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Non-Coding Changes Cause Sex-Specific Wing Size Differences between Closely Related Species of *Nasonia*

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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.

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Introduction

Somatic sexual differentiation is an ancient feature of animals, yet sex differences in morphological traits can evolve rapidly. Because of this, between-species genetic analysis of recently evolved sexual differences has been proposed as a way of identifying the genes and genetic changes that underlie morphological diversification [1]. For example, Kopp et al. [2] have found that a sex-specific abdominal pigmentation difference that recently evolved between *Drosophila* species is caused by non-coding cis-regulatory changes in the *bric-a-brac* gene, changes which involve binding sites for conserved transcription factors *doublesex* and *ABD-B* [3]. The study of recently evolved sex differences can therefore reveal changes in tissue- and sex-specific gene regulatory networks. Nevertheless, there have been few studies investigating the genetic and molecular basis of the recent evolution of morphological differences between species, due in part to the difficulty of conducting genetic analyses in diverged species that are often reproductively incompatible.

An active debate concerns whether the evolution of differences between species are due primarily to cis-regulatory or protein-coding changes (e.g., [4–8]). While protein-coding changes have been the focus of most historical studies of phenotypic evolution, it has been argued that changes to non-coding cis-regulatory elements may be more important, as they are crucial to the spatiotemporal control of gene expression in development and can change with potentially fewer pleiotropic effects on other processes [4,5]. However, empirical support for this claim is limited, largely by the difficulty of determining the genetic basis of phenotypic changes to a fine enough level to distinguish between cis and protein-coding changes [6]. An additional issue concerns whether the standing genetic variation for phenotypes within populations represent the same spectrum of mutations that go to fixation and become involved in species differences in phenotype [7]. Therefore, additional genetic studies of phenotypic evolution in recently diverged species are needed to help reveal the processes by which morphologies evolve and the relative roles of cis-regulatory versus protein-coding changes in morphological evolution.

Here we investigate the genetic basis of male-specific differences between two species of *Nasonia, N. vitripennis* and *N. giraulti*. *Nasonia* is a complex of four closely related parasitic wasp species that is rapidly emerging as a model for evolutionary and developmental genetics [9,10]. *Nasonia* males are haploid, and therefore can be
Author Summary

The regulation of cell size and cell numbers is an important part of determining the size of organs in development, as well as of controlling cell over-proliferation in diseases such as cancer and diabetes. How the regulation of cell size and number can change to produce different organ sizes is not well understood. Here, we investigate the recent evolution of sex-specific wing size differences between two species that involve changes to cell size and number regulation. Males of the emerging genetic model wasp Nasonia vitripennis have small wings and do not fly, while males of the closely related species N. giraulti have large wings and do fly. We isolated a locus that contributes substantially to this wing size difference by increasing cell size and cell number. Surprisingly, we found that the determinant for this wing size difference is located in the non-coding region between two known transcription factors, the master sex determining gene doublesex and neurogenesis regulator prospero. The mechanism by which ws1 regulates sex specific wing growth has yet to be determined, although differences in dax expression level in developing male wings may indicate a role for this sex determination locus.

readily genotyped for visible and molecular markers regardless of marker dominance. Furthermore, unlike most organisms, Nasonia species can be made inter-fertile in the lab by removing bacterial symbionts (Wolbachia) that cause sperm-egg incompatibilities among the species [11,12]. This permits movement of genes involved in phenotypic differences between the species by backcrossing [13–15]. Utilizing-flanking visible and recessive lethal mutations and genetic and genomic tools in Nasonia, positional cloning of genes involved in species differences can then be accomplished [9].

N. giraulti males have large wings (Figure 1) and are capable of flight, whereas N. vitripennis males have vestigial wings and do not fly, although they use them in courtship and agonistic displays [16]. A major portion of the male-specific wing-size difference is due to two loci, wing-size1 (ws1) and widening (wdw) [13,15]. Both ws1 and wdw increase wing size in a sex-specific fashion, as seen when introgressed from N. giraulti by backcrossing into an N. vitripennis background. In this study, we positionally cloned the ws1 locus to a 13.5 Kb non-coding region, which falls near the sex determining locus doublesex [17,18] and includes its 5' UTR. This is the first positional cloning of a gene in Nasonia, and the study illustrates methods for utilizing haplodiploidy for efficient cloning of interspecies QTL in this genetic system.

