Agrigenomics microarray publication compendium

Contents

Introduction

Agrigenomics is crucial to addressing the rising problems of climate change, food insecurity and growing population. The publications cited here highlight how Applied Biosystem™ Axiom™ genotyping solution is contributing to the advancement of agrigenomics by providing the required tools to the breeders and researchers to help them carry out efficient marker-assisted breeding, genomic selection, parentagem and characterization of genetically-modified organisms.

Keep reading to understand how genomics is paving the way for improved agriculture outcomes by promoting resilience, preservation, and productivity among livestock, crops, and aquaculture.

Aquaculture

1. Genotyping of two mediterranean trout populations in central-southern Italy for conservation purposes using a rainbow-trout-derived SNP array

Mediterranean trout, once a significant economic contributor is now one of the most threatened freshwater species due to the recent climatic changes. Understanding the genetic diversity of this population can help direct necessary breeding strategies to promote their conservation. The Applied Biosystems™ Axiom™ Rainbow Trout 57K array was used to genotype 288 trout specimens collected from the Volturno and Biferno rivers of Italy which allowed the researchers to perform the first genetic analysis of Mediterranean trout populations from this region. The identification of 900 polymorphic SNPs enabled the differentiation of native and non-native trout populations which can help breeders select the adult population for producing genetically pure juvenile trout and conserve the specie.

Basic animal or crop
Trout

Breeding goal
Perform the first genetic analysis of Midterranenean trout to conserve the threatened species.

Array used
Applied Biosystems™ Axiom™ Rainbow Trout 57K array

Link
https://www.mdpi.com/2076-2615/11/6/1803

Keywords
Trout breeding, SNP analysis, genetic diversity

Citation
Palombo V, De Zio E, Salvatore G, et al. (2021) Genotyping of Two Mediterranean Trout Populations in Central-Southern Italy for Conservation Purposes Using a Rainbow-Trout-Derived SNP Array. *Animals* 11(6):1803. DOI:10.3390/ani11061803

2. Accuracy of genotype imputation of a low-density SNP array for the Amazon fish *Colossoma macropomum*

In South America, the tambaqui fish is the primary target for aquaculture, yet costs can be prohibitive for high-density single nucleotide polymorphism (SNP) arrays that may be pivotal for aquaculture breeding. This study reports the development of the Applied Biosystems™ Axiom™ SerraSNP array, which is based on a low-density SNP array followed by genotype imputation to higher densities. Population analyses proved this array to be an efficient tool for genetic characterization, and potentially a valuable, lower-cost resource for genetic improvement programs targeting this Amazon native species.

Basic animal or crop
Fish

Breeding goal
A cost-effective solution for genetic improvement programs targeting this Amazon native species.

Array used
Applied Biosystems™ Axiom™ SerraSNP Array

Link
https://www.scielo.br/j/gmb/a/VhXRVkTJwbj3XjVXj7hvBqH/?lang=en

Keywords
Cost-effective genotyping, aquaculture breeding, SNP array imputation

Citation
Agudelo JFG, Mastrochirico-Filho VA, Garcia BF, et al. (2024) Accuracy of genotype imputation of a low-density SNP array for the Amazon fish Colossoma macropomum. *Genet Mol Biol* 47(3):e20230364.

3. Genetic architecture and genomic selection of fatty acid composition predicted by Raman spectroscopy in rainbow trout

The increased use of plant-based feed in the aquaculture industry is decreasing the amount of long-chain omega-3 polyunsaturated fatty acid (n-3 LC-PUFAs) in rainbow trout, which is important for their growth, reproduction, and immunity. To understand the genetic architecture of n-3 LC-PUFA's composition in rainbow trout, researchers used the Applied Biosystems™ Axiom™ Trout Genotyping 57K SNP array to analyze over 29,000 SNPs in 1382 rainbow trout. The GWAS identified 10 QTLs and 13 putative QTLs suggesting fatty acid proportions in rainbow trout are polygenic but exhibit moderate heritability indicating chances of improvement through genomic selection.

Basic animal or crop
Trout

Breeding goal
Enhance the capacity of rainbow trout to retain and synthesize long-chain omega-3 polyunsaturated fatty acids to increase their nutritional value.

Array used
Applied Biosystems™ Axiom™ Trout 57 K SNP Genotyping Array

Link
https://link.springer.com/article/10.1186/s12864-021-08062-7

Keywords
Genome-wide study, trout, heritability estimates

Citation
Blay C, Haffray P, D'Ambrosio J, et al. (2021) Genetic architecture and genomic selection of fatty acid composition predicted by Raman spectroscopy in rainbow trout. *BMC Genomics* 22:788. DOI: 10.1186/s12864-021-08062-7

4. Genomic selection and genome-wide association study for feed-efficiency traits in a farmed nile tilapia (*Oreochromis niloticus*) population

Nile tilapia is the third most globally farmed species with feed production representing the major cost for raising them. Due to the complexity of feed intake measurement, Nile tilapia's feed efficiency trait has been limitedly studied. The Applied Biosystems™ Axiom™ Nile Tilapia 65 K SNP array used in this study allowed researchers to analyze SNP data, conduct GWAS, and assess the performance of genomic selection models on fish sourced from Genetically Improved Farmed Tilapia (GIFT), Malaysia. It was found that feed efficiency is a polygenic trait and has significant heritability, indicating that genomic selection is a more practical and cost-effective approach to improve desirable feed efficiency traits.

Basic animal or crop
Tilapia

Breeding goal
Improve feed efficiency in Nile tilapia to increase growth performance and reduce the production cost of the feed.

Array used
Applied Biosystems™ Axiom™ Nile Tilapia 65 K SNP Array

Link
https://www.sciencedirect.com/science/article/pii/S235251342400228X

Keywords
Genome-wide study, genomic selection models, nile tilapia

Citation
Barría A, Benzie JA, Houston RD, et al. (2021) Genomic Selection and Genome-wide Association Study for Feed-Efficiency Traits in a Farmed Nile Tilapia (Oreochromis niloticus) Population. *Frontiers in Genetics* 12:737906. DOI: 10.3389/fgene.2021.737906

5. Validation of a QTL associated with resistance to *Vibrio anguillarum* in rainbow trout (*Oncorhynchus mykiss*)

Vibro anguillarum is a major disease affecting rainbow trout of Dutch water. The QTL on chromosome 21 has been found to be associated with vibro resistance but hasn't been analytically tested. To verify this, researchers used the Applied Biosystems™ Axiom™ Trout 57K array and genotyped the rainbow trout spawners for the presence of SNP AX-89,945,921, located on chromosome 21 which allowed them to select homozygous male fish carrying the resistance-associated SNP for breeding. The offspring from this male fish were found to have a higher frequency of the resistance allele exhibiting lower (50%) morbidity rates, demonstrating the practical application of marker-assisted breeding for increased disease resistance in rainbow trout aquaculture.

Basic animal or crop
Trout

Breeding goal
Marker-assisted selective breeding of rainbow trout populations resistant to vibriosis disease (caused by bacteria, *Vibro anguillarum*).

Array used
Applied Biosystems™ Axiom™ Trout 57K Array

Link
https://link.springer.com/article/10.1186/s13028-023-00692-z

Keywords
SNP selection, homozygous male, marker associated selective breeding

Citation
Karami AM, Marana MH, Mathiessen H, et al. (2023) Validation of a QTL associated with resistance to Vibrio anguillarum in rainbow trout (Oncorhynchus mykiss). *Acta Vet Scand* 65:28. DOI: 10.1186/s13028-023-00692-z

6. Use of whole-genome sequence data for fine mapping and genomic prediction of sea louse resistance in Atlantic salmon

Sea lice infestation in Atlantic Salmon causes significant economic losses to the aquaculture with the pathogen becoming resistant to the available medications with every passing day. Finding the genetic variations associated with resistance to the infection can help breeders develop Salmon species resistant to the parasite. Researchers used the Applied Biosystems™ Axiom™ NOFSAL03 50K array to perform a genome-wide association study on 3,185 genotyped salmon and provide imputation data for whole-genome sequencing. The genetic analysis from both methods demonstrated that resistance to sea lice is a polygenic trait with moderate heritability. It was also concluded that genomic predictions using the medium-density SNP genotyping array were even better than those obtained from whole-genome sequence (WGS).

Basic animal or crop
Salmon

Breeding goal
Use selective breeding to improve the resistance of Atlantic salmon to the sea lice infestation.

Array used
Applied Biosystems™ Axiom™ NOFSAL03 50K array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2024.1381333/

Keywords
Fish genotyping, GWAS analysis, medium-density SNP array

Citation
Onabanjo O, Meuwissen T, Aslam ML, et al. (2024) Use of whole-genome sequence data for fine mapping and genomic prediction of sea louse resistance in Atlantic salmon. *Frontiers in Genetics* 15:1381333. DOI: 10.3389/fgene.2024.1381333

7. Genome-wide association mapping and accuracy of predictions for amoebic gill disease in Atlantic salmon (Salmo salar)

Amoebic gills disease (AGD) is a serious threat to Tasmian Atlantic Salmon causing high morbidity in infected fish. Identifying the genetic basis of AGD resistance can help breed species with improved resilience. The Applied Biosystems™ Axiom™ NOFSAL2 57 K array was used to perform GWAS, identifying five significant SNPs three of which were found in correlation with genes involved in immunity and cellular adhesion. The study also demonstrated that genomic selection can improve prediction accuracy for AGD resistance by 9–17% and can be used for breeding resistant and sustainable Atlantic salmon.

Basic animal or crop
Salmon

Breeding goal
Identification of genomic regions associated with resistance to Amoebic gill disease (that causes respiratory distress) in Tasmanian salmons.

Array used
Applied Biosystems™ Axiom™ NOFSAL2 57 K Array

Link
https://www.nature.com/articles/s41598-020-63423-8

Keywords
Fish genotyping, quantitative trait loci analysis

Citation
Aslam ML, Boison SA, Lillehammer M, et al. (2020) Genome-wide association mapping and accuracy of predictions for amoebic gill disease in Atlantic salmon (Salmo salar). *Scientific Reports* 10(1):1–9. DOI: 10.1038/s41598-020-63423-8

8. Genome-wide association analysis of the resistance to infectious hematopoietic necrosis virus in two rainbow trout aquaculture lines confirms oligogenic architecture with several moderate effect quantitative trait loci

Infectious hematopoietic necrosis (caused by the IHNV virus) is a rainbow trout endemic in western North America increasing fish mortality. Examining the genetic architecture of the IHNV resistance trait can enable marker-assisted selection for producing IHNV resistance populations. Two distinct May and November commercial rainbow trout lines, naive to IHNV exposure, were genotyped using Applied Biosystems™ Axiom™ Rainbow Trout 65K array to obtain comprehensive SNP data. GWAS analysis helped identify 5 QTLs shared across the two lines, suggesting that this genomic region can play a role in IHNV resistance even in unrelated lines. It was concluded that IHNV resistance is a polygenic trait so genomic selection is an effective breeding strategy for improving trout species for this trait.

Basic animal or crop
Trout

Breeding goal
Improving North American trout's resistance to infectious hematopoietic necrosis which is one of the major causes of increased mortality.

Array used
Applied Biosystems™ Axiom™ Raibow Trout 65K Array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2024.1394656/full

Keywords
IHNV infection, quantitative trait loci analysis, GWAS

Citation
Palti Y, Vallejo RL, Purcell MK, et al. (2024) Genome-wide association analysis of the resistance to infectious hematopoietic necrosis virus in two rainbow trout aquaculture lines confirms oligogenic architecture with several moderate effect quantitative trait loci. *Frontiers in Genetics* 15:1394656. DOI: 10.3389/fgene.2024.1394656

9. Genomic evidence of recent European introgression into North American farmed and wild Atlantic salmon

Atlantic salmon is the major source of food in North America but the introgression of European alleles in them is a concern making their adaptation to the environment difficult. Previous studies exploring the extent of the introgression were performed using microsatellite markers but they have limited resolution. Using the Applied Biosystems™ Axiom™ Salmon Genotyping 220K array, scientists genotyped 6607 individuals to quantify the population structure of wild, farmed, and escaped farmed salmon. The results showed that 17% of American farmed salmon had more than 10% European alleles, two of the escaped farmed had 100% European alleles and wild juvenile Salmon found near aquaculture sites had a higher admixture.

Basic animal or crop
Salmon

Breeding goal
Provide a high-resolution method to identify the extent of European introgression in North American salmon.

Array used
Applied Biosystems™ Axiom™ Salmon Genotyping 220K array

Link
https://onlinelibrary.wiley.com/doi/full/10.1111/eva.13454

Keywords
Allele introgression, heritability, salmon genotyping

Citation
Bradbury IR, Lehnert SJ, Kess T, et al. (2022) Genomic evidence of recent European introgression into North American farmed and wild Atlantic salmon. *Evolutionary Applications* 15(9):1436-1448. DOI:10.1111/eva.13454

10. Estimates of autozygosity through runs of homozygosity in farmed coho salmon

Coho salmon farming is a significant industry in Chile. Understanding the genetic diversity and inbreeding levels of these populations is crucial for ensuring their long-term health, productivity, and sustainability. Researchers used a 200K Applied Biosystems™ Axiom™ Axiom myDesign Coho Salmon array to analyze the ROH (runs of homozygosity) and compare estimated inbreeding coefficients of the Coho Salmon populations. Comparison of inbreeding co-efficient from ROH and pedigree data revealed that the ROH-based method provides more accurate estimates of inbreeding coefficients compared to the pedigree-based method proving to be a valuable tool for effective management of genetic diversity.

Basic animal or crop
Coho Salmon

Breeding goal
Cost-effective yet accurate method for estimating inbreeding coefficients (a trait important for maintaining genetic diversity) in Coho salmon.

Array used
200K Applied Biosystems™ Axiom™ Axiom myDesign Coho Salmon Array

Link
https://www.mdpi.com/2073-4425/11/5/490

Keywords
Admixture, inbreeding, run of homozygosity

Citation
Yoshida GM, Cáceres P, Koop BF, et al. (2020) Estimates of Autozygosity Through Runs of Homozygosity in Farmed Coho Salmon. *Genes* 11(5):490. DOI: 10.3390/genes11050490

11. Population and clonal structure of *Acropora cf. hyacinthus* to inform coral restoration practices on the Great Barrier Reef

Acropora cf. hyacinthus is a key coral species for restoration efforts on the Great Barrier Reef. Assessing colonies' genotypic and genetic diversity is critical to avoid founder, inbreeding, or outbreeding effects. The Applied Biosystems™ Axiom™ AcropSNP allowed comprehensive SNP analysis, allowing researchers to differentiate between closely related Acropora species and identify the clonal colonies. It was also found that the samples had a high genetic diversity, but a low genetic differentiation between A. cf. hyacinthus populations suggesting a lack of population structure. Researchers were also able to identify species accurately.

Basic animal or crop
Coral

Breeding goal
To select genetically distinct *Acropora cf. hyacinthus* colonies for propagation and outplanting that could enhance the resilience of restored coral populations.

Array used
Applied Biosystems™ Axiom™ AcropSNP Array

Link
https://link.springer.com/article/10.1007/s00338-024-02520-w

Keywords
Colony selection, restoration

Citation
Howlett L, Camp EF, Locatelli NS, et al. (2024) Population and clonal structure of *Acropora cf. hyacinthus* to inform coral restoration practices on the Great Barrier Reef. *Coral Reefs* 43:1023–1035. DOI: 10.1007/s00338-024-02520-w

12. GRAMMAR-Lambda delivers efficient understanding of the genetic basis for head size in catfish

The head size in catfish is an important trait in aquaculture affecting the fillet yield and aesthetic value. There is a lack of understanding of genetic mechanisms controlling the head size. Researchers used the Applied Biosystems™ Axiom™ Catfish 250K SNP array to conduct GRAMMAR-Lambda driven GWAS on 556 genotyped catfish to identify genetic markers relating to the head size traits. The genetic analysis resulted in the Identification of quantitative trait nucleotides (QTNs) and candidate genes that influence head size, particularly those involved in bone development which can help direct breeding programs towards improving catfish populations.

Basic animal or crop
Catfish

Breeding goal
Identify the candidate genes relating to the head size in catfish to improve the fillet yield and aesthetic value.

