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基因芯片在猪育种中的应用进展

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摘要 基因芯片是利用DNA双链互补配对或DNA-RNA互补杂交检测特定DNA序列的高通量技术,可高效完成检测分型和支撑个体遗传评估与选育。目前主流商用育种芯片以SNPs标记为核心,标记位在基因组上均匀分布,又称SNP芯片,已广泛应用于猪(*Sus scrofa domestica*)重要经济性状遗传解析、基因组选择、分子标记辅助育种、品种鉴定及种质资源保护等领域,在肉质、生长、繁殖和抗病抗逆育种方面取得了显著进展,推动猪育种由传统表型选择向精准化、规模化和高效化转变。与此同时,结构变异(structural variations, SVs)等新型遗传标记的引入,有助于弥补常规SNP芯片在复杂基因组区域和大尺度变异检测方面的不足,为解析复杂性状提供了新的技术路径。本文综述了基因芯片的技术原理、类型划分与国产化发展进程,系统阐述其在猪肉品质改良、生长性能提升、繁殖效率优化及抗病抗逆育种中的应用成效与关键进展,分析了当前应用瓶颈,并展望了其通过多技术整合赋能猪种业自主可控、产业高质量发展的前景,为我国基因芯片在猪育种领域的创新研发与产业化落地提供理论参考与实践指引。

关键词 SNPs; 基因芯片; 猪育种; 分子育种; 基因组选择

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Application Progress of Gene Chip in Pig Breeding

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Abstract Gene chips are high-throughput tools that detect specific DNA sequences by leveraging DNA double-strand complementary pairing or DNA-RNA complementary hybridization, enabling efficient genotyping and supporting individual genetic assessment and selective breeding. Currently, mainstream commercial breeding chips primarily utilize SNPs—distributed evenly across the genome—and are widely applied in areas such as the genetic analysis of economically important traits in pigs (*Sus scrofa domestica*), genomic selection, marker-assisted breeding, breed identification, and germplasm conservation. These chips have facilitated significant progress in breeding for meat quality, growth, reproduction, and resilience (including disease and stress resistance), driving the transition of pig breeding from traditional phenotypic selection toward precision, large-scale, and high-efficiency operations. Meanwhile, the introduction of novel genetic markers, such as structural variations (SVs), helps address the limitations of conventional SNP chips regarding complex genomic regions and large-scale variation detection, offering new technical avenues for deciphering complex traits. This article reviews the technical principles, classification, and domestic

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development process of gene chips, systematically elaborating on their application efficacy and key advancements in improving pork quality, enhancing growth performance, optimizing reproductive efficiency, and developing disease-resistant and stress-tolerant pig breeds. It analyzes current application bottlenecks and envisions the prospects of gene chips, through multi-technology integration, empowering the independent and controllable development of the pig breeding industry and promoting its high-quality development. The aim is to provide theoretical reference and practical guidance for the innovative research and industrial application of gene chips in the field of pig breeding in China.

Keywords SNPs; Gene chip; Pig breeding; Molecular breeding; Genomic selection

随着猪(*Sus scrofa domestica*)育种目标由生长速度和胴体产量逐步拓展至肉质、繁殖力、抗病性与环境适应性等多性状协同改良,复杂经济性状的早期、准确遗传评估已成为现代猪育种的重要需求(Harlizius et al., 2020; Miar et al., 2014)。基因组选择利用全基因组标记和参考群信息估计候选个体的基因组育种值,能够为缺乏自身表型或表型测定成本较高性状的早期选择提供技术支持,但其预测准确性受到参考群规模及参考群与候选群遗传联系的显著影响(Wei et al., 2022)。2009年 PorcineSNP60 芯片的建立为猪全基因组高通量分型、全基因组关联分析和基因组选择提供了标准化工具,低密度 SNP 芯片结合基因型填充则进一步降低了大群体基因分型的实施成本(Grossi et al., 2018; Ramos et al., 2009)。然而,固定 SNP 芯片可能产生位点确定偏倚,对未参与芯片设计群体中的稀有变异代表性不足,并难以充分覆盖插入、缺失、重复、倒位和拷贝数变异等结构变异(Geibel et al., 2021; Yang et al., 2024)。因此,本文系统综述猪基因分型芯片的技术发展及其在肉质、生长、繁殖和抗病抗逆育种中的应用成果,分析 SNP 芯片的技术局限、结构变异的补充价值及产业化应用瓶颈,旨在为猪基因组育种技术优化与育种芯片研发提供参考。

1 基因芯片及芯片类型

1.1 基因芯片

基因芯片又称 DNA 微阵列或生物芯片,其雏形源于菌落杂交法(Amutha et al., 2022),酿酒酵母(*Saccharomyces cerevisiae*)是首个完成全基因组测序的真核生物(Goffeau et al., 1996),DeRisi 等(1997)利用覆盖几乎全部酵母基因的 DNA 微阵列开展了基因组尺度的表达研究,此前,Pease 等(1994)报道利用光刻技术制备寡核苷酸 DNA 芯片。基因芯片利用微阵列技术,将大量特定的寡核苷酸探针构建

于固相载体或悬浮于液相体系中,通过与标记后的样本 DNA 进行特异性杂交反应,再借助荧光信号检测系统对杂交信号进行捕获与分析,即可获取样本的基因信息(何志巍,姚开泰,1999)。基因芯片经历了明确的发展阶段,Bains (1991)运用杂交法固定短 DNA 片段,并基于杂交原理完成了序列测定。Fodor 等(1991)年建立光定向空间可寻址并行合成技术,为后续原位合成高密度寡核苷酸芯片奠定了基础,与低密度探针相比,Fodor 团队开发的光刻合成技术实现了原位高密度探针阵列,集成度提升千倍,可规模化生产并广泛应用于基因组分析。2009年,Illumina 公司开发出畜禽商业化基因芯片,并将其应用于奶牛(*Bos taurus*)的遗传育种工作(Matukumalli et al., 2009)。同年,专门用于猪的 SNPs 基因分型芯片—Illumina Porcine 60K Genotyping BeadChip 正式问世(Ramos et al., 2009)。2010年左右,该技术已在基因发现、疾病诊断和药理与新药开发等多个领域快速发展(黄丹凤,2012)。基因芯片技术凭借高通量、高灵敏度和高特异性的核心优势(李双双等,2024),可高效实现对基因组位点及基因表达特征的快速并行检测与系统性分析,为分子遗传学研究及猪基因组育种提供了技术支撑(汪佳豪等,2023)。如今,基因芯片已广泛应用于畜禽遗传育种与繁育领域,在猪育种中发挥着核心支撑作用,通过精准筛选优良功能基因、培育优质品种,显著提升了猪的肉质品质、繁殖能力以及抗病性能,为猪育种的高效化、精准化发展提供了关键的分子工具(丁向东等,2022;汪佳豪等,2023)(图1)。

1.2 基因芯片的类型

1.2.1 固相芯片

固相芯片是以玻璃等为固相支持物,通过光刻与固相 DNA 结合的光定向合成法,在小面积表面

精准合成数十至数万种寡核苷酸的二维阵列技术(Lipshutz et al., 1999),是集高通量、高效率、标准化于一体的基因分型技术。基于碱基互补配对的分子生物学原理,可实现对大批量样本的一次性高效基因型分析,进而实现一次性完成海量遗传位点信息检测的核心应用目标(王有栋等, 2025; Ma et al., 2000)。20世纪90年代,美国Affymetrix公司基于原位光刻技术推出首款商业化固相芯片(李丫丫, 2016),该芯片实现了光刻工艺的工程化优化、探针合成效率与芯片密度的提升,同时完成了固相基底修饰、探针固定流程的标准化设计,成功将实验室原理验证的技术转化为可批量制备、实际应用的商业化产品。随后Illumina公司开发出微球工艺芯片(Gunderson et al., 2004)。固相芯片凭借分型准确率高、检测速度快、分析流程简单的优势,已成为畜禽分子育种的核心工具,显著提升了群体遗传评估的时效性与规模化水平(王有栋等, 2025)。近年,我国在猪育种基因芯片的国产化研发和应用方面取得关键性突破:拉索生物联合高校研发出“华芯猪”系列芯片(李智, 2025);温氏集团与拉索生物联合研发的PorcineWENS 100K芯片实现100%国产化(邵泉尉, 2025),提高了基因组育种值预测的准确性,带动分子育种检测成本大幅下降,不仅打破了国外技术与成本垄断,更为推进我国猪育种的产业化提供了核心技术支撑和保障。

