

GEPHE SUMMARY

TICAM1 (https://www.gephebase.org/search-criteria?/and+GeneGephebase=^TICAM1^#gephebase-summary-title)	Gephebase Gene	GP00001128	GepheID
Published	Entry Status	Martin	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+TraitCategory=^Physiology^#gephebase-summary-title)	Trait Category		
Pathogen resistance (Trypanosoma) (https://www.gephebase.org/search-criteria?/and+Trait=^Pathogen resistance (Trypanosoma)^#gephebase-summary-title)	Trait		
Bos indicus (zebu) ; other breeds	Trait State in Taxon A		
Bos taurus (N'dama breed)	Trait State in Taxon B		
Data not curated	Ancestral State		
Domesticated (https://www.gephebase.org/search-criteria?/and+TaxonomicStatus=^Domesticated^#gephebase-summary-title)	Taxonomic Status		
		Taxon A	Taxon B
	Latin Name		Latin Name
Bos (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos^#gephebase-summary-title)		Bos taurus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms=^Bos taurus^#gephebase-summary-title)	
oxen, cattle	Common Name	cattle	Common Name
oxen, cattle	Synonyms	Bos bovis; Bos primigenius taurus; cattle; bovine; cow; dairy cow; domestic cattle; domestic cow; Bos taurus Linnaeus, 1758; Bos Taurus	Synonyms
genus	Rank	species	Rank
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Artiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos	Lineage
Bovinae () - (Rank: subfamily) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 27592)	Parent	Bos (oxen, cattle) - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)	Parent
9903 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9903)	NCBI Taxonomy ID	9913 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id= 9913)	NCBI Taxonomy ID
No	is Taxon A an Intraspecies?	Yes	is Taxon B an Intraspecies?
			Taxon B Description
		Bos taurus (N'dama breed)	

GENOTYPIC CHANGE

TICAM1	Generic Gene Name	Q8IUC6 (http://www.uniprot.org/uniprot/Q8IUC6)	UniProtKB Homo sapiens
TRIF; IIAE6; MyD88-3; PRVTIRB; TICAM-1	Synonyms	AAI51623 (https://www.ncbi.nlm.nih.gov/nucore/AAI51623)	GenebankID or UniProtKB
9606.ENSPO0000248244 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9606.ENSPO0000248244)	String		
-	Sequence Similarities		
GO:0019901 : protein kinase binding (https://www.ebi.ac.uk/QuickGO/term/GO:0019901)	GO - Molecular Function		
GO:0045087 : innate immune response (https://www.ebi.ac.uk/QuickGO/term/GO:0045087)	GO - Biological Process		

GO:0010628 : positive regulation of gene expression
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010628>)
GO:0051092 : positive regulation of NF-kappaB transcription factor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051092>)
GO:0006954 : inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0006954>)
GO:0051607 : defense response to virus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0051607>)
GO:0043123 : positive regulation of I-kappaB kinase/NF-kappaB signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043123>)
GO:0071222 : cellular response to lipopolysaccharide
(<https://www.ebi.ac.uk/QuickGO/term/GO:0071222>)
GO:0045429 : positive regulation of nitric oxide biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045429>)
GO:0030890 : positive regulation of B cell proliferation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030890>)
GO:0097190 : apoptotic signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0097190>)
GO:0010508 : positive regulation of autophagy
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010508>)
GO:0140052 : cellular response to oxidised low-density lipoprotein particle stimulus
(<https://www.ebi.ac.uk/QuickGO/term/GO:0140052>)
GO:0007249 : I-kappaB kinase/NF-kappaB signaling
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007249>)
GO:0031663 : lipopolysaccharide-mediated signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031663>)
GO:0002281 : macrophage activation involved in immune response
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002281>)
GO:0002756 : MyD88-independent toll-like receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002756>)
GO:0070266 : necroptotic process (<https://www.ebi.ac.uk/QuickGO/term/GO:0070266>)
GO:0034128 : negative regulation of MyD88-independent toll-like receptor signaling pathway (<https://www.ebi.ac.uk/QuickGO/term/GO:0034128>)
GO:0045080 : positive regulation of chemokine biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045080>)
GO:1900017 : positive regulation of cytokine production involved in inflammatory response
(<https://www.ebi.ac.uk/QuickGO/term/GO:1900017>)
GO:0045359 : positive regulation of interferon-beta biosynthetic process
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045359>)
GO:0032755 : positive regulation of interleukin-6 production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032755>)
GO:0002735 : positive regulation of myeloid dendritic cell cytokine production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0002735>)
GO:0032816 : positive regulation of natural killer cell activation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032816>)
GO:0032092 : positive regulation of protein binding
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032092>)
GO:0031398 : positive regulation of protein ubiquitination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0031398>)
GO:0032760 : positive regulation of tumor necrosis factor production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0032760>)
GO:0043496 : regulation of protein homodimerization activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043496>)
GO:0043330 : response to exogenous dsRNA
(<https://www.ebi.ac.uk/QuickGO/term/GO:0043330>)
GO:0034138 : toll-like receptor 3 signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034138>)
GO:0035666 : TRIF-dependent toll-like receptor signaling pathway
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035666>)