Array used
Applied Biosystems™ Axiom™ Catfish 250K SNP array

Link
https://pmc.ncbi.nlm.nih.gov/articles/PMC11760490

Keywords
GWAS, catfish breeding, quantitative trait nucleotide

Citation
Zhao Y, Gao J, Feng H, et al. (2025) GRAMMAR-Lambda Delivers Efficient Understanding of the Genetic Basis for Head Size in Catfish. *Biology* 14(1):63. DOI:10.3390/biology14010063

13. Genomic selection for growth traits in pacific oyster (*Crassostrea gigas*): Potential of low-density marker panels for breeding value prediction

The traditional pedigree method to select candidate genes for desirable traits in Pacific Oysters is time-consuming and expensive. To determine the capabilities of genomic prediction as a cost-effective way for estimating the breeding values for growth traits, the Applied Biosystems™ Axiom™ Oyster Genotyping array was used to genotype 820 oysters. The analysis of the genetic architecture of growth-related traits, such as, (shell height (SH), shell length (SL), and wet weight (WW) demonstrated that growth is a polygenic trait with moderate heritability. The genomic prediction outperformed pedigree methods that can be used to improve complex traits through marker-assisted oyster breeding.

Basic animal or crop
Oyster

Breeding goal
Demonstrate genomic prediction as a cost-effective method for improving the complex traits in Pacific oysters through marker-assisted breeding.

Array used
Applied Biosystems™ Axiom™ Oyster Genotyping Array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2018.00391/full

Keywords
Oyster breeding, genomic selection, SNP array

Citation
Gutierrez AP, Matika O, Bean TP, et al. (2018) Genomic Selection for Growth Traits in Pacific Oyster (Crassostrea gigas): Potential of Low-Density Marker Panels for Breeding Value Prediction. *Frontiers in Genetics* 9:391. DOI:10.3389/fgene.2018.00391

14. Signatures of selection for bonamiosis resistance in European flat oyster (*Ostrea edulis*): New genomic tools for breeding programs and management of natural resources

European flat oysters (Ostrea edulis) are an important seafood source but the long-term outbreak of Bonamia ostreae has severely affected their production. Investigating the genetics of the resistance to this disorder can help in sustainable aquaculture practices. The 95 oyster samples collected from six different beds were genotyped using the Applied Biosystems™ Axiom™ Oyster Genotyping array for Pacific and European oysters. The high-density testing resulted in the identification of 21 SNP associated with the immune function in oysters and a major putative QTL associated with Bonamia ostreae resistance providing valuable markers for improving the selective breeding of flat oysters towards parasite resistance.

Basic animal or crop
Oyster

Breeding goal
Improve selective breeding for producing oysters populations that are resistant to bonamiosis, a disorder that severely increases the mortality of European flat oysters.

Array used
Applied Biosystems™ Axiom™ Oyster Genotyping Array

Link
https://onlinelibrary.wiley.com/doi/full/10.1111/eva.12832

Keywords
QTL indentification, oyster genotyping, linkage disequilibrium

Citation
Vera M, Pardo BG, Cao A, et al. (2019) Signatures of selection for bonamiosis resistance in European flat oyster (Ostrea edulis): New genomic tools for breeding programs and management of natural resources. *Evolutionary Applications* 12(9):1781–1796. DOI: 10.1111/eva.12832

15. Consequences of domestication in eastern oyster: Insights from whole genomic analyses

The consistent hatchery practices can impose similar selection pressure on oysters which can decline their genetic diversity. The genetic effects of parallel domestication on bivalve organisms such as Eastern oysters have not been extensively studied. So researchers used the Applied Biosystems™ Axiom™ 566K Bi-allelic Oyster Array to genotype 960 oyster samples, including both wild and selected lines. The population analysis demonstrated reduced genetic diversity, increased inbreeding, and LD alterations in selectively bred oysters. 1174 outlier SNPs associated with cytoskeletal and muscular development were also identified, impacting the oyster adaptation to changing environments, and providing a foundation for future breeding programs.

Basic animal or crop
Oyster

Breeding goal
Select oysters with commercially valuable traits and direct selection of genetically diverse populations to minimize inbreeding.

Array used
Applied Biosystems™ Axiom™ 566K Bi-allelic Oyster Array

Link
https://onlinelibrary.wiley.com/doi/full/10.1111/eva.13710

Keywords
Runs of homozygosity, inbreeding in oyster, parallel domestication

Citation
Zhao H, Guo X, Wang W, et al. (2024) Consequences of domestication in eastern oyster: Insights from whole genomic analyses. *Evolutionary Applications* 17(6):e13710. DOI: 10.1111/eva.13710

16. Genetic diversity and population structure of farmed and wild Nile tilapia (*Oreochromis niloticus*) in Uganda: The potential for aquaculture selection and breeding programs

Nile tilapia holds significant importance in Uganda's economy but the genetic makeup of native Uganda Nile tilapia populations is poorly understood and there is a lack of improved strains available for aquaculture. The Applied Biosystems™ Axiom™ OreNil50 array was used to genotype 382 Nile tilapia samples from wild and farmed populations, to analyze the genetic structure, diversity, and admixture. While there was a clear genetic substructure between the wild Nile tilapia population, the SNP analysis also identified a genomic region on chromosome 5 associated with growth and immunity that can be targeted in marker-assisted breeding to develop resilient strains.

Basic animal or crop
Nile tilapia

Breeding goal
Explore the genetic diversity of Uganda's Nile tilapia to identify potential regions for selective breeding of improved fish strains.

Array used
Applied Biosystems™ Axiom™ OreNil50 array

Link
https://www.sciencedirect.com/science/article/pii/S0888754324000016

Keywords
Runs of homozygosity, Nile tilapia genetic diversity, SNP analysis

Citation
Robledo D, Ogwang J, Byakora E, et al. (2023) Genetic diversity and population structure of farmed and wild Nile tilapia (Oreochromis niloticus) in Uganda: The potential for aquaculture selection and breeding programs. *Genomics* 116(1):110781. DOI:10.1016/j.ygeno.2024.110781

Companion animal

1. Heritability and genome-wide association study of dog behavioral phenotypes in a commercial breeding cohort

The genetic architecture of behavior traits of dogs from commercial breeding facilities has not been explored yet. The Applied Biosystems™ Axiom™ CanineHD SNP array was used to genotype 615 dogs from these facilities to calculate inbreeding coefficients, perform genome-wide association studies, and calculate genetic risk scores for social fear (SF), non-social fear (NSF), and startle response (SR) traits. It was found that dogs from commercial breeding facilities had lower inbreeding co-efficient than those from other breeding sources. SF & NSF had moderate heritability whereas startle response possesses lower heritability indicating that these traits can be targeted for improving the overall behavior of the dogs and their relationship with humans.

Basic animal or crop
Dog

Breeding goal
To improve the desirable behavior traits in dogs through selective breeding.

Array used
Applied Biosystems™ Axiom™ CanineHD SNP array

Link
https://www.mdpi.com/2073-4425/15/12/1611

Keywords
Heritability estimate, inbreeding co-efficient, genome-wide association

Citation
Bhowmik N, Cook SR, Croney C, et al. (2024) Heritability and Genome-Wide Association Study of Dog Behavioral Phenotypes in a Commercial Breeding Cohort. *Genes* 15(12):1611. DOI:10.3390/genes15121611

2. Genome-wide variant analyses reveal new patterns of admixture and population structure in Australian dingoes

Previously reported population structure analysis and admixture patterns on Australian dingoes were reported using microsatellites that use a small number of markers and a geographically restricted genome. A genome-wide study was performed on Australian dingoes using Applied Biosystems™ Axiom™ Canine HD Genotyping array to understand the genomics more effectively. Results found five distinct dingo populations across Australia and lesser admixture patterns, revealing that Australian dingos are much purer than reported formerly. This indicates the need for change in conservation policies for dingoes.

Basic animal or crop
Dog

Breeding goal
Prevent introgression of alleles of domestic dogs into wild dingoes to maintain their distinct genetic lineage.

Array used
Applied Biosystems™ Axiom™ Canine HD Genotyping Array

Link
https://onlinelibrary.wiley.com/doi/full/10.1111/mec.16998

Keywords
GWAS analysis, genetic admiture

Citation
Cairns KM, Crowther MS, Parker HG, et al. (2023) Genome-wide variant analyses reveal new patterns of admixture and population structure in Australian dingoes. *Molecular Ecology* 32(15):4133-4150. DOI: 10.1111/mec.16998

3. Genetic inference of the mating system of free-ranging domestic dogs

Domestication has changed the social and reproductive traits of free-range dogs, including monogamy and extended parental care. Understanding the consequences of this shift is important for the genetic health and fitness of the population. The genomic analysis through Applied Biosystems™ Axiom™ Canine HD Genotyping Array allowed the investigation of kinship and reconstruction of pedigree lineage. It was concluded that FRDs exhibit a polygynandrous mating system, which has resulted in genetic diversity among the population. It's important to consider this diversity during breeding programs to avoid inbreeding.

Basic animal or crop

Dog

Breeding goal

Identify potential hybridization due to the polygynandrous mating system in free-range dogs (FRDs).

Array used

Applied Biosystems™ Axiom™ Canine HD Genotyping Array

Link

https://academic.oup.com/beheco/article/32/4/646/6208826

Keywords

Mating, dog pedigree

Citation

Natoli E, Bonanni R, Cafazzo S, et al. (2021) Genetic inference of the mating system of free-ranging domestic dogs. *Behavioral Ecology* 32(4):646-656. DOI: 10.1093/beheco/arab011

Livestock, poultry, and farm animals

1. Unravelling the genetic architecture of serum biochemical indicators in sheep

Despite their importance in livestock, the genetic mechanism underlying the biochemical indicators in Akkaraman sheep has not been explored yet. Using the Applied Biosystems™ Axiom™ Ovine 50 K SNP Genotyping array, researchers performed single-nucleotide polymorphism (SNP) on 422 genotyped lambs. The GWAS analysis allowed them to identify 23 SNP, 19 candidate genes, and 4 uncharacterized regions for the immune system, defense response, and cytoskeleton organization in sheep that can be used for developing targeted therapies and understanding disease pathophysiology.

Basic animal or crop
Sheep

Breeding goal
Understand the genetic basis of the serum biochemical markers in sheep so targeted interventions can be developed.

Array used
Applied Biosystems™ Axiom™ Ovine 50 K SNP array

Link
https://www.mdpi.com/2073-4425/15/8/990

Keywords
Serum biochemical markers, sheep genotyping, candidate genes

Citation
Kizilaslan M, Arzik Y, Behrem S, et al. (2024) Unravelling the Genetic Architecture of Serum Biochemical Indicators in Sheep. *Genes* 15(8):990. DOI:10.3390/genes15080990

2. Allelic and genotypic frequencies of SNP related to beef and carcass quality in Romosinuano cattle in Mexico

Romosinuano cattle are well adapted to high temperatures and humidity of tropical Mexico, but their meat is less tender than European cattle. There are currently no selection criteria for improving meat quality in these cattle. In this study, the Applied Biosystems™ Axiom™ BovMDv3 array was used to determine that several alleles associated with meat tenderness have similar genotypic frequencies in Romosinuano cattle as other breeds known for their meat tenderness. The authors conclude that marker-assisted selection may complement conventional selection methods to improve meat quality characteristics.

Basic animal or crop
Cattle

Breeding goal
Improve meat quality through marker-assisted selection.

Array used
Applied Biosystems™ Axiom™ BovMDv3 Array

Link
https://link.springer.com/article/10.1007/s11250-023-03643-y

Keywords
Marker-assisted selection, cattle genotyping, meat quality

Citation
Rocha RM, Ramírez-Valverde R, Núñez-Domínguez R, et al. (2023) Allelic and genotypic frequencies of SNP related to beef and carcass quality in Romosinuano cattle in Mexico. *Trop Anim Health Prod* 55:233. DOI: 10.1007/s11250-023-03643-y

3. Study of whole genome linkage disequilibrium patterns of Iranian water buffalo breeds using the Axiom Buffalo Genotyping 90K Array

The Iranian water buffalo breeds MAZ, AZI, and KHU hold prime importance because of their drought-resistance qualities. Understanding their genetic diversity is important to take informed measures for population genetics and retaining desirable traits. The Applied Biosystems™ Axiom™ Buffalo Genotyping 90K array, providing a large set of data (more than 52,000 SNPs), played a crucial role in understanding the linkage disequilibrium patterns and population size of these breeds. This eventually was important to understand the genetic relations between all three breeds, revealing AZI and KHU to be closer. The research finding also concluded that MAZ might be on the verge of extinction.

Basic animal or crop	**Breeding goal**	**Array used**
Buffalo	Understand genetic diversity in Iranian buffaloes to improve water resistance traits.	Applied Biosystems™ Axiom™ Buffalo 90K Genotyping Array
Link	**Keywords**	**Citation**
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0217687	Population, buffalo genotyping, genome-wide studies	Mokhber, Mahdi, Shahrbabak MM, Sadeghi M, et al. (2019) Study of Whole Genome Linkage Disequilibrium Patterns of Iranian Water Buffalo Breeds Using the Axiom Buffalo Genotyping 90K Array. *PLOS One* 14(5):e0217687. DOI: 10.1371/journal.pone.0217687

4. Inbreeding depression and runs of homozygosity islands in Asturiana de los Valles cattle breed after 30 years of selection

The Asturiana de los Valles cattle, a major meat source in Spain, has undergone selection for 30 years potentially causing inbreeding and affecting productive traits. Using the Applied Biosystems™ Axiom™ Bovine genotyping array to genotype 2693 cattle, researchers analyzed the inbreeding depression of reproductive and non-reproductive traits and compared the results with the pedigree method. The results from runs of homozygosity revealed a significant impact of the inbreeding on weaning weight and preweaning average daily gain. The identified 5 ROH islands containing candidate genes for growth development, intramuscular fat, body weight, and lipid metabolism can be targeted to reduce the effects of inbreeding.

Basic animal or crop	**Breeding goal**	**Array used**
Cattle	Reduce inbreeding and target the specific genetic regions to improve the productivity traits in the cattle.	Applied Biosystems™ Axiom™ Bovine genotyping array
Link	**Keywords**	**Citation**
https://onlinelibrary.wiley.com/doi/full/10.1111/jbg.12853	Runs of homozygosity, inbreeding depression, cattle genomic selection	Cortes O, Cañon J, Andrino S, et al. (2024) Inbreeding depression and runs of homozygosity islands in Asturiana de los Valles cattle breed after 30 years of selection. *Journal of Animal Breeding and Genetics* 141(4):440-452. DOI:10.1111/jbg.12853

5. Genome-wide analysis of milk production traits and selection signatures in serbian holstein-friesian cattle

Serbia has been relying on genetics from abroad to promote the breeding of Serbian Holstein-Friesian dairy cattle to enhance the quality of its milk. This research used the Applied Biosystems™ Axiom™ BovMDv3 array to perform SNP analysis on Holstein-Friesian natively and analyze the genetic traits that contribute to milk production. The gene identified in this research not only correlated with protein milk production in Serbian Holstein-Friesian cows but also aligns with the gene of American Holstein-Friesian.

Basic animal or crop	**Breeding goal**	**Array used**
Cattle	Improve the milk production traits in Serbian Holstein-Friesian dairy cattle.	Applied Biosystems™ Axiom™ BovMDv3 Array
Link	**Keywords**	**Citation**
https://www.mdpi.com/2076-2615/14/5/669	Milk production, milk protein, cattle genotyping	Ristanic M, Zorc M, Glavinic U, et al. (2023) Genome-wide analysis of milk production traits and selection signatures in Serbian Holstein-Friesian cattle. *Animals* 14(5): 669. DOI: 10.3390/ani14050669

6. Estimation of the genetic components of (Co)variance and preliminary genome-wide association study for reproductive efficiency in retinta beef cattle

Retina cattle breed hold prime importance as they can survive the harsh climate of Spain. Their fertility is crucial for the survival of the breed and the production of beef. Researchers used the Applied Biosystems™ Axiom™ Bovine Genotyping v3 array to genotype Retina cattle and locate the genes responsible for reproductive efficiency. GWAS analysis revealed 5 markers associated with this trait, located on chromosome BTA4 and BTA28 that can be used in MAS for improving fertility in this cow breed.

Basic animal or crop
Cattle

Breeding goal
Improving reproductive effectiveness in Retina cattle by locating genes responsible for fertility.

