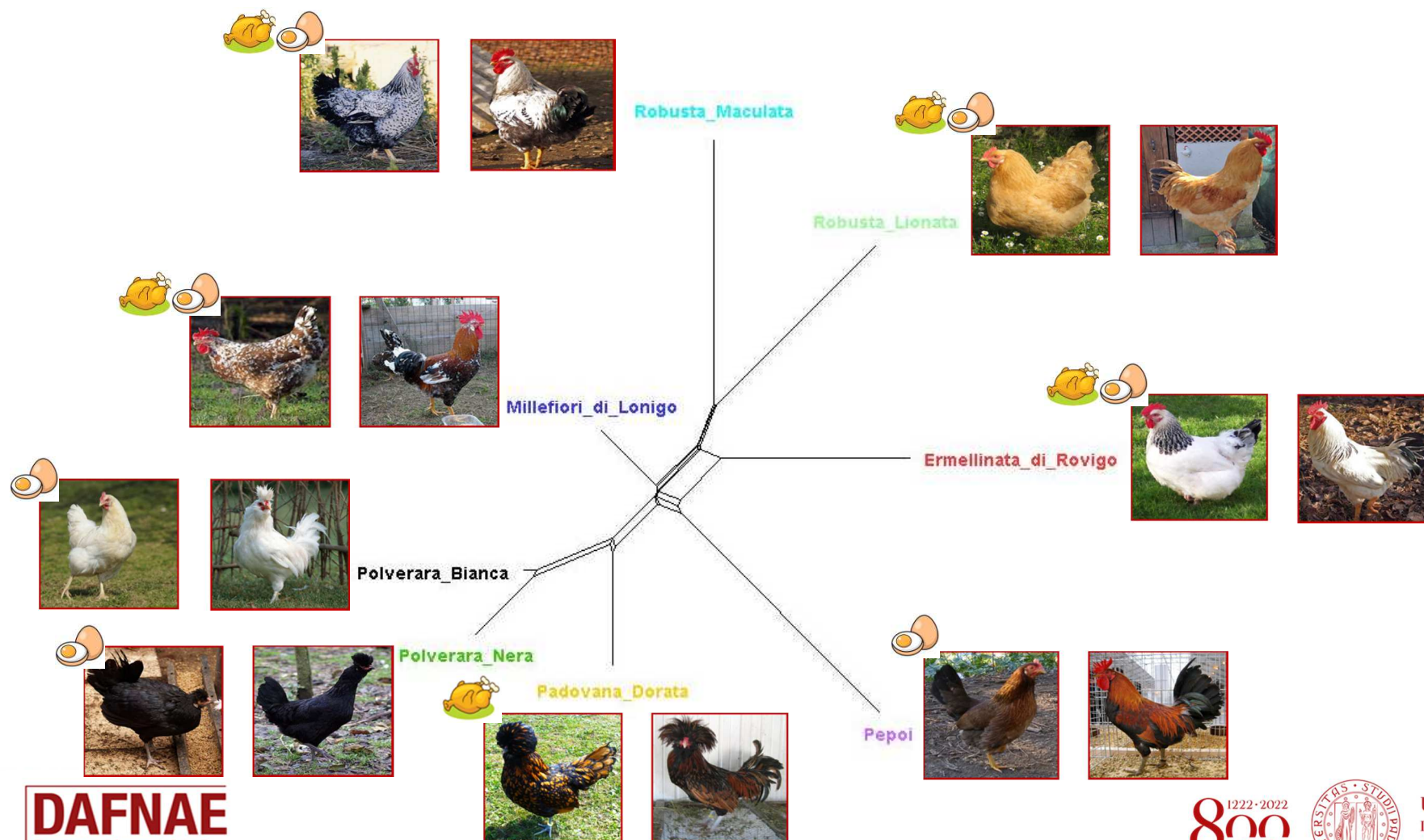
- SNPs with a call rate <95%
- MAF lower than 0.05%
- Animals with genotyping profile lower than 90%