GO - Cellular Component

GO:0005829 : cytosol (<https://www.ebi.ac.uk/QuickGO/term/GO:0005829>)
GO:0005739 : mitochondrion (<https://www.ebi.ac.uk/QuickGO/term/GO:0005739>)
GO:0010008 : endosome membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0010008>)
GO:0005776 : autophagosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0005776>)
GO:0097342 : ripoosome (<https://www.ebi.ac.uk/QuickGO/term/GO:0097342>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown~#gephebase-summary-title)	
Coding (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Coding~#gephebase-summary-title)	Molecular Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown~#gephebase-summary-title)	Aberration Type
unknown	Molecular Details of the Mutation
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping~#gephebase-summary-title)	
Genetic and expression analysis of cattle identifies candidate genes in pathways responding to Trypanosoma congolense infection. (2011) (https://pubmed.ncbi.nlm.nih.gov/21593421)	Main Reference

Noyes H; Brass A; Obara I; Anderson S; Archibald AL; Bradley DG; Fisher P; Freeman A; Gibson J; Gicheru M; Hall L; Hanotte O; Hulme H; McKeever D; Murray C; Oh SJ; Tate C; Smith K; Tapio M; Wambugu J; Williams DJ; Agaba M; Kemp SJ

African bovine trypanosomiasis caused by *Trypanosoma* sp., is a major constraint on cattle productivity in sub-Saharan Africa. Some African *Bos taurus* breeds are highly tolerant of infection, but the potentially more productive *Bos indicus* zebu breeds are much more susceptible. Zebu cattle are well adapted for plowing and haulage, and increasing their tolerance of trypanosomiasis could have a major impact on crop cultivation as well as dairy and beef production. We used three strategies to obtain short lists of candidate genes within QTL that were previously shown to regulate response to infection. We analyzed the transcriptomes of trypanotolerant N'Dama and susceptible Boran cattle after infection with *Trypanosoma congolense*. We sequenced EST libraries from these two breeds to identify polymorphisms that might underlie previously identified quantitative trait loci (QTL), and we assessed QTL regions and candidate loci for evidence of selective sweeps. The scan of the EST sequences identified a previously undescribed polymorphism in ARHGAP15 in the Bta2 trypanotolerance QTL. The polymorphism affects gene function in vitro and could contribute to the observed differences in expression of the MAPK pathway in vivo. The expression data showed that TLR and MAPK pathways responded to infection, and the former contained TICAM1, which is within a QTL on Bta7. Genetic analyses showed that selective sweeps had occurred at TICAM1 and ARHGAP15 loci in African taurine cattle, making them strong candidates for the genes underlying the QTL. Candidate QTL genes were identified in other QTL by their expression profile and the pathways in which they participate.

RELATED GEPHE

1 (ARHGAP15) (<https://www.gephebase.org/search-criteria?/or+Taxon ID=~9903~/and+Trait=Pathogen resistance/or+Taxon ID=~9913~/and+Trait=Pathogen resistance/and+groupHaplotypes=true#gephebase-summary-title>)

No matches found.

EXTERNAL LINKS

COMMENTS