Genomic diversity and population structure of twelve Italian local turkey (*Meleagris gallopavo*) populations

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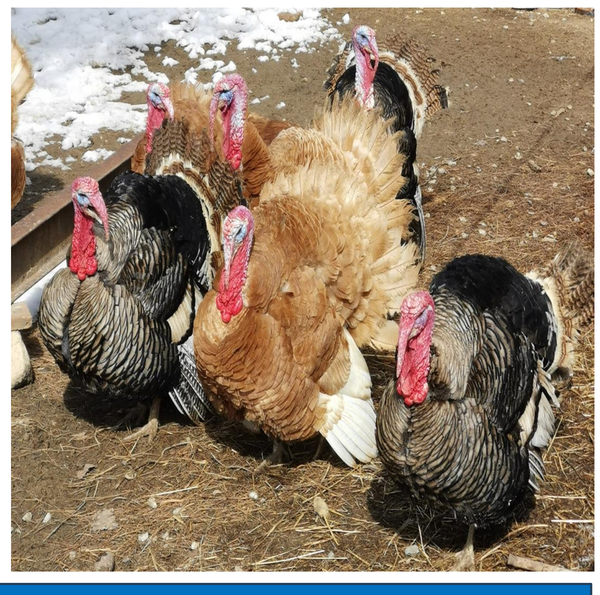
Introduction

Italian-origin turkey breeds are an important source of genetic diversity that should be preserved through an in vivo approach. Whole genome sequencing (WGS) datasets are produced from next-generation sequencing technologies. These technologies allow a comprehensive evolution of genomic variability within and across populations.

The Basilicata turkey population is widespread in the Basilicata region of southern Italy. There are two colors, one is buff, and the other is black plumage with buff and white streaks. Adult animals weight up to 9 kg for males and 4 kg for females. The female produces 50/60 eggs per year. The Basilicata population is rustic and adapted to harsh environment.

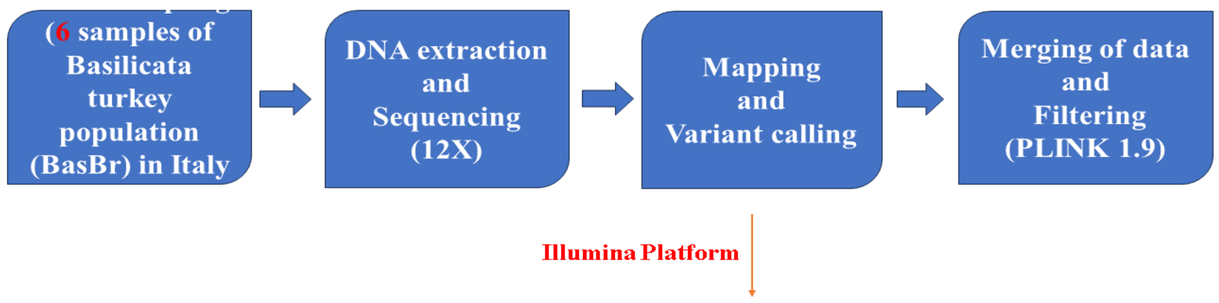


Objective

The aim of this study is to investigate the patterns of genetic diversity and population structure of Basilicata (BasBr) turkey population, and to conduct a genome-wide comparative analysis of 11 local Italian turkey populations.

Materials and Methods

Samples and Sequencing



The Turkey_5.0 genome assembly—GCA_000146605.1 was used in this study as a reference genome.

- The SNP data of BasBr population were merged with the genotypic data (Axiom® Turkey Genotyping Array (Affimetrix) containing 634,067 SNPs) retrieved from previous studies (Strillacci et al., 2019,2021).
- A total of 155,062 SNP markers passed the quality control.
- H_E, H_O, MAF and F_{ROH} for each breed were calculated.
- A multidimensional scaling (MDS) plot that represented the first 2 components identified with the mds-plot command of R software.
- PLINK 1.9 software was used to generate the input file to run ADMIXTURE analysis (Alexander et al., 2009).
- PLINK was used to explore Runs of homozygosity (ROH).

Results

Genetic diversity indices

The highest values of Ho (0.430), He (0.354), and MAF (0.272) were observed in IBRC, while the lowest values showed in ErRo (Table 1).

The inbreeding coefficients values ranged from 0.030 in IBRC to 0.269 in ErRo (Table 1).

Table 2. Genetic diversity indices (HO, HE, and MAF) and runs of homozygosity based inbreeding level (FROH) for each studied population

Population	N (113)	Ho ± SD	He ± SD	MAF ± SD	F_{ROH}±SD
Basilicata Comune It (BasBr)	6	0.401±0.402	0.24±0.216	0.2±0.201	0.033±0.001
Brianzolo (Br)	10	0.199±0.254	0.165±0.198	0.124±0.162	0.153±0.037
Bronzato Comune It (BrCI)	10	0.197±0.211	0.207±0.198	0.156±0.167	0.151±0.016
Bronzato Comune It. × Ibrido Commerciale (BrCI_IBRIDO)	5	0.21±0.238	0.26±0.186	0.191±0.157	0.165±0.067
Colli Euganei (COEU)	10	0.198±0.189	0.203±0.176	0.143±0.147	0.158±0.079
Ermellinato di Rovigo (ErRo)	10	0.091±0.175	0.094±0.173	0.072±0.141	0.269±0.026
Ermellinato di Rovigo × Ibrido Commerciale (ErRo_IBRIDO)	10	0.28±0.224	0.267±0.179	0.197±0.156	0.096±0.064
Ibrido Commerciale (IBRC)	10	0.413±0.219	0.354±0.147	0.272±0.144	0.030±0.005
Narragansett (NARR)	7	0.253±0.23	0.288±0.194	0.223±0.171	0.127±0.078
Nero Italiano (NI)	10	0.265±0.288	0.219±0.22	0.177±0.189	0.099±0.048
Parma E Piacenza (PrPc)	15	0.321±0.222	0.299±0.185	0.229±0.165	0.055±0.037
Romagnolo (ROM)	10	0.287±0.242	0.254±0.194	0.192±0.167	0.040±0.013