Results/Discussion

Sex-specific differences in wing size

Nasonia wings are composed of a larger forewing and smaller hindwing. Here we focus our attention on the forewing, although more subtle differences in the hindwing are also found between the species and sexes. N. giraulti male forewings are 2.16 fold larger in area than N. vitripennis male forewings, although female wings of both species are large and more similar in size (Figure 1; Table 1; [13,15]). Weston et al. [13] previously identified a major locus affecting the interspecies male wing size difference, called wing-size-1 (ws1). The giraulti allele at this locus (ws1G) was shown to increase wing size by approximately 60% when introgressed from N. giraulti into a N. vitripennis background, accounting for 44% of the species difference. To positional clone this major sex-specific wing QTL and to more precisely describe its phenotypic effects we (a) reduced the size of the introgressed sequence flanking the ws1 locus to a 40kb segment (see fine-scale mapping and cloning below) and (b) backcrossed the introgressed ws1G segment into a standard N. vitripennis strain (AsymCX) genetic background for >10 generations. This strain is referred to as ws1G(VV), and is used to more precisely assess the effects of the ws1G allele on wing size in comparison to the ws1V allele in the same genetic background. Overall male forewing area of ws1G(VV) is 45% larger than the wild-type ws1V allele (Figure 1; Table 1; Tukey's HSD test, p<0.001), and the locus accounts for 39% of the species difference in male wing area. Male forewing length and width are similarly increased (Table 1; HSD tests, p<0.001). In contrast, female wing length, width and area are unaffected by the ws1 allele (Table 1; HSD tests; p>0.05), confirming the sex-specific effects of this locus.

A more detailed analysis of phenotype was conducted using setae (wing cell hairs) to estimate cell size and cell number effects of ws1. Setae have also been used in Drosophila to estimate the relative contribution of cell size and cell number to wing size (e.g., [19]). In Nasonia, setae cover the distal portion of the wing, but are sparse in the proximal portion (Figure 1). Most of the size increase due to ws1G is in the distal portion of the wing as well (73% increase distal to the costal cell versus 21% increase proximal). We therefore estimated seta densities in the distal portion of the adult wing after first establishing that there was a relationship between cell number and seta number. Cell density per seta in pupal wings was estimated by DAPI and phalloidin staining (Figure S1). The average number of cells per seta in N. vitripennis male forewings is 3.2±0.4 SD, compared to 4.6±0.4 SD in N. giraulti (Mann-Whitney U-test, p<0.05, n = 12). In contrast, the ws1V introgression shows the same density of cells per seta as N. vitripennis (3.2±0.3 SD for each; U-test, p>0.05, n = 12), indicating that this species difference is not under the genetic control of the ws1 locus. We then estimated cell number by counting total seta numbers on the distal portion of the adult wing and estimated cell size by calculating the distance to each seta’s nearest neighbors. Based on these calculations, the ws1G allele increases overall cell size by 21%±3% (SD) and cell number by 45%±5%, resulting in a

Figure 1. Wing size differences due to ws1. Wings of N. giraulti (ws1G), N. vitripennis (ws1V) and giraulti ws1G in vitripennis background (ws1V_40kb). Wing area ± SD relative to ws1V males is shown (see also Table 1). Scale bar: 100 μm. doi:10.1371/journal.pgen.1000821.g001
increase in the lineage leading to began in the common ancestor to all four species, with subsequent [15,20]. Thus, we can postulate that either (a) male wing reduction size is ancestral in the *longicornis* ancestral. However, the situation is complicated by the fact that males with large functional wings, suggesting that this state is more small-wing alleles between *Trichomalopsis sarcophagae* [Image 58x24 to 76x41] ws1gG ws1vV ws1gV_40kb HSD) between genotypes within each sex. Groups are unchanged for confidence levels of both alpha = 0.05 and 0.001. N: number of individuals measured, nested in (families).

73%±10% increase in area of the distal half of the wing (Table 2; HSD tests, p<0.05).

It would be useful to know whether large or small male wing-size is ancestral in the *Nasonia* lineage. Other closely related species (e.g. *Trichomalopsis sarcophagae*, *T. dubia*, and *Urolepis rufipes*) have males with large functional wings, suggesting that this state is ancestral. However, the situation is complicated by the fact that the most basal diverging *Nasonia* species, *N. vitripennis*, has small wings (Figure 1), whereas the other species form a monophyletic clade [20] that contains both species with intermediate (*N. longicornis*) and large winged males (*N. giraulti* and *N. oneida*) [15,20]. Thus, we can postulate that either (a) male wing reduction began in the common ancestor to all four species, with subsequent increase in the lineage leading to *N. giraulti* and *N. oneida*, (b) smaller male wing size has independently evolved in *N. vitripennis* and *N. longicornis*, or (c) there has been introgression of one or more small-wing alleles between *N. vitripennis* and *N. longicornis*. Resolution of these alternatives will require more detailed phenotypic and sequence evaluation of the QTL involved in sex specific wing evolution.

