

## 利用高密度SNP检测不同猪品种间X染色体选择信号

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**摘要** 在家猪的培育过程中,许多重要的经济性状受到过高强度的人工选择,高密度SNP标记为通过选择信号检测追踪这些性状经历的选择提供了可能,并能根据选择信号利用生物信息学寻找到与选择相关的基因。X染色体由于其特殊性,在传统的遗传分析中许多针对常染色体的方法往往不适用,需要采取特殊的方法,选择信号检测可以作为一种行之有效的方法对X染色体进行分析。文章利用长白、松辽黑猪和大白3个猪品种,通过品种间选择信号检测方法XP-EHH,利用高密度SNP标记对X染色体进行选择信号检测,并通过生物信息学分析寻找选择信号区域内重要基因。在长白、松辽黑猪和大白3个品种中分别检测出29、13和15个选择信号区域,每个选择信号区域平均包含3.59、4.92、4.07个SNPs,长白和松辽黑猪、长白和大白有部分重叠选择信号区域,大白和松辽黑猪没有发现重叠选择信号区域。生物信息学分析发现各品种选择信号区域内有与繁殖、免疫等性状相关基因,其中部分在猪中尚未见报道,可作为研究猪相关性状的重要候选基因。

**关键词:** X染色体 选择信号 猪

**Abstract:** In the process of domestic pig breeding, many important economic traits were subject to strong artificial selection pressure. With the availability of high density single nucleotide polymorphism (SNP) markers in farm animals, selection occurring in those traits could be traced by detecting selection signatures on genome, and the genes experiencing selection can also be further mined based on selection signatures. Due to the special characteristic of X chromosome, many approaches of genetic analysis fitted for autosome are not plausible for X chromosome. Fortunately, detecting selection signature provides an effective tool to settle such situation. In this study, the Cross Population Extend Haplotype Homozygosity Test (XP-EHH) was implemented to identify selection signatures on chromosome X in three pig breeds (Landrace, Songliao, and Yorkshire) using high density SNPs, and the genes located within selection signature regions were revealed through bioinformatic analysis. In total, 29, 13, and 15 selection signature regions, with 3.59, 4.92, and 4.07 SNPs on average in each region, were identified in Landrace, Songliao, and Yorkshire, respectively. Some overlaps of selection signature regions were observed between Songliao and Landrace, and between Landrace and Yorkshire, while no overlaps between Yorkshire and Songliao were found. Bioinformatic analysis revealed that many genes in the selection signature regions were related to reproduction and immune traits, and some of them have not been reported in pigs, which might serve as important candidate genes in future study.

**Keywords:** X chromosome, selection signatures, pig

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[1] Price EO. Behavioral development in animals undergoing domestication. *Appl Anim Behav Sci*, 1999, 65(3): 245-271. 













[2] Megens HJ, Crooijmans RPMA, San Cristobal M, Hui X, Li N, Groenen MAM. Biodiversity of pig breeds from China and Europe estimated from