1.2.2 液相芯片

液相芯片技术又称xMAP技术(multiple-analyte profiling, MAP),是一项具有突破性的高通量生物芯片分子检测技术(Graham et al., 2019; 朱向博, 2012)。该技术以荧光编码微球作为载体,融合流式细胞术、激光检测、数字信号处理等多学科技术特性,摆脱固定载体限制,形成悬浮式基因分型路径,为畜禽育种等领域提供灵活、高效的基因检测方案(张格阳等, 2023; Reslova et al., 2017)。该方法以二代测序为基础开展基因型分型,与常规基因组测序相比,其核心差异在于液相芯片会先通过特异性探针捕获基因组上的特定目标区域再进行测序。这一靶向捕获可减少测序数据量和后续分析工作量,缩短检测周期,并降低数据存储与分析成本(丁文家等, 2025)。与固相芯片相比,液相芯片无需在固定载体上制备探针阵列,增减位点也无需重新设计芯片,可根据育种需求灵活调整检测靶

点,从而降低基因型分型的总体成本(丁文家等, 2025)。靶向测序基因型检测(genotyping by target sequencing, GBTS)是一种基于液相芯片的升级型靶向基因分型技术(徐勤圆, 2023),针对商业猪种筛选60 K关键SNPs位点,创新性地结合靶向捕获技术与高通量测序技术实现精准基因型分型,为商业猪种目标性状的定向选育与遗传改良提供技术支撑(王文文等, 2025)。在猪育种领域,液相芯片技术已实现规模化落地应用。“皖芯1号”为安庆六白猪等7个地方猪品种构建专属基因身份证,并提升保种精准度。该技术应用于安徽省浩宇保种场后,使种猪世代间隔由15个月缩短至9个月,场内种猪产能提高40%,为我国地方猪种资源的保护与产业化开发工作提供关键的技术支撑。

1.2.3 甲基化芯片

DNA甲基化是生物中关键的表观遗传修饰方式,在DNA甲基转移酶的催化作用下,甲基基团被特异性转移至DNA胞嘧啶残基上(Malygin, Hattman, 2012)。该修饰方式不改变DNA的核苷酸序列,却能通过调控基因表达影响生物学功能,其修饰位点通常位于胞嘧啶-磷酸-鸟嘌呤二核苷酸(cytosine-phosphate-guanine dinucleotide, CpG)中胞嘧啶的第五位碳原子上(张淼等, 2022)。DNA甲基化修饰具有至关重要的生物学功能,既可在分子与细胞层面调控基因表达水平、影响细胞分化进程(Meissner et al., 2008),也能延伸至机体整体层面,参与发育调控、生理稳态维持和疾病发生发展(蒋明等, 2015; Widschwendter, 2007)。2009年,Illumina公司首次将Infinium技术应用于Human-Methylation 27K芯片,该芯片可覆盖超过27 000个CpG位点的甲基化水平(Bibikova et al., 2009)。Wang等(2019)分别采用聚肌苷酸-聚胞苷酸(polyinosinic: polycytidylic acid, PolyI:C)、5-氮杂-2'-脱氧胞苷(5-aza-2'-deoxycytidine, Aza-CdR)及联合处理PK15细胞,并利用MeDIP-chip和转录组数据分析差异甲基化区域及相关宿主基因鉴定出与病毒复制、抑制相关的甲基化调控宿主基因。甲基化芯片的研究为哺乳动物疾病研究提供依据(Carreras-Gallo et al., 2024)。甲基化检测技术有助于精确识别与畜禽疾病抵抗力和生产性能等重要经济性状相关的差异甲基化区域,而将这些技术与表观基因组编辑和多组学分析相结合,可为推进畜禽精准育种提供

关键靶点支持(Zeng et al., 2025)。

总体而言,固相 SNP 芯片、液相芯片和甲基化芯片在检测对象、技术原理、功能定位及适用范围等方面存在明显差异(Ren et al., 2024; Peters et al., 2024)。固相 SNP 芯片将预先设计的寡核苷酸探针固定于固相载体表面(王有栋等, 2025),通过特异性杂交、延伸及荧光信号检测,对大量已知遗传变异位点进行并行分型(Ramos et al., 2009; Lipshutz et al., 1999)。该技术流程标准化、重复性较好,且数据便于统一分析,适用于基因组选择、全基因组关联分析和群体遗传研究;但检测位点相对固定,当芯片设计群体与目标群体遗传背景差异较大时,可能产生 SNP 确定偏倚(Geibel et al., 2021)。xMAP 悬浮微球芯片可在同一反应体系中同步检测多个已知核酸或蛋白质靶标,适合候选突变、病原体 and 生物标志物的联合检测,但靶标数量增加,会提高体系优化难度(Graham et al., 2019; Reslova et al., 2017)。GBTS 液相捕获芯片利用特异性探针富集目标区域并进行高通量测序,具有位点组合灵活、便于纳入新发现功能变异等特点,但对测序平台和生物信息分析能力要求较高(Ren et al., 2024; Zhang et al., 2025)。甲基化芯片主要检测预设 CpG 位点的甲基化水平,适用于差异甲基化分析和表观遗传标志物筛选,但其检测范围受探针覆盖限制,且结果明显依赖组织类型和生理状态(de Abreu et al., 2025; Peters et al., 2024)。

实际应用中,应根据研究目的、目标群体、样本规模、位点更新需求及实验条件选择合适的检测平台。对于商业猪种的大规模基因组选择、遗传评估和亲缘鉴定,可优先采用数据标准化程度较高的固相 SNP 芯片,但应提前评估其在目标群体中的位点检出率 and 多态性(Peters et al., 2024)。对于地方猪种,或需要根据新发现持续补充功能位点和性状关联位点的研究,GBTS 液相捕获芯片在构建品种特异性或性状特异性分型面板方面更具优势(Cao et al., 2026; Guo et al., 2021; Zhang et al., 2025)。若研究对象为预先确定的中低通量靶标集合,如已知突变、病原体或生物标志物,可选择 xMAP 悬浮微球芯片(Bongoni et al., 2013; Dunbar, Jacobson, 2005; Yan et al., 2017)。当研究重点是比较营养、环境、疾病或生长发育等条件下预设 CpG 位点的甲基化差异时,可采用甲基化芯片(Arneson et al., 2022; Bibikova et al., 2011);若需要发现未知甲基化位

点、获得单碱基分辨率信息或构建较为完整的全基因组甲基化图谱,则应选择全基因组亚硫酸氢盐测序或靶向甲基化测序技术(Hodges et al., 2009; Lister et al., 2009)。因此,不同平台不存在绝对优劣,应围绕具体研究问题,在位点覆盖范围、检测稳定性、样本规模、成本及实验与生物信息分析条件之间进行综合权衡。