152 animals and 449 837 SNP targets

Genetic diversity between breeds

- Genomic Runs of Homozygosity
- Gene Ontology

Considered chicken breeds



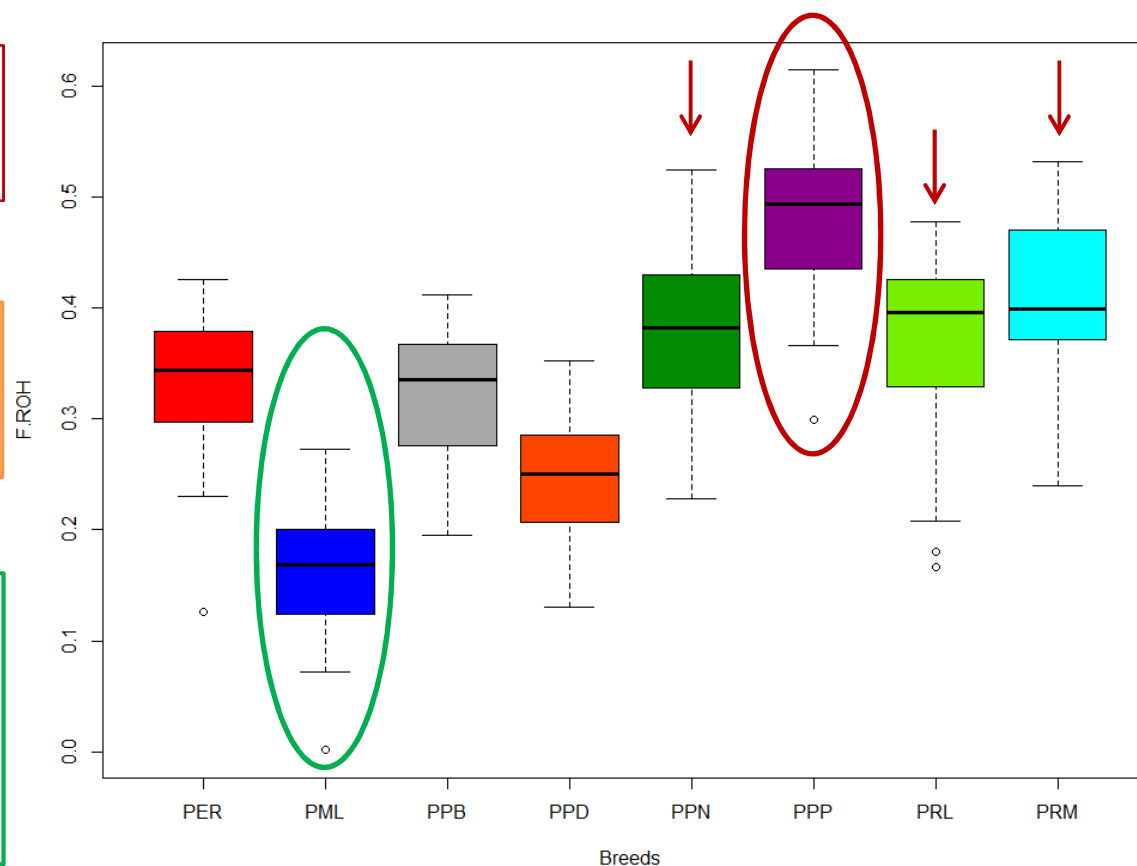
Distribution of Runs of Homozygosity in each breeds

To understand:

