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Genetic Polymorphism of the PAX7 Minisatellite Region in Italian Chicken

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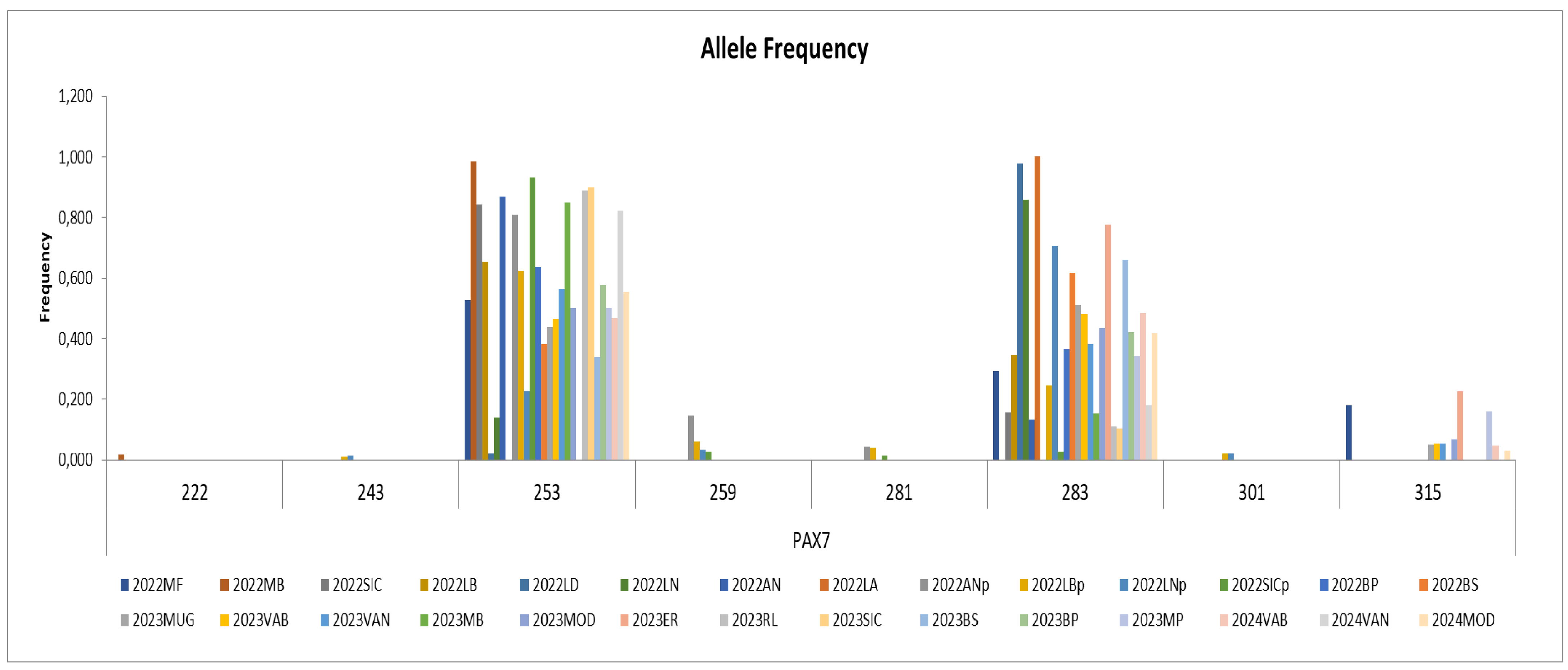
INTRODUCTION

In **local chicken breeds**, primarily raised for **meat production**, growth performance must be economically viable to ensure their sustainable utilization. However, it is crucial to maintain a balance with the preservation of biodiversity.

Investigating polymorphisms in the **Paired Box 7 *(PAX7)*** gene—proposed as a candidate marker for growth and meat quality—could provide a valuable tool for genetic improvement.



