

GEPHE SUMMARY

CXCL16 (https://www.gephebase.org/search-criteria?/and+Gene Gephebase= [^] CXCL16 [^] #gephebase-summary-title)	Gephebase Gene	GP00001591	GepheID
Published	Entry Status	Prigent	Main curator

PHENOTYPIC CHANGE

Physiology (https://www.gephebase.org/search-criteria?/and+Trait Category= [^] Physiology [^] #gephebase-summary-title)	Trait Category		
Pathogen resistance (lymphocyte susceptibility to virus) (https://www.gephebase.org/search-criteria?/and+Trait = [^] Pathogen resistance (lymphocyte susceptibility to virus) [^] #gephebase-summary-title)	Trait		
horse short-term carrier of Equine arteritis virus - CD3+T lymphocyte resistance to virus	Trait State in Taxon A		
horse long-term carrier of Equine arteritis virus - CD3+T lymphocyte susceptible to virus	Trait State in Taxon B		
Unknown	Ancestral State		
Intraspecific (https://www.gephebase.org/search-criteria?/and+Taxonomic Status= [^] Intraspecific [^] #gephebase-summary-title)	Taxonomic Status		
	Taxon A	Taxon B	
Equus caballus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Equus caballus [^] #gephebase-summary-title)	Latin Name	Equus caballus (https://www.gephebase.org/search-criteria?/and+Taxon and Synonyms= [^] Equus caballus [^] #gephebase-summary-title)	Latin Name
horse	Common Name	horse	Common Name
Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus Linnaeus, 1758	Synonyms	Equus przewalskii f. caballus; Equus przewalskii forma caballus; horse; domestic horse; equine; Equus caballus Linnaeus, 1758	Synonyms
species	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; Perissodactyla; Equidae; Equus; Equus	Lineage	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Deuterostomia; Chordata; Craniata; Vertebrata; Gnathostomata; Teleostomi; Euteleostomi; Sarcopterygii; Dipnotetrapodomorpha; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Boreoeutheria; Laurasiatheria; Perissodactyla; Equidae; Equus; Equus	Lineage
Equus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510)	Parent	Equus () - (Rank: subgenus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=35510)	Parent
9796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796)	NCBI Taxonomy ID	9796 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=9796)	NCBI Taxonomy ID
Yes	is Taxon A an Infrappecies?	Yes	is Taxon B an Infrappecies?
Horse short-term carrier of Equine arteritis virus - CD3+T lymphocyte resistance to virus	Taxon A Description	Horse long-term carrier of Equine arteritis virus - CD3+T lymphocyte susceptible to virus	Taxon B Description

GENOTYPIC CHANGE

CXCL16	Generic Gene Name	F7CTX0 (http://www.uniprot.org/uniprot/F7CTX0)	UniProtKB Equus caballus
-	Synonyms	0	GenebankID or UniProtKB
9796.ENSECAP00000015940 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=9796.ENSECAP00000015940)	String		
-	Sequence Similarities		
GO:0008009 : chemokine activity (https://www.ebi.ac.uk/QuickGO/term/GO:0008009)	GO - Molecular Function		
GO:0005044 : scavenger receptor activity (https://www.ebi.ac.uk/QuickGO/term/GO:0005044)			

GO:0005041 : low-density lipoprotein particle receptor activity
(<https://www.ebi.ac.uk/QuickGO/term/GO:0005041>)

GO - Biological Process

GO:0030307 : positive regulation of cell growth
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030307>)

GO:0030335 : positive regulation of cell migration
(<https://www.ebi.ac.uk/QuickGO/term/GO:0030335>)

GO:0034612 : response to tumor necrosis factor
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034612>)

GO:0034341 : response to interferon-gamma
(<https://www.ebi.ac.uk/QuickGO/term/GO:0034341>)

GO:0010818 : T cell chemotaxis (<https://www.ebi.ac.uk/QuickGO/term/GO:0010818>)

GO - Cellular Component

GO:0016021 : integral component of membrane
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016021>)

GO:0005615 : extracellular space (<https://www.ebi.ac.uk/QuickGO/term/GO:0005615>)

Presumptive Null

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

Molecular Type

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

Aberration Type

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

SNP Coding Change

Nonsynonymous

Molecular Details of the Mutation

4 candidate nonsynonymous substitutions within exon 1 (in 2 susceptible variants): (1)c.715A>T p.Tyr40Phe (2)c.801G>C w.Asp49His (3)c.804T>A/G p.Phe50Ile (4)c.810G>A p.Glu52Lys

Experimental Evidence

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

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

Main Reference

Allelic Variation in CXCL16 Determines CD3+ T Lymphocyte Susceptibility to Equine Arteritis Virus Infection and Establishment of Long-Term Carrier State in the Stallion. (2016)
(<https://pubmed.ncbi.nlm.nih.gov/27930647>)

Authors

Sarkar S; Bailey E; Go YY; Cook RF; Kalbfleisch T; Eberth J; Chelvarajan RL; Shuck KM; Artiushin S; Timoney PJ; Balasuriya UB

Abstract

Equine arteritis virus (EAV) is the causative agent of equine viral arteritis (EVA), a respiratory, systemic, and reproductive disease of horses and other equid species. Following natural infection, 10-70% of the infected stallions can become persistently infected and continue to shed EAV in their semen for periods ranging from several months to life. Recently, we reported that some stallions possess a subpopulation(s) of CD3+ T lymphocytes that are susceptible to in vitro EAV infection and that this phenotypic trait is associated with long-term carrier status following exposure to the virus. In contrast, stallions not possessing the CD3+ T lymphocyte susceptible phenotype are at less risk of becoming long-term virus carriers. A genome wide association study (GWAS) using the Illumina Equine SNP50 chip revealed that the ability of EAV to infect CD3+ T lymphocytes and establish long-term carrier status in stallions correlated with a region within equine chromosome 11. Here we identified the gene and mutations responsible for these phenotypes. Specifically, the work implicated three allelic variants of the equine orthologue of CXCL16 (EqCXCL16) that differ by four non-synonymous nucleotide substitutions (XM_00154756; c.715 A → T, c.801 G → C, c.804 T → A/G, c.810 G → A) within exon 1. This resulted in four amino acid changes with EqCXCL16S (XP_001504806.1) having Phe, His, Ile and Lys as compared to EqCXCL16R having Tyr, Asp, Phe, and Glu at 40, 49, 50, and 52, respectively. Two alleles (EqCXCL16Sa, EqCXCL16Sb) encoded identical protein products that correlated strongly with long-term EAV persistence in stallions (P<0.000001) and are required for in vitro CD3+ T lymphocyte susceptibility to EAV infection. The third (EqCXCL16R) was associated with in vitro CD3+ T lymphocyte resistance to EAV infection and a significantly lower probability for establishment of the long-term carrier state (viral persistence) in the male reproductive tract. EqCXCL16Sa and EqCXCL16Sb exert a dominant mode of inheritance. Most importantly, the protein isoform EqCXCL16S but not EqCXCL16R can function as an EAV cellular receptor. Although both molecules have equal chemoattractant potential, EqCXCL16S has significantly higher scavenger receptor and adhesion properties compared to EqCXCL16R.

Additional References

RELATED GEPHE

No matches found.

Related Genes

No matches found.

Related Haplotypes

EXTERNAL LINKS

COMMENTS

Non-null mutation. Susceptible variants are dominant