

DATABASE

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Development of a comprehensive GWAS atlas for chicken breeds

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Abstract

Modern poultry breeding requires integrated genomic and phenotypic data to optimize production traits, yet comprehensive resources remain fragmented and often inaccessible. We developed a comprehensive electronic Genome-Wide Association Studies (GWAS) Atlas for chicken breeds that consolidates genomic data with phenotypic information from both commercial and heritage breeds. This web-based platform addresses critical gaps in existing databases through a unified, cross-referenced system linking more than 2,500 SNPs and other DNA alterations to 454 documented traits across diverse chicken breeds. The Atlas features four integrated portals: breed profiles with visual catalogs, trait-based breed searches using hierarchical classification, genomic information with DNA alterations and affected genes linked to specific traits, and advanced search functionality. A key innovation is the platform's ability to reveal previously hidden cross-source genetic associations, such as connecting the GJA5 gene's roles in both egg production and feather coloration. This publicly accessible resource provides breeders and researchers worldwide with comprehensive tools for informed decision-making in poultry breeding programs.

Keywords: Chicken, Heritage Breeds, GWAS

Introduction

The global poultry industry comprises a complex network of interconnected components, spanning feed production, hatcheries, breeding programs, and processing facilities [1–5]. Within this system, modern poultry breeding confronts an urgent paradox: while genomic technologies have generated unprecedented data on beneficial traits, breeders lack the integrated tools to translate this knowledge into sustainable production improvements. Primary goals for the industry, including accelerating growth rates, improving feed conversion efficiency, and bolstering disease resistance [4, 6–9], increasingly depend on genomic-assisted selection, yet the required resources remain fragmented and inaccessible.

Over the past three decades, poultry breeding has undergone revolutionary transformation driven by Next-Generation Sequencing (NGS) technologies [10–22]. This has enabled the integration of NGS data with phenotypic observations through sophisticated database



systems and facilitated Genome-Wide Association Studies (GWAS) for identifying DNA variants linked to desirable production traits [10–17]. The extensive domestication history of chickens has produced a diverse array of heritage breeds, each adapted to specific environments [23–27]. The Middle Eastern Fayoumi exhibits exceptional heat resistance [28, 29], while the Canadian Chantecler demonstrates superior cold tolerance [30]. These breeds serve as living repositories of genetic variants with immense value for addressing current economic issues in poultry industry such as climate resilience challenges.

However, this wealth of genomic information remains trapped in a labyrinth of disconnected resources, creating insurmountable barriers for practical breeding applications. Consider a typical scenario: A producer seeking disease resistance or heat tolerance alleles to adapt their flock to evolving conditions must navigate multiple, incompatible databases to gather essential information. ChickenQTLdb [31, 32] might provide chromosomal regions associated with a desirable trait but only at low-resolution intervals, lacking the SNP-level precision needed for marker-assisted selection. To obtain specific variant data, the breeder must then consult Ensembl [33], which offers detailed genomic coordinates but divorces these variants from their phenotypic context and breed-specific validation.

The challenge deepens when attempting to verify these associations. Published GWAS studies contain the detailed SNP-trait relationships needed for confident selection decisions, yet remain scattered behind journal paywalls with inconsistent data formats that prevent systematic comparison [19]. Most critically, heritage breed characteristics, developed through centuries of natural selection and potentially harboring the most relevant adaptive variants, exist only in descriptive text within non-digital breed registries and historical archives. These valuable phenotypic observations cannot be computationally linked to modern molecular data.

No existing platform bridges these disparate resources to enable evidence-based selection decisions. Breeders are left to manually piece together fragments of information from multiple sources, without tools to validate which associations replicate across breeds or environmental conditions. This fragmentation transforms what should be a data-driven selection process into an exercise in incomplete information synthesis, undermining the promise of genomic-assisted breeding.