Array used
Applied Biosystems™ Axiom™ Bovine Genotyping v3 Array

Link
https://www.mdpi.com/2076-2615/13/3/501

Keywords
Linkage disequilibrium pruning, reproductive efficiencyy, cattle genotyping

Citation
Jiménez JM, Morales RM, Laseca N, et al. (2022) Estimation of the Genetic Components of (Co)variance and Preliminary Genome-Wide Association Study for Reproductive Efficiency in Retinta Beef Cattle. *Animals* 13(3):501. DOI: 10.3390/ani13030501

7. An integrative genomic prediction approach for predicting buffalo milk traits by incorporating related cattle QTLs

Genomic studies on buffaloes are lagging behind that of the cow despite buffalo being an important milk resource. But improving genetic analysis can help produce efficient breeding programs for buffalo milk selection traits. Researchers used the Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array to analyze the whole buffalo genome and locate SNPs relating to milk production. The identified QTLs along with genotyped data were used to develop an improved genomic prediction approach- pGBLUP that can make breeding programs efficient yet cost-effective.

Basic animal or crop
Buffalo

Breeding goal
Improve the quality of milk production in buffalo.

Array used
Applied Biosystems™ Axiom™ Buffalo 90K Genotyping Array

Link
https://www.mdpi.com/2073-4425/13/8/1430

Keywords
Genomic prediction. QTLs, buffalo genomics

Citation
Hao X, Liang A, Plastow G, et al. (2022) An integrative genomic prediction approach for predicting buffalo milk traits by incorporating related cattle QTLs. *Genes* 13(8):1430. DOI: 10.3390/genes13081430

8. Genomic population structure of the main historical genetic lines of Spanish merino sheep

Spanish Merino sheep, once known for its wool, experienced a drastic change in its selection criteria in the 1960s when sheep meat became a priority. Since then, the Merino sheep has been crossbred with local breeds around the globe and its wool quality is still underexplored. Using the Applied Biosystems™ Axiom™ 50K Ovine Genotyping array, researchers analyzed six historical lines of Merino sheep to identify the wool traits. The results not only revealed high genetic diversity in these historical lines but also identified SNPs for wool traits that can be crucial for breeding programs.

Basic animal or crop
Sheep

Breeding goal
To enhance the quality and quantity of wool production in Marino sheep.

Array used
Applied Biosystems™ Axiom™ Ovine 50K Genotyping Array

Link
https://www.mdpi.com/2076-2615/12/10/1327

Keywords
Genomic characterization, molecular variance, sheep genotyping

Citation
Granero A, Anaya G, Alcalde MJ, et al. (2022) Genomic population structure of the main historical genetic lines of spanish merino sheep. *Animals* 12(10):1327. DOI: 10.3390/ani12101327

9. Genetic parameters and genome-wide association studies for mozzarella and milk production traits, lactation length, and lactation persistency in Murrah buffaloes

Murrah buffaloes undergo a negative energy balance, especially during early lactation, which can result in health and fertility issues. There is a need to refine the current breeding goals for these water buffaloes by adding production efficiency and animal resilience traits. To achieve this, Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array was used to genotype 978 animals. The GWAS analysis identified the candidate genes for milk production, fat and protein content, mozzarella yield, lactation length, and lactation persistency. The genomic estimated breeding values verified moderate heritability for milk yield (MY), fat yield (FY), protein yield (PY), and somatic cell score (SCS) indicating that these regions can be selected to develop buffaloes with improved production traits.

Basic animal or crop
Buffalo

Breeding goal
Select Murrah buffaloes with imrpoved production and resilient traits.

Array used
Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array

Link
https://www.sciencedirect.com/science/article/pii/S0022030223006781

Keywords
Genome-wide assoication

Citation
Lázaro SF, Tonhati H, Oliveira HR, et al. (2024) Genetic parameters and genome-wide association studies for mozzarella and milk production traits, lactation length, and lactation persistency in Murrah buffaloes. *Journal of Dairy Science* 107(2):992-1021. DOI:10.3168/jds.2023-23284

10. Inter- and intra-breed genome-wide copy number diversity in a large cohort of European equine breeds

Copy number variations (CNVs) are a common genetic variation contributing to phenotypic traits in mammals, but they are not well-explored. Researchers used Applied Biosystems™ Axiom™ Equine HD Genotyping array to perform GWAS analysis of eight breeds of European horses. The genomic analysis identified breed-specific CNVs and novel CNVs relating to phenotypic diversity and disease resistance traits. These results are crucial to maintaining the horse species with desirable traits and persevering genetic diversity.

Basic animal or crop
Horse

Breeding goal
Facilitate selection strategies for improving important phenotypic traits (including, immunity, coat color, conformation, fertility, and temperament) in horses.

Array used
Applied Biosystems™ Axiom™ Equine HD Genotyping Array

Link
https://link.springer.com/article/10.1186/s12864-019-6141-z

Keywords
Copy number variations, genetic diversity, horse genotyping

Citation
Solé M, Ablondi M, Binzer-Panchal A, et al. (2019) Inter- and intra-breed genome-wide copy number diversity in a large cohort of European equine breeds. *BMC Genomics* 20:759. DOI: 10.1186/s12864-019-6141-z

11. A single-step genome-wide association study for semen traits of Egyptian buffalo bulls

Egyptian buffalo bulls are ranked fourth globally for their milk production and sixth for their meat production. Examining the genomic architecture for semen traits is vital to preserving the buffalo species through selection for sustainable growth. Utilizing Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array, researchers performed a single-step Genome-wide association study (ss-GWAS) to identify the SNPs crucial for semen traits. The identified five novel candidate genes for semen traits exhibited polygenic architecture, pinpointing new genetic targets for breeding programs.

Basic animal or crop
Buffalo

Breeding goal
Improve fertility traits in Egyptian buffalo bulls known for their meat and milk.

Array used
Applied Biosystems™ Axiom™ Buffalo 90K Genotyping Array

Link
https://www.mdpi.com/2076-2615/13/24/3758

Keywords
ss-GWAS, genomic selection, buffalo semen traits

Citation
EL Nagar AG, Salem MM, Amin AM, et al. (2023) A single-step genomewide association study for semen traits of Egyptian buffalo bulls. *Animals* 13(24):3758. DOI: 10.3390/ani13243758

12. Genome-wide scan of wool production traits in Akkaraman sheep

Akkaraman sheep, native to Tukey is an important breeding species because of its high-quality wool. Investigating the genetic basis of wool traits can improve future breeding programs of sheep. Applied Biosystems™ Axiom™Ovine 50K Genotyping Array was used to construct a genomic relationship and perform genome-wide analysis of Akkaraman sheep. As a result, the genomic heritability of five wool traits was estimated and the genomic location of SNPs for each trait was identified.

Basic animal or crop
Sheep

Breeding goal
Select sheep displaying quality wool traits through marker-assisted selection.

Array used
Applied Biosystems™ Axiom™Ovine Genotyping Array

Link
https://www.mdpi.com/2073-4425/14/3/713

Keywords
Sheep breeding, genomic heritability, wool trait QTL

Citation
Arzik Y, Kizilaslan M, Behrem S. et al. (2023) Genome-wide scan of wool production traits in akkaraman sheep. *Genes* 14(3):713. DOI: 10.3390/genes14030713

13. Genomic investigation of milk production in Italian buffalo

The Italian Mediterranean river buffalo, which is mainly farmed in southern Italy for milk and mozzarella production lacks an efficient genomic selection method for milk production. Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array was used to genotype 463 buffalo cows and 35 bulls to construct single-step genomic BLUP (ssGBLUP) and improve the accuracy of breeding value predictions for milk production traits. The inclusion of female genotypes along with that of the bull significantly improved prediction accuracy as compared to the pedigree method.

Basic animal or crop
Buffalo

Breeding goal
Improve the accuracy of genomic selection for milk production traits in Italian Mediterranean river buffalo by prioritizing female genotyping

Array used
Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array

Link
https://www.tandfonline.com/doi/full/10.1080/1828051X.2021.1902404#abstract

Keywords
Genomic selection, single-step genomic BLUP, buffalo genotyping

Citation
Cesarani A, Biffani S, Garcia A, et al. (2021) Genomic investigation of milk production in Italian buffalo. *Italian Journal of Animal Science* 20(1):539–547. DOI:10.1080/1828051X.2021.1902404

14. High-throughput genotype-based population structure analysis of selected buffalo breeds

India is the home of the best buffalo breeds but their genetic variability is not well understood. This research was carried out to understand the genetic diversity and population structure of seven buffalo breeds (Murrah, Nili-Ravi, Surti, Pandharpuri, Mehsana Banni, and Jaffarabadi). Applied Biosystems™ Axiom™ Buffalo Genotyping Array (designed based on SNPs discovered from Mediterranean, Murrah, Jaffarabadi, and Nili-Ravi breeds of buffaloes) was used to genotype 295 female buffaloes. The SNP analysis was instrumental in determining phenotypically different breeds i.e. Surti, Pandharpuri, and Jaffarabadi which showed distinct clustering patterns from others.

Basic animal or crop
Buffalo

Breeding goal
Explore the genetic diversity of Indian buffaloes to conserve breeds with desirable traits.

Array used
Applied Biosystems™ Axiom™ Buffalo Genotyping Array

Link
https://academic.oup.com/tas/article/5/2/txab033/6271363

Keywords
Buffalo genotyping, heterozygosity, SNP markers

Citation
Thakor PB, Hinsu AT, Bhatia DR, et al. (2021) High-throughput genotype-based population structure analysis of selected buffalo breeds. *Translational Animal Science* 5(2). DOI: 10.1093/tas/txab033

15. Signatures of selection reveal candidate genes involved in production traits in Chinese crossbred buffaloes

Chinese crossbred buffaloes have better milk yield than the local swamp buffaloes. Understanding the genetic mechanism underlying milk production can help improve the overall milk output. Using Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array, researchers generated the genotyped data for 133 buffaloes that helped identify 31 candidate selection regions associated with milk production and adaptation traits. These regions can further be used to improve milk production and other performance traits of the buffaloes through specialized breeding programs.

Basic animal or crop
Buffalo

Breeding goal
Improve milk production in Chinese crossbred buffaloes through marker-assisted selection.

Array used
Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array

Link
https://www.sciencedirect.com/science/article/pii/S0022030221010791

Keywords
Population structure, buffalo genotyping

Citation
Deng TX, Ma XY, Lu XR, et al. (2022) Signatures of selection reveal candidate genes involved in production traits in Chinese crossbred buffaloes. *Journal of Dairy Science* 105(2):1327-1337. DOI:10.3168/jds.2021-21102

16. Genetic architecture of body weight, carcass, and internal organs traits of Ghanaian local chickens

Chickens make up the livelihood of many households in Africa, but there is a limited understanding of the genetic architecture of production traits of indigenous chickens. To fill the gap, researchers used Applied Biosystems™ Axiom™ Chicken 600K Genotyping array to impute the genotypes of 1,113 Ghanaian chickens and performed GWAS. The SNP analysis resulted in the identification of 58 significant 1-Mb SNP windows containing several genes for carcass, growth, and internal organs possessing moderate heritability indicating that these traits can be improved through selective breeding.

Basic animal or crop
Chicken

Breeding goal
Improve the production traits of local Ghanaian chickens through selective breeding

Array used
Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2024.1297034/full

Keywords
SNP analysis, genome-wide association, growth traits

Citation
Kanlisi RA, Amuzu-Aweh EN, Naazie A, et al. (2024) Genetic architecture of body weight, carcass, and internal organs traits of Ghanaian local chickens. *Frontiers in Genetics* 15:1297034. DOI: 10.3389/fgene.2024.1297034

17. Exploring the genetic architecture of feed efficiency traits in chickens

Chicken is a global food source and improving feed efficiency can help reduce the use of resources. The previous studies of feed efficiency traits focused on the genetic architecture of each trait separately. To identify the common gene networks related to the feed efficiency trait, the Applied Biosystems™ Axiom™ Chicken 600K Genotyping array was used to genotype 1430 broiler chickens and perform a genome-wide association study (GWAS). The genetic analysis identified 33 genomic regions, containing 41 candidate genes associated with feed efficiency traits (feed intake, body weight gain, and feed conversion ratio). The consideration of non-additive genetic effects such as dominance and sex interactions allows more accurate models for the selection of birds with superior feed efficiency.

Basic animal or crop
Chicken

Breeding goal
Improve the feed efficiency of chickens to reduce the production cost.

Array used
Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link
https://www.nature.com/articles/s41598-021-84125-9#citeas

Keywords
GWAS, candidate genes, feed efficiency

Citation
Marchesi JAP, Ono RK, Cantão ME, et al. (2021) Exploring the genetic architecture of feed efficiency traits in chickens. *Scientific Reports* 11(1):1-12. DOI: 10.1038/s41598-021-84125-9

18. Genome-wide mapping of signatures of selection using a high-density array identified candidate genes for growth traits and local adaptation in chickens

With local Italian chicken populations at risk of extinction, identifying genes that influence its adaptation to stress conditions can help focus breeding programs toward its conservation. Researchers used the Applied Biosystems™ Axiom™ Chicken 600K Genotyping array to identify signatures of selection through a genome-wide study of backyard Italian chickens. The SNP analysis demonstrated several putative genomic regions, including genes related to immune response, disease resistance, and environmental stress tolerance as potentially under selection, covering most of the genome of local chickens. These findings can be used in future breeding programs to produce more resilient chickens that can adapt to changing conditions.

Basic animal or crop
Chicken

Breeding goal
Marker-assisted selection of Italian chicken demonstrating better adaptation to stress conditions.

Array used
Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link
https://link.springer.com/article/10.1186/s12711-023-00790-6

Keywords
Signatures of selection, chicken geneotype

Citation
Mastrangelo S, Ben-Jemaa S, Perini F, et al. (2023) Genome-wide mapping of signatures of selection using a high-density array identified candidate genes for growth traits and local adaptation in chickens. *Genet Sel Evol* 55:20. DOI: 10.1186/s12711-023-00790-6

19. High-density genotyping reveals candidate genomic regions for chicken body size in breeds of Asian origin

As a crucial food source in Asia, understanding the mechanism underlying the growth of chickens is the key to selecting superior traits. Researchers used the Applied Biosystems™ Axiom™ Genome-Wide Chicken Genotyping array to analyze 201 chickens from Asian Game and Asian Bantam breeds, which vary significantly in body size. GWAS analysis identified chromosome 4 (GGA4), containing candidate genes for muscle and bone development, as responsible for body size differences. These candidate genes, including MTM1 and SFRP2, can be a potential target for future breeding strategies aimed at influencing chicken body size.

Basic animal or crop
Chicken

Breeding goal
Selecting chickens with improved body size traits to enhance Asian chicken production.

Array used
Applied Biosystems™ Axiom™ Genome-Wide Chicken Genotyping array

Link
https://www.sciencedirect.com/science/article/pii/S0032579122005983

Keywords
Chicken genotyping, candidate genes, body size

Citation
Lyu S, Arends D, Nassar MK, et al. (2022) High-density genotyping reveals candidate genomic regions for chicken body size in breeds of Asian origin. *Poultry Science* 102(1):102303. DOI:10.1016/j.psj.2022.102303

20. Investigating the genetic determination of duration-of-fertility trait in breeding hens

Artificial insemination (AI) is the popular method of improving egg production for Chinese chicken but is often expensive requiring breeder males. As the duration of the fertility rate of chickens is directly correlated with intervals between AI, identifying genetic markers for fertility traits can reduce the number of required male breeders and the cost associated with AI. The research used Applied Biosystems™ Axiom™ HD chicken 600K genotyping array to perform a genome-wide association study (GWAS) on Jinghong breeding hens and identify 27 SNPs located on chromosomes 1, 3, and 8 related to the duration-of-fertility trait in hens. The four genes (CYP2D6, WBP2NL, ESR1, and TGFBR3) found to have higher mRNA expression levels can be used as genetic markers in chicken breeding programs to improve egg production.

Basic animal or crop
Chicken

Breeding goal
Provide a cost-effective method of improving egg production in Chinese chicken through marker-assisted selection of fertility traits.

