

丙酸通路基因多态性与猪肉质及胴体性状的关联分析

杨帆, 王琼萍, 何侃, 王明辉, 潘玉春

上海交通大学农业与生物学院, 上海 200240

YANG Fan, WANG Qiong-Ping, HE Kan, WANG Ming-Hui, PAN Yu-Chun

School of Agriculture and Biology, Shanghai Jiaotong University, Shanghai 200240, China

- 摘要
- 参考文献
- 相关文章

Download: PDF (392KB) HTML (596KB) Export: BibTeX or EndNote (RIS) Supplementary data

摘要 为了挖掘新的猪肉品质及胴体性状的候选基因, 揭示猪肉质及胴体性状的遗传机制, 文章将丙酸代谢通路作为候选通路, 将通路内基因与猪肉质及胴体性状进行关联分析。实验采用37头三元杂交商品猪作为研究对象, 首次针对丙酸通路中7个基因的36个SNP位点利用SNaPshot方法进行基因分型, 分别用最小二乘模型及MB-MDR模型与肉质及胴体性状进行关联分析。结果发现, 基因PCCB、MUT、MCEE及ACSS2上的4个SNP位点分别与肌内脂肪含量、背膘厚等性状显著相关($P<0.05$), ACSS2与猪脂肪含量显著相关; MCEE及MUT与猪的背膘厚显著相关; PCCB基因与脂重显著相关。通过MB-MDR方法检测到多个SNP位点具有互作效应, 并与背膘厚、水分含量、脂肪含量显著相关($P<0.05$)。另外, 丙酸代谢通路中的基因间的互作效应对猪肉品质有显著影响。

关键词: 丙酸代谢通路 多态性 肉质品质 胴体品质 SNaPshot

Abstract: In order to gain more extensive insight into detailed genetic control mechanisms of porcine meat quality and mine novel candidate genes, this study focused on the relationship between the genes of propanoate metabolism pathway and porcine meat quality as well as carcass traits based on the candidate gene set approach. Thirty-seven DLY pigs were tested in this study. A total of 36 SNPs within 7 candidate genes of propanoate metabolism pathway were genotyped and association analysis was conducted via Least Squares method, Multivariate multiple regression model, and a model-based multifactor dimensionality reduction method (MB-MDR). As a result, four SNPs in genes PCCB, MUT, MCEE, and ACSS2 were significantly associated with DLY pig meat quality or carcass traits ($P<0.05$). Results of MB-MDR analysis demonstrated that the interactions between multiple SNPs were significantly associated with the backfat thickness, water content, and fat content ($P<0.05$). ACSS2 was significantly associated with fat content; MCEE and MUT significantly influenced backfat thickness; and PCCB was related to fat weight. Moreover, the interactions between the genes in the propanoate metabolism pathway had remarkable influence in porcine meat quality and carcass traits.

Keywords: propanoate metabolism pathway, polymorphisms, meat quality, carcass traits, SNaPshot

收稿日期: 2011-11-29; 出版日期: 2012-07-25

基金资助:

国家重点基础研究发展计划(973计划)项目(编号 2006CB102102)和国家自然科学基金项目(编号31072003)资助

通讯作者 潘玉春 Email: panyc@sjtu.edu.cn


引用本文:

杨帆, 王琼萍, 何侃, 王明辉, 潘玉春. 丙酸通路基因多态性与猪肉质及胴体性状的关联分析. 遗传, 2012, 34(7): 872-878.

YANG Fan, WANG Qiong-Ping, HE Kan, WANG Ming-Hui, PAN Yu-Chun. Association between gene polymorphisms of propanoate metabolism pathway and meat quality as well as carcass traits in pigs. HEREDITAS, 2012, V34(7): 872-878.

链接本文:

http://www.chinagene.cn/Jwk_yc/CN/10.3724/SP.J.1005.2012.00872 或 http://www.chinagene.cn/Jwk_yc/CN/Y2012/V34/I7/872

[1] Kerstens HH, Kollers S, Kommadath A, Del Rosario M, Dibbits B, Kinders SM, Crooijmans RP, Groenen MA. Mining for single nucleotide polymorphisms in pig genome sequence data. *BMC Genomics*, 2009, 10: 4. 

[2] Hausman GJ, Champion DR, Buonomo FC. Concentration of insulin-like growth factors (IGF-I and IGF-II) in tissues of developing lean and obese pig fetuses. *Growth Dev Aging*, 1991, 55(1): 43-52.