The fragmentation of genomic resources presents specific bioinformatics challenges that extend beyond simple data availability. Current databases employ fundamentally incompatible data architectures: QTLdb stores QTL positions as linkage map intervals in centiMorgans [31, 32], while EVA requires precisely formatted VCF files with base-pair coordinates, making automated data integration computationally intractable [34]. This technical incompatibility is compounded by heterogeneous data models and ontologies across platforms.

To address these shortcomings, we developed a comprehensive GWAS Atlas for chicken breeds that consolidates fragmented genomic data from ChickenQTLdb, Ensembl, and peer-reviewed GWAS publications; incorporates diverse chicken breeds including heritage varieties with unique adaptive traits; provides cross-breed validation of genetic markers; and offers a unified platform with full traceability to primary sources. This integrated resource transforms the current fragmented landscape into a practical tool for genomic-assisted breeding, essential for meeting the demands of sustainable intensification in a changing climate.

Materials and methods

Data collection

A comprehensive research effort was conducted to compile data on various chicken breeds from multiple sources, including reputable chicken encyclopedias, scholarly publications, and specialized databases. The University of Sydney's Online Mendelian Inheritance in Animals (OMIA) website served as a particularly valuable resource for systematic documentation of Mendelian traits [35].

Our data curation focused on four major areas:

1. **Mendelian Traits Catalog:** We generated an extensive catalog of Mendelian traits observed across chicken breeds, systematically documenting phenotypic expression, associated breeds, and genetic abnormalities where possible [25, 35–37].
2. **Heritage Breed Characteristics:** We curated datasets describing distinguishing characteristics of historical chicken breeds, including size, egg production capacity, temperament, and breed-specific features [24–26, 38].
3. **Genomic Data Integration:** We integrated data from multiple online databases and peer-reviewed studies to build a cohesive resource for chicken genomics SNPs and other DNA alterations. This process involved linking phenotypes to GWAS-detected DNA anomalies and cataloging the breeds analyzed [37, 39–46]. Close to 2,300 SNPs have been documented in our current dataset.
4. **Visual Documentation:** We obtained images of chicken breeds from public domain and royalty-free sources, providing full attribution in accordance with license requirements.

All data were compiled with appropriate citations to original sources. Each trait included in the GWAS Atlas for Chicken Breeds platform is cross-referenced with either an external online database or a research paper. Given the extensive number of references used, the majority of these citations are included on the GWAS website rather than in this manuscript for brevity.

Data standardization and Integration

The primary challenge in constructing the user-friendly online GWAS Atlas lay in reconciling information from heterogeneous data sources, each employing different schemas, nomenclature, and file formats. We developed a comprehensive preprocessing framework that normalizes raw data from CSV exports, XML feeds, and PDF tables into a unified representation.

This involved creating source-specific parsers, automated transformation routines, and a manually curated synonym dictionary to resolve conflicting terminologies.

QTL intervals sourced from ChickenQTLdb were retained as chromosomal coordinates (start and end positions referenced to the GalGal6/GRCg6a assembly) and cross-referenced with Ensembl gene annotations to identify candidate genes falling within or immediately flanking each interval. Entries that could not be confidently mapped to a named gene are explicitly flagged in the database as locus-level associations to prevent misinterpretation as direct gene-trait links.

All genomic coordinates were standardized to the GalGal6 (GRCg6a) reference assembly. Where source data were reported against an earlier assembly (e.g., GalGal5), coordinates were remapped using the UCSC liftOver utility with the appropriate gallinaceous chain file; SNP liftOver was not used in this study. Gene identifiers were harmonized to NCBI Gene IDs as canonical references, with our manually curated synonym dictionary resolving naming conflicts and common aliases across QTLdb, Ensembl, EVA, and published GWAS sources.

Database architecture and technologies

We designed a flexible relational schema using MySQL to accommodate current and future data additions. Core entities like Breeds, Traits, SNPs, and Genes are represented in dedicated tables, while intermediary join tables capture many-to-many relationships and synonym mappings. Referential integrity is enforced through foreign-key constraints, and performance is optimized via targeted indexing on frequently queried fields.