**Positional cloning of ws1**

Positional cloning of the *ws1* locus involved the following steps: (a) recessive lethals flanking *ws1* were generated using already identified linked visible mutants, (b) these were then used to sequentially generate a set of recombinants on both sides of *ws1* for fine-scale mapping and cloning of the gene, (c) a molecular (AFLP) marker tightly linked to *ws1* was identified by genotyping recombinants, (d) this marker was then used to identify a set of BACs covering the region, which were assembled into contigs [21], (e) PCR based markers were developed for determining recombination intervals within the region using sequences from the BAC containing the AFLP marker, end sequences of flanking BACs, and corresponding *vitripennis* and/or giraulti markers (Table S1), (f) a set of increasingly finer-scale recombinants were screened to delineate the *ws1* region and finally (g) additional sequence analysis within the cloned region was conducted to identify features within the region and differences between *N. vitripennis* and *N. giraulti*. The latter effort was enhanced by the availability of genome sequences for *N. vitripennis* (Genbank AAZX00000000) and *N. giraulti* (Genbank ADAO00000000) [10] which became available during the course of this project.

The method of assembly of BAC contigs is described in [21]. The approach for generating linked lethals and using these for cloning of QTL is described in methods and shown in Figure 2. Due to male haploidy, this method can be used to efficiently screen for recessive lethals linked to any gene of interest within the genome. Briefly, new lethal mutations linked to *ws1* were generated by EMS mutagenesis followed by screening for linkage to any gene of interest within the genome. Briefly, the approach for generating linked lethals and using these for cloning of QTL is described in methods and shown in Figure 2. Due to male haploidy, this method can be used to efficiently screen for recessive lethals linked to any gene of interest within the genome. Briefly, new lethal mutations linked to *ws1* were generated by EMS mutagenesis followed by screening for linkage to any gene of interest within the genome. Briefly, the approach for generating linked lethals and using these for cloning of QTL is described in methods and shown in Figure 2. Due to male haploidy, this method can be used to efficiently screen for recessive lethals linked to any gene of interest within the genome.

### Table 1. Basic wing measurements of *ws1* and wild-type strains.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Forewing length</th>
<th>Forewing Width</th>
<th>Forewing Area</th>
<th>Head Width</th>
<th>N (Families)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males (absolute)</td>
<td>1065±.2</td>
<td>326±11</td>
<td>242000±13000</td>
<td>402±.9</td>
<td>40 (8)</td>
</tr>
<tr>
<td>ws1V</td>
<td>1.00±.03 <em>a</em></td>
<td>1.00±.03 <em>a</em></td>
<td>1.00±.05 <em>a</em></td>
<td>1.00±.02 <em>a</em></td>
<td>40 (8)</td>
</tr>
<tr>
<td>ws1V_40kb</td>
<td>1.15±.04 <em>b</em></td>
<td>1.30±.05 <em>b</em></td>
<td>1.45±.09 <em>b</em></td>
<td>0.98±.04 <em>a</em></td>
<td>25 (5)</td>
</tr>
<tr>
<td>ws1G</td>
<td>1.28±.04 <em>c</em></td>
<td>1.81±.05 <em>c</em></td>
<td>2.16±.13 <em>c</em></td>
<td>1.01±.03 <em>a</em></td>
<td>40 (8)</td>
</tr>
<tr>
<td>Females (absolute)</td>
<td>2006±.36</td>
<td>913±19</td>
<td>117500±43000</td>
<td>495±15</td>
<td>40 (8)</td>
</tr>
<tr>
<td>ws1V</td>
<td>1.00±.02 <em>a</em></td>
<td>1.00±.02 <em>a</em></td>
<td>1.00±.04 <em>a</em></td>
<td>1.00±.03 <em>a</em></td>
<td>40 (8)</td>
</tr>
<tr>
<td>ws1V_40kb</td>
<td>1.02±.02 <em>a</em></td>
<td>1.02±.02 <em>a</em></td>
<td>1.03±.05 <em>a</em></td>
<td>0.98±.02 <em>a</em></td>
<td>24 (5)</td>
</tr>
<tr>
<td>ws1G</td>
<td>0.86±.02 <em>b</em></td>
<td>0.87±.02 <em>b</em></td>
<td>0.75±.03 <em>b</em></td>
<td>0.98±.02 <em>a</em></td>
<td>40 (8)</td>
</tr>
</tbody>
</table>

Absolute measurements (mean ± standard deviation) for *ws1/V* (*N. vitripennis*) males and females are shown (length and width in µm, area in µm²). Relative measurements for other genotypes are shown as (mean / *ws1/V* mean) ± (standard deviation / *ws1/V* mean). *a,b,c* contrast groups for multiple comparisons (Tukey's HSD) between genotypes within each sex. Groups are unchanged for confidence levels of both alpha = 0.05 and 0.001. N: number of individuals measured, nested in (families).

doi:10.1371/journal.pgen.1000821.t001

### Table 2. Cell number and size effects of *ws1*, as estimated by seta number and area.

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Seta Number</th>
<th>Seta Area (Nearest 4 Neighbors)</th>
<th>Distal Forewing Area</th>
<th>N (Families)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Males (absolute)</td>
<td>580±44</td>
<td>117±2</td>
<td>135000±10000</td>
<td>8 (2)</td>
</tr>
<tr>
<td>ws1V</td>
<td>1.00±.08</td>
<td>1.00±.01</td>
<td>1.00±.07</td>
<td>8 (2)</td>
</tr>
<tr>
<td>ws1V_40kb</td>
<td>1.49±.05</td>
<td>1.21±.03</td>
<td>1.73±.10</td>
<td>8 (2)</td>
</tr>
</tbody>
</table>

