

GEPHE SUMMARY

BCMO1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=~BCMO1~#gephebase-summary-title)	Gephebase Gene	GP00000137	GepheID
	Entry Status	Courtier	Main curator
	Published		

PHENOTYPIC CHANGE

		Trait Category	
Morphology, Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=~Morphology~/and+TraitCategory=~Physiology~#gephebase-summary-title)		Trait	
Carotenoid content (https://www.gephebase.org/search-criteria?/and+Trait=~Carotenoidcontent~#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 (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=~Domesticated~#gephebase-summary-title)			
Taxon A		Taxon B	
Gallus gallus (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Gallusgallus~#gephebase-summary-title)		Gallus gallus (https://www.gephebase.org/search-criteria?/and+TaxonandSynonyms=~Gallusgallus~#gephebase-summary-title)	
chicken		chicken	
Gallus gallus domesticus; chicken; bantam; chickens		Gallus gallus domesticus; chicken; bantam; chickens	
species		species	
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) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9030)		Gallus () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9030)	
9031 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9031)		9031 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9031)	
No		No	

GENOTYPIC CHANGE

		Generic Gene Name	
BCO1		Q9HAY6 (http://www.uniprot.org/uniprot/Q9HAY6)	
BCO; BCDO; BCMO; BCDO1; BCMO1		GenebankID or UniProtKB	
9606.ENSPP00000258168 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPP00000258168)		XP_015148006 (https://www.ncbi.nlm.nih.gov/nuccore/XP_015148006)	
Belongs to the carotenoid oxygenase family.		Sequence Similarities	
GO:0046872 : metal ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0046872)		GO - Molecular Function	
GO:0003834 : beta-carotene 15,15'-monooxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0003834)			
GO:0010436 : carotenoid dioxygenase activity (https://www.ebi.ac.uk/QuickGO/term/GO:0010436)			
GO:0004744 : retinal isomerase activity			

(https://www.ebi.ac.uk/QuickGO/term/GO:0004744)

GO - Biological Process

GO:0001523 : retinoid metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0001523)
GO:1901810 : beta-carotene metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:1901810)
GO:0016121 : carotene catabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0016121)
GO:0042574 : retinal metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042574)
GO:0042572 : retinol metabolic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0042572)
GO:0035238 : vitamin A biosynthetic process
(https://www.ebi.ac.uk/QuickGO/term/GO:0035238)

GO - Cellular Component

GO:0005829 : cytosol (https://www.ebi.ac.uk/QuickGO/term/GO:0005829)

Mutation #1

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

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

Molecular Details of the Mutation

A to G at SNP1 (â~678 bp upstream of ATG)

Experimental Evidence

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

Main Reference

Detection of a Cis [corrected] eQTL controlling BCMO1 gene expression leads to the identification of a QTG for chicken breast meat color. (2011)
(https://pubmed.ncbi.nlm.nih.gov/21750696)

Authors

Le Bihan-Duval E; Nadaf J; Berri C; Pitel F; Graulet B; Godet E; Leroux SY; Demeure O; Lagarrigue S; Duby C; Cogburn LA; Beaumont CM; Duclos MJ

Abstract

Classical quantitative trait loci (QTL) analysis and gene expression QTL (eQTL) were combined to identify the causal gene (or QTG) underlying a highly significant QTL controlling the variation of breast meat color in a F2 cross between divergent high-growth (HG) and low-growth (LG) chicken lines. Within this meat quality QTL, BCMO1 (Accession number GenBank: AJ271386), encoding the Î²-carotene 15, 15'-monooxygenase, a key enzyme in the conversion of Î²-carotene into colorless retinal, was a good functional candidate. Analysis of the abundance of BCMO1 mRNA in breast muscle of the HG x LG F2 population allowed for the identification of a strong cis eQTL. Moreover, reevaluation of the color QTL taking BCMO1 mRNA levels as a covariate indicated that BCMO1 mRNA levels entirely explained the variations in meat color. Two fully-linked single nucleotide polymorphisms (SNP) located within the proximal promoter of BCMO1 gene were identified. Haplotype substitution resulted in a marked difference in BCMO1 promoter activity in vitro. The association study in the F2 population revealed a three-fold difference in BCMO1 expression leading to a difference of 1 standard deviation in yellow color between the homozygous birds at this haplotype. This difference in meat yellow color was fully consistent with the difference in carotenoid content (i.e. lutein and zeaxanthin) evidenced between the two alternative haplotypes. A significant association between the haplotype, the level of BCMO1 expression and the yellow color of the meat was also recovered in an unrelated commercial broiler population. The mutation could be of economic importance for poultry production by making possible a gene-assisted selection for color, a determining aspect of meat quality. Moreover, this natural genetic diversity constitutes a new model for the study of Î²-carotene metabolism which may act upon diverse biological processes as precursor of the vitamin A.

Additional References

Mutation #2

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

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

Molecular Details of the Mutation

A to G at SNP2 (â~621 bp upstream of ATG)

Experimental Evidence

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

Main Reference

Detection of a Cis [corrected] eQTL controlling BCMO1 gene expression leads to the identification of a QTG for chicken breast meat color. (2011)
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Authors

Le Bihan-Duval E; Nadaf J; Berri C; Pitel F; Graulet B; Godet E; Leroux SY; Demeure O; Lagarrigue S; Duby C; Cogburn LA; Beaumont CM; Duclos MJ

Abstract

Classical quantitative trait loci (QTL) analysis and gene expression QTL (eQTL) were combined to identify the causal gene (or QTG) underlying a highly significant QTL controlling the variation of breast meat color in a F2 cross between divergent high-growth (HG) and low-growth (LG) chicken lines. Within this meat quality QTL, BCMO1 (Accession number GenBank: AJ271386), encoding the Î²-carotene 15, 15'-monooxygenase, a key enzyme in the conversion of Î²-carotene into colorless retinal, was a good functional candidate. Analysis of the abundance of BCMO1 mRNA in breast muscle of the HG x LG F2 population allowed for the identification of a strong cis eQTL. Moreover, reevaluation of the color QTL taking BCMO1 mRNA levels as a covariate indicated that BCMO1 mRNA levels entirely explained the variations in meat color. Two fully-linked single nucleotide polymorphisms (SNP) located within the proximal promoter of BCMO1 gene were identified. Haplotype substitution resulted in a marked difference in BCMO1 promoter activity in vitro. The association study in the F2 population revealed a three-fold difference in BCMO1 expression leading to a difference of 1 standard deviation in yellow color between the homozygous birds at this haplotype. This difference in meat yellow color was fully consistent with the difference in carotenoid content (i.e. lutein and zeaxanthin) evidenced between the two alternative haplotypes. A significant association between the haplotype, the level of BCMO1 expression and the yellow color of the meat was also recovered in an unrelated commercial broiler population. The mutation could be of economic importance for poultry production by making possible a gene-assisted selection for color, a determining aspect of meat quality. Moreover, this natural genetic diversity constitutes a new model for the study of Î²-carotene metabolism which may act upon diverse biological processes as precursor of the vitamin A.

Additional References

RELATED GEPHE

1 (BCO2 = beta-carotene oxygenase 2) ([https://www.gephebase.org/search-criteria?/or+Taxon ID="+9031"/and+Trait=Carotenoid content/and+groupHaplotypes=true#gephebase-summary-title](https://www.gephebase.org/search-criteria?/or+Taxon+ID=))

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS