

# GEPHE SUMMARY

|   |                |              |
|---|----------------|--------------|
|   | Gephebase Gene | GephelD      |
| GRAMD3 ( <a href="https://www.gephebase.org/search-criteria?/and+Gene">https://www.gephebase.org/search-criteria?/and+Gene</a><br>Gephebase=^GRAMD3^#gephebase-summary-title) | GP00002391     | Main curator |
| Published   | Entry Status   | Courtier     |
|   |                |              |

## PHENOTYPIC CHANGE

|  | Trait Category   |  |                             |
|--|--|--|-----------------------------|
| Morphology ( <a href="https://www.gephebase.org/search-criteria?/and+Trait">https://www.gephebase.org/search-criteria?/and+Trait</a><br>Category=Morphology^#gephebase-summary-title)  | Trait  |  |                             |
| Coloration (skin) ( <a href="https://www.gephebase.org/search-criteria?/and+Trait=^Coloration">https://www.gephebase.org/search-criteria?/and+Trait=^Coloration</a><br>(skin)^#gephebase-summary-title)  | Trait State in Taxon A   |  |                             |
| Gallus gallus  | Trait State in Taxon B   |  |                             |
| Gallus gallus  | Ancestral State  |  |                             |
| Data not curated   | Taxonomic Status   |  |                             |
| Domesticated ( <a href="https://www.gephebase.org/search-criteria?/and+Taxonomic">https://www.gephebase.org/search-criteria?/and+Taxonomic</a><br>Status=^Domesticated^#gephebase-summary-title)   |  |  |                             |
| Taxon A  |  | Taxon B  |                             |
|  | Latin Name   |  | Latin Name                  |
| Gallus gallus<br>( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Gallus">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Gallus</a><br>gallus^#gephebase-summary-title)   | Gallus gallus<br>( <a href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Gallus">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=^Gallus</a><br>gallus^#gephebase-summary-title) |  |                             |
| chicken  | Common Name  |  | Common Name                 |
| Gallus gallus domesticus; chicken; bantam; chickens  | Synonyms   |  | Synonyms                    |
| species  | Rank   |  | Rank                        |
|  | Lineage  |  | Lineage                     |
| cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes; Phasianidae; Phasianinae; Gallus |  | cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Sauropsida; Sauria; Archelosauria; Archosauria; Dinosauria; Saurischia; Theropoda; Coelurosauria; Aves; Neognathae; Galloanserae; Galliformes; Phasianidae; Phasianinae; Gallus |                             |
| Gallus () - (Rank: genus)<br>( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9030">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9030</a> )   | Parent   | Gallus () - (Rank: genus)<br>( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9030">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9030</a> )   | Parent                      |
| 9031<br>( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9031">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9031</a> )  | NCBI Taxonomy ID   | 9031<br>( <a href="https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9031">https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9031</a> )  | NCBI Taxonomy ID            |
| No   | is Taxon A an Infraspecies?  | No   | is Taxon B an Infraspecies? |

## GENOTYPIC CHANGE

|  |                         |  |
|--|-------------------------|--|
|  | Generic Gene Name       | UniProtKB Gallus gallus  |
| GRAMD3   |                         | F1NDM3 ( <a href="http://www.uniprot.org/uniprot/F1NDM3">http://www.uniprot.org/uniprot/F1NDM3</a> )             |
| -  | Synonyms                | GenebankID or UniProtKB<br>Gallus gallus   |
| 9031.ENSGALP00000013389<br>( <a href="http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9031.ENSGALP00000013389">http://string-db.org/newstring_cgi/show_network_section.pl?identifier=9031.ENSGALP00000013389</a> ) | String                  | F1NDM3 ( <a href="https://www.ncbi.nlm.nih.gov/nuccore/F1NDM3">https://www.ncbi.nlm.nih.gov/nuccore/F1NDM3</a> ) |
|  | Sequence Similarities   |  |
| -  | GO - Molecular Function |  |
| -  | GO - Biological Process |  |
| -  | GO - Cellular Component |  |
| GO:0016021 : integral component of membrane<br>( <a href="https://www.ebi.ac.uk/QuickGO/term/GO:0016021">https://www.ebi.ac.uk/QuickGO/term/GO:0016021</a> )   |                         |  |