The application employs a multi-tier architecture:

- **Frontend:** HTML5, CSS3, and JavaScript for responsive, mobile-friendly interfaces [47].
- **Backend:** PHP running under Apache web server for request routing and business logic [48].
- **Database:** MySQL for robust data storage, indexing, and retrieval [49].

All curated data was organized into well-structured CSV files compatible with standard analysis tools, and cross-referenced with external databases or research papers to ensure scientific validity and traceability.

Results

Platform architecture and features

The GWAS Atlas website incorporates four major portals serving distinct research purposes (see Fig. 1):

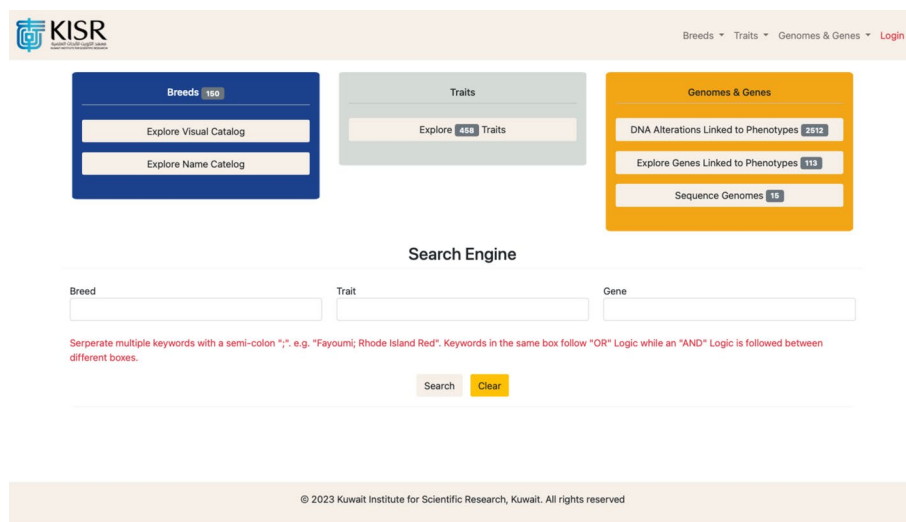


Fig. 1 Application search features of the GWAS Atlas website. Screenshot of the website page displaying the search features, showing all four major portals (Breed, Traits, Genome and Gene, and Advanced Search Engine)

1. **Breed Portal:** Users can select breeds of interest to access detailed profiles including physical characteristics, behavioral traits, and historical information (Fig. 1, upper left panel). The portal features two functional windows: a clickable visual catalogue where users can scroll through pictures of different breeds (Fig. 2A), and a clickable name catalogue where breed names are listed alphabetically (Fig. 2B). Additional detailed information about breed genetics, including inherited traits and genomic data, is displayed in the lower panel (Fig. 2C).
2. **Trait Portal:** Users can select specific traits (e.g., comb type, feather pattern, egg production capacity) to view all chicken breeds exhibiting those characteristics (Fig. 1, middle upper panel). We documented 454 traits exhibited across all known