2 猪育种基因芯片的设计与研发

猪作为全球最重要的家畜之一,其肉类及其他副产品是人类获取优质蛋白质的重要来源。优质种猪作为猪产业健康可持续发展的重要基础,对提升产业核心竞争力具有关键意义(段永邦, 2025)。基因芯片开发需以实际育种需求为导向,精准整合与生长、肉质、繁殖、抗病等性状相关的分子标记,涵盖功能基因位点,为定向选育提供精准的信息和技术支撑(范利, 2024; 黄路生等, 2024)。根据这些需求,可用基因组关联分析、标记筛选等技术手段,挖掘与猪生长、肉质、繁殖、抗病等性状显著相关的变异位点。例如通过全基因组关联分析(genome-wide association study, GWAS)分析已鉴定出骨形态发生蛋白 2 (bone morphogenetic protein 2, BMP2) 等与猪生长、胴体性状相关的候选基因(Blaj et al., 2018)。芯片的设计首先要收集核心育种种群与地方品种的全基因组重测序数据(高正杰等, 2024),以及猪经济相关的 QTL 区域与功能基因数据。位点筛选遵循“质量优先、分布均匀、功能导向”原则(Zhang et al., 2025),基于筛选出的目标位点,采用 GBTS 技术体系,通过探针与目标位点特异性结合实现高效基因型检测(Guo et al., 2022)。基于长白、大白和杜洛克商业猪种全基因组重测序数据,制备得到猪 60K 液相芯片,该芯片能够高效完成商业猪种基因分型(王文文等, 2025);武建亮等(2025)设计了包含 5 385 个 SNPs 位点的猪低密度芯片,将其填充至质控后的“中芯一号”44 506 个位点后,等位基因正确率和基因型正确率分别达到 99.46% 和 98.94%。研究人员基于姜曲海猪与其他猪种间的等位基因频率差异筛选品种鉴定 SNP 位点,并补充均匀分布的背景位点。北京康普森农业科技有限公司采用靶向捕获测序技术设计探针,研制出包含 50 014 个 SNP 位点的姜曲海猪 50K 液相芯片。该芯片具有较高的检出率和分型一致率,可用于品种

鉴定、亲缘关系分析和家系构建(高正杰等, 2024)。徐云碧等(2020)基于GBTS技术研发的20K液相芯片,其基因型检测可重复性达98%;对于多聚核苷酸多态性(multi-allelic single nucleotide polymorphism, mSNPs) 40K液相芯片可重复性达97.8%~99.7%,且与传统固相芯片相比,相同SNPs标记的平均一致性高达95.3%,在标记灵活性、检测高效性和成本等方面展现出显著优势。华南农业大学评估显示,纽勤50K、中芯一号50K等芯片经基因型填充后,位点准确性可提升至0.97以上,为猪生长、繁殖性状的遗传解析提供了高效工具(曾浩南等, 2022)。邱奥等(2021)以河北张家口大白猪为对象,对基于GBTS的液相50K芯片,Geneseek 50K SNPs和中芯一号固相商业芯片的基因型填充效果进行比较,结果显示,前两款芯片中相同位点数量最多,互相直接填充的平均基因型准确率约0.92,且液相50K作为参考群体时,Geneseek芯片与中芯一号芯片向其填充的准确性最高;合并填充方面,Geneseek与液相50K组合的填充效果最优,而扩大参考群体规模能显著提升直接填充和合并填充的准确性,证实3款猪50K芯片间的基因型填充可行,该研究为我国猪分子育种中不同芯片数据的应用提供了参考依据。

3 SNP芯片在猪育种上的应用

SNP芯片是猪基因组选择与遗传改良的核心工具,其发展关乎种源自主可控能力。早期全球商用市场以Neogen公司GGP 50K芯片、Affymetrix公司猪全转录组阵列芯片等国外固相芯片为主,国内外代表性猪育种SNP芯片在技术平台、标记密度、位点设计及应用场景等方面各具特点,其开发与应用概况见表1。但这类芯片存在位点适配性不足、技术垄断导致检测成本高昂等问题,我国猪育种曾长期依赖进口,核心技术与生产环节长期受制于人,形成“卡脖子”瓶颈(李利君等, 2025)。

近年来,在猪遗传育种领域,SNPs标记的应用十分广泛,成效显著。以“中芯一号”50K SNP芯片为代表的技术已应用于玉山黑猪等地方猪种的保种研究,通过分析其遗传多样性、近交水平、亲缘关系及家系结构,可精准评价保种效果、检测血统渗入情况,为优化保种方案和完善育种选配提供科学依据。该技术还可用于家畜遗传图谱构建、QTL定

位以及功能基因分析(杨彩琴等, 2018),为分子标记辅助育种的推进提供了有力的技术支撑(曲娟娟等, 2011)(图2)。SNPs标记在基因组中分布广、数量多,且易与猪经济性状建立稳定关联,可实现个体早期无表型筛选,显著缩短育种周期,在家畜遗传育种中具备极高应用价值(柴进等, 2024; 冯越等, 2024; 贾倩茹等, 2024)。现有猪液相育种芯片主要采用靶向测序基因分型技术,对预先筛选的SNPs及少量插入缺失位点进行检测;例如,猪GBTS50K面板由52 000个目标SNPs构成,位点筛选过程中还对低频变异进行了过滤,因此其主要功能是对已知目标位点进行规模化分型,而非发现目标区域之外的未知结构变异(Zhang et al., 2025)。除SNP外,拷贝数变异(copy number variation, CNV)作为猪基因组中重要的结构变异类型,也是影响表型差异和经济性状的重要遗传变异来源。研究表明,利用Porcine SNP60或80K SNP芯片的信号强度数据可在猪群体中鉴定大量CNV区域,且部分CNV区域与产仔数等繁殖性状相关,因此在常规SNP分型基础上进一步挖掘CNV信息,可补充SNP位点对复杂结构变异表征不足的问题(Wang et al., 2012; Wang et al., 2020)。对于插入、缺失、重复、倒位及复杂染色体重排等结构变异,可利用短读长全基因组测序开展群体水平筛查,并结合长读长测序、基因组组装或其他独立技术提高重复区域和复杂断点的解析能力;多平台联合分析能够明显提高结构变异的检出灵敏度和序列分辨率(Chaisson et al., 2019)。结构变异(structural variations, SVs)可通过破坏或重排基因编码序列、改变基因拷贝数与剂量、影响转录剪接,或扰动增强子等顺式调控元件及局部染色质结构,进而改变基因表达、转录本结构或蛋白质功能,并影响复杂性状(Abel et al., 2020; Chiang et al., 2017; Vialle et al., 2022; Yang et al., 2024)。Yang等(2024)在1 060头、101个猪品种的全基因组数据中构建了大规模结构变异图谱,鉴定了肌球蛋白VA(myosin VA, MYO5A)转录本中的SINE插入、约克夏猪特异性的ATP结合盒亚家族G成员2(ATP binding cassette subfamily G member 2, ABCG2)区域拷贝数增加,以及与脂肪酸去饱和酶3(fatty acid desaturase 3, FADS3)主效表达数量性状位点连锁的51 bp缺失。这些结构变异分别可能影响可变剪接、染色质互作和基因表达;其中FADS3表达与眼肌面积之间

的潜在关系,为解析结构变异影响猪经济性状提供了线索。因此,SVs 信息可作为 SNP 分型结果的补充,用于拓展猪复杂经济性状相关遗传变异的发现范围(Li et al., 2025; Li et al., 2024)。随着泛基因组和长读长测序技术的发展,猪育种芯片的标记类型开始由单一 SNP 向 SNP 与 SVs 联合检测拓展。李

响等(2026)开发的猪 50K 液相基因芯片整合了 45 113 个 SNPs 位点、4 910 个 SVs 位点及全长线粒体基因组捕获设计,在地方猪和商业猪样本中均表现出较好的捕获效率和检测稳定性,为复杂遗传变异的联合分析及猪分子育种提供了新的技术路径。鉴于靶向测序基因分型平台具有靶标选择相对灵

