

TuBAvI (2017-20)
TuBAvI-2 (2021-24)

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https://ec.europa.eu/agriculture/rural-development-2014-2020_en

Ministry of agriculture, food sovereignty and forestry –
National Rural Development Programme 2014/2022 – Measure 10.2 –
Conservation, use and sustainable development of genetic resources
in agriculture



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CONSERVATION OF BIODIVERSITY IN ITALIAN POULTRY BREEDS:
deepening and monitoring
TuBAvI-2



Breed data sheet

MILLEFIORI PIEMONTESE

Gallus gallus domesticus Sp.

**Origin and morphological,
genetic, reproductive,
and productive traits**



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



**MINISTERO DELL'AGRICOLTURA
DELLA SOVRANITÀ ALIMENTARE
E DELLE FORESTE**





The presented data were registered in nucleus populations conserved at the University of Turin (UniTO).

Latest update: November 25th, 2024

Millefiori piemontese male and female



UniTO



UniTO



Millefiori piemontese

Gallus gallus domesticus Sp.

Breed data sheet: origin and morphological, genetic, reproductive, and productive traits

Breed origin and development

Name of the breed	Millefiori piemontese
Synonyms or local names	-
Geographic origin	Piemonte (surroundings of Cuneo)
Geographic distribution	Unassessable
Estimated total population size	Not available
Extinction risk status (FAO, 1998)	Unassessable
Any other specific information	Quite large and stocky breed, similar to Bionda piemontese

Historical origin
Local breed, diffused around Cuneo (in the surroundings of Busca, Villafalletto, and Tarantasca) up to 1960s, it was reared in farms to be sold in local markets. Following uncontrolled crossbreedings and due to the abandonment of rural activities, the diffusion of the breed gradually reduced. Occasionally found in Piedmont's countryside up to the 1990s, it is now considered to be extinct, even if few birds may have survived somewhere in the area. Recover attempts are at present ongoing on behalf of local breeders.

Sitography

archivistoricoavicoltura.blogspot.com

agraria.org

Qualitative and quantitative morphological traits in adult breeders

Discrete or qualitative traits

Feather morphology	Normal
Feather distribution	Normal
Plumage structure	Abundant, soft
Plumage colours	Black mottled
Colour features	Bi-colour, without sexual dimorphism
Chick plumage colour	
Comb type	Simple comb , sometimes falling to one side in females during oviposition; less developed than in other Piedmont breeds
Comb points	
Ear-lobe colour	Red or red with whitish streaks
Beak colour	Yellow shaded with horn
Iris colour	
Muffs	Absent
Beard	Absent
Tuft	Absent
Skin colour	Yellow
Shank colour	
Shank feathering	
Skeletal variants	-
Other specific and distinct visible traits	-

Colour pattern
Ground colour black, with white spots, similar to Ancona breed pattern, but with less regular marking, sometimes with red traces.

Genetic traits

Characterisation of the breed with Single Nucleotide Polymorphisms (SNPs)

Molecular marker	Affymetrix Axiom 600K Chicken Genotyping Array
Laboratory that performed the analyses	Department of Agronomy, Food, Natural Resources, Animals and Environment (DAFNAE) University of Padua
Analysed parameters	MAF: minor allelic frequency Ho: observed heterozygosity He: expected heterozygosity F _{HOM} : inbreeding coefficient

Year		N**	MAF	Ho	He	F _{HOM}
2019	Mean	48	0.25	0.60	0.57	0.15
	SD*		0.20	0.12	0.12	0.41

*SD: standard deviation; **N: number of samples

Characterisation of nucleus populations with microsatellites and mating plans

Molecular marker	Microsatellites (26 markers)
Laboratory that performed the analyses	Laboratory of Animal Molecular Genetics Department of Veterinary Science (DSV) University of Turin
Analysed parameters	Ne: effective number of alleles Na: observed number of alleles I: Shannon diversity index H-Ind: individual variability index Ho: observed heterozygosity (average H-Ind) He: expected heterozygosity F: fixation index P: average kinship index
Indexes used to schedule mating plans	H-Ind P

Year		N**	Na	Ne	I	Ho	He	F	P
2020	Mean	52	4.214	2.703	1.059	0.586	0.586	-0.006	0.558
	SE*		0.366	0.227	0.093	0.057	0.041	0.064	0.013
2022	Mean	25	3.42	2.39	0.92	0.516	0.53	0.06	0.56
	SE*		0.24	0.14	0.07	0.045	0.04	0.07	0.01

*SE: standard error; **N: number of samples