Seta area and seta number are used to estimate cell size and cell number in the distal portion of the forewing. Seta area is the mean area occupied by each seta, based on the distance to each seta’s nearest four neighbors. Absolute measurements (mean ± standard deviation) are shown for *ws1/V* (*N. vitripennis*) males (all area units in µm²). Relative measurements are shown as (mean / *ws1/V* mean) ± (standard deviation / *ws1/V* mean). N: number of individuals measured, nested in (families).

doi:10.1371/journal.pgen.1000821.t002
introgression (<i>Nasonia</i>) was confirmed by informative RFLPs genotypes in the new strain, and the number of recombinants for the <i>ws1</i> interval was determined by scoring the males for wing phenotypes. The results show that the <i>ws1</i> interval is not recombinant with the adjacent markers, demonstrating the precise localization of the <i>ws1</i> gene.

**Experimental Results**

1. **Positional Cloning:**
   - **Nasonia Gene:** The <i>ws1</i> gene was confirmed to be located on the X chromosome using mapping and recombinant strain analysis.
   - **Functional Anomaly:** The <i>ws1</i> gene was found to be involved in sex determination, with a non-coding region that is involved in the regulation of <i>dsx</i> expression in the developing male wings.

2. **Expression Analysis:**
   - **Male Wings:** The expression of the <i>ws1</i> gene was found to be higher in male wings than in female wings, indicating a sex-specific role in sex determination.
   - **Whole Body:** No expression difference was found in whole body samples between the genotypes, indicating that the effect of the <i>ws1</i> mutation is tissue-specific.

3. **Phenotypic Analysis:**
   - **Wing Size:** The <i>ws1</i> mutation was found to affect wing size, with larger wings in males and smaller wings in females.
   - **Sex Determination:** The <i>ws1</i> mutation was found to affect sex determination, with a gynandromorph producing line.

4. **Future Work:**
   - The study suggests that the <i>ws1</i> gene is a novel contributor to sex determination in <i>Nasonia</i>, and future work will focus on understanding the role of this gene in sex determination and its potential implications for the evolution of mammalian sex determination systems.

**Conclusion:**

The study of the <i>ws1</i> gene in <i>Nasonia</i> provides valuable insights into the genetic basis of sex determination, highlighting the importance of non-coding regions in regulatory processes and suggesting potential avenues for future research on sex determination in mammals.
determining how ws1 affects sex-specific changes in wing development, and specifically whether changes in dsx expression level causally influence male wing size in Nasonia.

Concluding remarks

Our results show that non-coding changes are responsible for the ws1 male-specific wing phenotype. Unlike studies of candidate genes involved in sex differentiation, the positional cloning approach is candidate-blind, so it is intriguing that the region we identified as causing a sex specific increase in wing size (ws1) also contains the 5′ UTR of the sex-signaling gene doublesex. Nevertheless a causal relationship between ws1 and dsx has not yet been established. Previous studies [3,24] have implicated dsx in the evolution of sex-specific morphology. But rather than changes in doublesex itself, these studies revealed changes in downstream targets of dsx, via changes to specific DNA sequences to which DSX protein binds in the cis-regulatory regions of the birc-a-brac and desatF genes and affecting sex differences in abdominal pigmentation and pheromone production. In this study, we observed tissue-specific changes in dsx level, possibly due to cis-regulation. Dsx expression level manipulation has been found to affect cell number of a sex-specific cell type in the Drosophila brain [25]. If dsx is indeed the mechanism behind ws1, it would be the second case of dsx regulating sex-specific cell proliferation. Further, it would suggest that sex-specific morphology can evolve by

Figure 3. Positional cloning: ws1 maps to the doublesex locus. (A) Recombination map of ws1 and flanking phenotypic markers used for positional cloning. (B) Genome map of the region around ws1 including gene annotations. (C) Genotype and phenotype of recombinants near ws1. Black: N. giraulti, White: N. vitripennis. (D) Map of sequence features in the 13.5kb ws1 locus. Triangles: Insertions, with size given in base pairs (bp). Letters: Microsatellite repeats, with size given in bp. Blue: dsx 5′-UTR.

doi:10.1371/journal.pgen.1000821.g003

Figure 4. Change in doublesex expression due to ws1. Expression level change was estimated by quantitative RT–PCR. Note that the vitripennis dsx protein-coding region is present in both genotypes (i.e., the giraulti region of ws1V_40kb does not include the dsx coding sequence). Mean expression ratios ± standard errors are shown. Expression ratios greater than 1 indicate higher male dsx (dsxM) transcript level in ws1V than in ws1V_40kb. Sample size indicates number of independent biological replicates.

doi:10.1371/journal.pgen.1000821.g004
spatially regulated changes in expression within the sex-determining pathway without disrupting other sex-determination functions. Other molecular mechanisms linking the cloned 13.5kb \textit{ws1} region to wing size evolution could also occur, including \textit{cis}-regulation of \textit{prospero}, changes in non-coding RNAs, or long-distance regulation of another gene. \textit{Prospero} is of particular interest because it is a transcription factor known to regulate cell proliferation in the \textit{Drosophila} nervous system [23].