Array used
Applied Biosystems™ Axiom™ HD Chicken 600K genotyping array

Link
https://www.nature.com/articles/s41598-024-65675-0

Keywords
Reproductive traits, fertility rate, chicken SNP

Citation
Luo W, Huang X, Li J, et al. (2024) Investigating the genetic determination of duration-of-fertility trait in breeding hens. *Scientific Reports* 14(1):1-9. DOI:10.1038/s41598-024-65675-0

21. Genome-wide analyses identifies known and new markers responsible of chicken plumage color

Plumage color is an important qualitative trait in poultry and a phenotypic marker for breed identification. Understanding the genetic basis of this trait can make the breed identification efficient. Using the Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array, researchers genotyped 37 Polverara chickens (17 white and 20 black) to obtain a large dataset of SNP. The GWAS (genome-wide association study) and FST (genome-wide fixation index scan) conducted pinpointed 40 significant markers for already known and novel genes of plumage color laying the foundation for future breeding programs.

Basic animal or crop
Chicken

Breeding goal
Determine genetic markers assoicated with plumage color which is important for identifying breeds.

Array used
Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link
https://www.mdpi.com/2076-2615/10/3/493

Keywords
Breed identification, GWAS for chicken

Citation
Mastrangelo S, Cendron F, Sottile G, et al. (2020) Genome-wide analyses identifies known and new markers responsible of chicken plumage color. *Animals* 10(3):493. DOI: 10.3390/ani10030493

22. Genomics of Dwarfism in Italian local chicken breeds

Chicken body size is an important factor in determining the profitability of poultry meat with dwarfism being a sought-after trait for determining this trait. Identifying the genetic basis of dwarfism can help maintain the chicken's body size through genetic selection. Researchers compared three local Italian chicken breeds, Mericanel della Brianza (MERI), Pepoi (PPP), and Mugellese (MUG), through genotyping via Applied Biosystems™ Axiom™ Chicken 600K Genotyping array to examine the genetic basis of dwarfism. As a result, SNPs associated with dwarfism on chromosome 1 for MERI and MUF were identified, but none for Pepoi establishing Pepoi as non-dwarf and paving ways to maintain dwarfism in the other two breeds.

Basic animal or crop
Chicken

Breeding goal
Understand the genetic basis of dwarfism which is an important trait influencing growth and development in chicken.

Array used
Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link
https://www.mdpi.com/2073-4425/14/3/633

Keywords
Marker-assisted selection in chicken, dwarfism

Citation
Perini F, Cendron F, Wu Z, et al. (2023) Genomics of dwarfism in Italian local chicken breeds. *Genes* 14(3):633. DOI: 10.3390/genes14030633

23. Genome-wide association study of H/L traits in chicken

Chicken diseases are hindering the expansion of chicken breeds declining the growth of the poultry industry. Understanding the genetic basis of heterophil/lymphocyte (H/L) ratio traits associated with disease resistance is required to have improved breeds. To achieve this objective, the Applied Biosystems™ Axiom™ Chicken 55K array was used that allowed analyzing the genomic DNA profiles of 1650 white feather chicken broilers. Five significant SNPs associated with four novel genes influencing immune response and disease resistance were identified that can help develop marker-assisted selection strategies for breeding chickens with enhanced immunity.

Basic animal or crop
Chicken

Breeding goal
Selecting chicken with enhanced immunity.

Array used
Applied Biosystems™ Axiom™ Chicken 55K Array

Link
https://www.mdpi.com/2076-2615/9/5/260

Keywords
Marker-assisted selection in chicken, GWAS analysis, immune response

Citation
Zhu B, Li Q, Liu R, et al. (2019) Genome-wide association study of h/l traits in chicken. *Animals* 9(5):260. DOI: 10.3390/ani9050260

24. Genetics and genomic regions affecting response to newcastle disease virus infection under heat stress in layer chickens

Newcastle Disease Virus (NDV) is a highly contagious and economically significant avian pathogen that poses a threat to poultry producers in endemic zones. The effects of the virus are exacerbated in the presence of heat stress. To help breeders have genetically resistant chicken breeds, scientists used the Applied Biosystems™ Axiom™ Genome-Wide Chicken Array Kit and have high-density SNPs for genotyped Hy-Line Brown layer chicken samples. The examination of GWAS and genetic variations enabled the identification of several QTLs and candidate genes associated with viral tier, and chickens' immune response to the virus under heat stress which could inform future breeding strategies for resilient poultry populations.

Basic animal or crop

Chicken

Breeding goal

Produce chicken breeds with improved resistance to Newcastle Disease Virus (NDV) under heat stress as the virus aggravates in hot environment.

Array used

Applied Biosystems™ Axiom™ Genome-Wide Chicken Array

Link

https://www.mdpi.com/2073-4425/10/1/61

Keywords

Heritability estimate, Gene assisted marker selection, chicken breeding, heat stress

Citation

Saelao, P, Wang Y, Chanthavixay G. (2019) Genetics and genomic regions affecting response to Newcastle disease virus infection under heat stress in layer chickens. *Genes* 10(1):61. DOI: 10.3390/genes10010061

25. Loci associated with the chicken resistance to Salmonella enteritidis infection revealed by genome-wide association study

Salmonella enteritidis (bacteria) infection in poultry is one of the frequent outbreaks affecting meat quality and causing foodborne diseases. Researchers examined the genetic basis of Salmonella Enteritidis resistance in JiningBairi chicken breeds (local to China). They used Applied Biosystems™ Axiom™ Chicken 600K Genotyping array to perform a genome-wide study on 40 chickens (20 resistant and 20 susceptible to Salmonella Enteritidis infection) to identify SNPs associated with Salmonella enteritidis resistant. Consequently, genotypes of three SNPs were found to be associated with SE burden. These genetic markers can be used to enhance chicken resistance to SE through marker-assisted breeding.

Basic animal or crop

Chicken

Breeding goal

Select chickens that are resistant to salmonella enteritidis which otherwise affects the meat quality.

Array used

Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link

https://meddocsonline.org/journal-of-veterinary-medicine-and-animal-sciences/loci-associated-with-the-chicken-resistance-to-salmonella-enteritidis-infection-revealed-by-genome-wide-association-study.pdf

Keywords

Gene-assisted marker selection, chicken breeding, Salmonella resistance

Citation

Li X, Liu L, Yan Y, et al. (2020) Loci associated with the chicken resistance to Salmonella Enteritidis infection revealed by genome-wide association study. *Journal of Veterinary Medicine and Animal Sciences* 3(1):1018.

26. Genome-wide detection of CNVs and their association with performance traits in broilers

Copy number variations (CNVs) are a common genetic variation contributing to phenotypic and performance traits in chicken broilers, but not been well-explored in previous studies. Researchers used Applied Biosystems™ Axiom™ Chicken 600K Genotyping array to identify 23,214 autosomal CNV. The CNV-based GWAS conducted helped understand the association between these CNVs and eight performance-related traits (body weight at different ages, feed intake, feed conversion ratio, and body weight gain) and identify candidate genes near these CNVs involved in muscle development indicating that CNV integration can make the breeding programs efficient.

Basic animal or crop

Chicken

Breeding goal

Facilitate selection strategies for improving important performance traits (body weight, feed intake, body weight gain, and feed conversio ratio) in broilers.

Array used

Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link

https://link.springer.com/article/10.1186/s12864-021-07676-1

Keywords

Copy number variations, CNV-based GWAS, broiler

Citation

Fernandes AC, da Silva VH, Goes CP, et al. (2021) Genome-wide detection of CNVs and their association with performance traits in broilers. *BMC Genomics* 22:354. DOI:10.1186/s12864-021-07676-1

27. Detection of selection signatures among Brazilian, Sri Lankan, and Egyptian chicken populations under different environmental conditions

The sudden change in environmental conditions leaves chickens with reduced reproduction and immune function. To help the poultry industry thrive, it is important to Identify the selection signatures associated with the adaptation to extreme environmental conditions that can help produce resilient breeds. Chicken breeds sourced from tropical (Brazil, Sri Lanka) and arid (Egypt) regions were genotyped through Applied Biosystems™ Axiom™ Chicken 600K array to compare their allele frequencies and determine genetic differentiation. The results uncovered unique genomic regions associated with immune response, growth, and heat tolerance for the three regions suggesting adaptation to their climate.

Basic animal or crop
Chicken

Breeding goal
Develop chicken breeds with improved immune response, growth, and heat tolerance so they can thrive in extreme environmental conditions.

Array used
Applied Biosystems™ Axiom™ Chicken 600k Array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2018.00737/full

Keywords
Selection signatures, chicken genotyping

Citation
Walugembe M, Bertolini F, Dematawewa CM, et al. (2019) Detection of selection signatures among Brazilian, Sri Lankan, and Egyptian chicken populations under different environmental conditions. *Frontiers in Genetics* 9:385301. DOI: 10.3389/fgene.2018.00737

28. Novel polymorphisms in RAPGEF6 gene associated with egg-laying rate in Chinese Jing Hong chicken using genome-wide SNP scan

A decline in egg-laying rates in the later stages has become a concern for the poultry industry of China. There is a need to assess the genetic basis of egg-laying traits to extend laying cycles for increased productivity. Researchers used the Applied Biosystems™ Axiom™ Chicken HD 600K Genotyping array to perform GWAS on 120 Chinese Jing Hong chickens. Consequently, three SNPs located on chromosome 9 within the RAPGEF6 gene were found to be strongly associated with egg-laying rates in the later stages which can be used for improving egg production through marker-assisted breeding.

Basic animal or crop
Chicken

Breeding goal
Increase the egg-laying cycle in chickens.

Array used
Applied Biosystems™ Axiom™ Chicken HD 600K Genotyping Array

Link
https://www.mdpi.com/2073-4425/10/5/384

Keywords
Genome-wide study, SNP analysis, Chicken genotypes

Citation
Azmal SA, Bhuiyan AA, Omar AI, et al. (2019) Novel Polymorphisms in RAPGEF6 Gene Associated with Egg-Laying Rate in Chinese Jing Hong Chicken using Genome-Wide SNP Scan. *Genes* 10(5):384. DOI: 10.3390/genes10050384

29. Hybrid versus autochthonous turkey populations: Homozygous genomic regions occurrences due to artificial and natural selection

The Mexican turkey has undergone enormous changes due to natural and artificial selection. Understanding how varying natural and artificial selection pressures shape the genomes of different turkey populations can provide insights into the genetic basis of adaptation. Using the Applied Biosystems™ Axiom™ Turkey Genotyping array, researchers compared the genomic structure of traditional Mexican turkey with hybrid turkey and estimated inbreeding coefficients. The proportion of homozygous SNPs and runs of homozygosity (ROH) lead to the conclusion that genomes of Mexican turkeys show greater variability and evidence of adaptation to diverse environments whereas commercial hybrids have undergone selection for production traits. This information can be crucial for maintaining the genetic diversity in Mexican turkeys and for efficiently selecting desirable traits in commercial hybrid turkeys.

Basic animal or crop
Turkey

Breeding goal
To have commercial hybrid turkeys with diverse genomes so inbreeding can be prevented.

Array used
Applied Biosystems™ Axiom™ Turkey Genotyping Array

Link
https://www.mdpi.com/2076-2615/10/8/1318

Keywords
Run of homozygosity, SNPs, turkey, inbreeding

Citation
Strillacci MG, Marelli SP, Martinez-Velazquez G. (2020) Hybrid Versus Autochthonous Turkey Populations: Homozygous Genomic Regions Occurrences Due to Artificial and Natural Selection. *Animals* 10(8):1318. DOI: 10.3390/ani10081318

30. Genome-wide association study for frozen-thawed sperm motility in stallions across various horse breeds

Although there is a growing interest in artificial insemination for stallions, the molecular architecture of the genome relative to sperm formation and preservation after thawing is poorly understood. Identifying the genetic association between significant SNPs and the difference in sperm motility before and after freezing (DPM) can help in having high-quality cryopreserved semen for horse breeding programs. Researchers used the Applied Biosystems™ Axiom™ Equine Genotyping Array to carry out GWAS analysis and determine the frequency of minor alleles at the significant SNPs across different horse breeds. It was found that the presence of CC genotypes in these SNPs is responsible for improved cryopreservation and reduced initial progressive motility, indicating that cryotolerance of stallion sperm is not breed-dependent but rather an intraspecific trait associated with specific genetic variations.

Basic animal or crop
Horse

Breeding goal
Improve the reproduction of stallions by selecting genes for sperm motility after cryopreservation.

Array used
Applied Biosystems™ Axiom™ Equine Genotyping Array

Link
https://www.animbiosci.org/journal/view.php?doi=10.5713/ab.21.0504

Keywords
Sperm cryopreservation, horse breeding, male fertility

Citation
Nikitkina EV, Dementieva NV, Shcherbakov, YS, et al. (2022) Genome-wide association study for frozen-thawed sperm motility in stallions across various horse breeds. *Animal Bioscience* 35(12):1827–1838. DOI: 10.5713/ab.21.0504

31. A QTL for conformation of back and croup influences lateral gait quality in Icelandic horses

The Icelandic horse is known for its five gaits and functional & aesthetically pleasing conformation. There is a lack of selection criteria for improving the croup and back conformation of Icelandic horses, a trait significant to determining sound locomotion and riding ability. Utilizing the Applied Biosystems™ Axiom™ Equine Plus Genotyping Array, researchers identified a novel QTL on ECA22 gene associated with the conformation of the back and croup in Icelandic horses. It was concluded that this QTL not only affects the horse's back shape and structure but also the quality of their lateral gaits which can be instrumental in marker-assisted selection.

Basic animal or crop
Horse

Breeding goal
Select Icelandic horses with improved lateral gait by targeting superior croup and back conformation traits.

Array used
Applied Biosystems™ Axiom™ Equine Plus Genotyping Array

Link
https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-021-07454-z

Keywords
Horse genotyping, lateral gait quality

Citation
Rosengren, M.K., Sigurðardóttir, H, Eriksson S, et al. (2021) A QTL for conformation of back and croup influences lateral gait quality in Icelandic horses. *BMC Genomics* 22:267. DOI: 10.1186/s12864-021-07454-z

32. Genome-wide scans for signatures of selection in Mangalarga Marchador horses using high-throughput SNP genotyping

Mangalarga Marchador (MM) horse shares a significant position in Brazillian livestock and has undergone selection resulting in "batida" and "picada" gaits as the defining characteristics of the breed. Previously published studies lacked a genome-wide scan for regions under selection. Researchers used the Applied Biosystems™ Axiom™ Equine Genotyping array (Axiom MNEC670) to genotype 192 MM horses and conduct a genome-wide scan using Tajima's D, iHS, and ROH analysis to understand the genetic architecture of signatures of selection. The identified candidate genes within the regions of selection signatures were found to be involved in gait, temperament, conformation, and locomotor system but the population structure showed that the animals with different gaits were not genetically distinct.

Basic animal or crop
Horse

Breeding goal
Improve the phenotypic traits, including gait, conformation, and temperament of Mangalarga Marchador (MM) horses.

Array used
Applied Biosystems™ Axiom™ Equine Genotyping Array

Link
https://link.springer.com/article/10.1186/s12864-021-08053-8#Sec1

Keywords
High-throughput genotyping, runs of homozygosity, horse gait

Citation
Santos WB, Schettini GP, Maiorano AM, et al. (2021) Genome-wide scans for signatures of selection in Mangalarga Marchador horses using high-throughput SNP genotyping. *BMC Genomics* 22:737. DOI:10.1186/s12864-021-08053-8

33. Using high-density SNP data to unravel the origin of the Franches-Montagnes horse breed

Franches-Montagnes (FM) horses, the last native horse breed in Switzerland require the preservation of their unique genetic lineage. There has been no fine-scale population structure analysis done on FM which has resulted in less understanding of its diversity and impact of historical introgressions. 1268 horses of six different breeds were genotyped using Applied Biosystems™ Axiom™ Equine Genotyping array to conduct FM population structure analysis. The runs of homozygosity highlighted unexpectedly high levels of Thoroughbred admixture present and genes important for conformation and behavior in FM breeds. It was also found that the FM breed has experienced genetic bottlenecks due to intensive stallion selection, and restrictive mating choices indicating FM diversity should be prioritized in selection for the breed's survival.

Basic animal or crop
Horse

Breeding goal
Preserve genetic lineage of Franches-Montagnes (FM) horses, native to Switzerland.