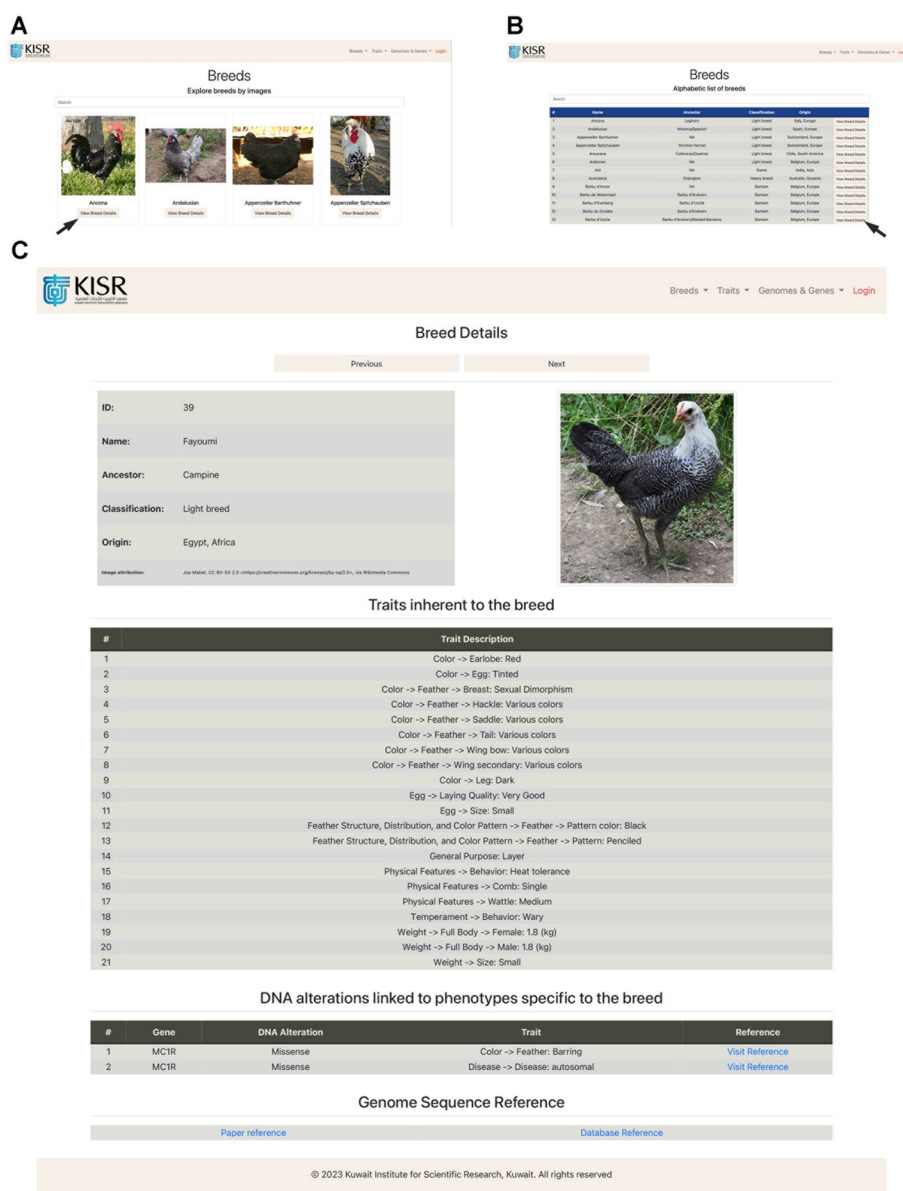


Fig. 2 Breed Profile Website Interface. Screenshot showing the results of clicking the GWAS Atlas breed window (Fig. 1, upper left), which opens two exploration options: (A) visual breed selection through images, and (B) text-based breed search by name. Both interfaces have clickable icons (arrows) that provide comprehensive breed information including phenotypic traits, country of origin, and available genomic data

chicken breeds, with each trait linked to references characterizing the associated genetic factors (Fig. 3A). To enhance clarity and facilitate efficient querying in the trait portal, we organized trait data into a four-level hierarchical schema: Main Category, Sub-Category-1, Sub-Category-2, and Value. Traits are first assigned to broad Main Categories (e.g., “Physical Features”), then progressively refined through Sub-Category-1 (e.g., “Comb Type”) and Sub-Category-2 (e.g., “Shape”) before specifying particular Values (e.g., “Single Comb”). By clicking the “view trait details” icon, further information is provided including the name of genes, breeds, and references linked to trait (Fig. 3B) [50–77].