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- pooled DNA samples: differences in microsatellite variation between two areas of domestication. *Genet Sel Evol*, 2008, 40(1): 103-128.
- [3] Johansson Moller M, Chaudhary R, Hellmén E, Høyheim B, Chowdhary B, Andersson L. Pigs with the dominant white coat color phenotype carry a duplication of the *KIT* gene encoding the mast/stem cell growth factor receptor. *Mamm Genome*, 1996, 7(11): 822-830. 
- [4] Van Laere AS, Nguyen M, Braunschweig M, Nezer C, Collette C, Moreau L, Archibald AL, Haley CS, Buys N, Tally M, Andersson G, Georges M, Andersson L. A regulatory mutation in *IGF2* causes a major QTL effect on muscle growth in the pig. *Nature*, 2003, 425(6960): 832-836.
- [5] Altshuler D, Brooks LD, Chakravarti A, Collins FS, Daly MJ, Donnelly P, Gibbs R, Belmont J, Boudreau A, Leal S. A haplotype map of the human genome. *Nature*, 2005, 437(7063): 1299-1320.
- [6] Hinds DA, Stuve LL, Nilsen GB, Halperin E, Eskin E, Ballinger DG, Frazer KA, Cox DR. Whole-genome patterns of common DNA variation in three human populations. *Science*, 2005, 307(5712): 1072-1079.
- [7] Steemers FJ, Gunderson KL. Whole genome genotyping technologies on the BeadArray™ platform. *Biotechnol J*, 2007, 2(1): 41-49. 
- [8] Tajima F. Statistical method for testing the neutral mutation hypothesis by DNA polymorphism. *Genetics*, 1989, 123(3): 585-595.
- [9] Gianola D, Simianer H, Qanbari S. A two-step method for detecting selection signatures using genetic markers. *Genet Res (Camb)*, 2010, 92(2): 141-155. 
- [10] Sabeti PC, Reich DE, Higgins JM, Levine HZP, Richter DJ, Schaffner SF, Gabriel SB, Platko JV, Patterson NJ, McDonald GJ, Ackerman HC, Campbell SJ, Altshuler D, Cooper R, Kwiatkowski D, Ward R, Lander ES. Detecting recent positive selection in the human genome from haplotype structure. *Nature*, 2002, 419(6909): 832-837.
- [11] Sabeti PC, Varilly P, Fry B, Lohmueller J, Hostetter E, Cotsapas C, Xie XH, Byrne EH, McCarroll SA, Gaudet R, Schaffner SF, Lander ES, Frazer KA, Ballinger DG, Stewart J. Genome-wide detection and characterization of positive selection in human populations. *Nature*, 2007, 449(7164): 913-918.
- [12] Walsh EC, Sabeti P, Hutcheson HB, Fry B, Schaffner SF, de Bakker PI, Varilly P, Palma AA, Roy J, Cooper R, Winkler C, Zeng Y, de The G, Lander ES, O'Brien S, Altshuler D. Searching for signals of evolutionary selection in 168 genes related to immune function. *Hum Genet*, 2006, 119(1-2): 92-102. 
- [13] Zhang C, Bailey DK, Awad T, Liu GY, Xing GL, Cao MQ, Valmeekam V, Retief J, Matsuzaki H, Taub M, Seielstad M, Kennedy GC. A whole genome long-range haplotype (WGLRH) test for detecting imprints of positive selection in human populations. *Bioinformatics*, 2006, 22(17): 2122-2128. 
- [14] Qanbari S, Pimentel EC, Tetens J, Thaller G, Lichtner P, Sharifi AR, Simianer H. A genome-wide scan for signatures of recent selection in Holstein cattle. *Anim Genet*, 2010, 41(4): 377-389.
- [15] Graf J, Hodgson R, van Daal A. Single nucleotide polymorphisms in the *MATP* gene are associated with normal human pigmentation variation. *Hum Mutat*, 2005, 25(3): 278-284. 
- [16] Lamason RL, Mohideen MAPK, Mest JR, Wong AC, Norton HL, Aros MC, Juryneć MJ, Mao XY, Humphreville VR, Humbert JE, Sinha S, Moore JL, Jagadeeswaran P, Zhao W, Ning G, Makalowska I, McKeigue PM, O'Donnell D, Kittles R, Parra EJ, Mangini NJ, Grunwald DJ, Shriver MD, Canfield VA, Cheng KC. *SLC24A5*, a putative cation exchanger, affects pigmentation in zebrafish and humans. *Science*, 2005, 310(5755): 1782-1786.
- [17] Bray SM, Mülle JG, Dodd AF, Pulver AE, Wooding S, Warren ST. Signatures of founder effects, admixture, and selection in the Ashkenazi Jewish population. *Proc Natl Acad Sci USA*, 2010, 107(37): 16222-16227. 
- [18] Ross MT, Grafham DV, Coffey AJ, Scherer S, McLay K, Muzny D, Platzer M, Howell GR, Burrows C, Bird CP, Frankish A, Lovell FL, Howe KL, Bentley DR. The DNA sequence of the human X chromosome. *Nature*, 2005, 434(7031): 325-337.
- [19] 杨广礼, 张淑红, 韩进诚, 张春梅, 郭艳, 闫永峰, 施传信, 王玉玲. 猪X染色体QTL定位和候选基因的研究进展. *黑龙江畜牧兽医*, 2010, 6(11): 38-40.
- [20] McVicker G, Gordon D, Davis C, Green P. Widespread genomic signatures of natural selection in hominid evolution. *PLoS Genet*, 2009, 5: e1000471. 
- [21] Pickrell JK, Coop G, Novembre J, Kudaravalli S, Li JZ, Absher D, Srinivasan BS, Barsh GS, Myers RM, Feldman MW, Pritchard JK. Signals of recent positive selection in a worldwide sample of human populations. *Genome Res*, 2009, 19(5): 826-837. 
- [22] Huang da W, Sherman BT, Lempicki RA. Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. *Nucleic Acids Res*, 2009, 37(1): 1-13. 
- [23] Choi Y, Seo H, Kim M, Ka H. Dynamic expression of calcium-regulatory molecules, *TRPV6* and *S100G*, in the uterine endometrium during pregnancy in pigs. *Biol Reprod*, 2009, 81(6): 1122-1130. 
- [24] 张树敏, 李娜, 李毅, 金鑫, 赵晓东, 张嘉保. 松辽黑猪繁殖性状遗传规律的研究. *沈阳农业大学学报*, 2007, 38(3): 349-352.
- [25] Chen P, Baas TJ, Mabry JW, Koehler KJ, Dekkers JC. Genetic parameters and trends for litter traits in U.S. Yorkshire, Duroc, Hampshire, and Landrace pigs. *J Anim Sci*, 2003, 81(1): 46-53.
- [26] Fontanella B, Russolillo G, Meroni G. *MID1* mutations in patients with X-linked Opitz G/BBB syndrome. *Hum Mutat*, 2008, 29(5): 584-594. 
- [27] Amaral AJ, Ferretti L, Megens HJ, Crooijmans RPMA, Nie HS, Ramos-Onsins SE, Perez-Enciso M, Schook LB, Groenen MAM. Genome-wide footprints of pig domestication and selection revealed through massive parallel sequencing of pooled DNA. *PLoS One*, 2011, 6(4): e14782.
- [28] Gu JJ, Orr N, Park SD, Katz LM, Sulimova G, MacHugh DE, Hill EW. A genome scan for positive selection in thoroughbred horses. *PLoS One*,

