

From genetic signals to regulatory genes

A chicken advanced intercross study

NATURE COMMUNICATIONS · 2025

01 QUESTION & STUDY DESIGN

How can genetic associations be connected to genes and tissues?

16

generations

4,671

samples

75

traits

RECOMBINATION → FINER MAPPING

Conceptual chromosome segments · not data

Early

Later

Genotypes + measured traits

↓

GWAS and QTL fine mapping

↓

Regulatory evidence integration

02 REPORTED RESULTS

154

single-gene QTLs

Out of 682 QTLs identified across 43 traits with significant signals.

TRAITS EXAMINED

Number of phenotypes in each category

Growth / development

36

Tissue / carcass

23

Feed intake / efficiency

9

Blood biochemistry

3

Feathers

4

Regulatory information helps prioritize genes beyond the nearest genomic neighbour.

03 FROM LOCUS TO MECHANISM

ASSOCIATION

Trait-associated locus

↓

REGULATION

eQTL + functional annotation

↓

INTEGRATION

SMR · colocalization · TWAS

↓

PRIORITIZATION

Candidate genes and tissues

INTERPRETATION

Prioritization is not proof of every causal mechanism. This is a growth-trait study, not a heat-stress experiment.

JOURNAL-CLUB QUESTION

Which experiment would test a candidate gene in your own chicken population?