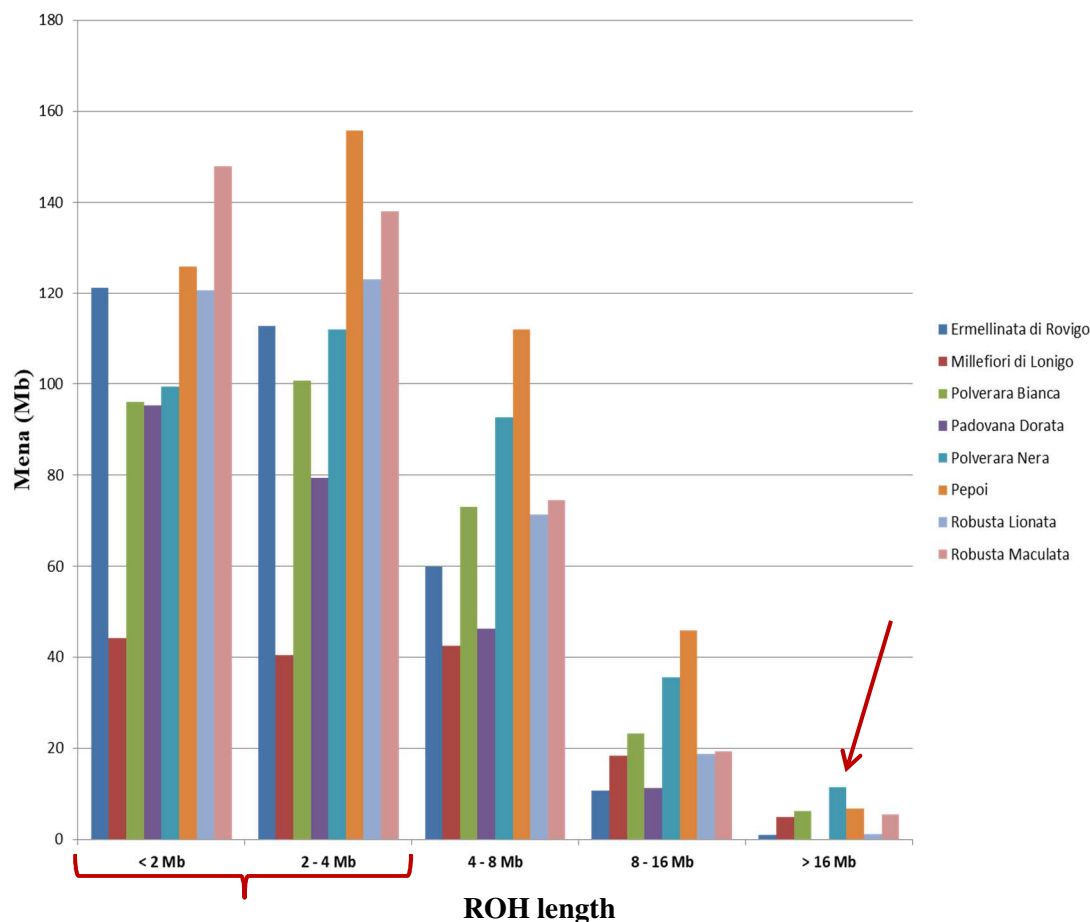
- I. Inbreeding value
- II. Level of inbreeding

- Max value in **Pepoi**
- High value on **Polverara Bianca** and **Robusta Lionata e Maculata**
- Min value in **Millefiori di Lonigo**

Animals with high levels of FROH, as observed in **Pepoi** breed, can be excluded or assigned a lower priority for mating purposes in endangered populations, to minimize the loss in genetic diversity and increase genetic diversity.



Classification of ROH according to their length in genomes



To understand:

- I. Demographic history;
- II. Inbreeding of population.

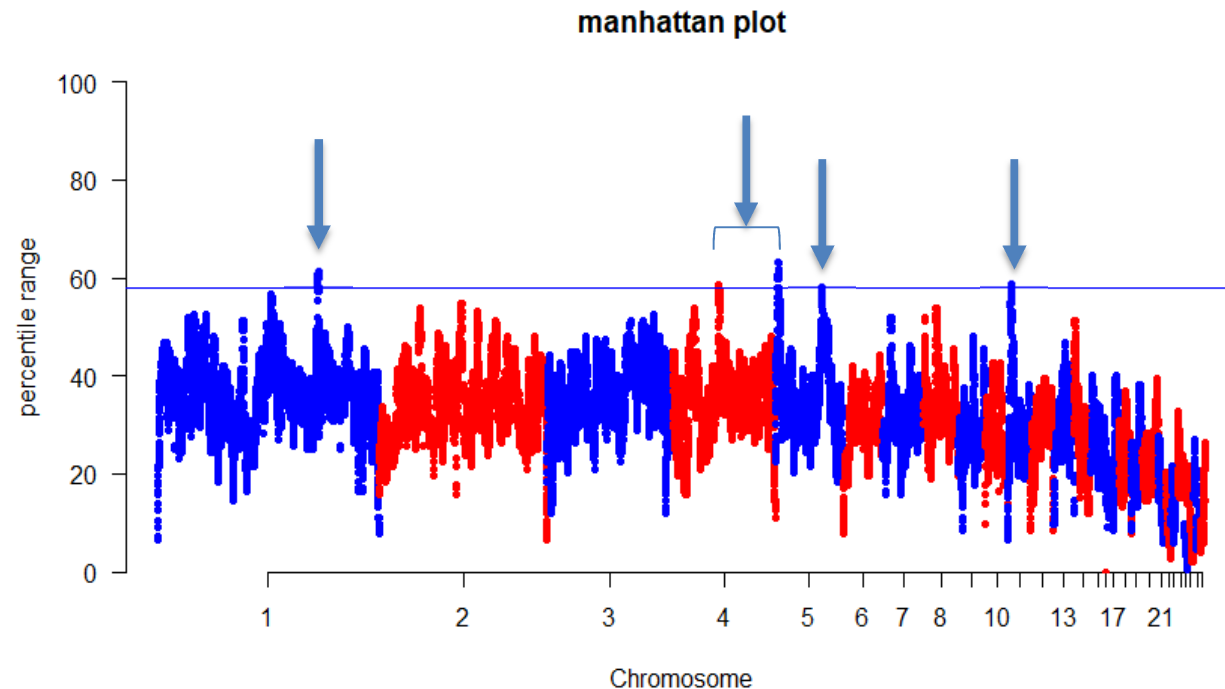
- All breeds showed the majority of ROH segments <4 Mb in length.
- PPN had a larger mean portion of their genome (11.4 Mb) covered in longer ROH (>16 Mb).

