

GEPHE SUMMARY

<p>Microphthalmia-associated transcription factor (#gephebase-summary-title)</p> <p>Published</p>	<p>Gephebase Gene</p> <p>GP00002127</p> <p>Santos</p> <p>Entry Status</p>	<p>GepheID</p> <p>Main curator</p>
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PHENOTYPIC CHANGE

<p>Morphology (#gephebase-summary-title)</p> <p>Coloration (feathers) (#gephebase-summary-title)</p> <p>Mallard pigmentation pattern</p> <p>Pekin pigmentation (white)</p> <p>Taxon A</p> <p>Domesticated (#gephebase-summary-title)</p>	<p>Trait Category</p> <p>Trait</p> <p>Trait State in Taxon A</p> <p>Trait State in Taxon B</p> <p>Ancestral State</p> <p>Taxonomic Status</p>	<p>Taxon A</p> <p>Latin Name</p> <p><i>Anas platyrhynchos</i> (#gephebase-summary-title)</p> <p>Common Name</p> <p>mallard</p> <p>Synonyms</p> <p><i>Anas boschas</i>; <i>Anas domesticus</i>; <i>Anas platyrhynchos f. domestica</i>; mallard; duck; mallard duck; mallard ducks; <i>Anas platyrhynchos</i> Linnaeus 1758; <i>Anas platyrhynchos</i></p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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; Anseriformes; Anatidae; Anatinae; <i>Anas</i></p> <p>Parent</p> <p><i>Anas</i> (ducks) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8835)</p> <p>NCBI Taxonomy ID</p> <p>8839 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8839)</p> <p>is Taxon A an Intraspecies?</p> <p>Yes</p> <p>Taxon A Description</p> <p>Wild mallard ducks</p>	<p>Taxon B</p> <p>Latin Name</p> <p><i>Anas platyrhynchos</i> (#gephebase-summary-title)</p> <p>Common Name</p> <p>mallard</p> <p>Synonyms</p> <p><i>Anas boschas</i>; <i>Anas domesticus</i>; <i>Anas platyrhynchos f. domestica</i>; mallard; duck; mallard duck; mallard ducks; <i>Anas platyrhynchos</i> Linnaeus 1758; <i>Anas platyrhynchos</i></p> <p>Rank</p> <p>species</p> <p>Lineage</p> <p>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; Anseriformes; Anatidae; Anatinae; <i>Anas</i></p> <p>Parent</p> <p><i>Anas</i> (ducks) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8835)</p> <p>NCBI Taxonomy ID</p> <p>8839 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=8839)</p> <p>is Taxon B an Intraspecies?</p> <p>Yes</p> <p>Taxon B Description</p> <p>Domesticated breed</p>
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GENOTYPIC CHANGE

<p>Mitf</p> <p>Wh; bw; mi; vit; BCC2; Bhlhe32; Gsfbcc2; Vitiligo; Bw; Mi; Vit</p> <p>10090.ENSMUSP00000044938 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=10090.ENSMUSP00000044938)</p> <p>Belongs to the MiT/TFE family.</p> <p>GO:0046983 : protein dimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0046983)</p>	<p>Generic Gene Name</p> <p>Synonyms</p> <p>String</p> <p>Sequence Similarities</p> <p>GO - Molecular Function</p>	<p>UniProtKB Mus musculus</p> <p>Q08874 (http://www.uniprot.org/uniprot/Q08874)</p> <p>GenebankID or UniProtKB</p> <p>()</p>
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GO:0003700 : DNA-binding transcription factor activity
 (https://www.ebi.ac.uk/QuickGO/term/GO:0003700)
 GO:0043565 : sequence-specific DNA binding
 (https://www.ebi.ac.uk/QuickGO/term/GO:0043565)
 GO:0003677 : DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003677)
 GO:0003682 : chromatin binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003682)
 GO:0000981 : DNA-binding transcription factor activity, RNA polymerase II-specific
 (https://www.ebi.ac.uk/QuickGO/term/GO:0000981)
 GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA
 polymerase II-specific (https://www.ebi.ac.uk/QuickGO/term/GO:0001077)
 GO:0000978 : RNA polymerase II proximal promoter sequence-specific DNA binding
 (https://www.ebi.ac.uk/QuickGO/term/GO:0000978)
 GO:0070888 : E-box binding (https://www.ebi.ac.uk/QuickGO/term/GO:0070888)
 GO:0003705 : transcription factor activity, RNA polymerase II distal enhancer sequence-
 specific binding (https://www.ebi.ac.uk/QuickGO/term/GO:0003705)