- [29] Grossman SR, Shylakhter I, Karlsson EK, Byrne EH, Morales S, Frieden G, Hostetter E, Angelino E, Garber M, Zuk O, Lander ES, Schaffner SF, Sabeti PC. A composite of multiple signals distinguishes causal variants in regions of positive selection. *Science*, 2010, 327(5967): 883-886.
- [30] Nonneman D, Rohrer GA, Wise TH, Lunstra DD, Ford JJ. A variant of porcine thyroxine-binding globulin has reduced affinity for thyroxine and is associated with testis size. *Biol Reprod*, 2005, 72(1): 214-220. 
- [31] Bordais A, Bolaños-Jimenez F, Fort P, Varela C, Sahel JA, Picaud S, Rendon A. Molecular cloning and protein expression of Duchenne muscular dystrophy gene products in porcine retina. *Neuromuscul Disord*, 2005, 15(7): 476-487. 
- [32] Smith AJ, Schacker TW, Reilly CS, Haase AT. A role for syndecan-1 and claudin-2 in microbial translocation during HIV-1 infection. *J Acquir Immune Defic Syndr*, 2010, 55(3): 306-315. 
- [33] Nielsen M, Hansen JH, Hedegaard J, Nielsen RO, Panitz F, Bendixen C, Thomsen B. MicroRNA identity and abundance in porcine skeletal muscles determined by deep sequencing. *Anim Genet*, 2010, 41(2): 159-168.
- [34] Ernkvist M, Persson NL, Audebert S, Lecine P, Sinha I, Liu ML, Schlueter M, Horowitz A, Aase K, Weide T, Borg JP, Majumdar A, Holmgren L. The Amot/Patj/Syx signaling complex spatially controls RhoA GTPase activity in migrating endothelial cells. *Blood*, 2009, 113(1): 244-253.
- [35] Liggins AP, Cooper CDO, Lawrie CH, Brown PJ, Collins GP, Hatton CS, Pulford K, Banham AH. MORC4, a novel member of the MORC family, is highly expressed in a subset of diffuse large B-cell lymphomas. *Br J Haematol*, 2007, 138(4): 479-486. 
- [36] Raychowdhury MK, Ramos AJ, Zhang P, McLaughlin M, Dai XQ, Chen XZ, Montalbetti N, Del Rocio Cantero M, Ausiello DA, Cantiello HF. Vasopressin receptor-mediated functional signaling pathway in primary cilia of renal epithelial cells. *Am J Physiol Renal Physiol*, 2009, 296(1): F87-F97.
- [37] Jack K, Bellodi C, Landry DM, Niederer RO, Meskauskas A, Musalgaonkar S, Kopmar N, Krasnykh O, Dean AM, Thompson SR, Ruggero D, Dinman JD. rRNA pseudouridylation defects affect ribosomal ligand binding and translational fidelity from yeast to human cells. *Mol Cell*, 2011, 44(4): 660-666. 
- [1] 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
- [2] 王艳允, 陈梅, 李斌.X染色体的剂量补偿机制[J]. 遗传, 2012,34(8): 977-984
- [3] 杨秀芹, 陈月婵, 汪亮, 李海涛, 刘娣, 关庆芝, 付博.猪Toll样受体4基因SNPs功能分析[J]. 遗传, 2012,34(8): 1050-1056
- [4] 郭良勇, 傅金奎, 王爱国.猪整合素 $\beta_1$ 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
- [5] 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
- [6] 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
- [7] 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
- [8] 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
- [9] 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
- [10] 林佳丽, 沈良才, 潘登科, 张瑾.猪GII1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
- [11] 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
- [12] 刘小磊, 杨松柏, Max F Rothschild, ZHANG Zhi-Wu, 樊斌.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[J]. 遗传, 2012,34(10): 1261-1270
- [13] 李秀领, 杨松柏, 唐中林, 李奎, 刘榜, 樊斌.大白猪和通城猪全基因组选择性清扫分析[J]. 遗传, 2012,34(10): 1271-1281
- [14] 孔庆然, 朱江, 黄波, 郇延军, 王峰, 石永乾, 刘仲凤, 武美玲, 刘忠华.TSA促进转基因猪体细胞核移植胚胎发育和外源基因表达[J]. 遗传, 2011,33(7): 749-756
- [15] 李莉, 贾同, 吴同山, 张守全.猪PEG1基因多态性及其遗传印记[J]. 遗传, 2011,33(7): 738-742