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利用紧缩线性模型和贝叶斯模型对猪总产仔数和产活仔数性状的全基因组关联研究

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摘要 全基因组关联分析策略已逐渐成为家畜重要经济性状研究的强有力工具。文章使用猪60K SNP芯片对一个具多胎繁殖性状记录的商业母猪群(n=820)进行分型检测, 共计57 814个SNP通过设定质控标准。主成分分析显示群体内不存在显著的群体分层现象, 而后分别运用两种统计模型Compressed Mixed Linear Model (GAPIT 程序包)、Bayes CPi(GenSel软件)进行第1和第2胎次总产仔数和产活仔数性状的全基因组关联分析。从两种分析方法所得结果中各取最显著的50个SNP位点进行比较：对于第1胎次总产仔数, 两种方法分析结果存在31个重合SNP位点, 对于第1胎次产活仔数, 有20个重合SNP位点; 且两种统计分析结果中最显著的SNP位点都在另一方法中得到验证。与第1胎次总产仔数显著关联的SNP位于1、2、3、7、13、16和18号染色体, 与第1胎次产活仔数显著关联的SNP位于1、3、4、13和16号染色体上的11个区域内。在1、3、13和16染色体上共有5个区域同时与这两个性状显著关联。与第2胎次总产仔数和产活仔数显著关联的区域主要位于7、10、12、13、14和16号染色体的6个重叠区域内。

关键词： 全基因组关联 总产仔数 产活仔数 SNP芯片 猪

Abstract： GWAS(Genome-wide association study) strategy has been extensively used for identification of economical trait loci in livestock animals. Using Illumina’s PorcineSNP60 BeadChip, a GWA study of 820 commercial pigs with reproductive traits recorded was performed. The PCA analysis showed that there was no significant population stratification. Two different statistical models Compressed Mixed Linear Model(GAPIT program package)and Bayes CPi (GenSel software) were used to implement GWAS on total number born and number born alive of the first and second parity. To compare the most significant 50 SNPs from each method, a total of 31 and 20 coincided SNPs for total number born in the first parity were identified, and there were 20 coincided SNPs for number born alive in the first parityinthe results of bothmethods. The most significant SNPs were also significant in the results of the other method. The most significantly associated regions for total number born in the first parity were located on SSC1, 2, 3, 7, 13, 16, and 18. The most significantly associated regions for number born alive in the first parity were locatedon SSC1, 3, 4, 13, and 16. There were 5 common regions significantly associated with bothtraits on SSC1, 3, 13, and 16. The most significantly associated regions forbothtotal number born and number born alive for the second parity were mainly located on six common regions on SSC7, 10, 12, 13, 14, and 16.

Keywords： GWAS, total number born, number born alive, SNP chip, pig

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[1] Rothschild M, Jacobson C, Vaske D, Tuggle C, Wang LZ, Short T, Eckardt G, Sasaki S, Vincent A, McLaren D, Southwood O, van der Steen

H, Mileham A, Plastow G. The estrogen receptor locus is associated with a major gene influencing litter size in pigs. *Proc Natl Acad Sci USA*, 1996, 93(1): 201-205.

[2] Li N, Zhao YF, Xiao L, Zhang FJ, Chen YZ. Candidate gene approach for identification of genetic loci controlling litter size in swine. In: Proceedings of the 6th World Con-gress Quatitative Genetics of Livestock. 1998, 26: 183-188.

[3] 赵要风, 李宁, 肖璐, 曹更生, 陈怡真, 张顺, 陈永福, 吴常信, 张建生, 孙士铨, 徐学清. 猪*FSHβ*亚基基因结构区逆转座子插入突变及其与猪产仔数关系的研究. 中国科学c辑, 1999, 29(1): 81-86.

[4] Fan B, Onteru SK, Du ZQ, Garrick DJ, Stalder KJ, Rothschild MF. Genome-wide association study identifies loci for body composition and structural soundness traits in pigs. *PLoS One*, 2011, 6(2): e14726.

[5] Gorbach DM, Cai W, Dekker JCM, Young JM. Whole-genome analyses for genes associated with residual feed intake and related traits utilizing the PorcineSNP60 BeadChip. In: Pig Genome III Conference. Hinxton, Cambridge, UK, 2009.

[6] Onteru SK, Fan B, Du ZQ, Garrick DJ, Stalder KJ, Rothschild MF. A whole-genome association study for pig reproductive traits. *Anim Genet*, 2012, 43(1): 18-26.

[7] Onteru SK, Fan B, Nikkilä MT, Garrick DJ, Stalder KJ, Rothschild MF. Whole-genome association analyses for lifetime reproductive traits in the pig. *J Anim Sci*, 2011, 89(4): 988-995.

[8] Purcell S, Neale B, Todd-Brown K, Thomas L, Ferreira MAR, Bender D, Maller J, Sklar P, de Bakker PIW, Daly MJ, Sham PC. PLINK: a tool set for whole-genome association and population-based linkage analysis. *Am J Hum Genet*, 2007, 81(3): 559-575.

[9] Zhang ZW, Ersoz E, Lai CQ, Todhunter RJ, Tiwari HK, Gore MA, Bradbury PJ, Yu JM, Arnett DK, Ordovas JM, Buckler ES. Mixed linear model approach adapted for genome-wide association studies. *Nat Genet*, 2010, 42(4): 355-360.

[10] Fernando RL, Garrick DJ. GenSel-User manualfor a Portfolio of genomic selection related analyses. *Anim Breed Genet*, Iowa State University, Ames. http://bigs.ansci. iastate.edu/bigsgui/login.html, 2008.