GO - Biological Process

GO:0043066 : negative regulation of apoptotic process
 (https://www.ebi.ac.uk/QuickGO/term/GO:0043066)
 GO:0045944 : positive regulation of transcription by RNA polymerase II
 (https://www.ebi.ac.uk/QuickGO/term/GO:0045944)
 GO:0006357 : regulation of transcription by RNA polymerase II
 (https://www.ebi.ac.uk/QuickGO/term/GO:0006357)
 GO:0006355 : regulation of transcription, DNA-templated
 (https://www.ebi.ac.uk/QuickGO/term/GO:0006355)
 GO:0030154 : cell differentiation (https://www.ebi.ac.uk/QuickGO/term/GO:0030154)
 GO:0043473 : pigmentation (https://www.ebi.ac.uk/QuickGO/term/GO:0043473)
 GO:0000122 : negative regulation of transcription by RNA polymerase II
 (https://www.ebi.ac.uk/QuickGO/term/GO:0000122)
 GO:0045893 : positive regulation of transcription, DNA-templated
 (https://www.ebi.ac.uk/QuickGO/term/GO:0045893)
 GO:0010628 : positive regulation of gene expression
 (https://www.ebi.ac.uk/QuickGO/term/GO:0010628)
 GO:0006351 : transcription, DNA-templated
 (https://www.ebi.ac.uk/QuickGO/term/GO:0006351)
 GO:0045165 : cell fate commitment (https://www.ebi.ac.uk/QuickGO/term/GO:0045165)
 GO:0010468 : regulation of gene expression
 (https://www.ebi.ac.uk/QuickGO/term/GO:0010468)
 GO:0030318 : melanocyte differentiation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0030318)
 GO:0043010 : camera-type eye development
 (https://www.ebi.ac.uk/QuickGO/term/GO:0043010)
 GO:0030316 : osteoclast differentiation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0030316)
 GO:0042127 : regulation of cell proliferation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0042127)
 GO:0046849 : bone remodeling (https://www.ebi.ac.uk/QuickGO/term/GO:0046849)
 GO:0044336 : canonical Wnt signaling pathway involved in negative regulation of apoptotic
 process (https://www.ebi.ac.uk/QuickGO/term/GO:0044336)
 GO:0030336 : negative regulation of cell migration
 (https://www.ebi.ac.uk/QuickGO/term/GO:0030336)
 GO:2000144 : positive regulation of DNA-templated transcription, initiation
 (https://www.ebi.ac.uk/QuickGO/term/GO:2000144)
 GO:0065003 : protein-containing complex assembly
 (https://www.ebi.ac.uk/QuickGO/term/GO:0065003)
 GO:0045670 : regulation of osteoclast differentiation
 (https://www.ebi.ac.uk/QuickGO/term/GO:0045670)
 GO:2001141 : regulation of RNA biosynthetic process
 (https://www.ebi.ac.uk/QuickGO/term/GO:2001141)
 GO:0016055 : Wnt signaling pathway
 (https://www.ebi.ac.uk/QuickGO/term/GO:0016055)

GO - Cellular Component

GO:0005634 : nucleus (https://www.ebi.ac.uk/QuickGO/term/GO:0005634)
 GO:0032991 : protein-containing complex
 (https://www.ebi.ac.uk/QuickGO/term/GO:0032991)

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

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

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

1-10 kb Insertion Size

6.6kb insertion between exon 1M and exon 2, leads to lower expression of isoform MITF M in pekin white ducks Molecular Details of the Mutation

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

An intercross population study reveals genes associated with body size and plumage color in ducks. (2018) (https://pubmed.ncbi.nlm.nih.gov/30018292) Main Reference

Zhou Z; Li M; Cheng H; Fan W; Yuan Z; Gao Q; Xu Y; Guo Z; Zhang Y; Hu J; Liu H; Liu D; Chen W; Zheng Z; Jiang Y; Wen Z; Liu Y; Chen H; Xie M; Zhang Q; Huang W; Wang W; Hou S; Jiang Y

Comparative population genomics offers an opportunity to discover the signatures of artificial selection during animal domestication, however, their function cannot be directly revealed. We discover the selection signatures using genome-wide comparisons among 40 mallards, 36 indigenous-breed ducks, and 30 Pekin ducks. Then, the phenotypes are fine-mapped based on resequencing of 1026 ducks from an F segregating population generated by wild–domestic crosses. Interestingly, the two key economic traits of Pekin duck are associated with two selective sweeps with fixed mutations. A novel intronic insertion most possibly leads to a splicing change in MITF accounted for white duck down feathers. And a putative long-distance regulatory mutation causes continuous expression of the IGF2BP1 gene after birth which increases body size by 15% and feed efficiency by 6%. This study provides new insights into genotype-phenotype associations in animal research and constitutes a promising resource on economically important genes in fowl.

RELATED GEPHE

2 (Endothelin receptor B2, MC1R) (<https://www.gephebase.org/search-criteria?/or+Taxon+ID=~8839~/and+Trait=Coloration/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS

@parallelism