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Preliminary Genome-Wide Association Study for Skin Traits in an Angora x Creole Backcross Population.

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Summary

Angora goat produce mainly mohair fiber but the Creole goats have a double hair coat: cashmere, fine and short seasonal down coat and coarser and longer guard hair. Both, mohair and cashmere fiber are determined by two types of skin hair follicle, primary and secondary and several phenotypes can be drawn from them like S/P ratio. The aim of this study was to identify polymorphisms associated with skin traits in a backcross Angora x Creole goats (n=477) using a SNP-based GWAS analysis. Significant regions on CHIR 1, 2, 6, and X exhibit a maximum signal for seven SNP markers with a p-value from 8.16E-06 to 1.26E-04. These results indicate that may be several genes that could be involved in skin traits close to the most significant SNP markers in this backross Angora x Creole population

Keywords: backcross goats, skin traits, SNPs, GWAS

Introduction

In mammals, skin hair follicles are found in a regular distribution with precise spacing between the primary hair follicles (P) and the secondary follicles (S).

Angora goat produce a single hair coat fiber (mohair), highly valued due to its resistance, flexibility, softness and luster. The Creole goats have a double hair coat: cashmere, fine and short seasonal down coat and coarser and longer guard hair. Both, mohair and cashmere fiber are determined mainly by two types of skin hair follicle, primary and secondary and several phenotypes can be drawn from them like S/P ratio. The local Angora and Creole goats skin histological characteristics were described by Carro et al. (2010) and Debenedetti et al. (2007).

Previous QTL mapping results based on microsatellite analyses affecting fleece and skin traits on several chromosomes in goats were carry out by (Cano et al., 2009; Debenedetti et al., 2014). Recently, the development by the International Goat Genome of the goatSNP50 chip data now allows us carry out genome wide association studies (GWAS). In this study, we used genome-wide SNP genotyping to indentify new markers associated with skin traits in an Angora x Creole backcross goat resource population.

Materials and methods

Animal population

The experimental population was generated at INTA Pilcaniyeu Experimental Farm, (north Patagonia, Argentina) in three batches (years 2006 to 2008). A backcross design was set up as follows: 5 F1 Angora x Creole bucks were backcrossed with 107 Creole (BCC) and 27 Angora (BCA) females.

Skin traits

The pre-treatment of skin samples, protocol and analyses were the same described by Debenedetti et al. (2014). Four phenotypic skin traits were measured by optical microscopy: number of primary follicles per group (P), number of secondary follicles per group (S), average secondary to primary follicle ratio (S/P) and SP coefficient of variation (CVS/P).

Genotype information and GWAS analysis

A total of 477 goats (10 grandparents, 5 F1 bucks, 134 dams and 328 backcross kids) were genotyped with the goatSNP50 chip. Quality Control (QC) from 53347SNP was carried out using PLINK program. Markers were removed based on: minor allele frequency (MAF less than 1%), genotype call rates per markers (GCR less than 90%), and deviation from Hardy-Weinberg equilibrium for each SNP ($p<1.10^{-6}$). Animal with pedigree inconsistency were removed. After the QC the final dataset contained 48057 SNP markers genotypes for 475 goats. The SNPs markers and positions were referred to CHIR_1.0 assembly.
To correct for population structure (BCC, BCA), gender (male, female), birth rank (single, multiple), age of dam (1-3) and year of birth (2006-2008) were fitted as fixed effects in SAS (proc Mixed) analysis. This model was used to generate phenotypic residuals. The GWAS was performed by using R/rrBLUP library (Yu et al, 2006).

Results and discussion

Table 1 show the phenotypes measurements (Mean, Minimum, Maximum and Standard Deviations) for four skin traits in BC progeny.

Table 1. Average values for four skin traits of BC goat progeny.