HO is observed heterozygosity, HE is expected heterozygosity, FIS is Wright's inbreeding coefficient and F_{ROH} is ROH based genomic inbreeding coefficient.

According to the first two components of inferred variance (Figure 1), the MDS analysis highlighted a clear separation for ErRo and BrCI breeds from all populations. Also, we can see a separation for BasBr, IBRC and NARR from the other breeds in the left side. The two crossbreds, Br, CoEU, NI, PrPc and ROM are very close with partial overlapping.

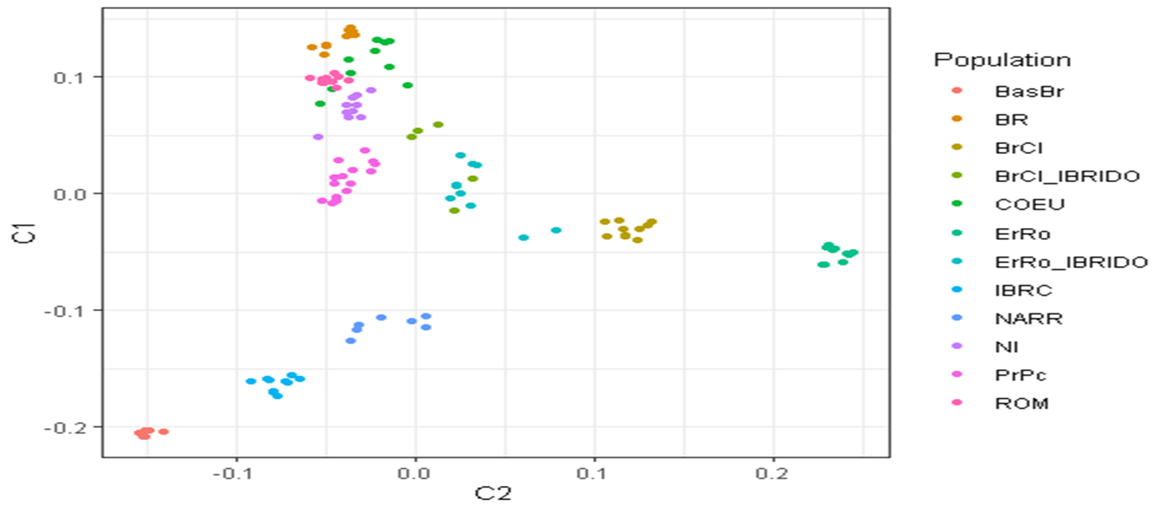


Figure 1. Genetic relationships among the Italian local chicken breeds defined through multidimensional scaling analysis. Populations abbreviations were described in the objectives section.

The optimal K values were from 2 to 12 to underline ancestral components shared among Italian turkey populations (Figure 2). The model assuming 2 ancestral populations, separated the ErRo breed from all populations, while other populations have the same ancestral of BrCI breed.

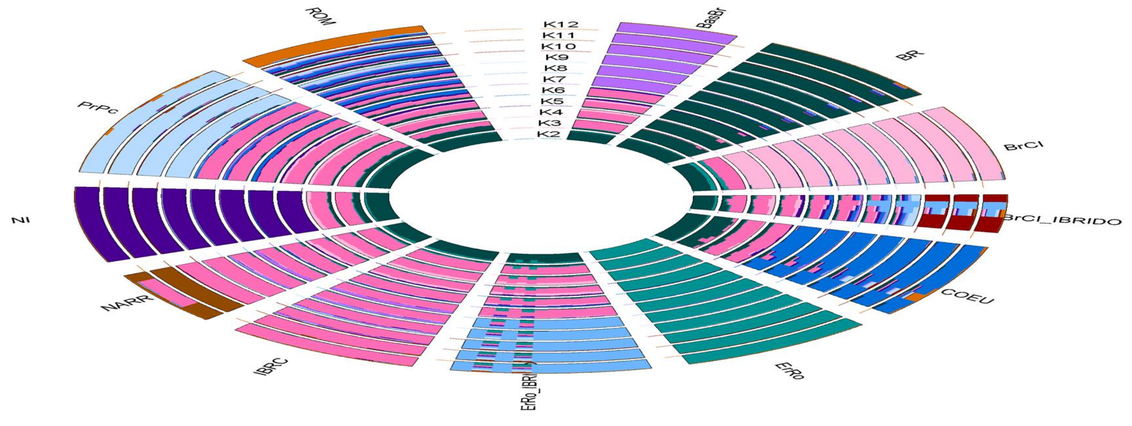


Figure 2. Circle plot showing ancestral clusters (K) inferred by Admixture analysis of the12 turkey populations. Populations abbreviations were described in the objectives section

Conclusions

The genetic diversity indices showed a moderate level of variability. The results from the several statistical approaches defined the genetic background for Basilicata turkey population.

Acknowledgments

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