SNP mapping of QTL affecting wool traits in a sheep backcross Sarda x Lacaune resource population

Daniel D. Allain, S. Miari, Mario Graziano Usai, Francis F. Barillet, Tiziana
Secchi, Rachel Rupp, Sara Casu, Antonello Carta

HAL Id: hal-02745624

https://hal.inrae.fr/hal-02745624v1

Submitted on 3 Jun 2020

Genes involved in hair follicle cycle of cashmere goat

W. Zhang[1,2,3], D. Allain[4], R. Su[1,3], J. Li[3] and W. Wang[2]
[1]Institute of ATCG, Nei Mongol Bio-Information, Hohhot, 010018 Hohot, China, P.R., [2]Chinese Academy of Sciences, Kunming Institute of Zoology, No.32 East Jiaochang Road, 650223 Kunming Yunnan, China, P.R., [3]Inner Mongolia Agricultural University, College of Animal Science, No. 306, Zhaowuda Road, 010018 Hohot, China, P.R., [4]INRA, UR631, SAGA, Auzeville, CS52627, 31326 Castanet Tolosan, France; atcgnmbi@aliyun.com

On behalf of International Goat Genome Consortium(IGGC) The hair follicle (HF) is central to most economically important fiber growth in livestock. However, the changes in expression of genes that drive these processes remain incompletely characterised. As model animal of hair biology, cashmere goat might help deciphering genes involved in primary and secondary HF of skin. We used RNA-seq to study gene expression profiles of HF including anagen, catagen and telogen in Nei Mongol Cashmere Goat (NMCG), which will increase our understanding of HF biology and contribute to the development of strategies to improve cashmere. Exome data from 7 secondary HFs and 11 primary HFs in NMCGs was mined. 22,176 annotated genes in reference genome were evaluated, 7,481 of which were shown to be expressed in HFs. Join together, 1,923 of 7,481 were expressed in all HFs, 3,219 and 2,339 of which were co-expressed in primary and secondary HFs exclusively. GO analysis showed that GO: (0044464, 0003824, 0032501, 0032502) were associated gene sets. High expressed gene in secondary and primary HFs are mainly involved in 14 GO categories which included in above mentioned GO items. High expressed genes in two type HFs of 1,923 are mainly located in CHI 7, 18 and 19 (P<0.01). Genes located in 4.6~4.9 Mb of CHI1 might be one gene cluster which has important function in HF development. Six SNPs related to hair follicle based on ~30K polymorphism loci different from reference, were functionally identified in CHI 1 and 19 respectively. Compare to secondary HF, primary HF expresses more genes to deal with stimulations from all-environment. Additionally, 13 HF specific expressed genes were identified according to comparative transcriptome analysis.

SNP mapping of QTL affecting wool traits in a sheep backcross Sarda × Lacaune resource population

D. Allain[1], S. Miari[2], M.G. Usai[2], F. Barillet[1], T. Sechi[2], R. Rupp[1], S. Casu[2] and A. Carta[2]
[1]INRA, UR631, SAGA, Auzeville, CS52627, 31326 Castanet Tolosan, France, [2]AGRIS-Sardegna, Settore genetica e biotecnologie, DiRPA, 07704 Olmedo, Italy; daniel.allain@toulouse.inra.fr

A QTL detection experiment was organized in a backcross Sarda × Lacaune sheep resource population. The aim of this experiment was primarily the search for loci influencing milk production and several other traits including wool traits through a whole genome scan on 968 females from 10 sire families. Ten fleece characteristics: greasy fleece weight, length of long and fine wool as well as fibre diameter (mean and CV), fibre curvature (mean and CV) and medullation content (objectionable, flat and medullated fibres) using OFDA methodology were measured on 892 6-months old females. For QTL detection, the Illumina OvineSNP50 beadchip that provided 44,859 SNP markers after quality control was used. Within and across families analyses were performed with the QTLMAP software. The statistical techniques used were linkage analysis, linkage disequilibrium analysis and joint linkage and association analysis (LDLA) using interval mapping. High significant QTL (P<0.001 at genome wide) affecting 7 wool traits: greasy fleece weight, fibre diameter (mean and CV), Fibre length, medullation content and CV of fibre curvature were found on chromosome 25 within a 2 cM interval suggestting that one or some genes with major effect on fleece characteristics are located on this chromosomal segment. Other high significant QTL's (P<0.001 at genome wide) influencing medullation content and, fibre length on chromosome 20 and 15 respectively were also detected. Other putative QTL's (P<0.01 at chromosome wide) were also observed on chromosome 3 and 6, 13 and 18, and 14 for greasy fleece weight, fibre length, and fibre curvature respectively. The linkage disequilibrium analysis and joint LDLA analysis confirmed the locations of the QTL mapped on OAR25, 20 15, 13 and 6 and all QTL found were discussed.

Book of Abstracts of the 64th Annual Meeting of the European Federation of Animal Science