METHODS

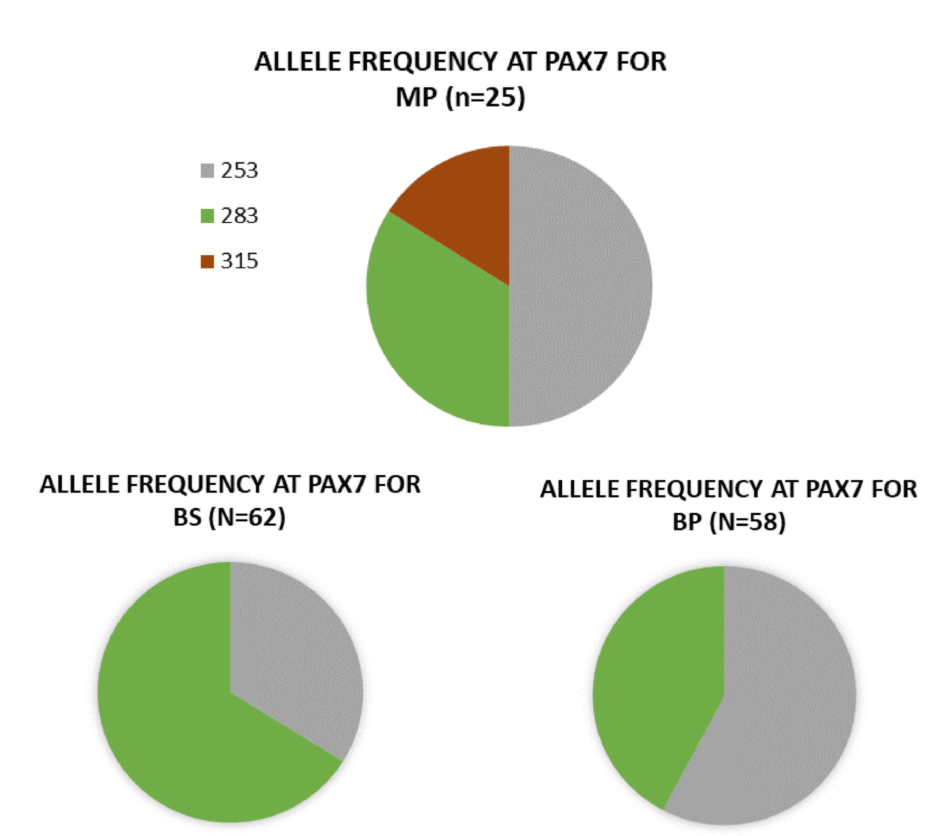
This study investigated the genetic polymorphism of the PAX7 gene's region in **1,131 individuals** from 17 Italian poultry breeds (AN, Ancona; BP, Bionda Piemontese; BS, Bianca di Saluzzo; ER, Ermellinata di Rovigo; LA, Livorno Argento; LB, Livorno Bianca; LD, Livorno Dorata; LN, Livorno Nera; MB, Mericanel della Brianza; MF, Millefiori di Lonigo; MP, Millefiori Piemontese; MUG, Mugellese; RL, Robusta Lionata; SIC, Siciliana; VAB, Valdarnese Bianca; VAN, Valdarno; MOD, Modenese), comprising **28 populations** from different origins or generational lineages.