Trait	Mean	Minimum	Maximum	Std. Dev.
P	2.9	2.2	3.9	0.2
S	24.6	13.7	41.8	4.6
S/P ratio	8.5	5.2	13.2	1.4
CVS/P	12.4	3.9	27.6	4.2

P: number of primary follicles per group
S: number of secondary follicles per group
S/P ratio: average S to P ratio
CVS/P: S/P coefficient variation

Table 2 provides the list of relevant SNPs markers for skin traits, the chromosome number (CHIR), the SNP where the maximum is reached and its position (Mb), the associated probability (p-value) the number of significant SNPs contributing to the peak and the interval of these SNPs.

Table 2. List of relevant SNP markers for skin traits.

Trait	Top SNP id	Number of significant SNPs	Chromosome (CHIR)	Physical position (Mb)	p-value	Significant interval (Mb)
P	rs268278725	1	3	35.06	1.70E-05	
	rs268280905	2	4	43.30	7.11E-05	43.30-110.90
	rs268236636	2	11	49.25	2.38E-05	49.25-49.32
	rs268267461	1	14	43.66	7.21E-05	
	rs268235802	2	29	10.09	4.78E-05	10.09-10.66
	rs268280053	**1**	**X**	**114.62**	**8.16E-06**	
S	rs268267989	1	2	44.28	2.58E-05	
	rs268257667	1	4	108.48	8.98E-05	
	rs268278353	**2**	**6**	**20.49**	**2.28E-06**	20.49-24.81
S/P ratio	**rs268235314**	**3**	**1**	**63.41**	**1.20E-05**	56.06-67.95
	rs268267989	1	2	44.28	2.24E-05	
	rs268265136	1	5	70.65	5.28E-05	
	rs268278353	1	6	20.49	6.56E-05	
	rs268281822	1	12	22.01	3.02E-05	
	rs268272924	2	14	21.06	2.06E-05	21.06-21.09
	rs268236827	1	16	64.54	3.38E-05	
	rs268245080	1	21	58.62	4.05E-05	
	rs268245619	2	22	50.34	9.84E-05	50.34-53.44
CVS/P	**rs268269814**	**1**	**2**	**99.19**	**1.26E-04**	
	rs268241796	1	5	84.31	4.02E-04	
	rs268268978	1	9	79.275	3.43E-04	
	rs268284509	4	11	48.15	3.64E-04	23.15-49.25
	rs268280733	3	13	31.52	3.28E-04	2.37-60.26
	rs268252169	2	14	2.98	1.46E-04	0.75-2.98
	rs268290014	1	20	60.22	3.18E-05	
	rs268280025	2	29	12.17	3.37E-04	7.62-12.17

Figure 1 shows by phenotypic traits the Manhattan plots the combined association signals ($-\log_{10}$(p-value)) on the y-axis versus position on chromosomes on the x-axis. Chromosomes are ordered from CHIR1 to CHIR29, the last one being the X chromosome.

Forty genome-wise significant SNP were detected on twenty six CHIR (Table 2). The highest signal for P, S, S/P ratio and CVS/P were detected on CHIR X, 6, 1 and 2 with a maximum obtain by genome-wise significant SNPs (rs268280053 ($-\log_{10}$(p-value) = 5.09), rs268278353 ($-\log_{10}$(p-value) = 5.64), rs268235314 ($-\log_{10}$(p-value) = 4.92) and rs268269814 ($-\log_{10}$(p-value) = 3.90)) respectively. Up to day the informed QTL affecting skin traits in goat are very limited.

Debenedetti et al. (2014) and Debenedetti (per. comm.) reported two QTL affecting S/P ratio and S on CHI19 and one QTL affecting S/P ratio on CHI1 by use microsatellites markers.

