Association between *rs427117280* genotypes and weaning weight and average daily gain until weaning weight in sheep

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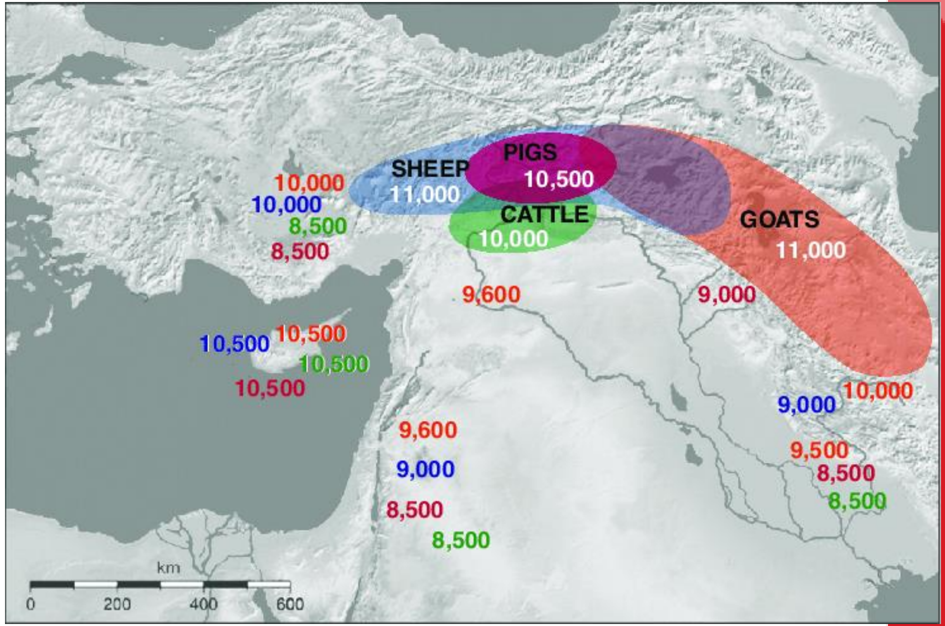
Outline

- Research background
- Materials and methods
- Results
- Discussion
- Conclusion

Research background

- Sheep farming has a crucial environmental role worldwide by reducing both the impact of greenhouse gas emissions.
- Carbon footprint of farming practices in sheep meat production is reported to be lower than beef (Mazzetto et al., 2023; Lal et al., 2022).
- Fixed and variable costs were the same for both species, however sheep had a substantially higher liveweight increase value than cattle ($4.79 vs. $1.46/kg) (Piltz et al., 2021).
- Valuable livestock for societies that meet their red meat needs from ruminants.




PNAS

Domestication and early agriculture in the Mediterranean Basin: Origins, diffusion, and impact

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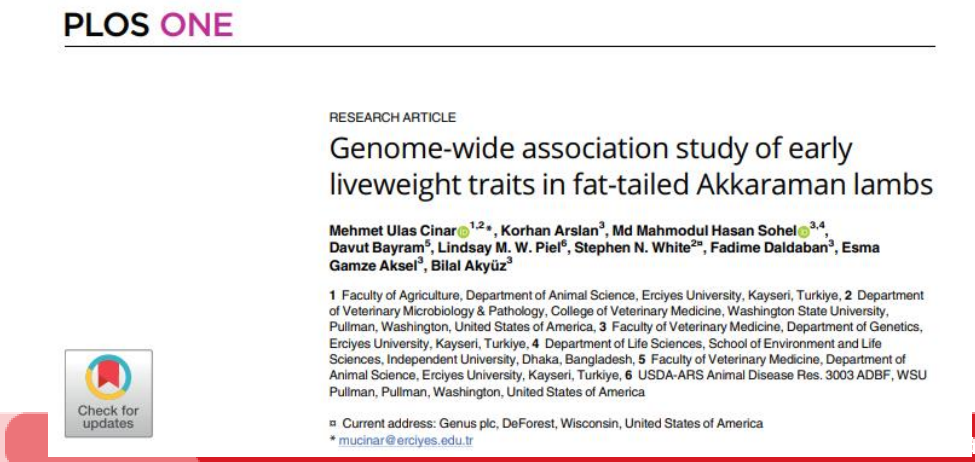
The past decade has witnessed a quantum leap in our understanding of the origins, diffusion, and impact of early agriculture in the Mediterranean Basin. In large measure these advances are attributable to new methods for documenting domestication in plants and