3. Genomic and Gene Portal: Provides access to genomic information (Fig. 1, upper right panel). The DNA alterations linked to phenotypes section primarily contains GWAS-identified variants associated with specific phenotypes. The portal lists potentially affected genes, types of genomic alterations detected, and their associated traits (Fig. 4A). Clicking the “view DNA alteration” icon reveals additional details (Fig. 4B). The “Explore genes linked to phenotypes” portal contains a curated list

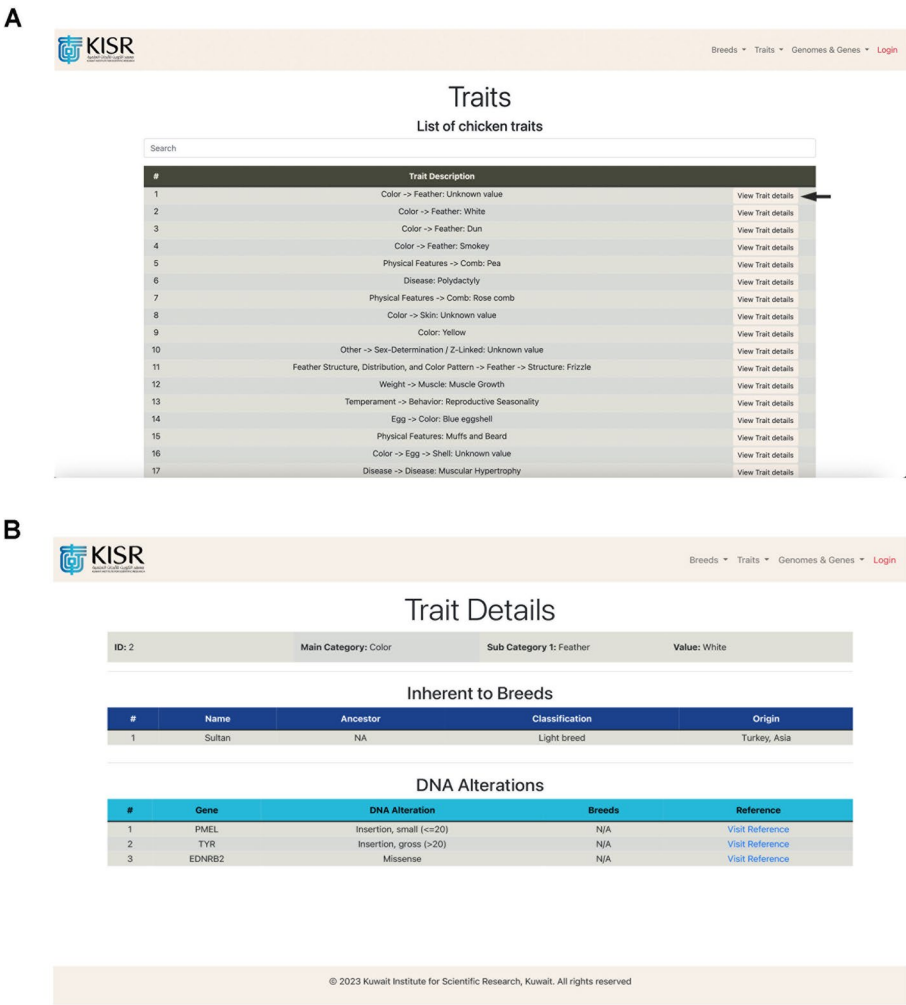
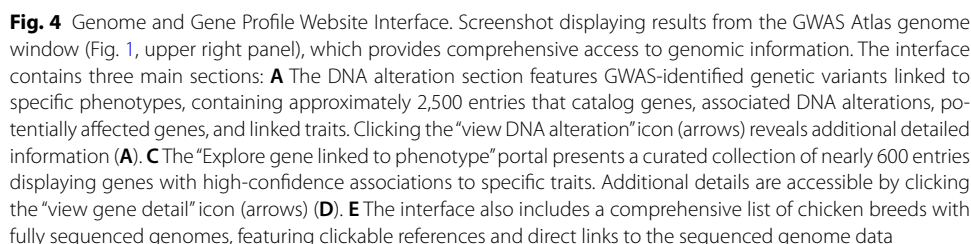


Fig. 3 Trait Profile Website Interface. Screenshot showing the results of clicking the GWAS Atlas trait window (Fig. 1, middle upper panel). This section of the GWAS Atlas website provides detailed descriptions of 454 traits documented across all known chicken breeds (A). Each trait entry includes a clickable reference icon (arrows) that links directly to the literature characterizing the associated genetic factors. By clicking the “view trait details” icon, further information is provided including the name of genes, breeds, and references linked to trait (B)



4. **Advanced Search Engine:** Enables direct queries by breed name, gene, or specific genetic markers, facilitating rapid targeted searches across the entire database (Fig. 1, lower panel).