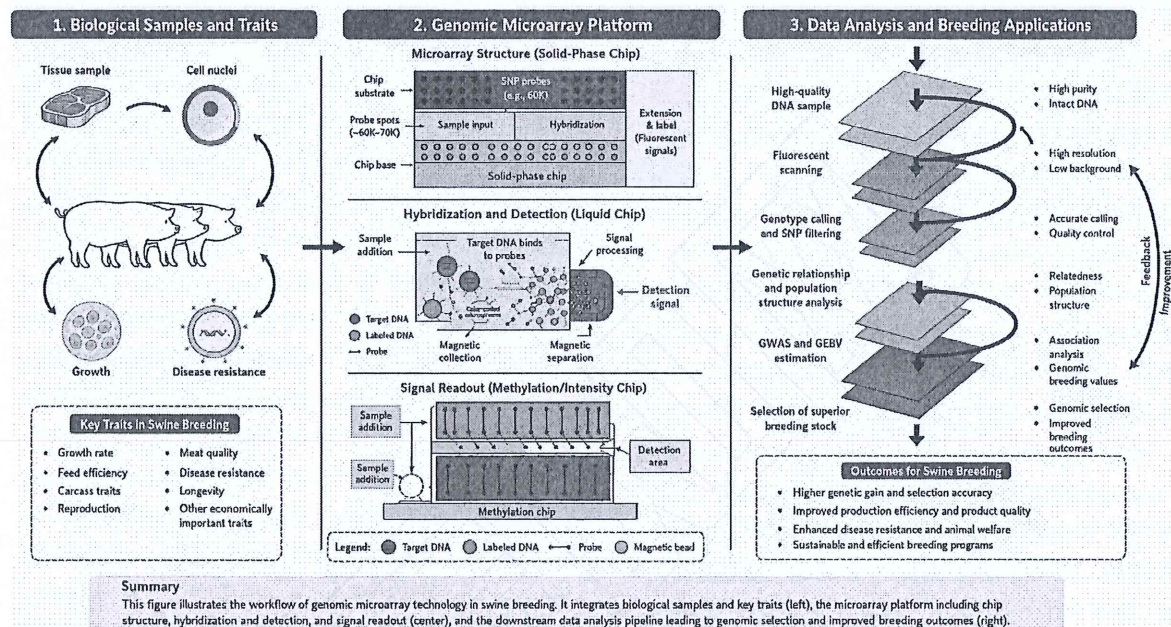


图1 基因芯片技术流程及生猪育种性状

Figure 1 Gene chip technology process and traits in pig breeding

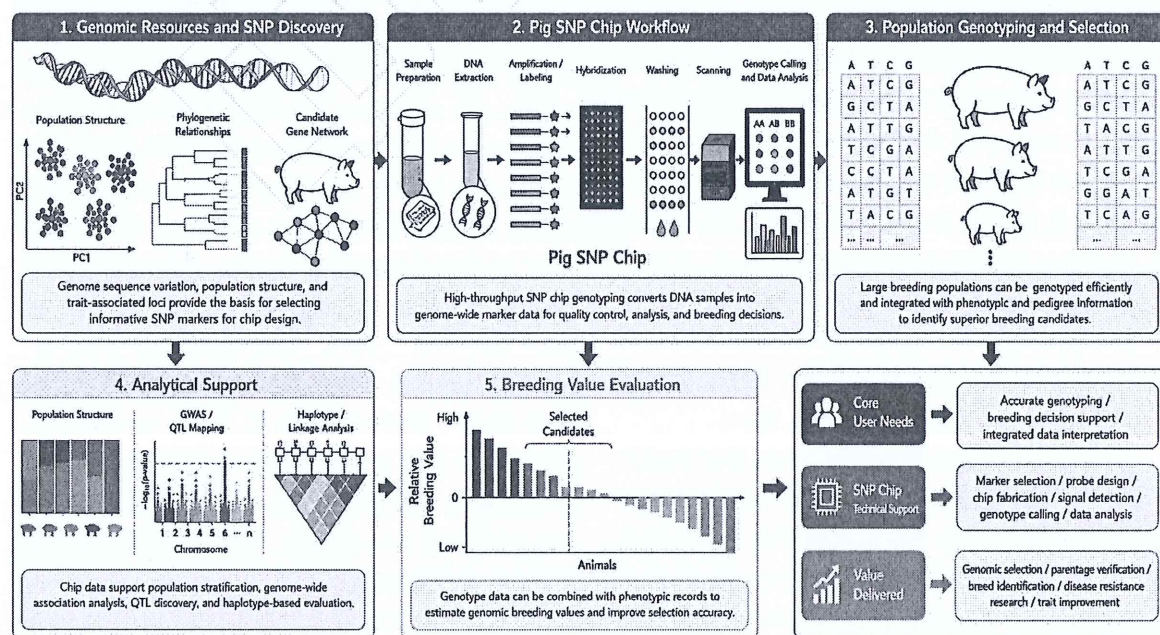


图2 猪育种芯片技术解析与育种应用路径图

Figure 2 Analysis of pig breeding chip technology and its application pathways in breeding programs

表 1 生猪育种的部分 SNPs 芯片开发概况

Table 1 Overview of SNPs chip development for swine breeding			
芯片名称(公开时间)	类型	位点数	位点设计特点
Chip name (Release date)	Type	Number of loci	Site design characteristics
Illumina Porcine SNP60 BeadChip (2009)	固相; 中高密度	64232	基于二代测序 SNP, 覆盖主要商业猪种及野猪, 强调全基因组覆盖
	Solid phase; Medium-high density		Based on next-generation sequencing SNP, the study covers major commercial pig breeds and wild boars, emphasizing whole-genome coverage
GeneSeek GGP-Porcine LD (2012)	固相; 低密度	设计 9390, 生产版约 8500	基于 13 个商业猪系的次要等位基因频率, 基因组位置及染色体末端覆盖筛选骨架位点
	Solid phase; Low density	Design version: 9390; Production version: 8500 approximately	Based on minor allele frequency, genomic location, and chromosome end coverage screening of 13 commercial pig lines, scaffold sites were selected
GeneSeek GGP-Porcine HD (2014)	固相; 中高密度	v1 为 68529; 后续版本 > 70000	全基因组高密度标记, 兼顾生产, 疾病及亲缘定位
	Solid phase; Medium-high density	v1 has 68529 bytes; Subsequent versions are > 70000	High-density whole-genome markers, taking into account site, and hybridization introgression analysis
GeneSeek GGP-Porcine 50K (v1/v2, 2020)	固相; 中密度	v1 为 50915; v2 为 50697; 现行产品 > 51000	基因组评估, GWAS, 亲缘关系及群体结构分析
	Solid phase; Medium density	v1 is 50915; v2 is 50697; current products > 51000	Genome assessment, GWAS, kinship and population structure analysis
“中芯一号”家猪育种芯片系列(2017)	固相; 中密度	早期核心设计 51368; KPS v2 研究版 57466	面向中国地方猪与商业猪; 早期含 29 个因果位点和 1642 个连锁位点, 覆盖 201 个性状
	Solid phase; Medium density	Early core design 51368; KPS v2 research version 57466	Targeting both local and commercial pigs in China; Early studies included 29 causal loci and 1642 linkage loci, covering 201 traits
PorcineWENS 100K (2024)	固相; 高密度	约 100K	采用国产固相技术, 提高中国猪群全基因组覆盖和变异代表性, 用于高分辨率育种
	Solid phase; High density	Approximately 100K	High-resolution GWAS, genome selection, genetic resource evaluation, and cross-population studies