Array used
Applied Biosystems™ Axiom™ Equine Genotyping Array

Link
https://gsejournal.biomedcentral.com/articles/10.1186/s12711-024-00922-6

Keywords
Run of homozygosity, admixture levels, high desnity SNP

Citation
Gmel AI, Mikko S, Ricard A, et al. (2024) Using high-density SNP data to unravel the origin of the Franches-Montagnes horse breed. *Genet Sel Evol* 56, 53. DOI: 10.1186/s12711-024-00922-6

34. Linkage disequilibrium and effective population size of buffalo populations of Iran, Turkey, Pakistan, and Egypt using a medium density SNP array

Buffaloes from Iran, Turkey, Pakistan, and Egypt share close ancestry. Genetic studies on these closely related populations can provide valuable insights into their shared ancestry, and genetic makeup to enhance breeding and conservation strategies. Researchers used Applied Biosystems™ Axiom™ Buffalo Genotyping array to generate comprehensive SNP data from samples of these buffalo populations and analyze the persistency of LD phase patterns (PLDP), effective population size, and population structure. The observed high correlation levels of LD patterns proved Applied Biosystems™ Axiom™ Buffalo 90K Genotyping array to be a suitable platform for GWAS and GS in these populations suggesting that genomic information from one population can be utilized to predict the diversity patterns in other populations.

Basic animal or crop
Buffalo

Breeding goal
Improve genetic diversity in buffalo populations so they adapt well to changing environments.

Array used
Applied Biosystems™ Axiom™ Buffalo Genotyping Array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2021.608186/full

Keywords
LD phase persistency, buffalo variability

Citation
Rahimmadar S, Ghaffari M, Mokhber M, et al. (2021) Linkage Disequilibrium and Effective Population Size of Buffalo Populations of Iran, Turkey, Pakistan, and Egypt Using a Medium Density SNP Array. *Frontiers in Genetics* 12:608186. DOI: 10.3389/fgene.2021.608186

35. Genome-wide association study of fiber diameter in alpacas

Alpaca fiber is the main source of income for alpaca producers in Peru. There were no selection markers identified for the fiber diameter in alpacas. So, researchers used a custom Applied Biosystems™ Axiom™ Alpaca genotyping array to genotype 1011 female Huacaya alpacas originating from two different regions in Peru and conducted GWAS. The genetic analysis led to the identification of four candidate regions associated with fiber diameter that can be used in alpaca breeding once verified.

Basic animal or crop
Camelid

Breeding goal
Select alpacas with favorable alleles associated with reduced fiber diameter to have fine fiber for textiles.

Array used
Custom Applied Biosystems™ Axiom™ Alpaca Genotyping Array

Link
https://www.mdpi.com/2076-2615/13/21/3316

Keywords
GWAS; alpaca genotyping, fiber diameter

Citation
More M, Veli E, Cruz A. (2023) Genome-Wide Association Study of Fiber Diameter in Alpacas. *Animals* 13(21):3316. DOI: 10.3390/ani13213316

36. Comparison of selection signatures between Korean native and commercial chickens using 600K SNP array data

Korean native chickens (KNCs) were restored to avoid extinction but the efforts weren't focused on economic traits. Prior studies lacked information on positive selection for adaptation to the backyard environment. The Applied Biosystems™ Axiom™ Chicken 600K Genotyping array was used to genotype 245 samples including Korean native chickens (KNCs) and commercial broilers and layers. This helped identify selection signals and candidate genes involved in traits such as reproductive organs, eggshell characteristics, immunity, and organ development with strong linkage disequilibrium patterns in the selective sweep region. These traits can be used to improve the productivity and economic value of the native chicken breeds.

Basic animal or crop
Chicken

Breeding goal
Improve the economic traits of Korean chickens by selecting genetic markers for reproductive organs and immunity.

Array used
Applied Biosystems™ Axiom™ Chicken 600K Genotyping Array

Link
https://www.mdpi.com/2073-4425/12/6/824

Keywords
Selection signatures, Korean chickens, quantitative trait locus

Citation
Cho S, Manjula P, Kim M, et al. (2021) Comparison of Selection Signatures between Korean Native and Commercial Chickens Using 600K SNP Array Data. *Genes* 12(6):824. DOI:10.3390/genes12060824

37. Evaluation of a chicken 600K SNP genotyping array in non-model species of grouse

The high cost of the commercially available genotyping array for grouse is often an obstacle to the genome-wide examination of grouse. The commercially available Applied Biosystems™ Axiom™ Genome-Wide Chicken Array Kit was used to genotype five North American prairie grouse species (belonging to Centrocercus and Tympanuchus genera). Principal component analysis with autosomal SNPs separated the two genera whereas gene ontology analysis identified genes involved in feather development, demonstrating the cross-species application of Applied Biosystems™ Axiom™ Genome-Wide Chicken Array Kit. The SNP results of grouses could be extended to other species within the Phasianidae family, including turkey.

Basic animal or crop
Grouse

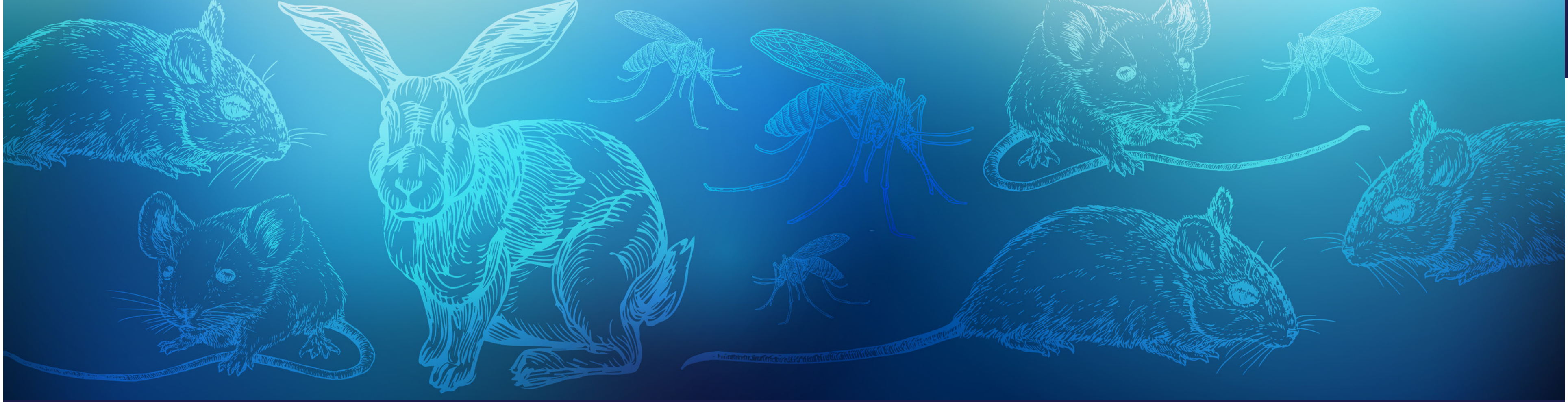
Breeding goal
Pave the way for genomic selection in threatened grouse species and conserve their desirable traits.

Array used
Applied Biosystems™ Axiom™ Genome-Wide Chicken Array

Link
https://www.nature.com/articles/s41598-019-42885-5

Keywords
Allele frequency differentiation, GWAS analysis

Citation
Minias P, Dunn PO, Whittingham LA, et al. (2019) Evaluation of a Chicken 600K SNP genotyping array in non-model species of grouse. *Sci Rep* 9:6407. DOI: 10.1038/s41598-019-42885-5



Model organisms*

1. Genome-wide Association study reveals new loci associated with pyrethroid resistance in Aedes aegypti

Aedes aegypti populations are developing resistance to pyrethroid, which is hindering mosquito control efforts. Understanding the resistance to pyrethroid beyond kdr mutations is required to develop effective control strategies. Applied Biosystems™ Axiom™ Aegypti1 array was used to genotype the two Aedes aegypti Brazilian populations to conduct a genome-wide association study (GWAS). Genomic analysis revealed two new loci acting synergistically with kdr alleles to increase resistance which can be used to further understand the global distribution of pyrethroid resistance.

Basic animal or crop
Mosquito

Breeding goal
To develop Aedes aegypti populations less resistant to Pyrethroid (a pesticide used worldwide to control mosquitoes and agricultural pests).

Array used
Applied Biosystems™ Axiom™ Aegypti1 Genotyping Array

Link
https://www.frontiersin.org/journals/genetics/articles/10.3389/fgene.2022.867231/full

Keywords
Pyrethroid Resistance, Aedes aegypti GWAS analysis

Citation
Cosme LV, Lima JB, Powell JR, et al. (2022) Genome-wide Association Study Reveals New Loci Associated With Pyrethroid Resistance in Aedes aegypti. *Frontiers in Genetics* 13. DOI: 10.3389/fgene.2022.867231

2. Genome-wide association studies for diarrhoea outcomes identified genomic regions affecting resistance to a severe enteropathy in suckling rabbits

Enteropathies are a significant problem in the rabbit meat industry, leading to high morbidity and mortality rates. There is no yet GWAS analysis performed to identify enteropathies resistant genetic markers in suckling rabbit populations. Applied Biosystems™ Axiom™ OrcunSNP 200K array was used to genotype 322 suckling rabbits and conduct GWAS alongside FST analysis. The high throughput genetic testing identified several genomic regions, including key loci on chromosome 13 containing genes for immunoglobulin Fc receptors. It was concluded that resistance to enteropathies is partially determined by genetics but upon further investigation, these markers can be used in breeding resistant rabbit populations.

Basic animal or crop
Rabbit

Breeding goal
To develop enteropathy resistance rabbit population and decrease their mortality rate.

Array used
Applied Biosystems™ Axiom™ OrcunSNP Array

Link
https://onlinelibrary.wiley.com/doi/full/10.1111/jbg.12844

Keywords
GWAS on rabbit, Fst analysis

Citation
Bovo S, Ribani A, Schiavo G. (2023) Genome-wide association studies for diarrhoea outcomes identified genomic regions affecting resistance to a severe enteropathy in suckling rabbits. *Journal of Animal Breeding and Genetics* 141(3):328-342. DOI: 10.1111/jbg.12844

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*Model organisms consist of shared biological processes across species, enabling researchers to explore and identify genetic markers relating to the key features such as growth, disease resistance, and environmental adaptability.

3. Novel genomic regions associated with intramuscular fatty acid composition in rabbits

Intramuscular fat is an important trait influencing the meat quality in rabbits. Understanding the genetic basis of this trait can direct breeders to produce rabbits with improved meat quality. The Applied Biosystems™ Axiom™ OrcunSNP array was used for genotyping the rabbits and performing a genome-wide association study (GWAS) to identify regions associated with intramuscular fatty acid composition. The linkage disequilibrium (LD) leads to the identification of multiple genomic regions related to the fatty acid composition (including those of lipid metabolism) of intramuscular fat (IMF) supporting its polygenic nature which means the meat quality can be improved through marker-assisted breeding.

Basic animal or crop
Rabbit

Breeding goal
To improve the meat quality through targeted selection for higher intramuscular fat content.

Array used
Applied Biosystems™ Axiom™ OrcunSNP Array

Link
https://www.mdpi.com/2076-2615/10/11/2090

Keywords
Rabbit meat quality, fatty acid composition, GWAS

Citation
Laghouaouta H, Sosa-Madrid BS, Zubiri-Gaitán A, et al. (2020) Novel Genomic Regions Associated with Intramuscular Fatty Acid Composition in Rabbits. *Animals* 10(11):2090. DOI:10.3390/ani10112090

4. Genome-wide association study of maternal genetic effects on intramuscular fat and fatty acid composition in rabbits

Intramuscular fat (IMF) and fatty acid composition in rabbits significantly impact the meat quality but there is no prior research investigating the effects of maternal genetics on these traits. The Applied Biosystems™ Axiom™ OrcunSNP array was used for genotyping the rabbits to perform the maternal genome-wide association study (GWAS). The study found several genomic regions associated with IMF and fatty acid composition on chromosomes OCU1, OCU5, and OCU19. It was also concluded that maternal genetics accounts for 8 to 22% of phenotypic variance for IMF and 10 to 45% for fatty acids providing new insights for the genetic improvement of meat quality in rabbits.

Basic animal or crop
Rabbit

Breeding goal
Improve the meat quality in rabbits by accounting the maternal genetic effects.

Array used
Applied Biosystems™ Axiom™ OrcunSNP Array

Link
https://www.mdpi.com/2076-2615/13/19/3071

Keywords
Maternal GWAS, fatty acids, intramuscular fat

Citation
EL Nagar AG, Heddi I, Sosa-Madrid BS, et al. (2022) Genome-Wide Association Study of Maternal Genetic Effects on Intramuscular Fat and Fatty Acid Composition in Rabbits. *Animals* 13(19):3071. DOI:10.3390/ani13193071

5. Disentangling the causal relationship between rabbit growth and cecal microbiota through structural equation models

The productivity and growth of rabbits depend on gut microbiota and host genetics. Previous studies on gut microbiota's effects on rabbit growth didn't account for the host genome. The Applied Biosystems™ Axiom™ OrcunSNP array was used to genotype 412 rabbits, assessing the causal relationship between the host genome, cecal microbiota, and average daily gain (ADG) through the structural equation model (SEM). Specific operational taxonomic units (OTU) in the cecal microbiota and host genetics were found to influence the average daily gain, with some microbial effects potentially counteracting direct genetic effects while others enhancing the growth. Considering these direct and indirect effects on growth is crucial for breeding rabbits with superior growth traits.

Basic animal or crop
Rabbit

Breeding goal
Select rabbits based on both direct genetic effects and indirect effects mediated by the gut microbiota to have their sustainable growth.

Array used
Applied Biosystems™ Axiom™ OrcunSNP array

Link
https://link.springer.com/article/10.1186/s12711-022-00770-2

Keywords
Structural equation mode, rabbit genotyping, average daily gain

Citation
Mora, M, Velasco-Galilea M, Sánchez JP, et al. (2022) Disentangling the causal relationship between rabbit growth and cecal microbiota through structural equation models. *Genetics Selection Evolution* 54(81). DOI:10.1186/s12711-022-00770-2

Plants and crops

1. Multi-model GWAS reveals key loci for horticultural traits in reconstructed garden strawberry

Modern strawberry cultivars lack the diversity and wider adaptability traits of early garden strawberries of America. So, researchers reconstructed the strawberry population through F. virginiana and F. chiloensis selection. The Applied Biosystems™ Axiom™ FanaSNP Array was used to generate the SNPs in these populations that helped understand the QTLs important for eight important horticulture traits. Trait loci bearing the harsh winter was identified that can play a crucial role in deciding the breeding goals.

Basic animal or crop
Strawberry

Breeding goal
Produce strawberry cultivars with improved adaptability to harsh winters.

Array used
Applied Biosystems™ Axiom™ FanaSNP Array

Link
https://onlinelibrary.wiley.com/doi/full/10.1111/ppl.14440

Keywords
Horticulture traits, strawberry breeding

Citation
Iso-Touru T, Junkers J, Rantanen M, et al. (2024) Multi-model GWAS reveals key loci for horticultural traits in reconstructed garden strawberry. *Physiologia Plantarum* 176(4), e14440. DOI: 10.1111/ppl.14440

2. Susceptibility evaluation to fire blight and genome-wide associations within a collection of Asturian apple accessions

While Asturias, Spain is the hub of apple cider production, the apples are growing under the serious threat of Fire Blight disease. It damages the apple tissues, hindering the apple production. This research used Applied Biosystems™ Axiom™ Apple 480K Array to analyze genome-wide association studies of these apples and understand their genetic diversities. The genetic markers identified revealed the location of Fire Blight resistant gene, signifying the genotyping of this particular gene for population breeding.

Basic animal or crop
Apple

Breeding goal
Produce apple cider cultivars that are less susceptible to fire blight disease (known for reducing apple production).

Array used
Applied Biosystems™ Axiom™ Apple 480K Array

Link
https://www.mdpi.com/2223-7747/12/23/4068

Keywords
Apple cider genotyping, population breeding

Citation
García-Fernández B, Dolcet-Sanjuan R, Micheletti D, et al. (2023) Susceptibility evaluation to fire blight and genome-wide associations within a collection of Asturian apple accessions. *Plants* 12(23):4068. DOI: 10.3390/plants12234068

3. Discovery of three loci increasing resistance to charcoal rot caused by Macrophomina phaseolina in octoploid strawberry

Charcoal rot, caused by Macrophomina phaseolina (fungus), is an increasing economic problem in the strawberry production industry worldwide. There is a lack of information on the genetic architecture of resistance to this disease in cultivated strawberries. Using the Applied Biosystems™ Axiom™ IStraw35, and Applied Biosystems™ Axiom™ FanaSNP 50 K array researchers genotyped reconstituted F. ananassa, elite lines, advanced selection, and commercial varieties of strawberry plants. The quantitative trait loci (QTL) analysis and genome-wide association studies (GWAS) identified two loci FaRMp1, and FaRMp2 in elite lines, and one loci FaRMp3 in reconstituted F. ananassa, associated with resistance to charcoal rot disease. The haplotype analysis further helped identify resistant and susceptible alleles demonstrating that resistant strawberries can be cultivated through marker-assisted selection.