Research background

- China produced approximately 2.68 million metric tons of lamb and mutton, accounting for about 26% of the world's total production. Followed by Australia (706,905 metric tons), Türkiye (489,354 metric tons), New Zealand (436,975 metric tons), and Algeria (344,937 metric tons).
- **Body weight** is one of the most important growth and development components in sheep as it both directly and indirectly influences lamb meat yield, wool production, and reproduction.
- **Lamb liveweight** and **liveweight gain** have been defined as the key drivers of profitability in international sheep production systems (Cocks et al., 2002; Conington et al., 2004).
- Each additional day a lamb requires to attain its desired slaughter weight results in an **economic loss of €1.41** per lamb per day for Irish sheep farmers (Byrne et al., 2010).

Genetics of bodyweight traits

- Estimated heritability for lamb daily weight gain and weaning weight was low to moderate depending on the sheep breed studied (Mortimer et al., 2017; Boujenane and Diallo, 2017).
- Few QTLs (4,072) have been identified using a genome scan based on marker-QTL linkage analysis in sheep while the number in cattle and pigs is 177,199 and 34,342, respectively (Hu et al., 2022).
- In our previous GWAS, a QTN (*rs427117280*; OAR2: 248863817G>T) was detected as genome-wide significantly associated with weaning weight and daily weight gain until weaning in Akkaraman lambs (Cinar et al., 2023).



PLOS ONE

RESEARCH ARTICLE

Genome-wide association study of early liveweight traits in fat-tailed Akkaraman lambs

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Aim

- **Objective:** The validation of GWAS results in multi-breed livestock is crucial for enhancing the accuracy of genomic selection and understanding genetic traits across different breeds.

- **Study aims** to investigate the associations of *rs427117280* SNP with lamb liveweight and lamb liveweight gain until weaning in points in multi-breed sheep population.

Materials and Methods (Study design)

Phenotyping (n=1973)

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Birth Weight (g)	BW30 (g)	BW60 (g)	BW90 (g)	ADGB-90 (g)

Genotyping

Statistical analysis
sasLM

$y_{imcjl} = \mu + G_i + O_m + F_c + T_j + N_l + e_{imcjl}$

y_{imcjl}: phenotype (birth, 30th, 60th ve 90th days weights and daily liveweight gain)

μ: population mean

G_i: fixed effect for genotype (3 levels; GG, TG, or TT)

O_m: sex (2 levels; male or female)

F_c: farm impact (17 levels)

T_j: fixed effect for birth type (2 levels; single, or twin)

N_l: fixed effect for ewe age

Results (association)