[3] Stinckens A, Luyten T, Bijttebier J, van den Maagdenberg K, Dieltiens D, Janssens S, de Smet S, Georges M, Buys N. Characterization of the

Service

- ▶ 把本文推荐给朋友
- ▶ 加入我的书架
- ▶ 加入引用管理器
- ▶ Email Alert
- ▶ RSS

作者相关文章

- ▶ 杨帆
- ▶ 王琼萍
- ▶ 何侃
- ▶ 王明辉
- ▶ 潘玉春

- [4] Burgos C, Carrodegua JA, Moreno C, Altarriba J, Tarrafeta L, Barcelona JA, López-Buesa P. Allelic incidence in several pig breeds of a missense variant of pig melanocortin-4 receptor (MC4R) gene associated with carcass and productive traits: its relation to IGF2 genotype. *Meat Sci*, 2006, 73(1): 144-150. 
- [5] Stachowiak M, Szydlowski M, Obarzanek-Fojt M, Switonski M. An effect of a missense mutation in the porcine melanocortin-4 receptor (MC4R) gene on production traits in Polish pig breeds is doubtful. *Anim Genet*, 2006, 37(1): 55-57. 
- [6] Song C, Gao B, Teng Y, Wang X, Wang Z, Li Q, Mi H, Jing R, Mao J. MspI polymorphisms in the 3rd intron of the swine POU1F1 gene and their associations with growth performance. *J Appl Genet*, 2005, 46(3): 285-289.
- [7] Yu TP, Sun HS, Wahls S, Sanchez-Serrano I, Rothschild MF, Tuggle CK. Cloning of the full length pig PIT1 (POU1F1) CDNA and a novel alternative PIT1 transcript, and functional studies of their encoded proteins. *Anim Biotechnol*, 2001, 12(1): 1-19. 
- [8] He K, Wang Q, Yang Y, Wang MPan Y. A comparative study of mouse hepatic and intestinal gene expression profiles under PPARalpha knockout by gene set enrichment analysis. *PPAR Res*, 2011, 2011: 629728.
- [9] Moffett SP. The PPA R pathway to obesity and type-2 diabetes: A multi-locus approach to understanding complex disease. University of Pittsburgh, 2002. 
- [10] Carrozzo R, Dionisi-Vici C, Steuerwald U, Luciolli S, Deodato F, Di Giandomenico S, Bertini E, Franke B, Kluijtmans LA, Meschini MC, Rizzo C, Piemonte F, Rodenburg R, Santer R, Santorelli FM, van Rooij A, de Vermunt Koning D, Morava E, Wevers RA. SUCLA2 mutations are associated with mild methylmalonic aciduria, Leigh-like encephalomyopathy, dystonia and deafness. *Brain*, 2007, 130(Pt 3): 862-874.
- [11] Sakamoto O, Ohura T, Murayama K, Ohtake A, Harashima H, Abukawa D, Takeyama J, Haginoya K, Miyabayashi S, Kure S. Neonatal lactic acidosis with methylmalonic aciduria due to novel mutations in the SUCLG1 gene. *Pediatr Int*, 2011, 53(6): 921-925. 
- [12] Chandler RJ, Aswani V, Tsai MS, Falk M, Wehrli N, Stabler S, Allen R, Sedensky M, Kazazian HH, Venditti CP. Propionyl-CoA and adenosylcobalamin metabolism in *Caenorhabditis elegans*: evidence for a role of methylmalonyl-CoA epimerase in intermediary metabolism. *Mol Genet Metab*, 2006, 89(1-2): 64-73. 
- [13] 王明辉. 候选基因集法及IGF1-FoxO通路及猪生长发育的关联研究[学位论文]. 上海: 上海交通大学, 2011.
- [14] Hu ZL, Dracheva S, Jang W, Maglott D, Bastiaansen J, Rothschild MF, Reecy JM. A QTL resource and comparison tool for pigs: PigQTLDB. *Mamm Genome*, 2005, 16(10): 792-800. 
- [15] Calle ML, Urrea V, Malats N, van Steen K. mbmdr: an R package for exploring gene-gene interactions associated with binary or quantitative traits. *Bioinformatics*, 2010, 26(17): 2198-2199. 
- [16] Perks CM, Denning-Kendall PA, Gilmour RS, Wathes DC. Localization of messenger ribonucleic acids for insulin-like growth factor I (IGF-I), IGF-II, and the type 1 IGF receptor in the ovine ovary throughout the estrous cycle. *Endocrinology*, 1995, 136(12): 5266-5273. 
- [17] Figueroa JA, Lee AV, Jackson JG, Yee D. Proliferation of cultured human prostate cancer cells is inhibited by insulin-like growth factor (IGF) binding protein-1: evidence for an IGF-II autocrine growth loop. *J Clin Endocrinol Metab*, 1995, 80(12): 3476-3482. 
- [18] Menuelle P, Binoux M, Plas C. Regulation by insulin-like growth factor (IGF) binding proteins of IGF-II-stimulated glycogenesis in cultured fetal rat hepatocytes. *Endocrinology*, 1995, 136(12): 5305-5310. 
- [19] Yoshii Y, Waki A, Furukawa T, Kiyono Y, Mori T, Yoshii H, Kudo T, Okazawa H, Welch MJ, Fujibayashi Y. Tumor uptake of radiolabeled acetate reflects the expression of cytosolic acetyl-CoA synthetase: implications for the mechanism of acetate PET. *Nucl Med Biol*, 2009, 36(7): 771-777. 
- [20] Luong A, Hannah VC, Brown MS, Goldstein JL. Molecular characterization of human acetyl-CoA synthetase, an enzyme regulated by sterol regulatory element-binding proteins. *J Biol Chem*, 2000, 275(34): 26458-26466. 
- [21] Sone H, Shimano H, Sakakura Y, Inoue N, Amemiya-Kudo M, Yahagi N, Osawa M, Suzuki H, Yokoo T, Takahashi A, Iida K, Toyoshima H, Iwama A, Yamada N. Acetyl-coenzyme A synthetase is a lipogenic enzyme controlled by SREBP-1 and energy status. *Am J Physiol Endocrinol Metab*, 2002, 282(1): E222-E230.
- [22] Bobik TA, Rasche ME. Identification of the human methylmalonyl-CoA racemase gene based on the analysis of prokaryotic gene arrangements. Implications for decoding the human genome. *J Biol Chem*, 2001, 276(40): 37194-37198.
- [23] Montgomery JA, Mamer OA, Scriver CR. Metabolism of methylmalonic acid in rats. Is methylmalonyl-coenzyme a racemase deficiency symptomatic in man? *J Clin Invest*, 1983, 72(6): 1937-1947.
- [24] Naranjo V, Acevedo-Whitehouse K, Vicente J, Gortazar C, de la Fuente J. Influence of methylmalonyl-CoA mutase alleles on resistance to bovine tuberculosis in the European wild boar (*Sus scrofa*). *Anim Genet*, 2008, 39(3): 316-320. 
- [25] Miller C, Wang L, Ostergaard E, Dan P, Saada A. The interplay between SUCLA2, SUCLG2, and mitochondrial DNA depletion. *Biochim Biophys Acta*, 2011, 1812(5): 625-629. 