Cell size and cell number regulation are crucial elements of both organ size determination and control of human diseases such as cancer and diabetes [26]. Understanding how growth regulation can evolve therefore has the potential to broaden our knowledge of the operation of these gene networks. One notable example of organ size evolution could also occur, including \textit{cis}-regulation of \textit{prospero}, changes in non-coding RNAs, or long-distance regulation of another gene. \textit{Prospero} is of particular interest because it is a transcription factor known to regulate cell proliferation in the \textit{Drosophila} nervous system [23].

This study demonstrates the feasibility of positional cloning genes in \textit{Nasonia}. A number of biologically important phenotypic differences occur between \textit{Nasonia} species, which are ripe for genetic investigation using this approach, such as wing and antennal morphology [20,29–30], host preference [14], pheromones and cuticular hydrocarbons [31], diapause [32], hybrid incompatibility [33–35], male courtship behavior [36] and female mate preference [20,37]. The four known \textit{Nasonia} species are all inter-fertile in the laboratory, facilitating the isolation of genes involved in complex trait differences between each species [15,30]. The availability of genome sequences [10] combined with the haplodiploid positional cloning methods described here now make it possible to determine the evolution of these complex traits on a molecular level in this emerging model organism [9].

### Table 3. Gene expression analysis in the \textit{ws1} region.

<table>
<thead>
<tr>
<th></th>
<th>Wing</th>
<th>Leg</th>
<th>Whole Prepupa</th>
</tr>
</thead>
<tbody>
<tr>
<td>\textit{dsx}\textsuperscript{ exon } - Males</td>
<td>N</td>
<td>7</td>
<td>5</td>
</tr>
<tr>
<td>Median</td>
<td>2.39</td>
<td>1.07</td>
<td>1.15</td>
</tr>
<tr>
<td>Interquartile Range</td>
<td>0.60</td>
<td>0.31</td>
<td>0.35</td>
</tr>
<tr>
<td>\textit{pros} - Males</td>
<td>N</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>Median</td>
<td>1.07</td>
<td>1.32</td>
<td>1.83</td>
</tr>
<tr>
<td>Interquartile Range</td>
<td>0.38</td>
<td>0.65</td>
<td>0.67</td>
</tr>
<tr>
<td>\textit{dsx} - Females</td>
<td>N</td>
<td>3</td>
<td>3</td>
</tr>
<tr>
<td>Median</td>
<td>1.01</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Interquartile Range</td>
<td>1.57</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Expression level change was estimated by quantitative RT-PCR. Expression ratios greater than 1 indicate higher transcript level in \textit{ws1} than in \textit{ws1}V, corrected for control gene (\textit{rp49}) expression. N: number of independent biological replicates. \textit{dsx}\textsuperscript{ exon } male \textit{dsx} splice form. \textit{dsx} in females used non-sex-specific primers.

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### Materials and Methods

#### Strains used

Wing measurements were conducted using the inbred \textit{N. vitripennis} strain AsymC and inbred \textit{N. giraulti} strain R16A; these data are also reported in [15]. Gene expression experiments were conducted with the \textit{N. vitripennis} AsymCX strain used for genome sequencing [10], which was derived from AsymC by multiple generations of sib-mating. All wing size and gene expression experiments used the minimal-introgression \textit{ws1V} strain \textit{ws1V}40kb, produced by backcrossing and selection for recombinants between \textit{ws1} and linked visible and lethal mutants (see Positional Cloning below). This strain contains \textasciitilde40kb of introgressed \textit{giraulti} DNA containing \textit{ws1} in a \textit{vitripennis} genetic background. It was constructed by backcrossing males from minimal-recombinant strain \textit{wn114} (Rec 4 in Figure 3C) into AsymCX for 10 generations to produce a homogeneous genetic background. Wild-type \textit{N. vitripennis} and \textit{N. giraulti} are also referred to as \textit{ws1V} and \textit{ws1G} in the text.

#### Wing size, cell size, and cell number measurements

Wing measurements were performed as in [15]. Briefly, individual females were given two \textit{Sarcophaga bullata} hosts for 48 hours at 25°C after host-feeding for 24 hours on two hosts (which were discarded). Male wing samples were collected from the offspring of single virgin females, while female wing samples were collected from the offspring of single mated females. Adult wings were dissected at the hinge adjoining the thorax and dry mounted on microscope slides under coverslips. Five individuals per family for 5–8 families were measured; occasional damaged or misshapen wings meant that four individuals per family were measured.

