

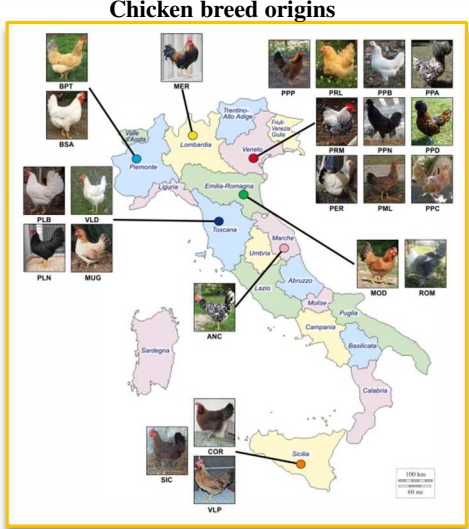
# Refining genetic structure and relationships of Italian Local Chicken breeds using genome-wide SNP data

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**Aim**  
 Give a high-resolution overview of the genome-wide diversity and population structure of 23 Italian local breeds and four commercial hybrids using Affymetrix 600 K Chicken SNP Array.



**Discussion**  
 Improving our knowledge of the genetic structure in livestock populations is fundamental for designing selection schemes, understanding environmental adaptation, enhancing the efficient use of the breeds, and implementing conservation programs. The advent of high-throughput genotyping arrays has considerably facilitated the study of genetic structure in livestock, but they are infrequently used and generally understudied in local breeds. The levels of genetic diversity, investigated through different approaches (expected and observed heterozygosity, and inbreeding coefficient), showed the lowest in the local chicken breeds, including PPA, PPC, PPP, PRM, and SIC, compared to the commercial stocks (Table 1). The level of genomic inbreeding estimated from runs of homozygosity (FROH) (Figure 1), was markedly different among the breeds and ranged from 0.121 (Valdarnese) to 0.607 (Sicilliana). These results could be explained by an increase in inbreeding, linked to their reduced demographic sizes over time due to selection events. BSA is the only indigenous chicken breed showing a lower inbreeding level, probably due to its larger population compared to the others. The analysis of genetic differentiation (Figures 1 and 3) showed that most breeds formed distinct clusters, but also indicated the gene flow events, especially among breeds that originated from the same geographical area, such as between the populations belonging to the Polverara and Padovana breeds, or among the three Sicilian populations (Figure 3). The genetic background of the commercial stocks is close to that of several breeds from the Veneto region, highlighting the story of their introgression with local breeds. Through the present study, we provided a complete overview of the Italian chicken breeds and contextualized them at a national level. Improvement of systems to record and monitor inbreeding in these breeds may contribute to their in situ conservation. This will promote conservation plans and highlight their role as a genetic reservoir. Consequently, a strategy to increase value for these breeds should be provided in order to guarantee a profit for farmers. The information obtained represents a useful tool for understanding correct genetic management and supervising conservation activity. In this context, the information from genomic analysis may play a crucial role in the development of mating plans to avoid the negative effects of inbreeding in these breeds.

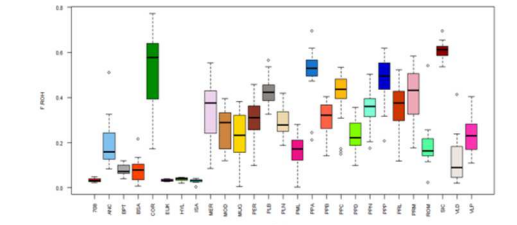
**Table 1.** Genetic diversity indices. Number of animals per breed (N), minor allele frequency (MAF) expected (He) and observed (Ho) heterozygosity, and inbreeding coefficient (FROH). For each value, the standard deviation (SD) is reported.

