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HIGH-RESOLUTION GENOMIC ANALYSIS OF SICILIAN CHICKEN POPULATIONS

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Aim of the research

In this study, we assessed the genetic variability and population structure of Cornuta di Sicilia (COS) and Val Platani (VLP) chicken populations using 600K SNP microarray data and compared them with other Italian local and commercial breeds.

Conclusion

Analysis of within-breed diversity showed moderate variability. The homozygosity hotspots harbored genes related to immune response and local adaptation traits. The COS formed a non-overlapping genomic cluster and clearly separated from the other populations. The VLP showed a complex genomic structure, due to the presence of two sub-populations that match with the different origin of the samples.

Introduction

Today, several populations are reared by smallholders in local extensive production systems and some of them do not have a defined genetic structure, such as Cornuta di Sicilia (COS) (also known as Cornuta di Caltanissetta) and Val Platani (VLP) (also known as Valplatani) chicken populations (**Figure 1**).

The exact origin of these populations is unknown. They represent local genetic resources historically present in the rural areas of the Sicily region (South Italy), but they are not officially recognized as breeds. The two populations have evolved over the centuries by natural adaptation, and are reared for egg deposition, for their tolerance to diseases and good adaptation to the local environment. The COS is also reared as ornamental chicken, due to its duplex-comb phenotype, which corresponds to a two-pronged horn or V-shaped comb that is restricted to the posterior portion of the comb developing region. To date, no official data are available on morphological and productive characteristics of these populations.

Material and methods

Samples consisted of 34 COS (7 males and 27 females) and 42 VPL (9 males and 33 females) chickens.

Genotyping was performed using the 600K Affymetrix Axiom Chicken Genotyping Array, which included 580,961 single nucleotide polymorphisms (SNPs). A total of 451,258 polymorphic SNPs and 72 animals were kept after filtering. The average minor allele frequency (MAF), observed (Ho) and expected (He) heterozygosity were estimated.

The runs of homozygosity (ROH) analysis was performed to estimate the molecular inbreeding and the homozygosity patterns.

The raw data of the two chicken populations were merged with the genotype data of 23 Italian local and 4 commercial populations (**Table 1**) retrieved from a previous study (Cendron et al., 2020), for a final dataset of 27 populations, 668 individuals and 419,475 SNPs. Multidimensional scaling (MDS), model-based clustering (Admixture), measurement of population differentiation, and neighbor networks were performed.

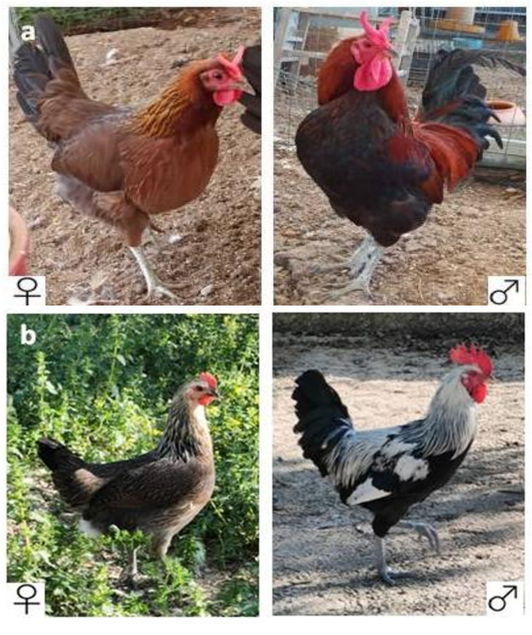

Figure 1. Female and male of COS (a) and VLP (b).

Population	Acronym	Population	Acronym
Ancona	ANC	Pepoi	PPP
Bianca di Saluzzo	BSA	Polverara Bianca	PPB
Bionda Piemontese	BPT	Polverara Nera	PPN
Cornuta Caltanissetta	**COR**	Robusta Lionata	PRL
Cornuta di Sicilia	**COS**	Robusta Maculata	PRM
Ermellinata di Rovigo	PER	Romagnola	ROM
Livorno Bianca	PLB	Siciliana	SIC
Livorno Nera	PLN	Valdarnese	VLD
Mericanel della Brianza	MER	**Valplatani**	**VLP**
Millefiori di Lonigo	PML	**Val Platani**	**VPL**
Modenese	MOD	708 Broiler Ross	708
Mugellese	MUG	Eureka	EUK
Padovana Argento	PPA	Hy-lyne white eggs	HYL
Padovana Camosciata	PPC	Isa Brown	ISA
Padovana Dorata	PPD		

Table 1. Population name and acronym of the 27 chickes populations.

