

GEPHE SUMMARY

	Gephebase Gene	GephelD
Doublesex (or neighbouring gene prospero) (<a +doublesex+(or+neighbouring+gene+prospero)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Gene+Gephebase=">https://www.gephebase.org/search-criteria?/and+Gene+Gephebase="+Doublesex+(or+neighbouring+gene+prospero)+"#gephebase-summary-title)	GP00000236	Main curator
	Martin	
Published	Entry Status	

PHENOTYPIC CHANGE

	Trait Category		
Morphology (<a +morphology+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait+Category=">https://www.gephebase.org/search-criteria?/and+Trait+Category="+Morphology+"#gephebase-summary-title)	Trait		
Wing shape (sex-specific) (<a +wing+shape+(sex-specific)+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Trait=">https://www.gephebase.org/search-criteria?/and+Trait="+Wing+shape+(sex-specific)+"#gephebase-summary-title)	Trait State in Taxon A		
Nasonia vitripennis	Trait State in Taxon B		
Nasonia giraulti	Ancestral State		
Data not curated	Taxonomic Status		
Interspecific (<a +interspecific+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxonomic+Status=">https://www.gephebase.org/search-criteria?/and+Taxonomic+Status="+Interspecific+"#gephebase-summary-title)			
	Taxon A		Taxon B
	Latin Name		Latin Name
Nasonia vitripennis (<a +nasonia+vitripennis+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Nasonia+vitripennis+"#gephebase-summary-title)	Nasonia giraulti (<a +nasonia+giraulti+"#gephebase-summary-title"="" href="https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms=">https://www.gephebase.org/search-criteria?/and+Taxon+and+Synonyms="+Nasonia+giraulti+"#gephebase-summary-title)		
	Common Name		Common Name
jewel wasp	-		
	Synonyms		Synonyms
jewel wasp; Nasonia vitripennis (Walker, 1836)	Nasonia giraulti Darling, 1990		
	Rank		Rank
species	species		
	Lineage		Lineage
cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita; Parasitoida; Chalcidoidea; Pteromalidae; Pteromalinae; Nasonia	cellular organisms; Eukaryota; Opisthokonta; Metazoa; Eumetazoa; Bilateria; Protostomia; Ecdysozoa; Panarthropoda; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Dicondylia; Pterygota; Neoptera; Holometabola; Hymenoptera; Apocrita; Parasitoida; Chalcidoidea; Pteromalidae; Pteromalinae; Nasonia		
	Parent		Parent
Nasonia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7424)	Nasonia () - (Rank: genus) (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7424)		
	NCBI Taxonomy ID		NCBI Taxonomy ID
7425 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7425)	7426 (https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=7426)		
	is Taxon A an Intraspecies?		is Taxon B an Intraspecies?
No	No		

GENOTYPIC CHANGE

	Generic Gene Name	UniProtKB Drosophila melanogaster
dsx	P23023 (http://www.uniprot.org/uniprot/P23023)	
	Synonyms	GenebankID or UniProtKB
CG11094; Dmdsx; Dmel\CG11094; Dsx; DSX; dsxF; dsxM; Hr; ix-62c	ACJ65512 (https://www.ncbi.nlm.nih.gov/nuccore/ACJ65512)	
	String	
7227.FBpp0303107 (http://string-db.org/newstring.cgi/show_network_section.pl?identifier=7227.FBpp0303107)		
	Sequence Similarities	
-		
	GO - Molecular Function	
GO:0042803 : protein homodimerization activity (https://www.ebi.ac.uk/QuickGO/term/GO:0042803)		
GO:0000977 : RNA polymerase II regulatory region sequence-specific DNA binding (https://www.ebi.ac.uk/QuickGO/term/GO:0000977)		
GO:0008270 : zinc ion binding (https://www.ebi.ac.uk/QuickGO/term/GO:0008270)		
GO:0001077 : proximal promoter DNA-binding transcription activator activity, RNA		

polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001077>)
GO:0001078 : proximal promoter DNA-binding transcription repressor activity, RNA
polymerase II-specific (<https://www.ebi.ac.uk/QuickGO/term/GO:0001078>)
GO - Biological Process