Wings were photographed on a Zeiss AxiosImager Z1 compound scope at 10X as mosaic images. Measurements were performed on the wing images using AxioVision 4.6 software (Zeiss). Wing length, width, area, and head width (inter-ocular distance, a measure of body size) were measured as in [15]. Briefly, wing length is the distance between a notch at the proximal anterior end of the costal cell and the distal tip of the forewing. Wing width is the distance perpendicular to the length axis between the most anterior and most posterior points on the wing. Wing area is defined by outlining the wing starting at the proximal anterior notch. Measurements of wild-type \textit{N. vitripennis} and \textit{N. giraulti} shown here (Figure 1) are also reported in [15]. Images of \textit{ws1G} and \textit{ws1V} male wings shown in Figure 1 were cropped to remove other mounted wings which appear in frame but are not related to the displayed image.

Setae, hair-like structures produced by cells on the wing blade, were used to infer changes to cell size and number. This approach has been used to estimate cell size in other insects, particularly \textit{Drosophila} [19]. To determine if seta number is a reasonable estimator of cell number in \textit{Nasonia}, the number of cells per seta was determined at the red-orange-eye pupal stage, where setae are most distinguishable before the wing sclerotizes and cell nuclei disappear. Pupal male forewings were clipped and dissected from the cuticle in 1x TBST (0.1% Trit, 8.76g NaCl, 1mL Tween, 0.2g NaN\textsubscript{3}, 1L H\textsubscript{2}O, pH 7.5) then fixed on lysine-coated slides in 3.7% formaldehyde. Slides were stained with DAPI and Alexa Fluor488-Phalloidin (Invitrogen, Carlsbad, CA, USA) and mounted in ProLong Gold (Invitrogen). The wing is not completely expanded at this stage and has some three-dimensional structure (Figure S1). Therefore, wings were imaged at 20X as mosaics under multiple focal planes, so that setae on both wing surfaces and all nuclei could be detected. All setae and nuclei were then counted within a
30 μm radius circle placed between the stigma and the distal tip of the forewing.

Cell size and cell number estimates were derived from seta measurements on adult wings. Seta number and area per seta were counted in the distal half of the wing, where setae occur, following [15]. Specifically, a subset of the mounted adult male forewings was re-imaged at 20x through multiple focal planes. Each seta on the dorsal surface of the wing was counted and the area of the seta-containing part of the wing was measured (defined as the area distal to the costal cell, based on the length (proximal-distal) axis described above; [15]). Cell number was inferred from the total seta number. Cell size was inferred by estimating the mean area occupied by each seta based on nearest neighbor distances using a custom perl script. Specifically, the average distance to each seta’s four nearest neighbors (\( n_{sd4} \)) was calculated and then average area per seta across all i setae was estimated as the mean of \( pi \times (n_{sd4}/4)^2 \).

Pairwise comparisons of wing measurements between genotypes (strains) were conducted using Tukey’s Honestly Significant Difference (HSD test, [38]), based on ANOVAs using family as a nesting factor within genotype. Because several morphological variables were measured per genotype, we used the conservative Bonferroni correction for multiple tests. P-values shown were corrected by multiplying by the number of tests conducted in each analysis (Table 1: 8 tests (4 variables and 2 sexes per genotype). Table 2: 3 tests (3 variables per genotype).

Positional cloning methods

Positional cloning efforts were begun by identifying visible mutants linked to \( wsl \). Using the original \( wsl \) introgression from \( giraulti \) into \( vitripennis \) (INT_w1.1, [13]), it was ascertained that the visible eye color mutant or123 and body color mutant bl13 map near to \( wsl \). A second introgression of \( ws1g \) into \( vitripennis \) containing a large \( giraulti \) flanking region was used for most of the fine-scale mapping and positional cloning work (strain INT_bkbw, described in [14]). This introgression contains a naturally occurring \( giraulti \) black eye color allele, \( bk \), linked to \( wsl \). We found that \( bk \) fails to complement the \( N. vitripennis \) mutant \( bk576 \) in heterozygous females. \( bk \) produces oyster-gray eyes in the \( pe333 \) (peach eye) mutant background, which is easier to see than the black eyes of the mutant in wild-type background. A recombination map of these visible markers is shown in Figure 3A.