[1] 李骞 刘舒媛 林克勤 孙浩 于亮 黄小琴 褚嘉祐 杨昭庆. EGLN1基因6个单核苷酸多态性与高海拔低氧适应的相关性[J]. 遗传, 2013, 35(8): 0-0

[2] 阮清伟 俞卓伟 保志军 马永兴. 免疫基因多态性与衰老和增龄相关疾病关系[J]. 遗传, 2013, 35(7): 813-822

[3] 夏正龙 俞菊华 李红霞 李建林 唐永凯 任洪涛 朱双宁. 建鲤肠型脂肪酸结合蛋白基因的分离及其SNPs与增重的相关分析[J]. 遗传, 2013, 35(5): 628-

- [4] 马晓军, 郭浩辉, 郝绍文, 孙首选, 杨小春, 余博, 金群华. 宁夏回族原发性膝骨性关节炎与瘦素受体基因多态性的相关性[J]. 遗传, 2013,35(3): 359-364
- [5] 邢凤, 秦孜娟, 王桂芝, 纪志宾, 王建民. 山羊 *GOLA-DQA2* 基因多态性与血液免疫性状的相关分析[J]. 遗传, 2013,35(2): 185-191
- [6] 郭良勇, 傅金鑫, 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
- [7] 游录鹏, 苗婧, 邹爱兰, 戚金亮, 杨永华. 马铃薯抗晚疫病基因 *Rpi-blb2* 的 LRR 区域多态性及分子进化分析[J]. 遗传, 2012,34(4): 485-494
- [8] 蒲连美, 南楠, 杨泽, 金泽宁. *SUMO4* 基因多态性与 2 型糖尿病的关系[J]. 遗传, 2012,34(3): 315-325
- [9] 汤敏中, 蔡永林, 郑裕明, 曾毅. 人类白细胞抗原与鼻咽癌的相关性[J]. 遗传, 2012,34(12): 1505-1512
- [10] 李佳慧, 姚永芳, 周亮, 徐怀亮. 藏酋猴 *Mhc-DPB1* 基因 exon 2 的多态性[J]. 遗传, 2012,34(11): 1417-1426
- [11] 彭冬铂, 姜正文, 孙斯平, 李才华, 卢大儒. 人类 Y 染色体 36 个新 STR 位点的筛选与鉴定[J]. 遗传, 2012,34(11): 1409-1416
- [12] 陈曦, 张慧, 王宇祥, 王守志, 程博涵, 李辉. 鸡视网膜母细胞瘤基因 1 (*RB1*) 多态性与体重性状的相关性[J]. 遗传, 2012,34(10): 1320-1327
- [13] 刘喜冬, 王志鹏, 樊惠中, 李俊雅, 高会江. 基于高密度 SNP 标记的肉牛人工选择痕迹筛查[J]. 遗传, 2012,34(10): 1304-1313
- [14] 朱媛媛, 梁宏伟, 李忠, 罗相忠, 李林, 张志伟, 邹桂伟. 黄颡鱼 *MSTN* 基因多态性及其与生长性状的相关性分析[J]. 遗传, 2012,34(1): 72-78
- [15] 杨宇晖, 梁旭方, 方荣, 彭敏燕, 黄志东. 鳕脂蛋白脂酶基因 SNP 及其与食性驯化相关性分析[J]. 遗传, 2011,33(9): 996-1002