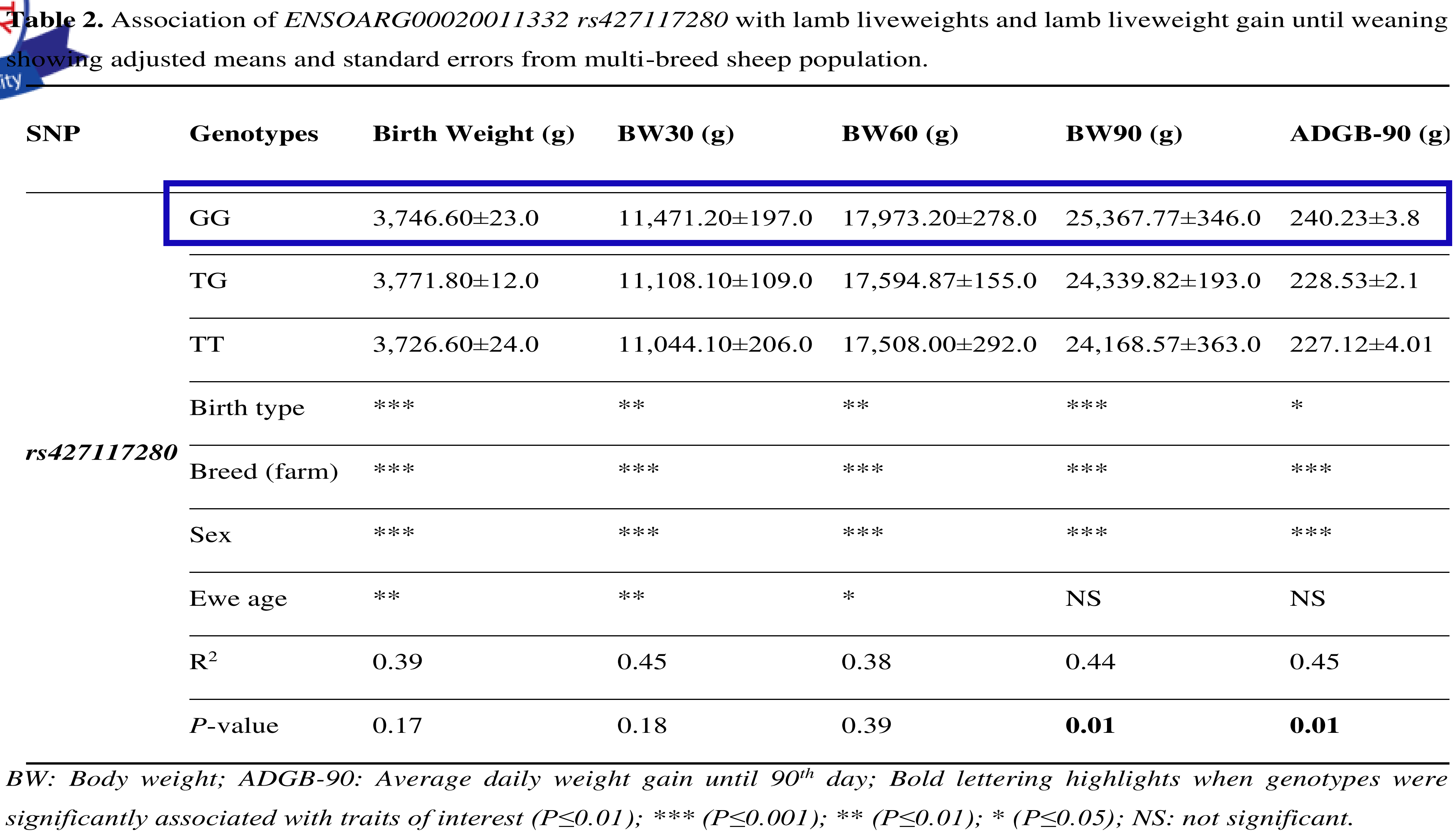


Table 2. Association of *ENSOARG00020011332 rs427117280* with lamb liveweights and lamb liveweight gain until weaning showing adjusted means and standard errors from multi-breed sheep population.

SNP	Genotypes	Birth Weight (g)	BW30 (g)	BW60 (g)	BW90 (g)	ADGB-90 (g)
rs427117280	GG	3,746.60±23.0	11,471.20±197.0	17,973.20±278.0	25,367.77±346.0	240.23±3.8
	TG	3,771.80±12.0	11,108.10±109.0	17,594.87±155.0	24,339.82±193.0	228.53±2.1
	TT	3,726.60±24.0	11,044.10±206.0	17,508.00±292.0	24,168.57±363.0	227.12±4.01
	Birth type	***	**	**	***	*
	Breed (farm)	***	***	***	***	***
	Sex	***	***	***	***	***
	Ewe age	**	**	*	NS	NS
	R^2	0.39	0.45	0.38	0.44	0.45
	P-value	0.17	0.18	0.39	**0.01**	**0.01**

*BW: Body weight; ADGB-90: Average daily weight gain until 90th day; Bold lettering highlights when genotypes were significantly associated with traits of interest (P≤0.01); *** (P≤0.001); ** (P≤0.01); * (P≤0.05); NS: not significant.*

Result and Discussion (genotype and allele freq.)