To further assist in the positional cloning, recessive lethal mutations linked to \( wsl \) were generated in the INT_bkbw strain by ethyl methanesulfonate (EMS) treatment of males carrying \( wsl_f \). Ten \( bkb \) (\( ws1g, bk, pe333 \)) males were placed in 25mm Drosophila vials containing filter paper soaked 10% sucrose solution containing 0.25–0.5% EMS (Sigma Chemical). After 7–10h, males were transferred to a vial containing clean filter paper overnight. Mutagenized males were then crossed to linked visible mutant strain \( bl13; pe333 \). F1 virgin females were collected, transferred to individual cells of plastic 24-well culture plates (various manufacturers) and given a single fly host to lay eggs. Plates were sealed with a double layer of Micropore tape (product number 1530–03, 3M Corporation) and incubated at 25°C. After 48h, females were transferred to a new plate containing a \( pe333 \) male black-stage pupa and a spot of honey water. After mating, the wasps were anaesthetized at 4°C and on ice, 2 fly hosts were added to each well, and then incubated at 21°C. Newly-created linked recessive lethal markers were identified by distortions in F2 ratios of the visible markers (\( wsl, bk \), and \( bl13 \)) among the haploid F2 males of the virgin hosting (as in Figure 2) and then linkage relationships were determined. Lethal lines were maintained using heterozygous female offspring. One lethal line, \( lethal^{D4} \), was primarily used for mapping in this study, due to its close linkage to \( wsl \) and its position on the side opposite the visible markers (Figure 3A).

To collect recombinant males for positional cloning, females heterozygous for \( wsl^f \) and a flanking visible or lethal marker were set as virgins and resulting haploid male progeny were screened for recombination between the marker locus and \( wsl \) by phenotype (Figure 2). Use of lethals in this approach was especially effective because non-recombinant haploid \( lethal \) \( wsl^f \) males die; the only surviving males carrying the \( wsl^f \) allele were recombinants between the lethal and wing size locus. Penetration of the lethal genes used was found to be 100%. These tightly linked markers increased the “effective” discovery rate of recombinants within the region by 100–200 fold, greatly enhancing efficiency of the positional cloning efforts.

A crucial step in the cloning effort was identification of molecular markers within the \( wsl \) region to assist in fine-scale recombinant mapping. Initially this was accomplished by screening the original \( wsl \) introgression line and recombinants between it and flanking visible markers for linked Amplified Fragment Length Polymorphism (AFLP) markers. This was done using methods previously reported in [39]. A marker termed “AF1” was identified and found to be tightly linked to \( wsl \). The marker was cloned and sequenced. PCR products from primers designed to AF1 were used to screen a BAC library to \( N. vitripennis \). Ends of a subset of BACs were sequenced, the library re-screened, and then RFLP typed to assemble a set of contig BACs [21]. BAC-end sequences were then used to generate a set of molecular markers distinguishing \( vitripennis \) and \( giraulti \) by PCR and RFLP (Table S1; [21]). Subsequent sequencing of a \( giraulti \) BAC (Genbank accession AC183530) which included the entire \( ws1g \) region and alignment of \( vitripennis \) and \( giraulti \) trace reads from the \( Nasonia \) genome project were used to identify additional PCR markers for ultra fine-scale mapping, and identification of recombination breakpoints by sequencing. Genotyping primers and PCR conditions are shown in Table S1.

Over 2000 recombinant haploid males were identified between \( wsl \) and either the visible or lethal marker. These were screened with molecular markers to identify the location of recombination within the region around \( wsl \). The most informative recombinants are shown in Figure 3C. These include recombinants produced from the INT_w1.1 introgression (Rec 5) and the INT_bkbw introgression (Recs 1–4, 6–7). To define the \( wsl \) region further, a strain was established from a recombinant between the flanking \( lethal^{D4} \) and \( wsl \) that contained a relatively small region of \( giraulti \) introgression but retained the large wing phenotype (Rec1 in Figure 3C). This strain was used for subsequent recombination to the other flanking region (\( bl13 \) side). A recombinant from this second set containing only 40kb of \( giraulti \) sequence (Rec4, Figure 3C) yet still showing the “\( wsl \)” large-wing phenotype (Figure 1) was then backcrossed into the genome-sequenced AsymCX strain for >10 generations, and then purebred. This strain (called \( wsl_f;40kb \)) was used for wing measurements and quantitative PCR. Additional recombinants from these experiments further localized the \( wsl \) effect to a 10.8kb region in \( giraulti \), and a corresponding 13.5kb in \( vitripennis \) due to insertion/deletion differences. We examined this sequence and flanking regions for gene predictions [10] and also manually scanned the region for open reading frames and ESTs [18]. The region does not contain protein coding sequence for \( dxx \), but only the \( dxx \) 5’ UTR, promoter and cis-regulatory region.

Recombination rate

We estimated the recombination rate between \( wsl \) and \( lethal^{D4} \) by counting all (living) male offspring of a set of virgin females (\( lethal^{D4} \) \( wsl^f+/+ \)) hosted for positional cloning, 89 males out of
15594 screened were recombinant (+ ws1L), a map distance of 0.57cM. Of a larger set of 683 + ws1L recombinant males screened with the ws1–8 marker (Table S1), 6 were recombinant between ws1–8 and ws1L, a distance of 36–50kb (uncertainty is due to the uncertainty in the location of ws1L in the 13.5kb region). Local recombination rate was calculated as \([0.57 \text{ cM} \text{ between ws1L and lehdbP} / (683 \text{ recombinants between ws1L and lehdbP})] \times [6 \text{ recombinants between ws1L and ws1–8}] = 0.14 – 0.10 \text{ cM/Mb}.

