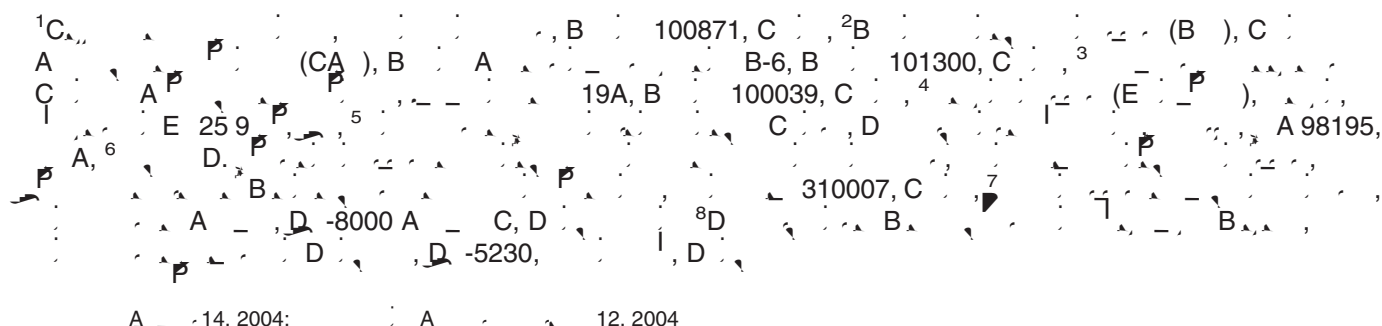


# ChickVD: a sequence variation database for the chicken genome

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## ABSTRACT

Working in parallel with the efforts to sequence the chicken (*Gallus gallus*) genome, the Beijing Genomics Institute led an international team of scientists from China, USA, UK, Sweden, The Netherlands and Germany to map extensive DNA sequence variation throughout the chicken genome by sampling DNA from domestic breeds. Using the Red Jungle Fowl genome sequence as a reference, we identified 3.1 million non-redundant DNA sequence variants. To facilitate the application of our data to avian genetics and to provide a foundation for functional and evolutionary studies, we created the 'Chicken Variation Database' (ChickVD). A graphical MapView shows variants mapped onto the chicken genome in the context of gene annotations and other features, including genetic markers, trait loci, cDNAs, chicken orthologs of human disease genes and raw sequence traces. ChickVD also stores information on quantitative trait loci using data from collaborating institutions and public resources. Our data can be queried by search engine and homology-based BLAST searches. ChickVD is publicly accessible at <http://chicken.genomics.org.cn>.

## INTRODUCTION

(*Gallus gallus*)

[illegible]

## DATA SOURCE

DATA SOURCE

## DATA CONTENT

[illegible]Table 1. *Mean values of the variables measured in the 1000 m and 2000 m races*

Figure 1: 3D scatter plot of simulated data points. The plot shows a dense cluster of points in a 3D space defined by axes x, y, and z. The points are distributed in a roughly spherical shape, with some outliers. The axes are labeled x, y, and z, and the plot is titled 'Figure 1: 3D scatter plot of simulated data points'.

## DATABASE USAGE AND ACCESS

The database is a collection of nucleic acid sequences, organized into a hierarchical structure. The sequences are stored in a relational database, and can be accessed using a variety of methods. The database is designed to be flexible and scalable, allowing for the storage and retrieval of large amounts of data. The sequences are organized into a hierarchical structure, with the top level being the species, and the bottom level being the individual sequences. The database is designed to be flexible and scalable, allowing for the storage and retrieval of large amounts of data. The sequences are organized into a hierarchical structure, with the top level being the species, and the bottom level being the individual sequences.

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## SYSTEM DESIGN AND IMPLEMENTATION

The system is designed to be flexible and scalable, allowing for the storage and retrieval of large amounts of data. The sequences are organized into a hierarchical structure, with the top level being the species, and the bottom level being the individual sequences. The database is designed to be flexible and scalable, allowing for the storage and retrieval of large amounts of data. The sequences are organized into a hierarchical structure, with the top level being the species, and the bottom level being the individual sequences.

Figure 1. A schematic diagram of the database structure, showing the hierarchy of species, sequences, and access methods.

## FUTURE DEVELOPMENTS

## ACKNOWLEDGEMENTS

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