Basic crop

Strawberry

Breeding goal

Cultivate strawberries that are resistant to charcoal rot disease that otherwise causes stunted growth and loss of the plant.

Array used

Applied Biosystems™ Axiom™ IStraw35, and Applied Biosystems™ Axiom™ FanaSNP 50 K array

Link

https://academic.oup.com/g3journal/article/11/3/jkab037/6132254

Keywords

Strawberry breeding, Haplotype analysis, QTLS,

Citation

Nelson JR, Verma S, Bassil NV, et al. (2021) Discovery of three loci increasing resistance to charcoal rot caused by Macrophomina phaseolina in octoploid strawberry. *G3 Genes|Genomes|Genetics* 11(3). DOI:10.1093/g3journal/jkab037

4. Development of a high-density genetic linkage map and identification of quantitativetrait loci (QTLs) associated with Botrytis cinerea resistance in strawberry(Fragaria × ananassa Duch.)

Botrytis cinerea (fungal pathogen) has been drastically affecting strawberry populations, reducing yield and quality of agronomic traits. This research aimed to identify the genome positions that might be susceptible to Botrytis cinerea. The use of Applied Biosystems™ Axiom™ FanaSNP helped construct linkage maps for maternal and paternal species of Fortuna × Rubygem's F1 population. As a result, 5 significant QTLs associated with resistance to B. cinerea were identified that can help in future marker-assisted selection for strawberry breeding.

Basic animal or crop

Strawberry

Breeding goal

Grow strawberries with resistance to Botrytis cinerea (the fungal pathogen that causes mechanical damage) through marker-assisted selection.

Array used

Applied Biosystems™ Axiom™ FanaSNP Array

Link

https://journals.tubitak.gov.tr/agriculture/vol48/iss5/5/

Keywords

Strawberry genotyping, SNP markers, linkage groups

Citation

Ayvaz Sönmez D, Karcı H, Topçu H, et al. (2024) Development of a high-density genetic linkage map and identification of quantitative trait loci (QTLs) associated with Botrytis cinerea resistance in strawberry (Fragaria × ananassa Duch.). *Turkish Journal of Agriculture and Forestry* 48(5):677–691. DOI: 10.55730/1300-011X.3211

5. Identification of QTLs for powdery mildew (*Podosphaera aphanis*; syn. *Sphaerotheca macularis f.* sp. *fragariae*) susceptibility in cultivated strawberry (*Fragaria ×ananassa*)

Powdery mildew (fungal pathogen) is affecting the strawberry cultivars, particularly Sonata' x 'Babette' population in the UK, reducing the yearly yield and quality of the fruit. Researchers used the Applied Biosystems™ Axiom™ iStraw90K array to genotype Sonata' x 'Babette' existing populations map with high-density SNPs and understand the genes that are more resistant to the fungi. Population genetics resulted in the identification of three distinctive QTLs and genes resistant to powdery mildews that can be used in strawberry breeding to produce more resistant cultivars.

Basic animal or crop
Strawberry

Breeding goal
Grow Sonata' x 'Babette' population of UK strawberries that are more resistant to powdery mildew fungi.

Array used
Applied Biosystems™ Axiom™ iStraw90K Array

Link
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0222829

Keywords
Population mapping, SNP genotyping for strawberry, fungal resistant

Citation
Sargent DJ, Buti M, Šurbanovski N, et al. (2019) Identification of QTLs for powdery mildew (Podosphaera aphanis; syn. Sphaerotheca macularis f. Sp. Fragariae) susceptibility in cultivated strawberry (Fragaria ×ananassa). *PLOS ONE* 14(9), e0222829. DOI: 10.1371/journal.pone.0222829

6. Accelerating genetic gains for quantitative resistance to verticillium wilt through predictive breeding in strawberry

Verticillium wilt is one of the most devastating diseases of strawberries in this century. Traditional breeding has shown negligible genetic gains for VW resistance. To demonstrate the efficacy of genomic prediction, researchers genotyped the training population using the Applied Biosystems™ Axiom™ FanaSNP 50 K array. The GWAS analysis and calculated genomic-estimated breeding values allowed the identification of genetic markers associated with Verticillium wilt resistance and the prediction of the resistance. It was concluded that using GEBV to select parents leads to more resistant offspring than selection based on phenotypic observation, demonstrating genomic prediction as a viable tool to accelerate the breeding of wilt-resistant cultivators.

Basic animal or crop
Strawberry

Breeding goal
Use genomic prediction to accelerate the breeding of Verticillium wilt resistant strawberries.

Array used
Applied Biosystems™ Axiom™ FanaSNP 50 K Array

Link
https://acsess.onlinelibrary.wiley.com/doi/full/10.1002/tpg2.20405

Keywords
Genomic prediction, GWAS analysis, genome-estimated breeding value, genomic prediction, GWAS analysis, genome-estimated breeding value

Citation
Feldmann MJ, Pincot DDA, Vachev MV, et al. (2024) Accelerating genetic gains for quantitative resistance to verticillium wilt through predictive breeding in strawberry. *The Plant Genome* 17(1):e20405. DOI:10.1002/tpg2.20405

7. Exploration of a European-centered strawberry diversity panel provides markers and candidate genes for the control of fruit quality traits

European strawberry accessions hold great genetic diversity but their fruit quality traits are underexplored. Researchers emphasized on GWAS analysis of 233 strawberry accessions, using the Applied Biosystems™ Axiom™ FanaSNP to understand the molecular basis of fruit traits. Genetic mapping found 71 associations of desirable traits, identifying new QTLs for glossiness, and skin resistance that can direct future breeding programs focused on increased shelf-life preserving the color and quality of the fruit.

Basic animal or crop
Strawberry

Breeding goal
Produce strawberry cultivars with improved fruit quality and increased shelf life traits.

Array used
Applied Biosystems™ Axiom™ FanaSNP Array

Link
https://academic.oup.com/hr/article/11/7/uhae137/7672963

Keywords
Marker-assisted selection, genetic diversity, strawberry evolution

Citation
Prohaska A, Rey-Serra P, Petit J, et al. (2024) Exploration of a European-centered strawberry diversity panel provides markers and candidate genes for the control of fruit quality traits. *Horticulture Research* 11(7):uhae137. DOI: 10.1093/hr/uhae137

8. Using high-density SNP array to investigate genetic relationships and structure of apple germplasm in Bosnia and Herzegovina

Bosnia and Herzegovina (B&H) apple consists of a significant genetic diversity but it was studied using SSR markers which is limited in its capacity to reveal the intricacies of apple germplasm genetic structure. With the Applied Biosystems™ Axiom™ Apple 480K array, researchers were able to use high-density SNP markers to identify the minute details not revealed by SSR. Apple genotyping enabled researchers to reconstruct pedigree that can further help in the genetic characterization of B&H cultivators.

Basic animal or crop
Apple

Breeding goal
Genetic analysis of Bosnia and Herzegovina (B&H) apples to identify the desirable traits and inform breeding programs accordingly.

Array used
Applied Biosystems™ Axiom™ Apple 480K Array

Link
https://www.mdpi.com/2311-7524/9/5/527

Keywords
Apple genetic diveristy, SNP markers

Citation
Konjić A, Kurtović M, Grahić, et al. (2023) Using High-Density SNP Array to Investigate Genetic Relationships and Structure of Apple Germplasm in Bosnia and Herzegovina. *Horticulturae*, 9(5):527. DOI: 10.3390/horticulturae9050527

9. Identification of stable and multiple environment interaction QTLs and candidate genes for fiber productive traits under irrigated and water stress conditions using intraspecific RILs of Gossypium hirsutum var. MCU5 X TCH1218

Cotton's productivity under water stress is the sought-after trait but quite complex genetically. Applied Biosystems™ Axiom™ Cotton 50K Genotyping array provided high-throughput SNPS to allow genotyping of this water stress-bearing cotton population and characterize it genetically. Genetic mapping revealed 85 QTLs associated with cotton productivity that can be fine-mapped to produce drought-resistant breeds through marker-assisted selection.

Basic animal or crop
Cotton

Breeding goal
Produce drought-resistant cotton breeds through marker-assisted selection.

Array used
Applied Biosystems™ Axiom™ Cotton 50K Genotyping Array

Link
https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2022.851504/full

Keywords
recombinant inbred line, population mapping

Citation
Boopathi NM, Tiwari G J, Jena SN, et al. (2022). Identification of Stable and Multiple Environment Interaction QTLs and Candidate Genes for Fiber Productive Traits Under Irrigated and Water Stress Conditions Using Intraspecific RILs of Gossypium hirsutum var. MCU5 X TCH1218. *Frontiers in Plant Science* 13:851504. DOI: 10.3389/fpls.2022.851504

10. Genetic diversity and selection signatures in a gene bank panel of maize inbred lines from Southeast Europe compared with two West European panels

Southeast Europe's maize population has a long history of genetic material swapping following the modern trends in the US. Although these populations developed the desired trait but still sustained some genes important for their survival. Researchers genotyped such 572 inbred maize lines, using the Applied Biosystems™ Axiom™ 600K Maize Genotyping array to analyze genomic structure and genetic diversity. The analysis revealed genomic regions rich in selection signatures that indicated adaptation to modern environments and changing climatic conditions. These selection signatures exhibiting stress tolerance and nutrient use efficacy traits could become an important component of breeding programs.

Basic animal or crop
Maize

Breeding goal
Develop cultivars exhibiting superior abiotic stress tolerance and optimized nutrient use efficiency.

Array used
Applied Biosystems™ Axiom™ Maize Genotyping Array

Link
https://link.springer.com/article/10.1186/s12870-023-04336-2

Keywords
Selection signatures, genetic swapping, maize genotyping

Citation
Galić V, Anđelković V, Kravić N, et al. (2023) Genetic diversity and selection signatures in a gene bank panel of maize inbred lines from Southeast Europe compared with two West European panels. *BMC Plant Biol* 23:315. DOI: 10.1186/s12870-023-04336-2

11. Additive and heterozygous (dis)advantage GWAS models reveal candidate genes involved in the genotypic variation of maize hybrids to *Azospirillum brasilense*

Azospirillum brasilense (plant-growth-promoting bacteria) is widely used for maize inoculation to promote maize growth under nitrogen stress. However, the genes responding to A. brasilense are not well-known due to the absence of GWAS studies on maize interaction with Azospirillum brasilense. Researchers used the Applied Biosystems™ Axiom™ Maize Genotyping array to obtain SNP markers for identifying the root and shoot trait genes that recognize and promote growth through A. brasilense. Additive and heterozygous (dis)advantage GWAS models analysis revealed 25 responsive maize genes helping its defense, hormone biosynthesis, and root growth that can be used for marker-assisted breeding of the maize population.

Basic animal or crop	**Breeding goal**	**Array used**
Maize	Develop maize populations possessing root and shoot traits that respond well to the plant growth-promoting bacteria (*Azospirillum brasilense*).	Applied Biosystems™ Axiom™ Maize 600K Genotyping Array

Link	**Keywords**	**Citation**
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0222788	GWAS analysis, maize marker-assisted breeding, inbred lines	Vidotti MS, Lyra DH, Morosini JS, et al. (2019) Additive and heterozygous (dis)advantage GWAS models reveal candidate genes involved in the genotypic variation of maize hybrids to Azospirillum brasilense. *PLOS ONE* 14(9):e0222788. DOI: 1371/journal.pone

12. Population structure analysis and identification of genomic regions under selection associated with low-nitrogen tolerance in tropical maize lines

Low nitrogen is often a threat to maize growth and the grain it produces. While research has been conducted on temperate regions, tropical Brazil maize is under-explored. To understand the genomic diversity reflecting low nitrogen tolerance, researchers genotyped tropical maize inbred lines using Applied Biosystems™ Axiom™ Maize Genotyping array. The population identified 29 SNPs exhibiting differences in allele frequencies between maize populations tolerant to low nitrogen and those intolerant. These SNPs can be crucial in marker-assisted genetic selection for producing low nitrogen tolerant maize populations.

Basic animal or crop	**Breeding goal**	**Array used**
Maize	Select maize cultivars tolerant to low nitrogen conditions through marker-assisted breeding.	Applied Biosystems™ Axiom™Maize Genotyping Array

Link	**Keywords**	**Citation**
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0239900	population genetics, maize breeding, low-N efficiency	Espolador FG, Correia Granato ÍS, Mendonça LF, et al. (2020) Population structure analysis and identification of genomic regions under selection associated with low-nitrogen tolerance in tropical maize lines. *PLOS ONE* 15(9):e0239900. DOI: 10.1371/journal.pone.0239900

13. *In silico* quality assessment of SNPs—A case study on the Axiom® Wheat genotyping arrays

Bread wheat genotyping, crucial to producing cultivars that adapt to changing climatic conditions and increasing consumption demand, requires precision and accuracy. The comprehensive assessment of SNPs on the commercially available array can make the genotyping process quicker and more accurate. Researchers used Applied Biosystems™ Axiom™ Wheat Breeders Genotyping Array and Applied Biosystems™ Axiom™ Wheat HD genotyping array to extract information about SNPs and their flanking sequences important for bread wheat marker-assisted selection. The genomic analysis led them to classify SNP into three classes based on their quality which can help breeders create more accurate desirable traits for bread wheat.

Basic animal or crop	**Breeding goal**	**Array used**
Wheat Bread	Produce desirable traits in bread wheat efficiently through marker-assisted selection.	Applied Biosystems™ Axiom™ Wheat Breeders Genotyping Array

Link	**Keywords**	**Citation**
https://www.sciencedirect.com/science/article/pii/S2214662820300219	SNP classification, single nucleotide polymorphism, bread wheat genetic analysis	Lange TM, Heinrich F, Enders M, et al. (2019) In silico quality assessment of SNPs—A case study on the Axiom® Wheat genotyping arrays. *Current Plant Biology* 21:100140. DOI: 10.1016/j.cpb.2020.100140

14. Using whole-genome SNP data to reconstruct a large multi-generation pedigree in apple germplasm

Apple is one of the important crops in temperate regions of Europe. The already available apple pedigree was built using SSR which limits the ability to infer parentages between genotypes with widely occurring alleles. Researchers wanted to conduct the largest analysis on European apples through SNP analysis so a wider understanding of genetic diversity could be made. They used Applied Biosystems™ Axiom™ Apple480K array to examine the genetic correlation of desirable traits. A reconstructed largest apple pedigree spanning seven generations provided insights into a parent-offspring trio, parent-offspring duo, and grandparent-parent-offspring group which is instrumental in the genetic selection of desirable traits and breeding programs.

Basic animal or crop
Apple

Breeding goal
Construct the largest apple pedigree to obtain information on traits important for survival and growth.

Array used
Applied Biosystems™ Axiom™ Apple480K Array

Link
https://link.springer.com/article/10.1186/s12870-019-2171-6#Sec18

Keywords
Apple pedigree, SNP analysis

Citation
Muranty H, Denancé C, Feugey L, et al. (2020) Using whole-genome SNP data to reconstruct a large multi-generation pedigree in apple germplasm. *BMC Plant Biol* 20:2. DOI: 10.1186/s12870-019-2171-6

15. Molecular diversity within a Mediterranean and European panel of tetraploid wheat (T. turgidum subsp.) landraces and modern germplasm inferred using a high-density SNP array

Wheat, the third most important cereal grain globally has undergone a significant reduction in genetic diversity due to domestication. This is leading to the development of wheat varieties that are less nutritious and resilient. Using the Applied Biosystems™ Axiom™ Wheat Breeders 35K array, researchers genotyped 265 tetraploid wheat samples from Mediterranean and European areas to assess their genetic diversity and population structure. It was concluded that the landraces are a valuable source of genetic variability and can be used to cultivate wheat with improved genetic diversity.

Basic animal or crop
Wheat

Breeding goal
Improve the genetic diversity of domesticated wheat so it adapts to the varying conditions and provides more nutrition.