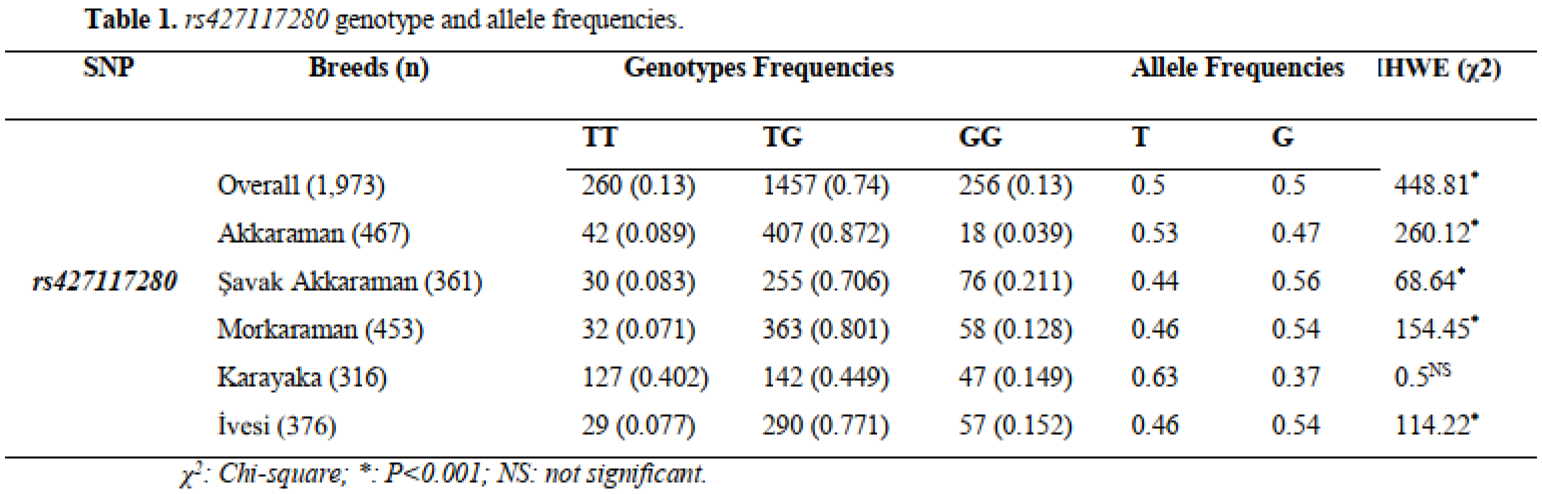
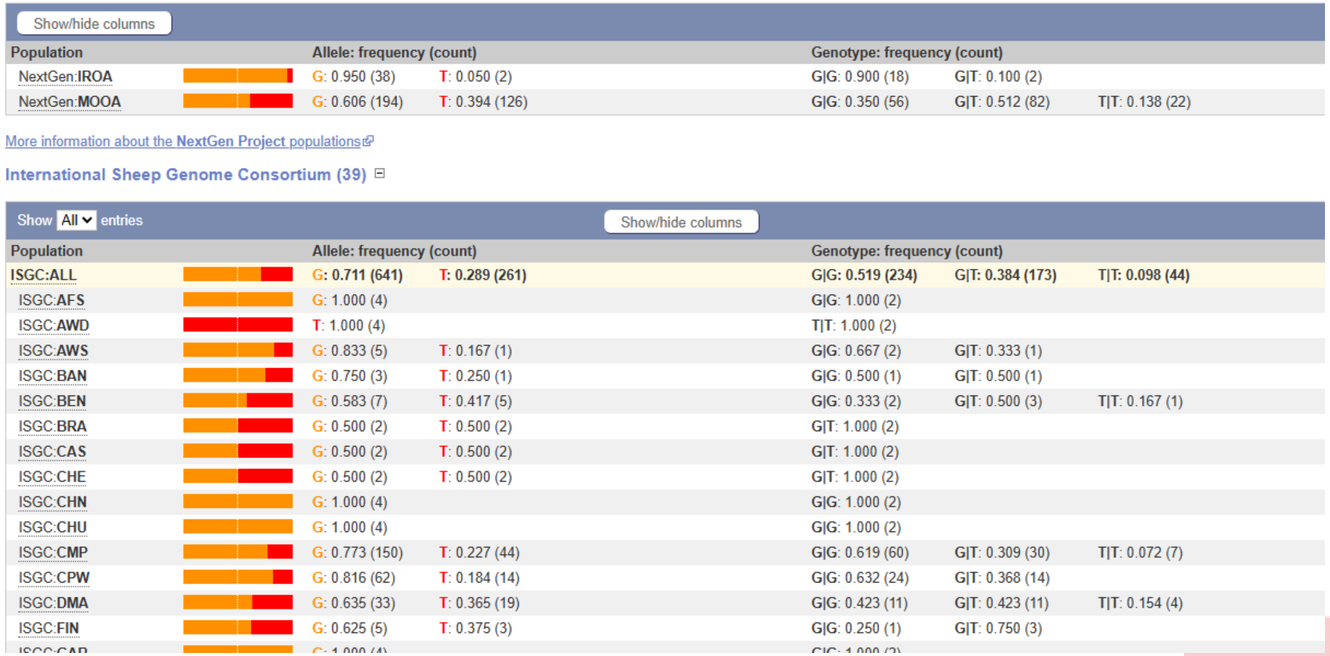