we can improve the whole genome coverage and variation representativeness of Chinese pig herds for high-resolution breeding				Low-cost genotyping, genotype filling, and genome breeding	
猪全基因组低密度9K SNP芯片(2018)	固相; 低密度	8846	整合 GGP-Porcine HD, GWAS/QTL 及生长、繁殖、抗病等功能位点	低成本基因分型、基因型填充和基因组育种	
Low-density 9K SNP microarray of the whole pig genome (2018)	Solid phase; Low density		Integrate GGP-Porcine HD, GWAS/QTL, and functional sites related to growth, reproduction, and disease resistance	Low-cost genotyping, genotype filling, and genome breeding	
杜洛克猪全基因组低密度10K SNP芯片(2022)	固相; 低密度	9731	基于杜洛克核心群, 整合 GWAS, BayesB, 遗传缺陷及高密度芯片位点; 平均MAF为0.31	杜洛克猪基因组选择, 亲缘关系, 遗传多样性和高密度填充	
Duroc pig whole genome low-density 10K SNP chip (2022)	Solid phase; Low density		Based on the Duroc core group, it integrates GWAS, BayesB, genetic defects and high-density chip sites; The average MAF is 0.31	Duroc pig genome selection, kinship, genetic diversity, and high-density filling	
猪全基因组低密度3K/5K SNP芯片(2024)	固相; 低密度	5K 验证版 5385; 填充目标 44506	基于 KPS v2, 采用前向顺序特征选择和多目标局部优化, 兼顾较高MAF与较低标记冗余	低成本早期分型, 基因组选择及中高密度填充	
Low-density 3K/5K SNP microarray of the whole pig genome (2024)	Solid phase; Low density	5K validation version 5385; Population target 44506	Based on KPS v2, it adopts forward sequential feature selection and multiple-objective local optimization to balance higher MAF and lower label redundancy	Low-cost early typing, genome selection, and medium-to-high density filling	
“华芯猪”Pro/Mini (2025)	固相; 高密度/低密度	Pro 约 73K; Mini 约 13K	Pro 用于高密度参考群和精准选种, Mini 用于大群体低成本检测并向Pro填充	规模化基因组选择, 亲缘分析, 参考种群构建和基因型填充	
"Huaxin Pig" Pro/Mini (2025)	Solid phase; High density/ Low density	Pro: Approximately 73K; Mini: Approximately 13K	Pro is used for high-density reference groups and precise seed selection, while Mini is used for low-cost detection of large populations and to fill in Pro	Large-scale genome selection, parentage analysis, reference population construction, and genotype filling	
猪 80K 功能位点液相芯片(2023)	液相; 高密度	80483 个目标 SNPs	全基因组背景上强化生长、繁殖、肉质等功能位点, 采用靶向捕获, 可灵活增删位点	基因组选择, 功能变异筛选及经济性状辅助育种	
80K functional site liquid-phase chip for pigs (2023)	Liquid phase; High density	80483 target SNPs	It enhances functional sites related to growth, reproduction, and meat quality against the whole genome background, employs targeted capture, and allows for flexible addition or deletion of sites	Genomic selection, functional variant screening, and economic trait-assisted breeding	
GenoBaits Porcine SNP50K (2021)	液相; 中密度	50885	基于靶向捕获测序, 位点组合可调整, 是后续GBTS产品的重要技术阶段	基因组选择, 群体遗传, 品种鉴定及功能位点检测	
	Liquid phase; Medium-high density		Based on targeted capture sequencing, the combination of sites can be adjusted, which is an important technological stage for subsequent GBTS products	Genomic selection, population genetics, variety identification, and functional site detection	

GBTS50K 猪液相芯片 (2023)	液相; 中密度 Liquid phase;	52000 个 SNPs	采用 GBTS/mSNP 策略; 约 8.8K 个位点位于重要经济性状 QTL 区, 可获取邻近 SNP 信息	基因组选择, GWAS, 品种鉴定和种质资源评价 Genome selection, GWAS, variety identification, and germ-plasm resource evaluation
GBTS50K porcine liquid phase chip (2023)	Medium density	52000 SNPs	The GBTS/mSNP strategy was adopted; Approximately 8.8K sites are located in the QTL region of important economic traits, and neighboring SNP information can be obtained	plasm resource evaluation
mSNP 猪 10K 液相芯片 (2023)	液相; 低密度 liquid phase; Low density	约 9400 个位点 Approximately 9400 target sites	单靶区可获取多个相邻 SNP; 与 50K 形成“低密度早选—高密度核心区”体系 A single target region can acquire multiple adjacent SNPs; Together with 50K, it forms a "low-density early selection-high-density core group" system	低成本大群体分型, 亲缘关系分析, 基因组选择和高密度填充 Low-cost large-scale population typing, kinship analysis, genome selection, and high-density filling
北京黑猪分子育种 50K SNP 芯片 (2023)	固相; 中密度 Solid phase;	49563	基于 Illumina Infinium iSelect, 整合北京黑猪特异, 肉质及全基因组背景位点 Based on Illumina Infinium iSelect, we integrated specific, meat quality, and whole-genome background loci of Beijing Black Pig	北京黑猪品种鉴定, 亲缘关系, 种质评价和分子育种 Identification, kinship, germplasm evaluation, and molecular breeding of Beijing Black Pig breeds
50K SNP chip for molecular breeding of Beijing Black pigs (2023)	Medium density			
姜曲海猪 50K SNP 液相芯片 (2024)	液相; 中密度 Liquid phase;	50014 (11169 个品种鉴定位点 + 38845 个背景位点)	基于 41 个猪种, 769 个体筛选品种鉴定位点, 并配置全基因组背景标记, 采用靶向捕获 Based on 41 pig breeds and 769 individuals, breed identification loci were screened and whole-genome background markers were configured, and targeted capture was employed	姜曲海猪品种鉴定, 亲缘关系分析和家系构建 Identification, kinship analysis and pedigree construction of Jianguhai pig breed
50K SNP liquid phase chip for Jianguhai pig (2024)	Medium density	50014 (11169 varietal identification loci + 38845 background loci)		
“陕芯一号”猪 50K 液相育种芯片 (2025)	液相; SNP/SV 联合 Liquid phase; SNP/SV combined	45113 个 SNP + 4910 个 SV, 并含线粒体捕获设计 45113 SNPs + 4910 SVs, including mitochondrial capture design	整合 161 个猪种及多源短/长读长数据, 同时覆盖 SNP 和 SV It integrates data from 161 pig breeds and multiple sources of short/long reads, covering both SNPs and SVs	地方猪和商业猪联合分型, 品种鉴定, 遗传资源保护及基因组育种 Joint typing, breed identification, genetic resource protection, and genome breeding of local and commercial pigs
"Shaanxi Chip No. 1" 50K liquid phase breeding chip for pigs (2025)				

活的特点,未来可探索将经独立群体和功能试验验证的候选SVs断点,或与其高度连锁的标记,纳入品种特异性或性状特异性靶向分型面板(Zhang et al., 2025)。

3.1 基因芯片在猪肉品质改良中的应用

猪肉品质的评定需综合考量感官特性、理化性质、营养价值及食品安全等维度,其中肉色、大理石纹、嫩度、肌肉脂肪(intramuscular fat, IMF)含量是该领域主要的评价指标(马衍旋, 2018; Nonneman et al., 2013)。在这些指标中,IMF含量是评价猪肉品质的关键指标之一(Wang et al., 2022; Wood et al., 2008),其含量水平影响肉类的抗氧化特性、嫩度、风味、多汁性和可接受性(Yu et al., 2023)。多数肉质指标属于中低遗传力性状,传统选育周期长、效率低,而借助SNP芯片技术开展遗传评估与定向选育,已成为精准提升猪肉品质的有效途径(Miar et al., 2014)。早期研究多聚焦于“关键基因特异性芯片”的开发,核心思路是围绕调控肉质的核心基因设计检测工具。随着高密度SNP芯片技术的成熟,GWAS与SNP芯片结合的技术方案,逐渐成为挖掘肉质相关遗传标记的主要技术路径(Wang et al., 2023)。Gao等(2021)使用GeneSeek Porcine SNP50K BeadChip对582头杂交猪进行基因分型,并通过GWAS分析肉质性状,最终鉴定出32个与肉质性状显著关联的SNPs位点,同时在显著SNPs所在基因组区域筛选到多个肉质性状相关候选基因。Zhang等(2019)在莱芜猪、二花脸猪、巴马香猪、苏太猪、白杜洛克×二花脸F₂群体及杜长大三元杂交猪等6个群体共2446头猪中,对38项肌肉脂肪酸组成性状开展多群体GWAS和Meta分析,并将芯片基因型填充至序列水平,鉴定到285个显著关联的先导SNP(lead SNP)。研究进一步筛选出FADS2、ATP结合盒亚家族D成员2(ATP binding cassette subfamily D member 2, ABCD2)、超长链脂肪酸延长酶5(ELOVL fatty acid elongase 5, ELOVL5)、超长链脂肪酸延长酶6(ELOVL fatty acid elongase 6, ELOVL6)、超长链脂肪酸延长酶7(ELOVL fatty acid elongase 7, ELOVL7)、硬脂酰辅酶A去饱和酶(stearoyl-CoA desaturase, SCD)和甲状腺激素反应蛋白(thyroid hormone responsive, THRSP)等脂质代谢相关候选基因。中国农业科学