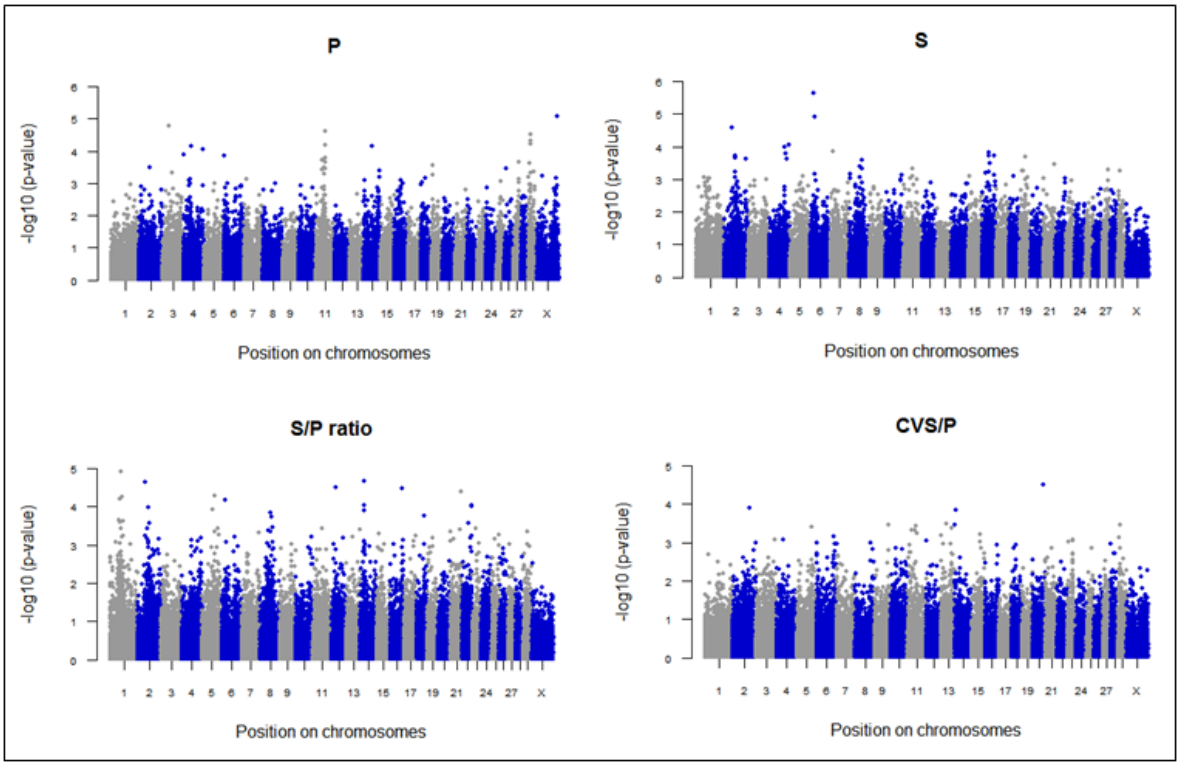

Figure 1. Genome-wide Manhattan plot for skin traits.

Conclusion

In this preliminary GWAS study several SNP markers have been shown to be associated with skin phenotypes traits. Significant regions on CHIR 1, 2, 6, and X exhibit a maximum signal for seven SNP markers with a p-value from 8.16E-06 to 1.26E-04. These results indicate that may be several genes could be involved in skin traits close to the most significant SNP markers in this backcross Angora x Creole population.

List of Reference

Carro, N.D., Debenedetti, S. & Taddeo H.R., 2010. Efecto de la edad sobre la población de folículos pilosos y su relación con características de mohair en caprinos de Angora. In. Vet., 12(2): 161-172.

Cano, E.M., Debenedetti, S., Abad, M., Allain, D., Taddeo, H.R.& Poli, M.A., 2009. Chromosomal segments underlying quantitative trait loci for mohair production in Angora goats. Anim.Gen. Res. Inf. , 445: 107-112.

Debenedetti S., Lombardo, D., Giovaninni, N. & Taddeo, H.R. 2007. Caracterización folicular de la piel y su relación con características de fibra en caprinos Angora, Criollo Neuquino y su cruza. Resultados preliminares. ALEPRYCs, Malargüe, Mendoza. p. 196-198.

Debenedetti, S., Cano, E. M., Poli, M.A. &Taddeo, H.R. 2014. QTL affecting skin traits on CHI19 in an Angora x Creole goat backcross population. In Proc 10thWCGALP, p.0764-0766

Yu, J., Pressoir G., Briggs,W.H., Vroh Bi I.et al. 2006. An unified mixed-model method for association mapping that accounts for multiple levels of relatedness. Genetics, 38:203-208.