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Fat-tail sheep still represent twenty-five percent of the world sheep population; they are predominant in pastoral, transhumant and low input systems. In Western countries and in high input systems they are generally endangered.

Fat-tail sheep preserved genetic variability for functional adaptation.

The identification of the genes with a role in the fat-tail phenotype contributes to the understanding of the physiology of fat deposition as well as the mechanisms of adaptation and is essential for maintaining future breeding options.

AIM Identify signals of fat deposition and adaptation through genome-wide scan of the Barbaresca fat-tail sheep.

ANIMALS Barbaresca in an ancient Sicilian fat-tail sheep, highly endangered at present. Of the 35 000 heads of 1980, about 1 300 are left nowadays in 20 flocks. The breed originated from crosses between Barbary sheep from North Africa and the Pinzirita breed at times of the Arab settling in Sicily (9th century). The breed is reared in a very restricted area in central Sicily on small- and medium-sized farms under a semi-extensive farming system. It is a dual-purpose breed: milk for cheese and meat. Barbaresca is one of the only two fat-tail sheep of Italy.

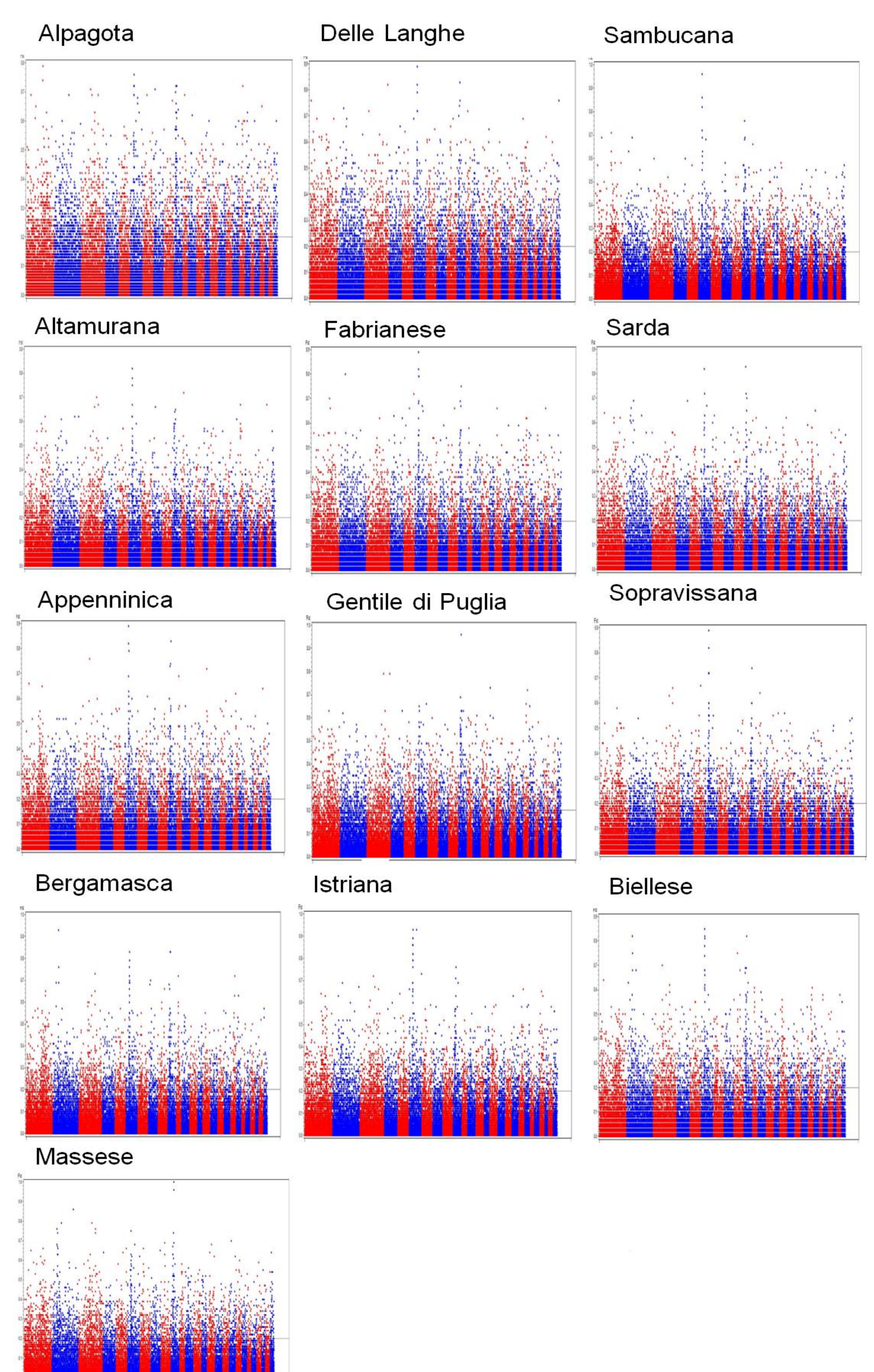
METHODS Genotypic data were obtained with the OvineSNP50K array. Fst values of differentiation for 43072 markers were calculated in pairwise comparisons of Barbaresca with each of 13 Italian thin tail breeds.