院深圳农业基因组研究所开发的“天鹏香芯V2”75K液相芯片,在V1版本(70K液相芯片)基础上迭代优化,删除捕获特异性不足、分型准确性低、检出率不达标及最小等位基因频率过低的位点,新增猪肉量、产仔数等产量相关及肌肉脂肪含量、脂肪酸组成等品质相关关键功能位点,同时配置新一代基因组选择算法,显著提升分型准确性与捕获特异性,强化位点的育种信息价值,有效实现产量与品质性状的协同改良,突破传统芯片难以兼顾双类经济性状的痛点,已在多家猪育种企业推广应用并推动性状持续提升(李奎, 2025)。邱奥等(2022)利用50K液相芯片对商品猪群体进行基因分型,结合生长、繁殖性状表型数据开展基因组选择效果分析,发现该芯片对100 kg体重日龄、背膘厚的基因组预测准确性分别达0.68和0.72,显著高于传统育种值估计效率。从产业应用角度看,肉质性状遗传改良的重要瓶颈之一是高质量表型获取成本较高,肌肉脂肪含量、嫩度、肉色、pH及部分精细胴体组成和胴体分割性状通常需要在屠宰后通过取样、胴体解剖或实验室分析获得,因而难以在留种候选猪本身直接、大规模记录(Buitenhuis et al., 2026; Davoli, Braglia, 2007; Lozada-Soto et al., 2022; Gao et al., 2021);已有研究表明,将具有目标肉质表型和基因型信息的商品杂交猪纳入参考群,有助于提高对商品猪肉质和胴体性状的预测能力(Emmanuel, 2022)。大规模纯种猪与三元杂交猪研究发现,背膘厚、眼肌深度和平均日增重在两类群体间的遗传相关分别为0.81、0.79和0.56,且相关性状在纯种和杂交群体中受到部分重叠、部分不同的基因组区域影响,提示仅依据核心纯种群中的关联结果,可能不足以完全反映商品杂交猪的实际表现(Bergamaschi et al., 2020)。在技术发展方面,将SNP芯片数据与肠道微生物组信息联合分析,可改善脂肪沉积、肌肉脂肪和肉色等部分性状的表型预测,但其增益具有明显的性状和采样阶段依赖性,且加入宿主基因组与微生物组互作项并未稳定提高预测准确性;因此,未来应以连接纯种核心群与商品杂交群的肉质参考群为基础,对活体辅助表型和多组学信息的增益进行性状特异性及独立群体验证,而不能仅以候选位点数量评价芯片的肉质育种价值(Khanal et al., 2020)。

3.2 基因芯片在猪生长性能与发育性状改良中的应用

动物生长发育是从胚胎形成到个体成熟过程中,细胞生长、增殖和分化,以及组织器官形态发生与体量增长相互协调的连续过程(Boulan, Leopold, 2021; Kaldis, Richardso, 2012)。作为养猪业中至关重要的经济指标,生长性能与发育性状直接决定猪肉生产效率,对产业经济效益具有关键影响(柯思琪, 2025)。随着对猪生长发育相关 QTL 及候选基因的挖掘工作的不断深入,越来越多的芯片技术被研发并应用于育种实践(Sun et al., 2025),如早期研究发现磷脂酶 C β 4 (phospholipase C beta 4, *PLCB4*) 基因是猪生长和日增重性状的候选基因之一(Zhao et al., 2021)。Blaj 等(2018)采用 Illumina PorcineSNP60 BeadChip 对 3 个 F₂ 代猪群体的 2 380 只猪进行全基因组基因分型,同时进行基于逆方差策略的 Meta 分析,发现了 *BMP2* 基因为胴体长度的强候选基因,这为解析猪生长与胴体性状的遗传基础提供了新线索,丰富了相关候选基因库。阮栋林等(2023)联合温氏集团团队,利用猪 GeneSeek 50K SNPs 芯片对温氏集团某核心猪场 3 334 头美系杜洛克种猪进行基因分型,采用 GCTA 软件的约束极大似然法(restricted maximum likelihood, REML)系统分析 10 个生长与体尺性状的遗传力及性状间遗传相关性,精准明确美系杜洛克种猪生长与体尺性状的遗传参数特征,为其遗传评估提供了科学数据支撑,优化了杜洛克猪目标性状的选育策略。蒲蕾等(2020)利用 Illumina SNP60 芯片对杜洛克猪群体的 458 个个体进行基因分型,在 13 号染色体全羧化酶合成酶(holocarboxylase synthetase, *HLCS*)基因的内含子区检测到 4 个与生长发育性状显著相关的 SNPs 位点;这些位点分别与剩余采食量、100 kg 背膘、平均日采食量、平均日增重及 100 kg 日龄显著关联;张笑科等(2023)发现,3-羟基酰基辅酶 A 脱水酶 1 (3-hydroxyacyl-CoA dehydratase 1, *HACD1*) 和骨形态发生蛋白与激活素膜结合抑制因子(BMP and activin membrane bound inhibitor, *BAMBI*)基因作为杜洛克猪生长发育的“核心调控因子”,*HACD1* 基因可通过调控肌母细胞融合与骨骼肌生长参与肌肉纤维形成,*BAMBI* 基因可通过调节转化生长因子- β (transforming growth factor beta, TGF- β)及 Wnt 信号通路,参与肌肉再生和脂肪细胞分化,明确了

这些 SNPs 位点与杜洛克猪生长性状的强关联性,为生长性状的分子标记辅助选择提供了精准靶点。基因芯片在猪生长和胴体性状改良中的重要价值之一,是利用全基因组 SNP 信息估计候选猪的基因组育种值,使年轻候选猪在尚未获得完整自身表型或后代表型时即可开展早期遗传评估,并提高日增重、背膘厚和眼肌深度等性状的选择效率(Guo et al., 2016; Jiao et al., 2014; Jibrila et al., 2022; Zhang et al., 2018)。Melnikova 等(2021)利用高密度 SNP 芯片和 ssGBLUP 方法评估大白猪繁殖、生长、脂肪和肌肉性状。结果表明,基因组信息对低遗传力繁殖性状育种值可靠性的提升更为明显,增幅约为 40%;对肌肉深度、100 kg 日龄和背膘厚等性状,初步基因组育种值与最终育种值保持一定相关性,说明基因组信息可为候选猪早期选择提供补充依据。但芯片预测模型的应用效果具有明显的群体依赖性。Zhao 等(2023)在两个杜洛克群体中发现,群体间遗传联系及因果变异效应的一致性会影响联合基因组评估效果,当群体间遗传相关较弱时,合并参考群并不一定提高所有性状的预测准确性。在芯片位点优化方面,Wei 等(2023)以 1 018 头大白猪的 50K 芯片数据为基础,将基因型填充至序列水平,并根据大规模 GWAS meta 分析结果预选与 100 kg 体重日龄、日增重和背膘厚等性状相关的变异;与常规芯片数据相比,不同位点预选方案使基因组预测准确性平均提高 0.3%~2%,且提升幅度随性状、位点比例和预测模型而变化。因此,猪生长性状芯片的产业化发展不应仅追求标记数量增加,而应围绕目标品种建立持续更新的基因型—表型参考群,筛选并验证具有稳定预测贡献的生长和胴体性状相关位点,同时在独立群体和连续世代中评价基因组育种值的准确性及偏倚,以提高芯片在实际种猪选择中的稳定性和适用性(Melnikova et al., 2021; Wei et al., 2023; Zhao et al., 2023)。