High coverage within the short category of ROH may indicate a relatively high contribution of ancient inbreeding in the breeds, whereas the higher coverage of long ROH suggests a more recent inbreeding effect.

Occurrence of SNPs in ROH across genomes

Percentage of SNP residing within a ROH was estimated to identify the genomic regions of high homozygosity. Six genomic regions were identified among all breeds.

58 % threshold limit to consider ROH Island



Genomic regions of extended homozygosity (ROH islands) identified and Quantitative Trait Loci (QTL) associated

Results and discussion

GGA	N° of SNPs	Start	End	Length (bp)	Genes	QTL
1	17	141583475	141639278	55803	<i>LOC107050425</i>	Breast muscle pH QTL (157157)
1	144	141921559	142517751	596192	<i>LOC107051457</i> , <i>LOC101748187</i>	Muscle dry matter content QTL (24459) Muscle dry matter content QTL (24460) Muscle dry matter content QTL (24461) Muscle dry matter content QTL (24462) Breast muscle pH QTL (157157)
4	39	41007013	41128124	121111	TENM3 , <i>LOC101748815</i>	Ileum weight QTL (96634)
5	261	2090157	3519023	1428866	<i>PRMT3</i> , NELL1 , <i>SLC6A5</i> , <i>MIR1775</i> , <i>LOC107053351</i> , <i>LOC107053350</i> , ANO5 , <i>SLC17A6</i> , <i>FANCF</i> , <i>GAS2</i> , <i>SVIP</i> , <i>ANO3</i> , <i>SLC5A12</i> , <i>FIBIN</i> , BBOX1 , <i>LOC107053349</i> , <i>LOC107053348</i>	Body weight (28 days) QTL (95416) Body weight (28 days) QTL (95415)
11	16	3344808	3389428	44620	<i>ESRP2</i>	Feed intake QTL (64558)
11	71	3596573	3760321	163748	<i>SLC12A4</i> , <i>LOC107054268</i> , <i>LOC101752262</i> , <i>SLC6A2</i> , <i>LPCAT2</i>	Feed intake QTL (64559)

TENM3: developing nervous system;

ANO5: develop muscle tissue;

NELL1: growth factor linked to bone tissue formation and skeleton integrity;

BBOX1: feed efficiency.

Conclusions

- Pepoi breeds needs urgent conservation plan in order to revive them and reduce the inbreeding. **However, the number of individuals in the population is really low.**
- The analysis of ROH highlights the importance of novel marker based information to prevent future loss of diversity;
- **Genes found in ROH islands could be useful for selection signatures.**
- In conclusion, the breeds are currently experiencing reduced representatives, **inbreeding depression and recent inbreeding events.** Past conservation needs to be adjusted if the numbers of representatives of each breed must be increased, preserved and prevented from moving towards extinction.

Acknowledgments

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THANK YOU ALL