Table 1. *rs427117280* genotype and allele frequencies.

SNP	Breeds (n)	Genotypes Frequencies			Allele Frequencies		HWE ($\chi 2$)
		TT	TG	GG	T	G	
	Overall (1,973)	260 (0.13)	1457 (0.74)	256 (0.13)	0.5	0.5	448.81^{*}
	Akkaraman (467)	42 (0.089)	407 (0.872)	18 (0.039)	0.53	0.47	260.12^{*}
rs427117280	Şavak Akkaraman (361)	30 (0.083)	255 (0.706)	76 (0.211)	0.44	0.56	68.64^{*}
	Morkaraman (453)	32 (0.071)	363 (0.801)	58 (0.128)	0.46	0.54	154.45^{*}
	Karayaka (316)	127 (0.402)	142 (0.449)	47 (0.149)	0.63	0.37	0.5^{NS}
	İvesi (376)	29 (0.077)	290 (0.771)	57 (0.152)	0.46	0.54	114.22^{*}

*χ^2: Chi-square; *: $P<0.001$; NS: not significant.*



Population	Allele: frequency (count)		Genotype: frequency (count)		
NextGen:IROA	G: 0.950 (38)	T: 0.050 (2)	G|G: 0.900 (18)	G|T: 0.100 (2)	
NextGen:MOOA	G: 0.606 (194)	T: 0.394 (126)	G|G: 0.350 (56)	G|T: 0.512 (82)	T|T: 0.138 (22)