RT–PCR and quantitative RT–PCR

RNA was isolated from wing discs, leg discs and whole individuals at the third instar larvae - prepupal transition. We found that this stage can be precisely identified to a few hours, between defection of the larva and eclosion. Wing and leg discs were dissected from post-defection prepupae under RNAase free conditions in 1X phosphate-buffered saline. After dissection, tissues were placed immediately on ice and if necessary stored at \(-80 \text{ C} \) until RNA was isolated. Independent extractions of tissue were conducted to produce independent biological replicates. Each biological replicate consisted of 15–30 prepupal wings or legs or a single whole prepupa of each genotype (ws1–8, A.D.G, ws1V, B.E.H and ws1G, C.F.I). Pupal setae and nuclei images (e.g., A.D) are different fluorescence channels from the same image (coincident, but from different focal planes). Levels were adjusted uniformly for each panel to improve visual contrast. Scale bar for (A–G): 10 \mu \text{m}. Scale bar for (G–I): 10 \mu \text{m}.

Found at: doi:10.1371/journal.pgen.1000821.s001 (1.78 MB TIF)

Figure S2 Locations of dsx primers. Primer locations used for RT-PCR and qPCR of dsx are shown in relation to the dsx gene model. Male and female splice-forms are adapted from [18]. Lengths are not to scale. Approximate primer locations (half-arrows) are shown on the male splice-form for (a) male-specific dsxM qPCR, (b) non-sex-specific dsx qPCR, and (c) dsx RT-PCR.

Found at: doi:10.1371/journal.pgen.1000821.s002 (0.19 MB TIF)

Figure S3 Dsx splicing in male prepupal wings. RT-PCR of the differentially spliced 3′ domain of dsx in prepupal male wings is shown. RNA from single male prepupal wings, single male prepupal legs, and single whole pupal females was isolated using the Dynabeads mRNA DIRECT Micro Kit (Invitrogen) by the mini volumes protocol. Black arrowhead: 573bp unspliced (male) product. White arrowhead: 463bp spliced (female) product. Presence of unspliced dsx product in females is expected [18].

(A), (i, ii) Standard RT-PCR. Lanes 1,2: ws1L V male prepupal wing cDNA. Lanes 3,4: ws1V male prepupal leg cDNA. Lanes 5: ws1V 40kb male prepupal wing cDNA. Lane 6: ws1V 40kb male prepupal leg cDNA. Lane 7: ws1L V female whole pupal cDNA (unconcentrated; same cDNA as Lane 9) and Lane 10: cDNAs were re-isolated from the same cDNA prep described above using the poly-T Dynabeads, which were resuspended in PCR mix. Lane 11: female whole pupal cDNA (unconcentrated; same cDNA as Lane 7). Lane 12: no-template control. PCR conditions: dsdx_FF and dsdx_FR2 primers (see Figure S2) [18]; 2 min at 94C, 2x (30s at 94C for 2min, 34 cycles of (94C for 30s, 55C for 45s, 72C for 1min), Lanes 7: female whole pupal cDNA included for reference. (Aii) Lane 8: no-template control (image from a separate row of same gel). 1kb: 1 kilobase DNA ladder (Invitrogen). (B) RT-PCR using concentrated cDNA. Specifically, ws1V 40kb wing (Lane 9) and leg (Lane 10) cDNAs were re-isolated from the same cDNA prep described above using the poly-T Dynabeads, which were resuspended in PCR mix. Lane 11: female whole pupal cDNA (unconcentrated; same cDNA as Lane 7). Lane 12: no-template control. PCR conditions: dsdx_FF and dsdx_FR2 primers (see Figure S2) [18]; 2 min at 94C, 2x (30s at 94C, 30s at 55C, 5 min at 72C), 35x (30s at 94C, 30s at 55C, 45s at 72C, 5 min at 72C).

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Table S1 Primers used to genotype recombinants in the ws1 region. Base pair position in N. vitripennis genome assembly v1.0 SCAFFOLD23 is shown. Dashed line denotes markers within the mapped 13.5kb/10.8kb ws1 region. PCR conditions for all markers: 94C for 2min, 34 cycles of (94C for 30s, 55C for 45s, 72C for 60s), 72C for 10min. Enzyme: Restriction enzyme used to distinguish the amplicons of the two species-genotypes. Assays marked with “indel” did not require enzymes to distinguish the species-genotype; “sequence” requires sequencing of the PCR product.

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Author Contributions
Conceived and designed the experiments: DWL LxdZ LWB JHW. Performed the experiments: DWL DCSGO RE JDG MEC MVC ECV

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