One of the Atlas’s most significant features is its ability to reveal cross-source associations previously unavailable in any single resource. For example, the GJA5 gene appears to be significantly associated with egg number [57], while the OMIA database implicates the same gene in feather-color variation [78]. By linking both observations to the canonical GJA5 record, our database uncovers relationships that would otherwise remain obscured across separate databases.

Accessibility and user features

The platform includes advanced search functionality for complex queries combining traits, breeds, and genetic markers simultaneously. User login functionality enables registered researchers to contribute new data following verification processes, bookmark entries, and participate in expanding the knowledge base.

The resource is publicly available through Amazon Web Services with a subdomain from the Kuwait Institute for Scientific Research (KISR) at <http://cga.kisr.edu.kw/>, broadening accessibility to scientists and researchers worldwide.

Discussion

We report the development and release of the GWAS Atlas for Chicken Breeds, a comprehensive genomic resource addressing significant gaps in poultry genetics research and breeding. By consolidating fragmented data, integrating diverse breed information, and providing an intuitive interface, this resource facilitates more efficient and targeted breeding programs.

The integration of heritage breed information alongside commercial varieties represents a particular strength of our platform. While commercial breeds have been extensively studied for production traits, heritage breeds often harbor unique genetic adaptations that remain largely undocumented electronically. By capturing adaptations such as heat resistance in Fayoumi chickens or cold tolerance in Canadian breeds, our Atlas provides valuable genetic resources for climate-resilient breeding programs.

The comprehensive cross-referencing system addresses common limitations in existing databases by ensuring every entry links to peer-reviewed publications or established external databases. This enhances reliability and enables critical evaluation of underlying evidence before incorporating genetic associations into breeding programs.

Our hierarchical trait organization system and flexible database architecture enable sophisticated comparative analyses while maintaining user accessibility. Unlike specialized repositories focusing primarily on genetic variants or QTLs, our platform provides holistic integration of phenotypic, genetic, and visual information accessible to diverse user groups from genomics specialists to small-scale breeders.

It is also worth stating that integrated analysis revealed an important example of pleiotropy in poultry genetics: GJA5 gene, initially identified through GWAS for egg production traits [57], also influences feather color variation in the OML4 breed [78]. This discovery exemplifies the power of comprehensive database integration in uncovering pleiotropic effects that might be overlooked when analyzing traits in isolation. Such findings are particularly significant for poultry breeding programs, as they highlight potential unintended consequences of selection: selecting for improved egg production via GJA5 variants could inadvertently alter feather coloration phenotypes.

The ability of our GWAS Atlas to reveal these pleiotropic relationships through cross-database validation demonstrates a key advantage over fragmented resources. By integrating data from multiple sources and breeds, our platform enables researchers to identify genes with multiple phenotypic effects, facilitating more informed breeding decisions. This holistic view of gene function is essential for sustainable breeding strategies, as it allows breeders to anticipate and manage correlated responses to selection. Future updates to the Atlas will specifically highlight known pleiotropic loci to assist breeders in understanding the full phenotypic consequences of their selection decisions.