Results

The genetic diversity indices, estimated using different approaches, displayed moderate levels of genetic diversity in both populations (**Table 2**).

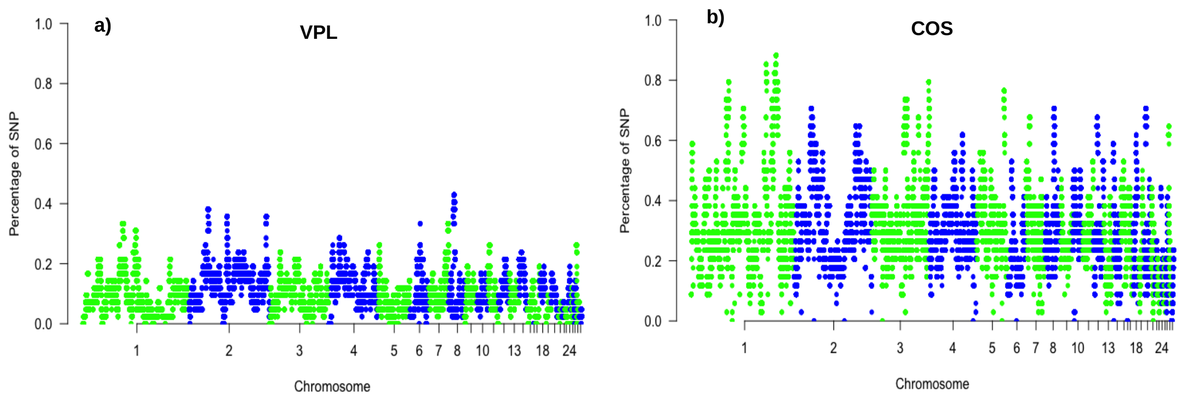

Figure 2. Manhattan plot of SNP frequency (%) in ROH islands of Val Platani (VPL) and Cornuta (COS) chickens

Population	Ho±s.d	He±s.d	MAF±s.d	F_{ROH}±s.d
VPL	0.362±0.150	0.368±0.124	0.279±0.131	0.103±0.126
COS	0.253±0.211	0.240±0.188	0.259±0.132	0.307±0.174

We investigated the ROH islands using the top 0.999 SNPs in ROH of the percentile distribution within each population. Figures 2a and 2b showed the Manhattan plots of SNPs in ROH occurrence in VPL and COS, respectively. Several outstanding peaks with a high percentage of ROH were identified, especially in COS population.

A total of 7 ROH islands were identified in the two populations. COS reported five ROH islands detected on two chromosomes (GGA01 and GGA03), containing 1,280 SNPs. The VPL showed two hotspots on GGA02 and GGA08, containing 1,217 markers.

Within ROH islands, a total of 28 genes for COS and 24 genes for VPL were mapped, associated with production traits, immune responses and environmental adaptation.

The MDS plot (**Figure 3**) allowed us to separate the three Sicilian chickens, and in particular the Siciliana (SIC) breed and the COS from the other populations. The VPL was on the gradient between the two Sicilian populations (SIC and COS) and the other breeds involved in the study. In the Admixture analysis (**Figure 4**), SIC and COS were the first to separate at K = 3 (yellow). From K = 5 and for subsequent K values, the VPL population started clustering apart from all other populations, and showed shared genomic components with other populations, and the presence of substructure.