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:0007530 : sex determination (<https://www.ebi.ac.uk/QuickGO/term/GO:0007530>)
GO:0045892 : negative regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045892>)
GO:0045893 : positive regulation of transcription, DNA-templated
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045893>)
GO:0046660 : female sex differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046660>)
GO:0048086 : negative regulation of developmental pigmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048086>)
GO:0048071 : sex-specific pigmentation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0048071>)
GO:0035215 : genital disc development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0035215>)
GO:0007485 : imaginal disc-derived male genitalia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007485>)
GO:0016199 : axon midline choice point recognition
(<https://www.ebi.ac.uk/QuickGO/term/GO:0016199>)
GO:0007619 : courtship behavior (<https://www.ebi.ac.uk/QuickGO/term/GO:0007619>)
GO:0045497 : female analia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045497>)
GO:0019101 : female somatic sex determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0019101>)
GO:0007486 : imaginal disc-derived female genitalia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0007486>)
GO:0045496 : male analia development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045496>)
GO:0008049 : male courtship behavior
(<https://www.ebi.ac.uk/QuickGO/term/GO:0008049>)
GO:0045433 : male courtship behavior, veined wing generated song production
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045433>)
GO:0046661 : male sex differentiation
(<https://www.ebi.ac.uk/QuickGO/term/GO:0046661>)
GO:0045498 : sex comb development
(<https://www.ebi.ac.uk/QuickGO/term/GO:0045498>)
GO:0018993 : somatic sex determination
(<https://www.ebi.ac.uk/QuickGO/term/GO:0018993>)

GO - Cellular Component

GO:0005634 : nucleus (<https://www.ebi.ac.uk/QuickGO/term/GO:0005634>)

	Presumptive Null
Unknown (https://www.gephebase.org/search-criteria?/and+Presumptive Null=~Unknown^#gephebase-summary-title)	
	Molecular Type
Cis-regulatory (https://www.gephebase.org/search-criteria?/and+Molecular Type=~Cis-regulatory^#gephebase-summary-title)	
	Aberration Type
Unknown (https://www.gephebase.org/search-criteria?/and+Aberration Type=~Unknown^#gephebase-summary-title)	
	Molecular Details of the Mutation
various	
	Experimental Evidence
Linkage Mapping (https://www.gephebase.org/search-criteria?/and+Experimental Evidence=~Linkage Mapping^#gephebase-summary-title)	
	Main Reference
Non-coding changes cause sex-specific wing size differences between closely related species of <i>Nasonia</i> . (2010) (https://pubmed.ncbi.nlm.nih.gov/20090834)	
	Authors
Loehlin DW; Oliveira DC; Edwards R; Giebel JD; Clark ME; Cattani MV; van de Zande L; Verhulst EC; Beukeboom LW; Muñoz-Torres M; Werren JH	

Abstract

The genetic basis of morphological differences among species is still poorly understood. We investigated the genetic basis of sex-specific differences in wing size between two closely related species of *Nasonia* by positional cloning a major male-specific locus, wing-size1 (*ws1*). Male wing size increases by 45% through cell size and cell number changes when the *ws1* allele from *N. giraulti* is backcrossed into a *N. vitripennis* genetic background. A positional cloning approach was used to fine-scale map the *ws1* locus to a 13.5 kilobase region. This region falls between *prospero* (a transcription factor involved in neurogenesis) and the master sex-determining gene *doublesex*. It contains the 5'-UTR and cis-regulatory domain of *doublesex*, and no coding sequence. Wing size reduction correlates with an increase in *doublesex* expression level that is specific to developing male wings. Our results indicate that non-coding changes are responsible for recent divergence in sex-specific morphology between two closely related species. We have not yet resolved whether wing size evolution at the *ws1* locus is caused by regulatory alterations of *dsx* or *prospero*, or by another mechanism. This study demonstrates the feasibility of efficient positional cloning of quantitative trait loci (QTL) involved in a broad array of phenotypic differences among *Nasonia* species.

Additional References

RELATED GEPHE

	Related Genes
1 (Unpaired-like) (https://www.gephebase.org/search-criteria?/or+Taxon ID=~7425^/and+Trait=Wing shape/or+Taxon ID=~7426^/and+Trait=Wing shape/and+groupHaplotypes=true#gephebase-summary-title)	

No matches found.

EXTERNAL LINKS

COMMENTS

@SexualTrait