

# Genome-wide association mapping and functional analysis of body weight, feed intake and walking ability in turkeys

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## Introduction

- The underlying genetic mechanisms affecting turkey growth traits have not been widely investigated
- Genome-wide association studies (GWAS) and pathway-based analysis became the primary approaches to identify candidate genes associated with complex traits

## Objectives

Identify regions associated with growth traits, feed intake and walking ability in a breeding turkey line using GWAS  
*and*  
Study the functional evidence that may support the impact of identified regions on these economic traits in turkeys

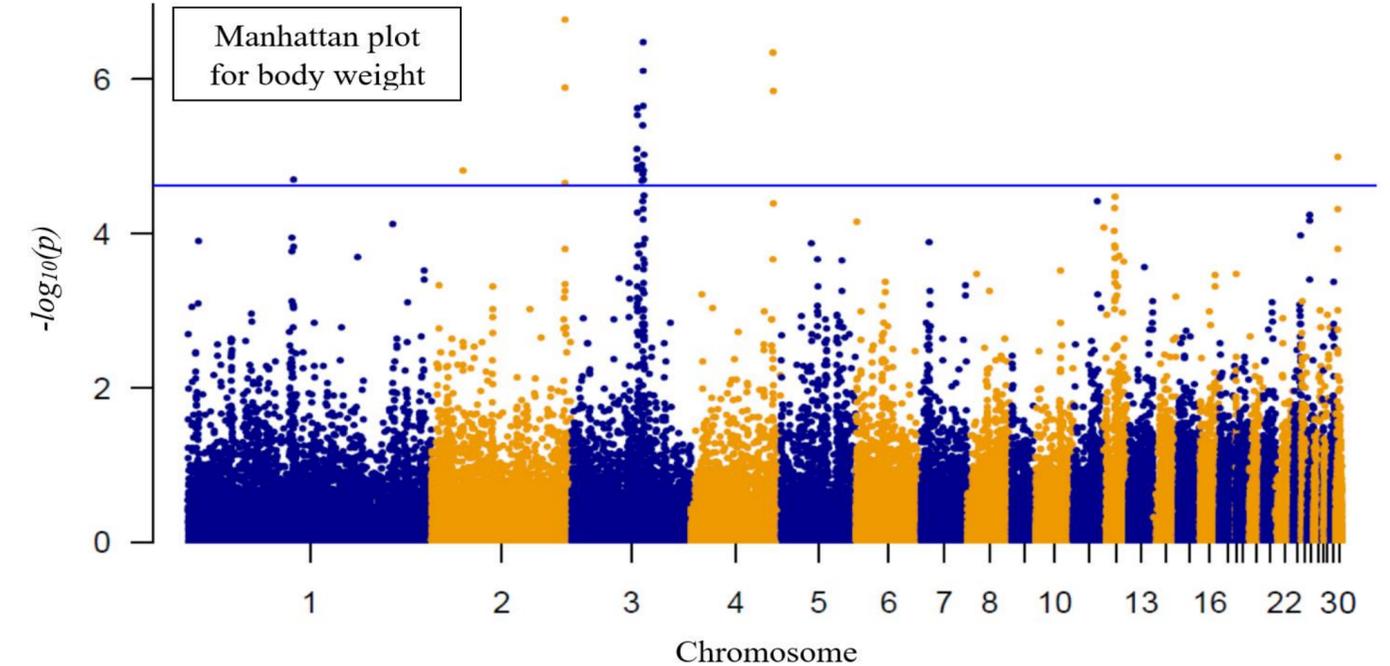
## Materials and Methods

- 31,950 turkeys phenotyped and genotyped (56,393 SNP)
- A mixed model was fitted:
  - **Fixed:** hatch-week-year and sex
  - **Random:** polygenic effect
- Significant (FDR = 0.05) markers were assigned to genes
- Databases



## Results

- Interesting functional terms were uncovered. e.g.,
  - Skeletal muscle tissue growth and regulation of digestive system process
  - Walking behavior and leg progression



- Candidate genes were identified. e.g.,
  - *COL8A1* and *RBPM2* associated with body weight
  - *PPARA* related to feed efficiency

## Conclusion

The uncovered candidate genomic regions and genes are novel and associated with economic traits in turkeys. These functional categories may contribute in developing turkey breeding strategies