[11] Meuwissen THE, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps. *Genetics*, 2001, 157(4): 1819-1829.

[12] Kizilkaya K, Fernando RL, Garrick DJ. Genomic prediction of simulated multibreed and purebred performance using observed fifty thousand single nucleotide polymor-phism genotypes. *J Anim Sci*, 2010, 88(2): 544-551.

[13] Pritchard JK, Stephens M, Rosenberg NA, Donnelly P. Association mapping in structured populations. *Am J Human Genet*, 2000, 67(1): 170-181.

[14] Patterson N, Price AL, Reich D. Population structure and eigenanalysis. *PLoS Genet*, 2006, 2(12): e190.

[15] Price AL, Patterson NJ, Plenge RM, Weinblatt ME, Shadick NA, Reich D. Principal components analysis cor-rects for stratification in genome-wide association studies. *Nat Genet*, 2006, 38(8): 904-909.

[16] Yu JM, Pressoir G, Briggs WH, Bi IV, Yamasaki M, Doe-bley J, McMullen M, Gaut BS, Nielsen DM, Holland JB, Kresovich S, Buckler ES. A unified mixed-model method for association mapping that accounts for multiple levels of relatedness. *Nat Genet*, 2005, 38(2): 203-208.

[17] 许志峰. 选殖猪母源性胚胎拉链状白胺酸蛋白质激酶之调控区域及其特性分析[学位论文]. 台湾大学动物科学技术学研究所, 2010.

[18] Hickson JA, Fong B, Watson PH, Watson AJ. *PP2Cδ* (*Ppm1d*, WIP1), an endogenous inhibitor of p38 MAPK, is regulated along with *Trp53* and *Cdkn2a* following p38 *MAPK* inhibition during mouse preimplantation development. *Mol Reproduct Dev*, 2007, 74(7): 821-834.

[19] Ewing RM, Chu P, Elisma F, Li HY, Taylor P, Climine S, McBroon-Cerajewski L, Robinson MD, O' Connor L, Li M, Taylor R, Dharsee M, Ho Y, Heilbut A, Moore L, Zhang SD, Ornatsky O, Bukhman Y, Ethier M, Sheng YL, Vasilescu J, Abu-Farha M, Lambert JP, Duewel HS, Stewart I, Kuehl B, Hogue K, Colwill K, Gladwish K, Muskat B, Kinach R, Adams SL, Moran MF, Morin GB, Topaloglou T, Figeys D. Large-scale mapping of human protein-protein interactions by mass spectrometry. *Mol Syst Biol*, 2007, 3: 89.

[1] 郑伟 季林丹 邢文华 涂巍巍 徐进.肺结核全基因组关联研究进展[J]. 遗传, 2013,35(7): 823-829

[2] 曹随忠 岳成鹤 李西睿 冯冲 龙川 潘登科.锌指核酸酶技术制备肌肉生长抑制素基因敲除的五指山小型猪成纤维细胞[J]. 遗传, 2013,35(6): 778-785

[3] 杨秀芹，陈月婵，汪亮，李海涛，刘娣，关庆芝，付博.猪TolI样受体4基因SNPs功能分析[J]. 遗传, 2012,34(8): 1050-1056

[4] 许睿玮，严卫丽.原发性高血压全基因组关联研究进展[J]. 遗传, 2012,34(7): 793-809

[5] 郭良勇，傅金銮，王爱国.猪整合素β_1基因CRS-PCR多态性与产仔数的关联性分析[J]. 遗传, 2012,34(7): 879-886

[6] 沈君叶，俞英，王茜，马裴裴，朱士恩，史文清，王雅春，张勤.母猪繁殖力性状影响因素分析及遗传参数估计[J]. 遗传, 2012,34(5): 591-596

[7] 李聪，孙东晓，姜力，刘剑锋，张勤，张沅，张胜利.奶牛重要经济性状全基因组关联分析研究进展[J]. 遗传, 2012,34(5): 545-550

[8] 陈时锦，范晶，蒋钦杨，兰干球，郭晓萍，郭亚芬.广西巴马小型猪小RNA启动子*U6*和*7SK*的克隆及功能验证[J]. 遗传, 2012,34(4): 445-453

[9] 秦祖兴，黄高波，罗军，宁淑芳，卢晟盛.TSA和VPA处理对食蟹猴-猪异种体细胞核移植胚胎早期发育的影响[J]. 遗传, 2012,34(3): 342-347

[10] 解炳腾，纪光臻，孔庆然，毛剑，石永乾，刘世超，武美玲，王娟，刘林，刘忠华.曲古抑菌素A对克隆猪端粒长度的影响[J]. 遗传, 2012,34(12): 1583-1590

[11] 李俊燕，谭英姿，冯国鄞，贺林，周里钢，陆灏.糖尿病肾病遗传学研究进展[J]. 遗传, 2012,34(12): 1537-1544

[12] 于辉，刘荣辉，李华，左启祯，李岩，吴珍芳.猪5个群体SLA微卫星遗传多样性[J]. 遗传, 2012,34(11): 1427-1433

[13] 林佳丽，沈良才，潘登科，张瑾.猪*Gli1*基因的克隆、表达谱分析及脂肪组织特异性表达载体的构建[J]. 遗传, 2012,34(10): 1291-1297

[14] 马云龙，张勤，丁向东.利用高密度SNP检测不同猪品种间X染色体选择信号[J]. 遗传, 2012,34(10): 1251-1260

[15] 张杰，尚宗民，曹建华，樊斌，赵书红.Otterlace软件在猪全基因组序列人工注释分析中的应用[J]. 遗传, 2012,34(10): 1339-1347