To contextualize the contribution of our GWAS Atlas, it is important to explicitly compare it with existing chicken genomic resources. As stated before, currently available databases each serve specific but limited functions. Chicken QTLdb [31, 32], while comprehensive in cataloging QTL regions across numerous traits, provides only chromosomal intervals without SNP-level resolution, making it difficult for breeders to identify specific variants for marker-assisted selection. Ensembl offers extensive genomic annotation and variant data but lacks phenotypic associations and breed-specific validation, requiring users to manually cross-reference with external sources [33]. The European Variation Archive (EVA) contains millions of chicken SNPs but presents them without trait associations or functional context [34]. Published GWAS studies, though containing valuable SNP-trait associations, remain scattered across journals with inconsistent data formats and limited accessibility [31, 32]. Perhaps most critically, heritage breed data, which represents centuries of natural selection for locally adapted traits, exists primarily in non-digital archives or breed registries. Our GWAS Atlas fundamentally differs by integrating these disparate resources into a unified platform that provides: (1) direct SNP-to-trait associations with full literature traceability, (2) a potential for cross-breed validation showing which associations replicate across genetic backgrounds, (3) digitized heritage breed characteristics linked to molecular markers, and (4) a single query interface that eliminates the need for manual cross-referencing between databases.

This integration transforms what currently requires hours of manual searching across multiple databases into a single, evidence-based query, directly addressing the practical needs of modern poultry breeding programs. The platform enables breeders to identify not just any genetic variants, but specifically those that have been validated across different genetic backgrounds and environmental conditions. By incorporating heritage breed data, we preserve invaluable genetic resources while making them computationally accessible for the first time. This comprehensive approach ensures that genomic discoveries can finally be translated into practical breeding decisions, fulfilling the long-standing promise of genomic-assisted selection in poultry production.

To illustrate the practical utility of the Atlas, consider the scenario described in the Introduction: a breeder seeking heat-tolerance alleles for a commercial laying flock. Beginning at the Trait Portal, the user queries “heat tolerance” and retrieves all documented breeds exhibiting this characteristic, including the Middle Eastern Fayoumi. Navigating to the Genomic and Gene Portal, the breeder can view GWAS-identified SNPs and candidate genes associated with thermotolerance phenotypes, together with the source publications supporting each association. The Advanced Search Engine allows simultaneous filtering by trait, breed, and gene to narrow results to the most replicated markers. The identified variants and their chromosomal coordinates can then be exported and submitted directly to a genotyping service or incorporated into a marker-assisted selection pipeline, achieving in a single session what previously required hours of manual cross-referencing across incompatible databases.

The public availability of this resource represents our commitment to open science and global collaboration. As climate change and food security challenges intensify, the need for resilient, productive chicken breeds becomes increasingly critical. The GWAS Atlas for Chicken Breeds contributes to addressing these global challenges by providing comprehensive, accessible genomic information that enhances poultry breeding capabilities worldwide.

By enabling greatly enhanced cross-source genetic associations and maintaining rigorous scientific traceability, this platform represents a significant advancement in poultry genomics research and practical breeding applications.

Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s12859-026-06427-x>.

Supplementary Material 1

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Author contributions

1. BA was responsible for writing the manuscript, identify the major databases required for this project2. NA was responsible for manually curating the Mendelian traits and SNPs dataset3. AA was responsible for manually curating datasets that describes the core traits of various chicken breeds4. HA was responsible for collation and curation of big data types generated by BA, NA, and AA into a singular and unified cloud application.

Data availability

The GWAS Atlas for Chicken Breeds is publicly accessible at <http://cga.kisr.edu.kw/>. All curated datasets, including breed profiles, trait classifications, genomic variants, and associated metadata, are freely available through the web interface without registration requirements. The underlying database structure, data processing scripts, and comprehensive documentation are available upon reasonable request from the corresponding author. All original data sources are properly cited and linked within the database, ensuring full traceability to primary publications and external databases.

Declarations

Ethics approval and consent to participate

Not applicable. This study involved the compilation and curation of publicly available genomic and phenotypic data from existing databases and published literature. No human subjects, animal experiments, or collection of primary biological samples were involved in this research.

Consent for publication

Not applicable. This manuscript does not contain any individual person's data in any form (including individual details, images, or videos).

Competing interests

The authors declare no competing interests.

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