Breed	Accession	N	MAF		He		Ho		F <sub>ROH</sub>	
			Mean	SD	Mean	SD	Mean	SD	Mean	SD
Ansouze	ANSC	24	0.267	0.242	0.263	0.181	0.274	0.187	0.284	0.1
Bianca di Salizo	BSA	24	0.286	0.19	0.339	0.172	0.336	0.151	0.076	0.059
Bionda Piemontese	BPT	22	0.283	0.21	0.325	0.188	0.317	0.164	0.116	0.025
Cinotta Calabrese	CCR	22	0.267	0.301	0.167	0.162	0.221	0.178	0.345	0.18
Ercellinata di Rovigo	PER	23	0.309	0.321	0.199	0.192	0.222	0.198	0.459	0.044
L'orno Bianca	PLB	24	0.269	0.295	0.205	0.196	0.218	0.186	0.465	0.061
Lisorno Nera	PLN	24	0.263	0.279	0.231	0.211	0.231	0.195	0.365	0.062
Merisano della Brianza	MER	24	0.282	0.288	0.232	0.18	0.261	0.186	0.368	0.127
Milford di Longgo	PML	23	0.281	0.238	0.263	0.199	0.201	0.178	0.302	0.08
Modenese	MCD	24	0.273	0.252	0.26	0.197	0.27	0.181	0.296	0.083
Miraflores	MFG	24	0.284	0.231	0.281	0.182	0.3	0.175	0.236	0.115
Padovana Argentina	PPA	24	0.241	0.331	0.151	0.198	0.146	0.185	0.588	0.098
Padovana Camosciata	PPC	24	0.238	0.303	0.169	0.191	0.179	0.193	0.538	0.095
Padovana Dorsata	PPD	24	0.247	0.264	0.219	0.194	0.232	0.187	0.404	0.081
Pepoi	PPP	24	0.277	0.341	0.154	0.191	0.168	0.196	0.379	0.039
Polverara Bianca	PPB	24	0.26	0.261	0.216	0.179	0.248	0.187	0.41	0.052
Polverara Nera	PPN	24	0.257	0.29	0.201	0.193	0.213	0.194	0.454	0.062
Robusta Lanata	PRL	23	0.165	0.185	0.181	0.199	0.185	0.195	0.308	0.039
Robusta Marchetta	PRM	24	0.304	0.358	0.157	0.149	0.166	0.193	0.272	0.032
Romagnola	ROM	24	0.271	0.241	0.281	0.197	0.278	0.182	0.235	0.091
Sicilliana	SIC	24	0.259	0.361	0.129	0.205	0.123	0.189	0.648	0.034
Valdarnese	VLD	24	0.283	0.204	0.221	0.181	0.222	0.16	0.127	0.098
Valdarnese	VLP	20	0.281	0.268	0.26	0.224	0.261	0.184	0.239	0.086
708 Broiler Ross	708	13	0.317	0.234	0.369	0.219	0.324	0.162	-0.005	0.009
Eureka	ELK	9	0.329	0.261	0.374	0.26	0.305	0.177	-0.018	0.013
Hy-line white eggs	HVL	10	0.333	0.278	0.375	0.286	0.289	0.285	-0.020	0.008
Ista Brown	ISA	9	0.332	0.261	0.378	0.276	0.298	0.182	-0.028	0.017

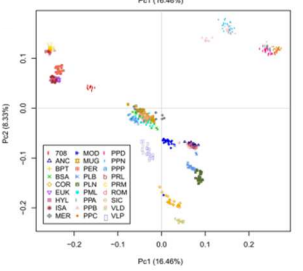
## Results



**Figure 2.** Neighbor-joining tree constructed on the Reynold's genetic distance based on individual allele-sharing distances. Breed acronyms are reported in Table 1.



**Figure 1.** Boxplot of the inbreeding coefficient (FROH) estimated from runs of homozygosity for each breed considered in this study. Breed acronyms are reported in Table 1.



**Figure 3.** Genetic relationships among the 27 chicken breeds in this study as inferred by multidimensional scaling (MDS) analysis using all of the individuals per breed. Breed acronyms are reported in Table 1.

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