3.3 基因芯片在猪繁殖性状改良中的应用

选种是猪繁殖的初始环节,影响繁殖效率与养猪业经济效益,而基因组选择技术为繁殖性状的精准选种提供了有效手段(阳文攀等, 2025)。Muñoz 等(2019)以 20 个欧洲地方猪品种及少量西班牙野猪(*S. scrofa*)为研究对象,利用 GeneSeek Genomic Proiler HD 猪基因分型芯片进行基因分型,分析基因组多样性、群体结构等特征,检测到与生长、繁殖

等性状相关的候选基因,如精子顶体相关蛋白1 (sperm acrosome associated 1, *SPACA1*)和溶质载体有机阴离子转运蛋白家族成员4C1 (solute carrier organic anion transporter family member 4C1, *SLCO4C1*)等,为欧洲地方猪品种的保护、可持续利用及分子育种提供了科学依据。在长白母猪群体中,研究人员以国家某核心育种场1 063头长白母猪为对象,利用50K SNPs芯片结合其断奶至配种间隔记录开展GWAS分析,通过GEMMA软件混合线性模型检测到第1胎次和第3胎次共5个显著关联的SNPs位点;对显著位点进行单倍型分析后构建4个单倍型区块,并鉴定出BTG抗增殖因子1 (BTG anti-proliferation factor 1, *BTGI*)、岩藻糖基转移酶1 (H血型) (fucosyltransferase 1 [H blood group], *FUT1*)、岩藻糖基转移酶2(H血型) (fucosyltransferase 2 [H blood group], *FUT2*)、上皮钠通道1 γ 亚基 (sodium channel epithelial 1 subunit gamma, *SCNN1G*)、Cbl原癌基因B (Cbl proto-oncogene B, *CBLB*)等候选基因,这些基因通过调控子宫内膜修复与发情周期影响配种效率,为缩短繁殖间隔提供了精准遗传靶点(陈信佑等, 2023)。王源等(2023)以5 701头大白猪为研究对象,系统收集繁殖性状表型数据,包括母猪窝产活仔数,同时兼顾大白猪繁殖性状研究常规测定指标,完善表型记录体系,采用GeneSeek GGP 80K芯片对试验群体进行基因分型及全基因组关联分析,成功检测到12号染色体上的rs81399457位点。该位点的C等位基因可使母猪平均每窝产活仔数增加0.8头,该研究通过精准匹配基因型与繁殖表型,明确了大白猪产仔数及仔猪断奶重相关的关键遗传位点。齐丽娜等(2024)选取103头沙乌头猪母猪,利用50K SNPs芯片进行DNA分型,质控后保留44 739个SNPs用于GWAS分析,同步收集窝产活仔数、出生窝重、断奶窝重等核心繁殖性状表型数据,结合群体亲缘关系分析,功能注释推测细胞因子信号转导抑制因子2 (suppressor of cytokine signaling 2, *SOCS2*)和醌型二氢蝶啶还原酶 (quinoid dihydropteridine reductase, *QDPR*)为改善沙乌头猪繁殖性能的关键基因。Lan等(2023)使用GeneSeek Porcine 50K SNPs芯片对190头沙子岭猪进行了基因分型,获得41 857个高质量SNPs,鉴定出31个与繁殖性状相关的显著SNPs,其中包含18个注释候选基因。刘燕玲等(2024)基于靶向捕获测序技术,利用猪50K液相芯

片对大白猪开展研究,对比单SNPs与单倍型两种基因组育种值估计方法,结果显示基于单倍型的分析方法准确性显著优于单个SNPs分析,其中靶向block划分法的预测效果最佳,为基因组选择技术的优化升级提供了高效方案。藏麻猪为甘肃甘南原始藏系地方猪种,张丰霞等(2024)以140头藏麻母猪为研究样本,利用50K液相SNPs芯片进行基因分型,结合广义线性模型 (generalized linear model, GLM) 与混合线性模型 (mixed linear model, MLM) 开展GWAS分析,共检出14个与总产仔数、1个与产活仔数显著关联的SNPs位点,并鉴定出CCHC型锌指蛋白24 (zinc finger CCHC-type containing 24, *ZCCHC24*)等3个核心候选基因,为藏麻猪专用繁殖性状检测芯片的开发及高繁核心种群的精准选育奠定了基础。繁殖性状产业化改良面临的重要困难是,多数产仔和仔猪存活性状的遗传力较低,且窝产仔数、仔猪存活率和平均出生重等育种目标之间可能存在拮抗性遗传关系,因此需要采用兼顾产仔数、仔猪活力和存活率的多性状平衡选择策略(Knap et al., 2023; Nguyen et al., 2021; Ogawa et al., 2022; Putz et al., 2015)。Boonkum等(2025)基于4 465头母猪的9 969窝记录发现,窝产仔数及窝内出生重整齐度相关性均表现为低遗传力,增加窝产仔数还可能伴随仔猪平均出生重和整齐度下降,因而繁殖育种不宜仅以总产仔数为单一目标。窝内出生重整齐度本身具有可选择的遗传变异,Sell-Kubiak等(2015)的预测结果显示,通过针对该性状进行选择,仔猪出生重的窝内标准差在一个世代中具有降低约10%的潜力,说明将整齐度纳入综合育种目标具有数量遗传学依据。在参考群建设方面,两条母系猪群的研究表明,群体内预测通常需要约3 000~6 000头参考个体才能使多数母系性状获得较高预测准确性,而将参考群扩大至约30 000头仍可进一步提高总产仔数和死胎数的预测准确性;跨品系参考个体的贡献则明显低于同品系个体(Kjetsa et al., 2024)。因此,未来繁殖芯片应用应重点建设持续更新的母系品系内参考群,并将产活仔数、死胎数、仔猪出生重及窝内整齐度纳入多性状综合评价,而不是依赖少数繁殖候选基因进行选择。

3.4 基因芯片在猪抗逆育种中的应用

猪的抗逆性指对不良环境的抵抗能力,这既是

未来猪育种计划的理想目标,也是猪适应复杂养殖环境、降低疫病和极端环境的核心保障,这类性状遗传力低、表型测定难度大,传统选育进展缓慢(Harlizius et al., 2020)。随着对猪免疫调控及环境适应相关基因挖掘的深入,SNP芯片凭借高通量、精准化优势,实现了从单基因靶向检测到全基因组精准选育的跨越(苗娜等, 2025)。晁哲等(2015)采用PCR-RFLP对120头五指山猪进行检测,结果显示FUT1基因A+307G位点均为仔猪腹泻易感型GG基因型,表明该群体缺乏相应抗性位点基因。Illumina PorcineSNP60 v2为猪群体拷贝数变异(copy number variation, CNV)检测提供核心工具,助力解析群体遗传结构(Kim et al., 2025);蒋征(2014)克隆糖皮质激素受体(glucocorticoid receptor, GR)基因启动子,探究其在脂多糖(lipopolysaccharide, LPS)处理下的转录调控机制,为应激相关基因功能解析提供基础;Dong等(2021)通过SNPs分型发现,CD163分子、唾液酸结合免疫球蛋白样凝集素1(编码蛋白又称CD169)、G蛋白信号调节因子16(regulator of G protein signaling 16, RGS16)基因的自然多态性与仔猪对猪蓝耳病毒(Porcine reproductive and respiratory syndrome virus, PRRSVs)单独感染及PRRSVs/猪圆环病毒2b亚型(Porcine circovirus type 2b, PCV2b)共感染的抗性显著关联,且部分位点与鸟苷酸结合蛋白(guanylate binding protein 5, GBP5)基因存在遗传互作,说明候选基因变异可能影响病毒载量、增重等感染反应性状。陶璇等(2022)在地方猪研究中,采用“中芯一号”SNP芯片,对四川8个地方猪种共562头健康种猪进行基因分型,分析群体遗传结构与重要经济性性状关联位点,揭示丫杈猪、乌金猪等群体遗传分化显著但核心经济性性状关联位点保守的特征。在海南地方猪抗逆适应性研究中,冯雪燕等(2022)采用SNP芯片对五指山猪、临高猪等4个海南地方猪种及参考群体共300余头猪进行全基因组选择信号分析,定位受选择区域并注释到鸟苷酸结合蛋白5(guanylate binding protein 5, PLIN1)、肝脂酶(lipase C, hepatic type, LIPC)等脂质代谢相关候选基因,这些基因通过调控能量代谢助力其适应热带环境,为解析猪抗热机制及后续抗热育种提供潜在靶点。辛文水等(2024)以海南地方猪为研究对象,采用50K SNP芯片分型技术,经DNA提取、SNP分型及质控后,以相关杂交猪和巴马香猪为参考群体,进行群