RESULTS Strong signals of selection were detected on chromosome 6, in a region encoding the SLIT homolog 2 gene, this gene acting as a molecular guidance cue in cellular migration.

The signature on OAR 10:29.0-30.7 Mb had been previously identified as fat-tail signature by Yuan et al. (2016) in Chinese sheep, and was also reported by Seroussi et al. (2017) as signal of climate adaptation, this conclusion being supported by the presence of the ALOX5AP gene, which encodes a protein that is required for the synthesis of lipid mediators involved in various types of inflammatory responses (Seroussi et al. 2017).



The signature on OAR 7:82 Mb was located in proximity of the Vertnin gene, a candidate for variation in vertebral number, and was already revealed in Iranian and Mediterranean fat-tailed breeds (Moradi et al., 2012; Moioli et al., 2015).



OAR	start	end	Genes in the region
1	161588670	161912812	ST3GAL6, DCBLD2, LOC101107320
1	163538737	163965269	ABI3BP, ADGRG7, TMTM45A, LOC101109067
2	56006296	56331862	LOC101111526
2	87286590	87291060	PLIN2, DENND4C, RPS6, ACER2
3	122515163	122887650	MGAT4C
3	136341082	136433664	FAIM2, BCDIN3D, NCKAP5L, LOC105612627, TMBIM6, PRPF40B, FMNL3, FAM186B, KCNH3, MCRS1, SPATS2, C1QL4, DNAJC22, PRPH
3	154033734	154318689	MSRB3, LOC105609947, LEMD3, WIF1, TBC1D30
3	169813339	169988856	ANO4
5	59126508	59475280	CAMK2A, TCOF1, CD74, LOC105606717, RPS14, NDST1
6	36034915	36390529	HERC3, PYURF, PIGY, HERC5, HERC6, PPM1K, ABCG2, PKD2, SPP1, MEPE
6	37126564	39487124	IHSP, LAP3, MED28, LOC105615455, LOC105608051, MED28, FAM184B, NCAPG, LCOR1, DCAF16, FAM184B, LOC105615456, LOC105608050, LOC105608049, LOC101122950, SLIT2
6	69675370	69867326	CHIC2, LOC105613061, PDGFRA, GSX2, KIT
6	77012913	77459287	ADGRL3, LOC101114018
6	115244531	115439490	GRK4, NOP14, LOC106991221, LOC106991246, MFSN10, ADD1, SH3BP2, FAM193A
7	33565208	33736820	RHOV, VPS18, DLL4, CHAC1, INO80, EXD1, CHP1, MGA, LOC10561677, MARKBP1, JIMD7, PLAG2G4B, PLAG2G4E, EDH4, SPTBN5
7	82172198	82279625	ELMSAN1, PNMA1, PTGR2, ZNF410, FAM16B, COQ6, ENTPD5, BBOF1, ALDH6A1, LINS2, VSX2, ABCD4, VRTN SYNDIG1L
9	36057235	36326237	PLAG1, CHCHD7, SDR16C5, SDR16C5, LOC101116323, PENK
10	17765501	17904934	SUCLA2
10	19626592	20969799	DLEU7, FAM124A, LOC101119651
10	22012281	23976329	FOXO1, MRPS31, LOC105616150, LOC105608777, LOC105608775, LOC105608779, LOC105608780, LOC101122286, COG6, LHFP, NHLRC3, PROSER1, STOLM3, FREM2, LOC101108400, UFM1
10	27402323	27623690	LOC101109717, LOC101109981, RFC3, STARD13
10	29101583	30823905	BRCA2, ZAR1, FRY, LOC106991357, RXFP2, LOC101110773, LOC106991379, B3GLCT, HSPH1, LOC105616258, TEX26, MEDAG, LOC105610262, ALOX5AP, USPL1, LOC11112330, LOC101112071, KATNAL1, LOC106991380, UBL3
12	29027811	29441975	SMYD3, LOC105616512, LOC105616511
14	12515054	12841601	MAP1, LC3B, ZCCHC14, JPH3, KLHDC4, SLC7A5, LOC106991585, CASA, BANP
15	30012057	30425982	TRIM29, OAF, POU2F3, TMEM136, ARHGEF12
17	70788082	70947463	SMARCB1, SLC2A11, MIF, DERL3, MP11, ZNF70, VPRES3, CHCHD10, CABIN1, SUSD2, GGT5, SNRPD3, GUCD1, ADORA2A, UPB1, SPECC1L, BCR, RSPH14, GNAZ
19	31614145	31942689	LOC105607729, LOC105603449, MITF
19	33342669	33399965	FAM19A1

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