Array used
Applied Biosystems™ Axiom™ Wheat Breeders 35K Array

Link
https://www.mdpi.com/2073-4395/11/3/414

Keywords
Wheat Breeders array, genetic diversity, population structure

Citation
Ganugi P, Palchetti E, Gori M, et al. (2021) Molecular Diversity within a Mediterranean and European Panel of Tetraploid Wheat (T. Turgidum subsp.) Landraces and Modern Germplasm Inferred Using a High-Density SNP Array. *Agronomy* 11(3):414. DOI:10.3390/agronomy11030414

16. Genome-wide association study (GWAS) reveals an SNP associated with waxy trait and development of a functional marker for predicting waxy maize (*Zea mays* L. var. ceratina)

Waxy maize is popular in China and Southeast Asia for fresh consumption. The lack of a reliable marker for the waxy trait and the recessive nature of the waxy allele have made the traditional selection methods for waxy maize complicated. Researchers performed GWAS on 213 inbred lines and recombinant inbred lines (RILs) of field maize and waxy maize which were genotyped using Applied Biosystems™ Axiom™ Maize 600K Genotyping array. The comprehensive analysis of genetic variation successfully demonstrated SNP AX-90613979 on chromosome 9 based on which a functional marker was developed and analytically tested to predict waxy phenotype. The identification of this marker provides a cost-effective and efficient method for selecting waxy varieties, demonstrating its potential for advanced waxy maize breeding.

Basic animal or crop
Maize

Breeding goal
Cost-effective and efficient method for selecting waxy maize varieties.

Array used
Applied Biosystems™ Axiom™ Maize 600K Genotyping Array

Link
https://www.mdpi.com/2073-4395/12/10/2289

Keywords
Quantitative trait loci, SNP, waxy maize

Citation
Ruanjaichon V, Yin KK, Thunnom B. (2022) Genome-Wide Association Study (GWAS) Reveals an SNP Associated with Waxy Trait and Development of a Functional Marker for Predicting Waxy Maize (Zea mays L. Var. Ceratina). *Agronomy* 12(10): 2289. DOI: 10.3390/agronomy12102289

17. Development of an inclusive 580K SNP array and its application for genomic selection and genome-wide association studies in rice

The existing rice genotyping array often consists of random SNPs that are not effective in dissecting the genetic architecture of key traits including starch synthesis, blast resistance, and yield-related traits. By integrating the SNPs from Applied Biosystems™ Axiom™ Rice Genotyping 44K array and other databases, researchers developed a custom Applied Biosystems™ Axiom™ Rice Genotyping 580 K array consisting of SNP for key rice traits. The custom array was used in GWAS and genomic selection to identify the candidate genes for lum length, heading date, and panicle length. The array was also able to achieve predictability for these traits demonstrating it to be an accurate yet cost-effective solution for advancing rice breeding programs.

Basic animal or crop

Rice

Breeding goal

Provide an efficient and high-throughput genotyping tool to cultivate rice populations with desirable traits such as lum length, heading date, and panicle length.

Array used

Applied Biosystems™ Axiom™ Rice Genotyping 44K array

Link

https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2022.1036177/full

Keywords

Rice genotyping, custom array, genomic selection

Citation

Kim KW, Nawade B, Nam J, et al. (2022) Development of an inclusive 580K SNP array and its application for genomic selection and genome-wide association studies in rice. *Frontiers in Plant Science* 13:1036177. DOI:10.3389/fpls.2022.1036177

18. Prediction accuracy of genomic estimated breeding values for fruit traits in cultivated tomato (Solanum lycopersicum L.)

Tomato's fruit traits hold prime importance in cultivation and often are the choice of interest in breeding. Genomic selection (GS) is an efficient method for improving tomato fruit traits, but its success relies on the accuracy of GEBV values' predictions. Researchers used the Applied Biosystems™ Axiom™ Tomato 51K Genotyping array to genotype the sample germplasm collections of tomatoes and assess the accuracy of GEBV for five fruit traits using six GS models. It was concluded that strategically choosing the smaller set of SNP marker density provides greater prediction accuracy for GEBV values for fruit weight, fruit width, fruit height, pericarp thickness, and brix that can facilitate the genomic selection in developing elite cultivars.

Basic animal or crop

Tomato

Breeding goal

Efficiently improve the fruit traits (height, width, pericarp thickness, weight, and Brix) in tomato cultivars through genomic selection.

Array used

Applied Biosystems™ Axiom™ Tomato 51K Genotyping Array

Link

https://link.springer.com/article/10.1186/s12870-024-04934-8

Keywords

Genomic selection, prediction model, SNP

Citation

Yeon J, Nguyen TTP, Kim M, et al. (2024) Prediction accuracy of genomic estimated breeding values for fruit traits in cultivated tomato (Solanum lycopersicum L.). *BMC Plant Biol* 24:222. DOI: 10.1186/s12870-024-04934-8

19. Genetic dissection of seedling root system architectural traits in a diverse panel of hexaploid wheat through multi-locus genome-wide association mapping for improving drought tolerance

Wheat is an important crop in India but often has to go through drought conditions that adversely affect its growth. Wheat cultivators with efficient root systems architecture (RSA) play a crucial role in water absorption and tolerating drought. Targeting RSA in breeding can facilitate the production of cultivars with drought-tolerance abilities. Researchers used Applied Biosystems™ Axiom™ Wheat Breeders 35k array to genotype a diverse range of 136 wheat and perform multi loci genome-wide association study (ML-GWAS). The genetic analysis identified novel genes and loci associated with seedling RSA that can be targeted to improve root traits and drought tolerance in wheat cultivars.

Basic animal or crop
Wheat

Breeding goal
Develop wheat cultivars with efficient RSA (root system architecture) to survive through water scarcity.

Array used
Applied Biosystems™ Axiom™ Wheat Breeders 35k Array

Link
https://www.mdpi.com/1422-0067/22/13/7188

Keywords
Quantitative trait nucleotides, ML-GWAS

Citation
Danakumara T, Kumari J, Singh AK, et al. (2021) Genetic Dissection of Seedling Root System Architectural Traits in a Diverse Panel of Hexaploid Wheat through Multi-Locus Genome-Wide Association Mapping for Improving Drought Tolerance. *International Journal of Molecular Sciences* 22(13):7188. DOI: 10.3390/ijms22137188

20. Low-density SNP markers with high prediction accuracy of genomic selection for bacterial wilt resistance in tomato

Bacterial wilt (BW) causes severe damage to the tomato populations and the host resistance to this disease is a complex trait. Improving the genomic selection method to identify the genes associated with BW can help produce BW-resistant tomato populations. Researchers used the Applied Biosystems™ Axiom™ Tomato 51K array to evaluate the accuracy of prediction values (GEBV) by comparing six GS models. The identification of high-performing low-density SNP markers for predicting GEBV offers a cost-effective approach to predicting BW resistance, promising more efficient tomato breeding strategies.

Basic animal or crop
Tomato

Breeding goal
Cost-effective tomato breeding for producing populations resistant to bacterial wilt disease.

Array used
Applied Biosystems™ Axiom™ Tomato 51K Genotyping Array

Link
https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2024.1402693/full

Keywords
Genomic selection, prediction values, SNP

Citation
Yeon J, Le NT, Heo J. (2024) Low-density SNP markers with high prediction accuracy of genomic selection for bacterial wilt resistance in tomato. *Frontiers in Plant Science* 15:1402693. DOI: 10.3389/fpls.2024.1402693

21. Germplasm screening using DNA markers and genome-wide association study for the identification of powdery mildew resistance loci in tomato

Tomato cultivars show a weak resistance to powdery mildew (fungus disease), which reduces their yield. Since it mainly occurs in wild tomatoes they have better resistance to it. Researchers used Applied Biosystems™ Axiom™ Tomato 52K Genotyping array to genotype 290 tomato accessions, including both cultivated and wild species, and identify novel quantitative trait loci (QTL) for powdery mild dew resistant (PMR) trait. The GWAS analysis led to the identification of three candidate genes associated with powdery mildew resistance that can be used in breeding programs for producing PMR-resistant cultivars.

Basic animal or crop
Tomato

Breeding goal
Develop tomato varieties with better resistance to powdery mildew.

Array used
Applied Biosystems™ Axiom™ Tomato 52K Genotyping Array

Link
https://www.mdpi.com/1422-0067/23/21/13610

Keywords
QTL, SNP analysis, disease resistance, tomato genoyping

Citation
Park J, Lee S, Choi Y, et al. (2021) Germplasm Screening Using DNA Markers and Genome-Wide Association Study for the Identification of Powdery Mildew Resistance Loci in Tomato. *International Journal of Molecular Sciences* 23(21):13610. DOI: 10.3390/ijms232113610

22. Optimizing genomic selection of agricultural traits using K-wheat core collection

Wheat is a staple food globally and understanding its genetic diversity is crucial to producing wheat with superior traits. To achieve this, researchers genotyped a diverse Korean wheat accession using Applied Biosystems™ Axiom™ Wheat Breeders 35K Genotyping array which helped create a mini core collection (miniCC) of wheat accession representing more diversity. Population structure analysis identified genetic markers associated with ten important agricultural traits (awn color, awn length, culm color, culm length, ear color, ear length, days to heading, days to maturity, leaf length, and leaf width) which were then used in six GS models to predict the accuracy of GEBV values, providing an efficient way of selecting superior populations.

Basic animal or crop
Wheat

Breeding goal
Efficiently select important agricultural traits in wheat through genomic selection.

Array used
Applied Biosystems™ Axiom™ Wheat Breeders 35K Genotyping Array

Link
https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2023.1112297/full

Keywords
Genetic diversity, wheat genotyping, genomic selection

Citation
Kang Y, Choi C, Kim JY, et al. (2023) Optimizing genomic selection of agricultural traits using K-wheat core collection. *Frontiers in Plant Science* 14: 1112297. DOI: 10.3389/fpls.2023.1112297

23. Korean soybean core collection: Genotypic and phenotypic diversity population structure and genome-wide association study

Soybean is an important food and feed crop that requires conserving its genetic variability for breeding high-quality soybean populations. Previous efforts to preserve the genetic variations relied on a limited number of markers that didn't represent a diverse variability. Applied Biosystems™ Axiom™ SoyaSNP array was used to perform SNP analysis on 2,872 Korean soybean collections and construct a Korean soybean core collection representing 99% of the genetic diversity of the original collection. This core collection proved to be a valuable genetic resource for breeding programs as it identified candidate genes and markers for important agricultural traits including stress tolerance.

Basic animal or crop
Soybean

Breeding goal
Preserve genetic diversity of soybean to select desirable traits including stress tolerance.

Array used
Applied Biosystems™ Axiom™ SoyaSNP Array

Link
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0224074

Keywords
GWAS, soybean SNP

Citation
Jeong N, Kim S, Jeong S, et al. (2019) Korean soybean core collection: Genotypic and phenotypic diversity population structure and genome-wide association study. *PLOS ONE* 14(10):e0224074. DOI: 10.1371/journal.pone.0224074

24. Genome-wide association study for ultraviolet-B resistance in soybean (*Glycine max L.*)

Due to the depletion of the ozone layer, UV-B rays are becoming a stressor for the growth of soybean- a major global legume crop. Understanding the UV-B response via genome-wide studies can provide stronger markers for producing UV-B resistance populations. Using Applied Biosystems™ Axiom™ SoyaSNP, researchers genotyped 688 soybean germplasms, including landraces, breeding lines, varieties, and collections that helped identify five candidate genes related to UV-B resistance. It was established that CRY and CRY1 genes associated with DNA repair, are the most likely candidates for UV-B resistance that can be used in marker-assisted selection for breeding resistant soybean populations.

Basic animal or crop
Soybean

Breeding goal
Prevent yield losses in soybean populations through marker-assisted selection UV-B resistant traits.

Array used
Applied Biosystems™ Axiom™ SoyaSNP Array

Link
https://www.mdpi.com/2223-7747/10/7/1335

Keywords
Genome-wide study, UV-B resistance, soybean genotypes

Citation
Lee T, Kim KD, Kim J, et al. (2021) Genome-Wide Association Study for Ultraviolet-B Resistance in Soybean (Glycine max L.). *Plants* 10(7):1335. DOI: 10.3390/plants10071335

25. Associative mapping for exotic soybean germplasm grain yield in high temperatures

Heat stress is a major abiotic stressor that can significantly reduce soybean yields in high-temperature regions like MATOPIBA, Brazil. Identifying the SNP associated with heat tolerance can help grow soybean varieties resistant to high temperatures. Soybean collections (consisting of plant introductions from 32 countries and control cultivars) were genotyped using Applied Biosystems™ Axiom™ SoyaSNP to conduct associative mapping for locating desirable SNPs. Genomic studies revealed 16 variations associated with four high-temperature traits (plant height, agronomic value, seed weight, and grain yield) which can be valuable tools for marker-assisted selection in soybean breeding programs.

Basic animal or crop
Soybean

Breeding goal
Select soybeans with improved plant height, agronomic value, seed weight, and grain yield traits capable of surviving high temperatures.

Array used
Applied Biosystems™ Axiom™ SoyaSNP Array

Link
https://www.scielo.br/j/rcaat/a/NXKsbykgMChtsKddBTGsmrp/

Keywords
Marker-assisted selection, associative mapping, heat tolerance

Citation
Sousa CC, Assunção US, Ferreira MC, et al. (2022) Associative mapping for exotic soybean germplasm grain yield in high temperatures. *Revista Caatinga* 35(3):567–573. DOI: 10.1590/1983-21252022v35n307rc

26. GWAS of adventitious root formation in roses identifies a putative phosphoinositide phosphatase (*SAC9*) for marker-assisted selection

Rose propagation using stem cuttings is often inconsistent as the ability to form adventitious roots varies significantly among different rose genotypes. Identifying the genetic variations in rooting ability is essential to cultivating roses with efficient propagation ability. Applied Biosystems™ Axiom™ WagRhSNP was used to examine tetraploid allele dosages for each SNP for garden and cut rose populations. GWAS analysis facilitated the identification of SNP on the SAC9 gene and the development of a KASP marker associated with adventitious root formation for efficient rose propagation.

Basic animal or crop
Rose

Breeding goal
Efficient rose propagation by targeting genes associated with adventitious root formation using marker-assisted selection.

Array used
Applied Biosystems™ Axiom™ WagRhSNP Array

Link
https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0287452

Keywords
Tetraploid allele dosages, KASP marker, rose SNP

Citation
Wamhoff D, Patzer L, Schulz DF, et al. (2023) GWAS of adventitious root formation in roses identifies a putative phosphoinositide phosphatase (SAC9) for marker-assisted selection. *PLOS ONE* 18(8):e0287452. DOI: 10.1371/journal.pone.0287452

27. Rose Rosette disease resistance loci detected in two interconnected tetraploid garden rose populations

Rose Rosette Disease (RRD) is a major threat to the rose in the United States affecting plant growth and causing death within a few years. Understanding the genetic basis of resistance to the pathogen (*Rose rosette emaravirus*) in tetraploid roses can facilitate the development of resistant species. The genotyped data provided through Applied Biosystems™ Axiom™ WagRhSNP enabled the researchers to create high-density linkage maps for two garden rose populations and isolate individuals carrying the resistance locus. A partial resistance locus to RRV on linkage group 5, inherited from the Brite Eyes rose cultivar, was identified that can accelerate marker-assisted selection for developing RRV-resistant rose.

Basic animal or crop
Rose

Breeding goal
Develop rose populations resistant to RRV (*rose rosette emaravirus*) which is a threat to the plant's growth.

Array used
Applied Biosystems™ Axiom™ WagRhSNP Array

Link
https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2022.916231/full

Keywords
Linkage group, rose rosette emaravirus, quantitative trait loci

Citation
Lau J, Young EL, Collins S, et al. (2022) Rose Rosette Disease Resistance Loci Detected in Two Interconnected Tetraploid Garden Rose Populations. *Frontiers in Plant Science* 13:916231. DOI: 10.3389/fpls.2022.916231

28. Association of single nucleotide polymorphisms (SNPs) to black spot resistance in roses

Black spot (caused by Diplocarpon rosae fungus) is a prevalent yet severe disease of garden roses worldwide reducing plant production and growth. There is a lack of studies on the genetic basis of this disease. To fill this gap, Applied Biosystems™ Axiom™ WagRhSNP was sued to conduct GWAS on 96 rose genotyped cultivars sourced from Hannover, Germany greenhouse. The genomic analysis identified 149 SNPs significantly associated with resistance to black spot field mixtures indicating it to be a multi-loci trait. This information can potentially be used for efficient breeding of black spot-resistant rose varieties.