体结构、血缘渗入及选择信号检测等分析,选择信号分析筛选出556个显著SNPs位点,注释得到的126个候选基因主要富集在脂质合成与代谢等抗逆相关通路,发现海南地方猪具备优良抗逆性,能适应热带环境;袁瀚豪等(2025)采用GGP 50K SNP芯片,对湘西黑猪、宁乡猪、黔邵花猪、大围子猪共2676头湖南地方猪的血样进行基因分型,经质控和基因组品种构成(genomic breed composition, GBC)筛选纯种个体后,群体遗传和选择信号分析发现了部分与环境适应、免疫和能量代谢相关的候选区域,为解析地方猪潜在抗逆性遗传基础提供了线索。纯种候选猪通常饲养于高生物安全环境,其疾病韧性难以充分表达,而商品杂交猪所处的病原和管理压力更加复杂(Madad et al., 2026)。Madad等(2026)利用5个纯种群体27880头公猪的日采食数据构建韧性指标后发现,这些指标与1818头自然多病原挑战杂交猪的死亡率、治疗率和生长表现之间的遗传相关变异较大且平均接近于零,因此目前尚不能直接使用核心场常规采食波动指标选择商品猪疾病韧性。在自然多病原挑战条件下,日采食量及采食时间的波动可以形成可遗传的韧性表型,其遗传力约为0.15~0.26,并与死亡率和治疗率呈0.37~0.85的遗传相关,说明疾病压力环境下的纵向生产记录能够为抗病育种提供比单次健康检查更直接的表型依据(Putz et al., 2019)。饮水量、饮水时间、采食量和采食行为等自动监测性状也表现出中等至较高遗传力,部分性状与生长速度及临床疾病指标存在遗传联系,可作为疾病韧性评价的候选指示性状(Cheng et al., 2021)。此外,健康仔猪血浆中的部分代谢物具有中高遗传力,并与后续疾病挑战中的治疗次数、死亡率和生产性能存在遗传相关,但其作为育种指标的稳定性仍需扩大群体进行验证;因此,未来抗病芯片育种应加强商品场健康记录和自然疾病挑战群建设,将死亡、治疗、增重、采食和饮水行为等表型与芯片数据联合分析,并将代谢物等分子指标定位为需要进一步验证的辅助信息(Dervishi et al., 2021)。

4 总结与展望

在技术层面,我国猪育种芯片已由依赖进口逐步转向自主研发。早期,国内猪基因组育种主要依赖国外商业固相SNP芯片,受价格较高、位点设计

针对性不足以及核心技术掌握有限等因素制约,芯片研发与应用的自主性相对不足目前。“中芯一号”“陕芯一号”等国产芯片实现关键技术自主可控,其中国产芯片的研发有助于减少对进口平台的依赖,并在规模化检测、位点定制和服务成本方面提供更多选择;“陕芯一号”为50K液相育种芯片,具备自主知识产权,可显著提升检测效率并降低应用成本。“皖芯1号”为安徽地方猪种优化,提高SNP位点捕获效率,且依托基因型填充技术可降低中小猪场检测成本,填补了国内中部地区地方猪专用育种芯片空白(钟经文, 2025)。总体上,SNP芯片具有分型效率高、检测流程标准化和适合大规模群体应用等优势,但其检测范围取决于预先设计的探针和位点集合,因而对未纳入芯片设计的低频变异、品种特异性变异以及插入、缺失、重复和倒位等结构变异的识别能力有限(Li et al., 2017)。SVs可通过改变编码序列、基因剂量或基因调控元件影响基因表达。已有猪基因组研究发现部分SVs与繁殖性状、肉质及肌肉发育相关(Du et al., 2021; Li et al., 2024)。因此,SVs并非对SNP芯片的替代,而是对现有SNP标记体系的重要补充;未来可利用全基因组测序和长读长测序发现潜在功能SVs,并将经独立群体和功能试验验证的SVs纳入品种特异性或性状特异性分型面板,从而提高猪复杂经济性状遗传解析和基因组育种的完整性(Li et al., 2017; Li et al., 2024)。基因组信息可支持候选猪的早期遗传评估,使育种场能够在部分生产性状尚未完全表达前开展预选,从而减少低潜力个体的后续饲养和性能测定投入;在抗病育种领域,集成抗腹泻、抗蓝耳病等与抗病相关候选位点和宿主反应性状研究的积累,未来可将经过独立群体和功能验证的候选变异纳入性状特异性分型面板,为抗病抗逆性状的基因组评估提供补充信息(陈泽芳, 赵爱莉, 2017);同时,低成本国产芯片的推广应用,让中小养殖场得以便捷开展科学选种,加速了行业整体育种水平的升级,为我国猪产业核心竞争力的提升提供了核心支撑。

当前,基因芯片在猪育种中的规模化应用仍受到成本、群体适配性和数据整合等因素制约。首先,基因分型成本及参考群建设投入仍是制约基因组选择推广的重要因素,中小规模猪场尤其难以积累充足的基因型—表型参考数据,我国多数种猪场尚缺乏系统化的基因组选择实施方案(Grossi et

al., 2018; Wei et al., 2022; Yin et al., 2024);其次,部分商业芯片主要依据欧美猪种等发现群体设计,在中国地方猪种中可能存在SNP发现偏倚,影响其对地方猪遗传变异的代表性;同时,基因组育种值的预测准确性还受参考群规模、群体间遗传关系及预测模型等因素影响(周隽等, 2022; Chen et al., 2018);此外,技术整合协同性欠缺,体现为三个层面,一是商用芯片多仅提供原始基因型数据,缺乏配套的优化基因组预测模型,导致遗传评估准确性受限(Chen et al., 2025; Wang et al., 2025),二是芯片与自动化表型鉴定设备间无标准化数据接口,依赖人工录入易引发数据误差,延长育种周期(Baldin et al., 2025; Billah et al., 2025),三是与基因编辑等前沿技术的协同性有限,难以形成“检测-筛选-培育”的闭环育种系统(Chen et al., 2025; Ju et al., 2025; Mueller, Van Eenennaam, 2022)。

未来,随着基因组学、大数据技术与人工智能算法的深度融合,基因芯片将成为猪种业创新的重要技术平台。一方面,应强化基因芯片与基因组选择模型、高通量表型鉴定设备、分子设计育种工具的协同整合,打通多维度数据接口,构建从基因型检测、表型验证到品种选育的闭环技术体系(周光亮等, 2024);另一方面,应加快构建标准化共享基因型数据库、规模化参考群体与专业化分析平台,搭建用户友好型在线分析系统。此外,低深度全基因组重测序(low-coverage whole-genome sequencing, LCWGS)结合基因型填充,可通过减少单个个体的测序数据量,在获得全基因组高密度变异信息的同时,有望进一步降低大规模群体的基因分型成本,成为固定SNP芯片的有效补充,从而大幅提升基因芯片技术在中小规模猪场的可及性。随着芯片技术的迭代,基因芯片将继续提高猪育种效率,并支持自主可控种业“中国芯”建设、猪产业生物安全屏障和我国猪种业全球市场竞争力提升,为我国养猪业的高质量可持续发展奠定坚实的遗传基础。

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