

GEPHE SUMMARY

Gephebase Gene
tyrosinase-related protein 1 (TYRP1)

Entry Status
Published

GepheID
GP00001149

Main curator
Martin

PHENOTYPIC CHANGE

Trait Category
Morphology

Trait
Coloration (coat)

Trait State in Taxon A
Columba livia - blue/black

Trait State in Taxon B
Columba livia - brown b1 allele

Ancestral State
Taxon A

Taxonomic Status
Domesticated

Taxon A

Latin Name
Columba livia

Common Name
rock pigeon

Synonyms
Columba livia domestica; rock pigeon; carrier pigeon; domestic pigeon; rock dove; Columba livia Gmelin, JF, 1789

Rank
species

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; Columbiformes; Columbidae; Columba

Parent
Columba () - (Rank: genus)

NCBI Taxonomy ID
8932

is Taxon A an Intraspecies?
No

Taxon B

Latin Name
Columba livia

Common Name
rock pigeon

Synonyms
Columba livia domestica; rock pigeon; carrier pigeon; domestic pigeon; rock dove; Columba livia Gmelin, JF, 1789

Rank
species

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; Columbiformes; Columbidae; Columba

Parent
Columba () - (Rank: genus)

NCBI Taxonomy ID
8932

is Taxon B an Intraspecies?
No

GENOTYPIC CHANGE

Generic Gene Name
Tyrrp1

Synonyms
b; isa; Oca3; TRP1; Tyrrp; TRP-1; brown; Tyrrp-1

String
10090.ENSMUSP00000006151

Sequence Similarities
Belongs to the tyrosinase family.

GO - Molecular Function
GO:0042803 : protein homodimerization activity
GO:0046982 : protein heterodimerization activity
GO:0046872 : metal ion binding
GO:0004497 : monooxygenase activity

GO - Biological Process
GO:0032438 : melanosome organization
GO:0043473 : pigmentation
GO:0048023 : positive regulation of melanin biosynthetic process

UniProtKB Mus musculus
P07147

GenebankID or UniProtKB
NP_001302454

GO:0006583 : melanin biosynthetic process from tyrosine
GO:0030318 : melanocyte differentiation
GO:0043438 : acetoacetic acid metabolic process
GO:0006582 : melanin metabolic process

GO - Cellular Component

GO:0016021 : integral component of membrane
GO:0030669 : clathrin-coated endocytic vesicle membrane
GO:0010008 : endosome membrane
GO:0042470 : melanosome
GO:0033162 : melanosome membrane

Presumptive Null

No

Molecular Type

Coding

Aberration Type

SNP

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

Ala23Pro

Experimental Evidence

Linkage Mapping

	Taxon A	Taxon B	Position
Codon	-	-	-
Amino-acid	-	-	-

Main Reference

Epistatic and combinatorial effects of pigmentary gene mutations in the domestic pigeon. (2014)

Authors

Domyan ET; Guernsey MW; Kronenberg Z; Krishnan S; Boissy RE; Vickrey AI; Rodgers C; Cassidy P; Leachman SA; Fondon JW; Yandell M; Shapiro MD

Abstract

Understanding the molecular basis of phenotypic diversity is a critical challenge in biology, yet we know little about the mechanistic effects of different mutations and epistatic relationships among loci that contribute to complex traits. Pigmentation genetics offers a powerful model for identifying mutations underlying diversity and for determining how additional complexity emerges from interactions among loci. Centuries of artificial selection in domestic rock pigeons (*Columba livia*) have cultivated tremendous variation in plumage pigmentation through the combined effects of dozens of loci. The dominance and epistatic hierarchies of key loci governing this diversity are known through classical genetic studies, but their molecular identities and the mechanisms of their genetic interactions remain unknown. Here we identify protein-coding and cis-regulatory mutations in *Tyrp1*, *Sox10*, and *Slc45a2* that underlie classical color phenotypes of pigeons and present a mechanistic explanation of their dominance and epistatic relationships. We also find unanticipated allelic heterogeneity at *Tyrp1* and *Sox10*, indicating that color variants evolved repeatedly through mutations in the same genes. These results demonstrate how a spectrum of coding and regulatory mutations in a small number of genes can interact to generate substantial phenotypic diversity in a classic Darwinian model of evolution.

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Additional References

RELATED GEPHE

Related Genes

3 (MC1R, SLC45A2=MATP, SOX10)

Related Haplotypes

3

EXTERNAL LINKS

COMMENTS

@Epistasis Multiple alleles