More information about the NextGen Project populations

International Sheep Genome Consortium (39) ⊟

Population	Allele: frequency (count)		Genotype: frequency (count)		
ISGC:ALL	**G: 0.711 (641)**	**T: 0.289 (261)**	**G|G: 0.519 (234)**	**G|T: 0.384 (173)**	**T|T: 0.098 (44)**
ISGC:AFS	G: 1.000 (4)		G|G: 1.000 (2)		
ISGC:AWD	T: 1.000 (4)		T|T: 1.000 (2)		
ISGC:AWS	G: 0.833 (5)	T: 0.167 (1)	G|G: 0.667 (2)	G|T: 0.333 (1)	
ISGC:BAN	G: 0.750 (3)	T: 0.250 (1)	G|G: 0.500 (1)	G|T: 0.500 (1)	
ISGC:BEN	G: 0.583 (7)	T: 0.417 (5)	G|G: 0.333 (2)	G|T: 0.500 (3)	T|T: 0.167 (1)
ISGC:BRA	G: 0.500 (2)	T: 0.500 (2)	G|T: 1.000 (2)		
ISGC:CAS	G: 0.500 (2)	T: 0.500 (2)	G|T: 1.000 (2)		
ISGC:CHE	G: 0.500 (2)	T: 0.500 (2)	G|T: 1.000 (2)		
ISGC:CHN	G: 1.000 (4)		G|G: 1.000 (2)		
ISGC:CHU	G: 1.000 (4)		G|G: 1.000 (2)		
ISGC:CMP	G: 0.773 (150)	T: 0.227 (44)	G|G: 0.619 (60)	G|T: 0.309 (30)	T|T: 0.072 (7)
ISGC:CPW	G: 0.816 (62)	T: 0.184 (14)	G|G: 0.632 (24)	G|T: 0.368 (14)	
ISGC:DMA	G: 0.635 (33)	T: 0.365 (19)	G|G: 0.423 (11)	G|T: 0.423 (11)	T|T: 0.154 (4)
ISGC:FIN	G: 0.625 (5)	T: 0.375 (3)	G|G: 0.250 (1)	G|T: 0.750 (3)	

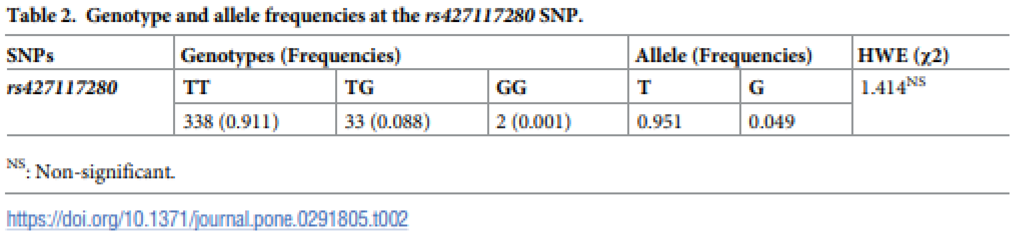


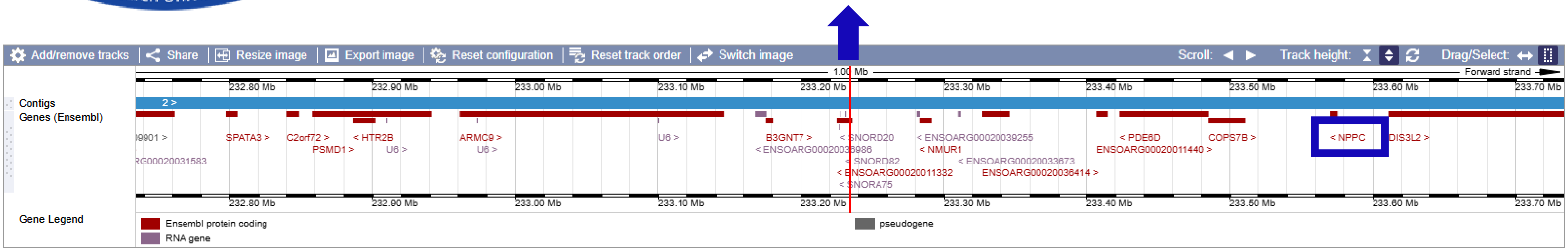
Table 2. Genotype and allele frequencies at the *rs427117280* SNP.

SNPs	Genotypes (Frequencies)			Allele (Frequencies)		HWE ($\chi 2$)
rs427117280	TT	TG	GG	T	G	1.414^{NS}
	338 (0.911)	33 (0.088)	2 (0.001)	0.951	0.049	

^{NS}: Non-significant.

https://doi.org/10.1371/journal.pone.0291805.t002

Discussion



rs427117280

- natriuretic peptide precursor-C (*NPPC*) gene encoding C-type natriuretic peptide.
- NPPC plays a critical role in growth in mammals, as it is expressed in the growth plate (Olney, 2006; Peng et al., 2013; Vasques et al., 2014).