Basic animal or crop
Rose

Breeding goal
Efficient breeding of rose cultivars that are resistant to black spot disease caused by fungus.

Array used
Applied Biosystems™ Axiom™ WagRhSNP Array

Link
https://ejournal.unipas.ac.id/index.php/Agro/article/view/1316

Keywords
Diplocarpon rosae, rose GWAS, black spot

Citation
Yemer GK, Debener T, Linde M. (2024) Association of Single Nucleotide Polymorphisms (SNPs) to Black Spot Resistance in Roses. *Agro Bali: Agricultural Journal* 7(1):1–16. DOI: 10.37637/ab.v7i1.1316

29. Genetic analysis of callus formation in a diversity panel of 96 rose genotypes

Callus formation via In-vitro propagation is a common strategy for developing rose cultivators with desirable traits, but the process is labor-intensive and complex due to the genetic variability of this trait. Understanding the genetic factors associated with callus formation can help make in-vitro propagation efficient. Researchers used the Applied Biosystems™ Axiom™ WagRhSNP array to analyze the genetic variations in a diverse panel of 96 rose genotypes. GWAS analysis resulted in the identification of 4 SNPs strongly associated with callus formation that can serve as a starting point in locating candidate genes for callus formation which is important to make the *in-vitro* propagation quick.

Basic animal or crop
Rose

Breeding goal
To make *in-vitro* propagation of rose cultivars faster by tagreting the genes associated with callus formation.

Array used
Applied Biosystems™ Axiom™ WagRhSNP Array

Link
https://link.springer.com/article/10.1007/s11240-020-01875-6

Keywords
Rosa x hybrida, callus induction

Citation
Nguyen THN, Winkelmann T, Debener T. (2020) Genetic analysis of callus formation in a diversity panel of 96 rose genotypes. *Plant Cell Tiss Organ Cult* 142:505-517. DOI: 10.1007/s11240-020-01875-6

30. Genome-wide association study of healthful flavonoids among diverse Mandarin accessions

The amount of flavonoids in Mandarian citrus is significant for its nutritional content and disease resistance. However, traditional citrus breeding didn't explore the genetics of flavonoids in Mandarin accession. The Applied Biosystems™ Axiom™ Citrus 56AX array was used for a genome-wide study on 137 diverse genotyped Mandarin accessions. Genetic analysis identified 4 candidate genes associated with the biosynthesis of specific flavonoids in the peel, pulp, and seed samples that can be used in breeding mandarins with higher levels of flavonoids through marker-assisted selection.

Basic animal or crop
Citrus

Breeding goal
Breed Mandaran citrus with higher levels of flavaniod content as it imparts immunity and nutritional value to the plant

Array used
Applied Biosystems™ Axiom™ Citrus 56AX Array

Link
https://www.mdpi.com/2223-7747/11/3/317

Keywords
Citrus genotyping, candidate genes, polyphenols

Citation
Mattia MR, Du D, Yu Q, et al. (2022) Genome-Wide Association Study of Healthful Flavonoids among Diverse Mandarin Accessions. *Plants* 11(3):317. DOI: 10.3390/plants11030317

31. Exploring the phylogenetic relationship among citrus through leaf shape traits: A morphological study on citrus leaves

Citrus phylogeny is a complex process due to which its breeding has been focused on fruit traits only overlooking the inheritance of foliar traits. This research explored the relationship between leaf morphology and the evolutionary history of citrus to understand its origins, domestication, and adaptation. Applied Biosystems™ Axiom™ Citrus HD Genotyping Array genotyped the entire Givaudan Citrus Variety Collection consisting of 1000 accessions that enabled researchers to identify 382 genetically distinct accessions that were not part of the clonal lineage. The leaf morphology analysis conducted on these accessions found that variations in citrus leaf blade width contribute to the diversity observed among citrus species that can potentially facilitate breeders to produce cultivars with superior traits.

Basic animal or crop
Citrus

Breeding goal
Using leaf morphology anallysis among original and hybrid citurs to advance citrus breeding focused on selecting superior traits.

Array used
Applied Biosystems™ Axiom™ Citrus HD Genotyping Array

Link
https://www.mdpi.com/2311-7524/9/7/793

Keywords
Citrus evolution, leaf morphology

Citation
Traband RC, Wang X, Lui J, et al. (2023) Exploring the Phylogenetic Relationship among Citrus through Leaf Shape Traits: A Morphological Study on Citrus Leaves. *Horticulturae* 9(7):793. DOI: 10.3390/horticulturae9070793

32. Revealing genetic determinants of photosynthesis-related traits in citrus via genome-wide association studies

The photosynthesis traits, including chlorophyll content, absorbance, fluorescence, and photochemical efficiency play an important in determining the ability of citrus plants to convert sunlight into fruits. Understanding the genetic basis of photosynthesis can help breeders produce varieties with improved traits. Using a tailored Applied Biosystems™ Axiom™ Citrus56AX array, researchers conducted GWAS that identified 125 genomic loci and 189 potentially associated genes responsible for variations in 11 distinct photosynthesis-related traits. These genetic markers can facilitate marker-assisted breeding once analytically evaluated.

Basic animal or crop
Citrus

Breeding goal
Select citrus breeds that are better at converting sunlight into fruits by targeting their photosynthesis trait.

Array used
Tailed Applied Biosystems™ Axiom™ Citrus56AX Array

Link
https://www.maxapress.com/article/doi/10.48130/frures-0024-0013

Keywords
Photosynthesis, citrus genotyping

Citation
Wang X, Traband R, Hiraoka Y, et al. (2024) Revealing genetic determinants of photosynthesis-related traits in citrus via genome-wide association studies. *Fruit Research* 4:e020. DOI: 10.48130/frures-0024-0013

33. Mining and genomic characterization of resistance to tan spot, Stagonospora nodorum blotch (SNB), and Fusarium head blight in Watkins core collection of wheat landraces

Tan spot, Stagonospora nodorum blotch (SNB), and Fusarium Head Blight (FHB) are common fungal disorder of wheat landraces. Despite their prevalence, their genetics have not been explored. Researchers used the Applied Biosystems™ Axiom™ Wheat Breeders Genotyping Array to genotype Watkins collection of wheat landraces and identify new quantitative trait loci (QTLs). GWAS analysis identified 30 significant SNPs associated with resistance to these disorders, including novel QTLs for tan spot resistance, providing valuable information for marker-assisted selection (MAS) for wheat breeding programs.

Basic animal or crop
Wheat

Breeding goal
Use marker-assisted breeding to produce wheat varieties resistant to fungal disorders (Tan spot, Stagonospora nodorum blotch, and Fusarium Head Blight).

Array used
Applied Biosystems™ Axiom™ Wheat Breeders Genotyping Array

Link
https://link.springer.com/article/10.1186/s12870-019-2093-3

Keywords
Watkins landrace cultivars, genome-wide association study

Citation
Halder J, Zhang J, Ali S, et al. (2019) Mining and genomic characterization of resistance to tan spot, Stagonospora nodorum blotch (SNB), and Fusarium head blight in Watkins core collection of wheat landraces. *BMC Plant Biol* 19:480. DOI: 10.1186/s12870-019-2093-3

34. Deciphering of the genetic control of phenology, yield, and pellicle color in Persian walnut (*Juglans regia L.*)

Persian walnut while native to Central Asia is widely cultivated in temperate regions of America, Europe, and Asia. The molecular pathways controlling the yield, nut quality, and ability to adapt to specific climate conditions are not known yet. The Applied Biosystems™ Axiom™J. regia 700K SNP array was used to genotype 896 Persian walnuts to perform quantitative trait loci (QTL) mapping and genome-wide association studies (GWAS). The process helped identify the loci, candidate genes, and molecular pathways associated with leafing date, harvest date, yield, lateral fruit-bearing, and pellicle color traits that can help improve the Persian walnut's breeding programs.

Basic animal or crop
Walnut

Breeding goal
Develop Persian walnut cultivars that are better adapted to the varying environment conditions.

Array used
Applied Biosystems™ Axiom™J. regia 700K SNP array

Link
https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2019.01140/full

Keywords
High-density linkage maps, QTL mapping, GWAS

Citation
Marrano A, Sideli GM, Leslie CA, et al. (2019) Deciphering of the Genetic Control of Phenology, Yield, and Pellicle Color in Persian Walnut (Juglans regia L.). *Frontiers in Plant Science* 10:470068. DOI:10.3389/fpls.2019.01140

35. QTL analysis and CAPS marker development linked with russet in pear (Pyrus spp.)

The formation of russet in pear skin is a significant trait attributing to the resistance against external stresses and commercial value. Understanding the genetics of russeting through a high-density SNP can help improve pear breeding. Using Applied Biosystems™ Axiom™ 70K Genotyping array, researchers genotyped 'Whangkeumbae', 'Minibae' pear cultivars and their 183 F1 progeny to create a high-density genetic linkage map. The genetic analysis facilitated the identification of a specific QTL on chromosome 8 associated with russeting and the development of a CAPS marker which can be used in pear breeding programs for distinguishing between cultivars with high and low russet coverage.

Basic animal or crop
Pear

Breeding goal
Select cultivars with high russet coverage to have resilient and commercially valuable pear populations.

Array used
Applied Biosystems™ Axiom™ 70K Genotyping Array

Link
https://www.mdpi.com/2223-7747/11/23/3196

Keywords
Pear genotyping, linkage map, russet formation loci

Citation
Kim Y, Oh S, Han H, et al. (2021) QTL Analysis and CAPS Marker Development Linked with Russet in Pear (Pyrus spp.). *Plants* 11(23):3196. DOI: 10.3390/plants11233196

36. Identification of consistent QTL for time to maturation in Virginia-type peanut (*Arachis hypogaea L.*)

Time-to-maturation (TTM) is an important trait contributing to adaptability, yield, and quality in peanuts (Arachis hypogaea L). Little is known regarding the genetic control of TTM in Virginia market-type peanuts. Using the Applied Biosystems™ Axiom™ Arachis 47K SNP array, recombinant inbred lines (RILs) were genotyped to construct a high-density genetic map. This analysis led to the identification of two consistent quantitative trait loci (QTLs) for TTM, located on chromosomes A04 and B03 that can be targeted in marker-assisted breeding for Virginia-type peanut cultivars with greater adaptability.

Basic animal or crop
Peanut

Breeding goal
Improve adaptability of Virginia-type peanut cultivars by targeting time to maturation genes.

Array used
Applied Biosystems™ Axiom™ Arachis 47K SNP Array

Link
https://link.springer.com/article/10.1186/s12870-021-02951-5

Keywords
Time-to-maturation, Virginia market-type peanut, recombinant inbred line

Citation
Kunta S, Agmon S, Chedvat I, et al. (2021 Identification of consistent QTL for time to maturation in Virginia-type Peanut (Arachis hypogaea L.). *BMC Plant Biol* 21:186. DOI: 10.1186/s12870-021-02951-5

37. Genetic mapping and QTL analysis for peanut smut resistance

South American peanuts are highly susceptible to smut disease (caused by Thecaphora frezii). The genetic resistance to this has been explored in wild Arachis species only, and not in tetraploid genetic background. Using the Applied Biosystems™ Axiom™ 48K Arachis2 array, researchers genotyped 103 recombinant inbred lines (RILs) derived from a cross between a susceptible and resistant synthetic amphidiploid peanut line. The genetic analysis identified a major QTL on chromosome A08 and a minor QTL on A02/B02 (ntrogressed from wild Arachis species) which were found to increase the resistance to smut by 57%. The findings of this research can potentially make the marker-assisted selection for smut-resistant peanuts efficient.

Basic animal or crop
Peanut

Breeding goal
Smut resistance

Array used
Applied Biosystems™ Axiom™ 48K Arachis2 Array

Link
https://link.springer.com/article/10.1186/s12870-021-03023-4#Sec8

Keywords
Linkage map, smut resistance, peanut SNP

Citation
de Blas FJ, Bruno CI, Arias RS, et al. (2021) Genetic mapping and QTL analysis for peanut smut resistance. *BMC Plant Biol* 21:312. DOI: 10.1186/s12870-021-03023-4

38. Genome-wide association study reveals candidate genes involved in fruit trait variation in Persian walnut (Juglans regia L.)

Understanding the genetic determinants of fruit quality traits in walnuts is essential to breeding new cultivars and meeting the producers' and consumers' needs. Previous studies lacked the combination of accurate phenotypic data and the use of the unique INRAE walnut germplasm collection. The Applied Biosystems™ Axiom™ J. regia 700K SNP array was used to genotype 170 accessions of walnut that allowed the researchers to perform GWAS to identify multiple marker-trait associations (MTAs) for 25 fruit traits, including morphometrics, shape, volume, weight, cracking, and nutritional components, along with a highly significant SNP on chromosome 14. A few candidate genes for cell wall function and calcium signaling were also proposed that can be used as molecular markers in walnut breeding programs.

Basic animal or crop
Walnut

Breeding goal
Develop walnut cultivars with improved fruit quality traits that increase their economic value.

Array used
Applied Biosystems™ Axiom™ J. regia 700K SNP array

Link
https://www.frontiersin.org/journals/plant-science/articles/10.3389/fpls.2020.607213/full

Keywords
Linkage disequilibrium, GWAS, fruit traits

Citation
Bernard A, Crabier J, Donkpegan AS, et al. (2021) Genome-Wide Association Study Reveals Candidate Genes Involved in Fruit Trait Variation in Persian Walnut (Juglans regia L.). *Frontiers in Plant Science* 11:607213. DOI:10.3389/fpls.2020.607213

39. Reconstruction of the largest pedigree network for pear cultivars and evaluation of the genetic diversity of the USDA-ARS national pyrus collection

The USDA-ARS National Clonal Germplasm Repository (NCGR) houses one of the world's largest and most diverse pear collections but lacks comprehensive, high-density genetic characterization. The Applied Biosystems™ Axiom™ Axiom Pear 70K Genotyping array was used to perform population structure analysis and get clarity on the genetic diversity of Pyrus. As a result, the largest pedigree of pear cultivars was reconstructed which revealed a high degree of inbreeding. Researchers also discovered new synonyms, and mutants and identified potential labeling errors, providing valuable information for peer breeding programs.

Basic animal or crop
Pear

Breeding goal
Reconstruct the largest pedigree of pear cultivars and understand the genetic diversity to inform future breeding programs.

Array used
Applied Biosystems™ Axiom™ Axiom Pear 70K Genotyping Array

Link
https://academic.oup.com/g3journal/article/10/9/3285/6060139

Keywords
Pear genotyping, pedigree construction, population structure, germplasm characterization

Citation
Montanari S, Postman J, Bassil NV. (2020) Reconstruction of the Largest Pedigree Network for Pear Cultivars and Evaluation of the Genetic Diversity of the USDA-ARS National Pyrus Collection. *G3 Genes|Genomes|Genetics* 10(9):3285-3297. DOI: 10.1534/g3.120.401327

40. Genome-wide analysis highlights genetic admixture in exotic germplasm resources of Eucalyptus and unexpected ancestral genomic composition of interspecific hybrids

Eucalyptus tree makes up most of the forest landscape in Australia, but due to the complex genotyping of these plants, they have been underexplored. Hybrid eucalyptus are widely planted due to their fast growth but their genetic makeup is unknown. Using Applied Biosystems™ Axiom™ Eucalyptus 72K Genotyping array, scientists explored genetic variation between 440 eucalyptus. The SNP-based hybrid analysis showed the prevalence of unintentional hybridization and demonstrated genomic patterns deviating from the expected pedigree due to selection patterns toward the fast-growing E. grandis genome.

Basic animal or crop

Eucalyptus

Breeding goal

Identify the actual ancestral origin of superior hybrids and discard unwanted hybrid combinations.

Array used

Applied Biosystems™ Axiom™ Eucalyptus 72K Genotyping Array

Link

https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0289536

Keywords

Hybridization, directional selection

Citation

Novaes E, Grattapaglia D. (2023) Genome-wide analysis highlights genetic admixture in exotic germplasm resources of Eucalyptus and unexpected ancestral genomic composition of interspecific hybrids. *PLOS ONE* 18(8):e0289536. DOI: 10.1371/journal.pone.0289536

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