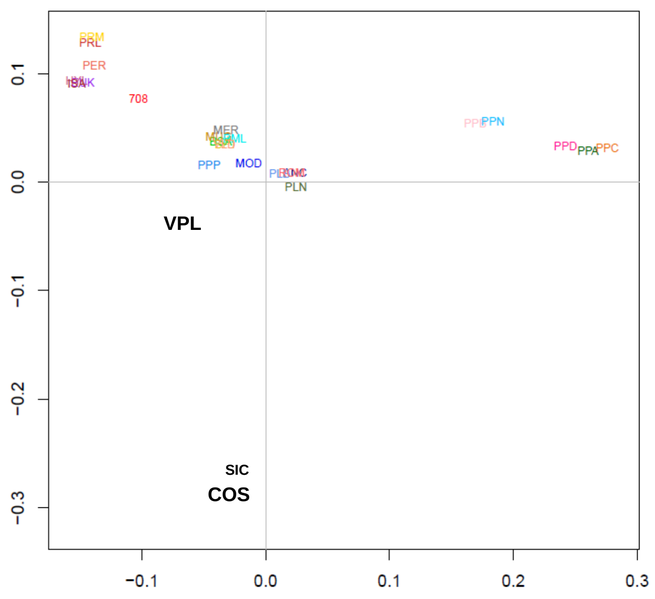

Figure 3. Multidimensional scaling analysis plot of the 27 chicken populations.

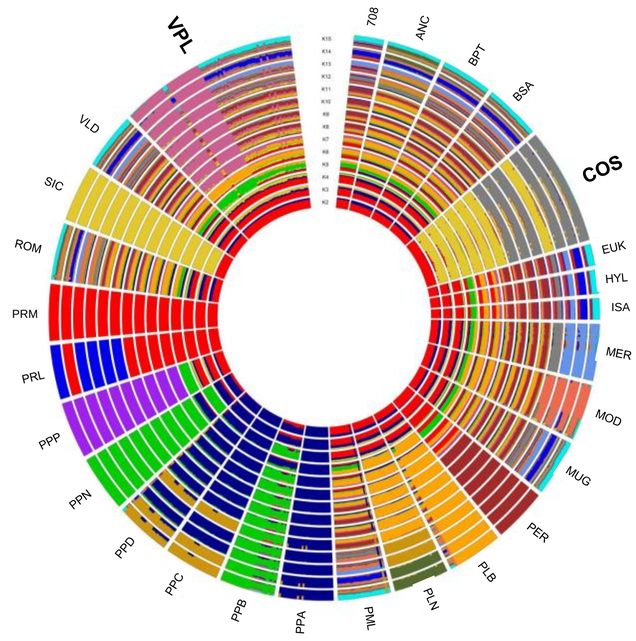

Figure 4. Model-based clustering of the 27 chicken populations (K = 2-15).

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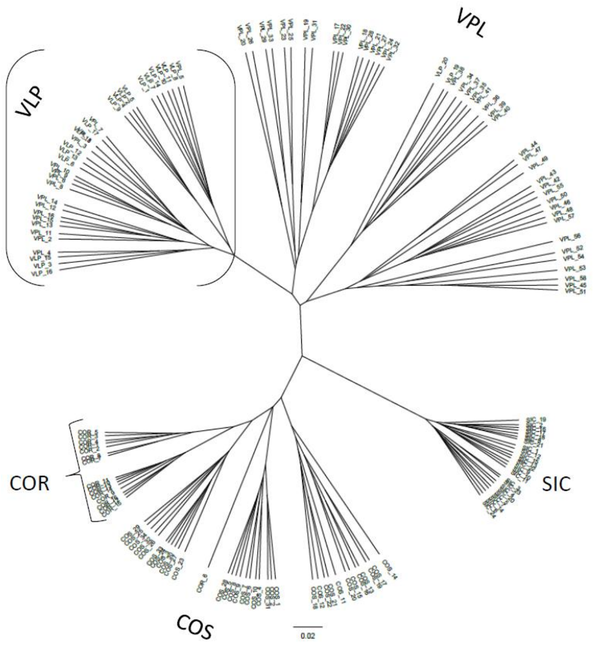

Figure 5. NJ tree based on allele sharing distance

Analyses were also performed to explore in detail the relatedness among Sicilian chickens, to evaluate any differences between the individuals of COS and VPL sampled in this study and those present in the dataset of Cendron et al. (2020) (here COR - Cornuta and VLP - Valplatani).

The NJ tree based on allele sharing distance (ASD) separated Valplatani's individuals according to their population of origin, whereas the two Cornuta's groups (COR and COS) shared a similar genetic background. (**Figure 5**).

References: Cendron et al., (2020). Animals, 10, 1441. doi.org/10.3390/ani10081441.
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