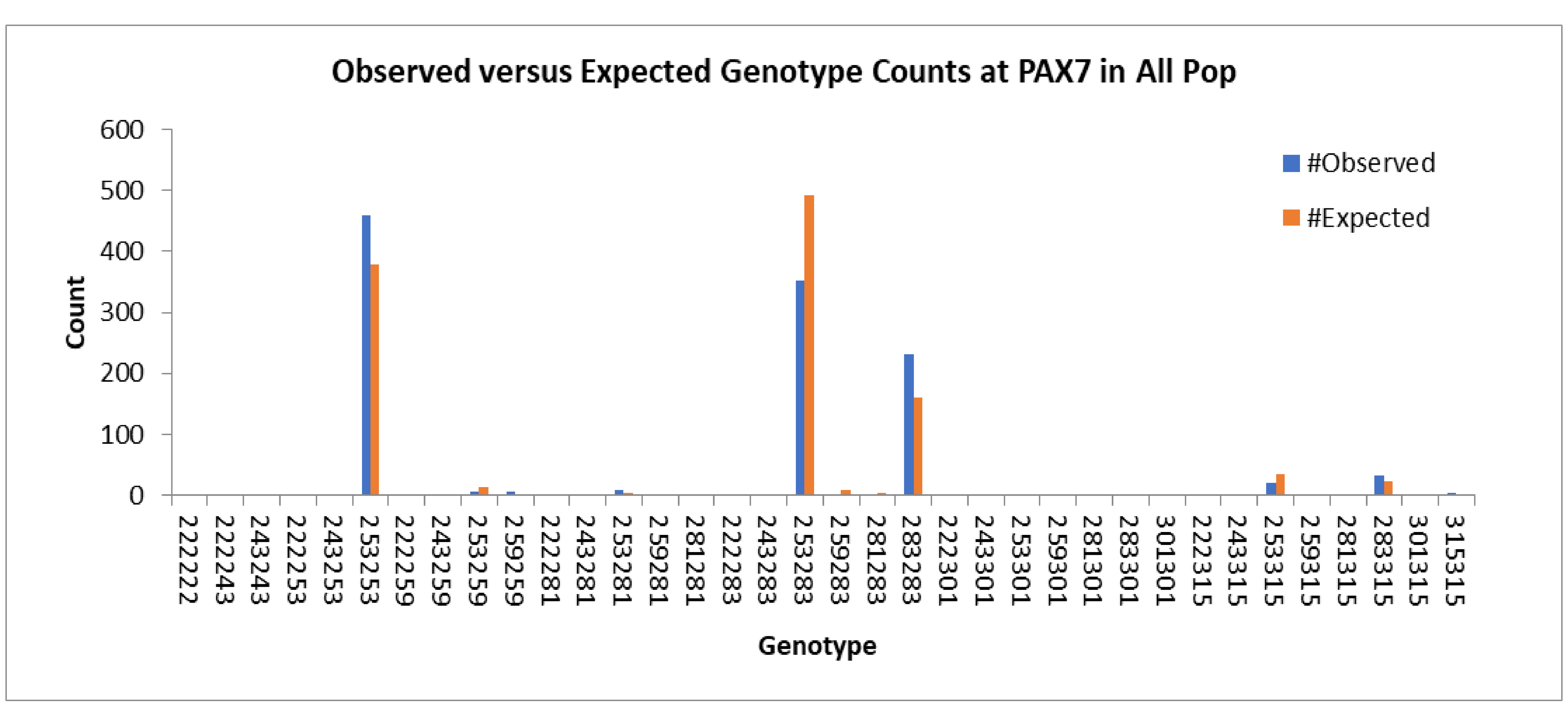
RESULTS

Analysis of the minisatellite region identified **eight alleles** (222, 243, 253, 259, 281, 283, 301, and 315). Among these, the most prevalent were 253 and 283, potentially linked to improved fitness.

Genotype distribution highlighted the prevalence of three genotypes: homozygotes 253 (41%) and 283 (21%), and heterozygote 253/283 (31%), with an excess of homozygosity.

Observed and expected heterozygosity were 0.36±0.04 and 0.37±0.04, respectively. Among Piedmontese breeds, Millefiori Piemontese (MP) had the highest polymorphism, with three alleles (253, 283, 315) and five genotypes; unlike Bionda Piemontese (BP) and Bianca di Saluzzo (BS) which lacked allele 315.





DISCUSSIONS & CONCLUSIONS

The dominance of alleles 253 and 283 may reflect past selection for desirable traits, as these variants correlate with growth performance in literature.

Low-frequency genotypes observed may be due to the application of genetic variability-preservation mating plan and also to the introduction of breeders from local farms into conservation centres.

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