Open Access

Association Between Natriuretic Peptide Receptor 2 (*NPR2*) *RS208158047* Polymorphism and Fattening Performance of Young Bulls

Jale Metin Kıyıcı, Zeki Emre Şenöz and Mehmet Ulaş Çınar | Feb 04, 2022

ANNALS OF ANIMAL SCIENCE

animals MDPI

- Animals (Basel). 2020 Dec 15;10(12):2391. doi: 10.3390/ani10122391

Association of *TMEM8B* and *SPAG8* with Mature Weight in Sheep

Mehmet Ulas Cinar[1,2], Michelle R Mousel[3,4], Maria K Herndon[1], J Bret Taylor[5], Stephen N White[1,3,6]

- Author information
- Article notes
- Copyright and License information

PMCID: PMC7765121 PMID: 33333720

PLOS Biology

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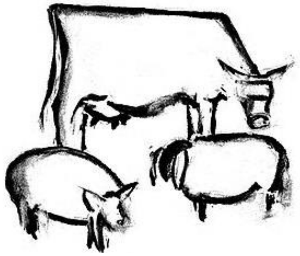
RESEARCH ARTICLE

Genome-Wide Analysis of the World's Sheep Breeds Reveals High Levels of Historic Mixture and Strong Recent Selection

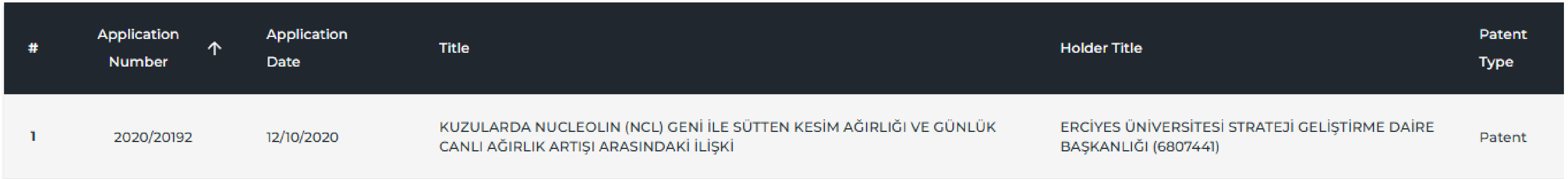
James W. Kijas, Johannes A. Lenstra, Ben Hayes, Simon Boitard, Laercio R. Porto Neto, Magali San Cristobal, Bertrand Servin, Russell McCulloch, Vicki Whan, Kimberly Gietzen, Samuel Paiva, William Barendse, Elena Ciani, [...], other members of the International Sheep Genomics Consortium [view all]

Published: February 7, 2012 • https://doi.org/10.1371/journal.pbio.1001258

Conclusion



- *rs427117280-GG* genotype frequency was still very low in the five different sheep breeds examined.
- Selection studies to increase the frequency of this genotype in sheep breeds will make a positive contribution to increasing the liveweight at weaning.
- More extensive research may be designed to validate association of *rs427117280* with pre-weaning and weaning growth traits in different sheep breeds worldwide.



#	Application Number ↑	Application Date	Title	Holder Title	Patent Type
1	2020/20192	12/10/2020	KUZULARDA NUCLEOLIN (NCL) GENİ İLE SÜTTEN KESİM AĞIRLIĞI VE GÜNLÜK CANLI AĞIRLIK ARTIŞI ARASINDAKİ İLİŞKİ	ERCİYES ÜNİVERSİTESİ STRATEJİ GELİŞTİRME DAİRE BAŞKANLIĞI (6807441)	Patent

Future work

- Selection signatures of Türkiye sheep breeds based on tail type.
- Association of selection signatures with economical traits.
- Machine learning assisted GWAS.
- Quantitative genetics.
- Novel phenotypes.
- **Erasmus+ internship** availability.
- Collaboration is looking…

Thank you and Questions??

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- The National Community-based Small Ruminant Breeding Programme.
- General Directorate of Agricultural Research and Policies.
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