GO:0005881 : cytoplasmic microtubule  
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005881>)

Presumptive Null

No (<https://www.gephebase.org/search-criteria?/and+Presumptive+Null=^No^#gephebase-summary-title>)

Molecular Type

Cis-regulatory (<https://www.gephebase.org/search-criteria?/and+Molecular+Type=^Cis-regulatory^#gephebase-summary-title>)

Aberration Type

Unknown (<https://www.gephebase.org/search-criteria?/and+Aberration+Type=^Unknown^#gephebase-summary-title>)

Molecular Details of the Mutation

No coding mutation in GRAMD3. The expression of GRAMD3 gene in the dermis tissues of the shank was significantly ( $P = 0.010738 < 0.05$ ) higher in 350-day-old Gushi chickens characterized by the dermal shank pigmentation than in one-day-old Gushi chickens. Variation in the flanking region of GRAMD3 probably leads to the abnormal expression of GRAMD3.

Experimental Evidence

Association Mapping (<https://www.gephebase.org/search-criteria?/and+Experimental+Evidence=^Association+Mapping^#gephebase-summary-title>)

Main Reference

Mapping of Id locus for dermal shank melanin in a Chinese indigenous chicken breed. (2017) (<https://pubmed.ncbi.nlm.nih.gov/29321357>)

Authors

Xu J; Lin S; Gao X; Nie Q; Luo Q; Zhang X

Abstract

The dermal shank pigmentation, one of the defining traits of chicken breeds, is caused by an abnormal deposition of melanin in the dermis of the shank. The abnormal deposition is controlled by the sex-linked inhibitor of dermal melanin (Id). In this study, we aim to locate the gene responsible for the dermal shank pigmentation in chickens by an association analysis and a differential expression analysis. Based on our results, 72 single-nucleotide polymorphisms (SNPs) located in Z chromosome (chrZ): 71-73 Mb (galGal3) were selected to further explore their relationships with the dermal shank pigmentation in pure lines of 96 Gushi hens and 96 Gushi hens with a yellow shank skin colour. The results of the association analysis showed that the SNPs located in chrZ: 72.58-72.99 Mb (galGal3) (chrZ: 79.02-79.44 Mb (galGal4)) are significantly associated with the dermal shank pigmentation. Based on the results of our previous studies and the present association analysis, the zinc-finger protein 608 (ZNF608), GRAM domain containing 3 (GRAMD3), aldehyde dehydrogenase 7 family member A1 (ALDH7A1), fem-1 homologue C (FEM1C), beta-1,4-galactosyltransferase 1 (B4GALT1) and versican (VCAN) genes were selected for the differential expression analysis. The gene expression profiles showed that the expression of GRAMD3 gene in the dermis tissues of the shank was significantly ( $P = 0.010738 < 0.05$ ) higher in 350-day-old Gushi chickens characterized by the dermal shank pigmentation than in one-day-old Gushi chickens. The dermal shank pigmentation was not present in the one-day-old Gushi chickens. Additionally, the results of the association analysis and the expression analysis showed that GRAMD3 could be the most likely candidate gene for the Id locus. However, we did not detect a mutation, i.e. significantly associated with this trait within GRAMD3. Therefore, we concluded that the variations located in the flanking region of GRAMD3 led to the abnormal expression of GRAMD3, which requires further study.

Additional References

## RELATED GEPHE

Related Genes

14 (ABCA1, Agouti (ASIP), CDKN2A, CYP19A1, EDN3, Endothelin receptor B2, MC1R, Melanophilin (MLPH), PMEL17, SLC45A2-MATP, SLCO1B3, SOX10, tyrosinase (TYR), tyrosinase-related protein 1 (TYRP1)) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=^9031^/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

Related Haplotypes

No matches found.

## EXTERNAL LINKS

## COMMENTS