

1 **Evolutionary genetics of cytoplasmic incompatibility genes**

2 ***cifA* and *cifB* in prophage WO of *Wolbachia***

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24 **Abstract**

25 The bacterial endosymbiont *Wolbachia* manipulates arthropod reproduction to facilitate its  
26 maternal spread through populations. The most common manipulation is cytoplasmic  
27 incompatibility (CI): *Wolbachia*-infected males produce modified sperm that cause embryonic  
28 mortality, unless rescued by eggs harboring the same *Wolbachia*. The genes underlying CI, *cifA*  
29 and *cifB*, were recently identified in the eukaryotic association module of *Wolbachia*'s prophage  
30 WO. Here, we use transcriptomic and genomic approaches to address three important  
31 evolutionary facets of these genes. First, we assess whether or not *cifA* and *cifB* comprise a  
32 classic toxin-antitoxin operon, and show they do not form an operon in strain *wMel*. They  
33 coevolve but exhibit strikingly distinct expression across host development. Second, we provide  
34 new domain and functional predictions across homologs within *Wolbachia*, and we show amino  
35 acid sequences vary substantially across the genus. Lastly, we investigate conservation of *cifA*  
36 and *cifB* and find degradation and loss of the genes is common in strains that no longer induce  
37 CI. Taken together, we find no evidence for the operon hypothesis in *wMel*, provide functional  
38 annotations that broaden the potential mechanisms of CI induction, illuminate recurrent erosion  
39 of *cifA* and *cifB* in non-CI strains, and advance an understanding of the most widespread form of  
40 reproductive parasitism.

41

42 **Key words**

43 symbiosis, reproductive manipulation, gene loss, bacteriophage

44

## 45 **Introduction**

46 The genus *Wolbachia* is the most widespread group of maternally transmitted endosymbiotic  
47 bacteria (Zug and Hammerstein 2012). They occur worldwide in numerous arthropods and  
48 nematodes and can selfishly manipulate reproduction (Werren, et al. 2008), confer antiviral  
49 defense (Bian, et al. 2010; Teixeira, et al. 2008), and assist reproduction and development of  
50 their hosts (Dedeine, et al. 2001; Hoerauf, et al. 1999; Hosokawa, et al. 2010). The most  
51 common parasitic manipulation is cytoplasmic incompatibility (CI), whereby *Wolbachia*-  
52 infected males produce modified sperm that can only be rescued by eggs infected with the same  
53 *Wolbachia* strain (Yen and Barr 1971). If the modified sperm fertilize eggs infected with no  
54 *Wolbachia* (unidirectional CI) or a genetically-incompatible *Wolbachia* strain (bidirectional CI),  
55 then delayed histone deposition, improper chromosome condensation and cell division  
56 abnormalities result in embryonic mortality (Landmann, et al. 2009; Lassy and Karr 1996;  
57 Serbus, et al. 2008; Tram and Sullivan 2002). Other described reproductive manipulations  
58 include parthenogenesis (Stouthamer, et al. 1990), male-killing (Hurst, et al. 1999), and  
59 feminization (Rousset, et al. 1992), all of which give a fitness advantage to *Wolbachia*-infected  
60 females and thus assist the spread of the infected matriline through a population. These  
61 manipulations, once sustained, can also impact host evolution including speciation (Bordenstein,  
62 et al. 2001; Brucker and Bordenstein 2013; Jaenike, et al. 2006) and mating behaviors (Miller, et  
63 al. 2010; Moreau, et al. 2001; Randerson, et al. 2000; Shropshire and Bordenstein 2016).

64

65 In addition to the aforementioned reproductive manipulations, *Wolbachia* strains affect host  
66 biology by provisioning nutrients (Hosokawa, et al. 2010), altering host survivorship (Min and  
67 Benzer 1997) and fecundity (Dedeine, et al. 2001; Stouthamer and Luck 1993), and importantly,

68 protecting the host against pathogens (Bian, et al. 2010; Hughes, et al. 2011; Kambris, et al.  
69 2009; Moreira, et al. 2009; Teixeira, et al. 2008; Walker, et al. 2011). The combination of  
70 reproductive manipulations that enable *Wolbachia* to spread in a population, and the ability to  
71 reduce vector competence through pathogen protection, have placed *Wolbachia* in the forefront  
72 of efforts to control target arthropod populations (Bourtzis, et al. 2014; Hoffmann, et al. 2011;  
73 Turelli and Hoffmann 1991; Walker, et al. 2011; Zabalou, et al. 2004). Despite these important  
74 applications, the widespread prevalence of *Wolbachia* across arthropod taxa (Hilgenboecker, et  
75 al. 2008; Werren and Windsor 2000; Zug and Hammerstein 2012), and decades of research, only  
76 recently have the genes underlying CI been determined (Beckmann, et al. 2017; LePage, et al.  
77 2017).

78  
79 Two studies converged on the same central finding: coexpression of a pair of syntenic genes  
80 recapitulates the CI phenotype (Beckmann, et al. 2017; LePage, et al. 2017). Uninfected  
81 *Drosophila melanogaster* males transgenically expressing the two genes from *wMel Wolbachia*  
82 caused CI-like embryonic lethality when crossed with uninfected females that was notably  
83 rescued by *wMel*-infected females (LePage, et al. 2017). Additionally, the two *wMel* genes  
84 separately enhanced *Wolbachia*-induced CI in a dose dependent manner when expressed in  
85 *Wolbachia*-infected males (LePage, et al. 2017). In a separate study, CI-like embryonic lethality  
86 was also recapitulated through transgenic coexpression in *D. melanogaster* males of homologous  
87 transgenes encoded by the *Wolbachia wPip* strain (which infects *Culex* mosquitoes) (Beckmann,  
88 et al. 2017). These two genes occur in the recently discovered eukaryotic association module of  
89 temperate phage WO (Bordenstein and Bordenstein 2016), which was previously implicated in  
90 influencing CI (Bordenstein, et al. 2006; Duron, et al. 2006; Masui, et al. 2000; Sinkins, et al.

91 2005). The presence of these genes within prophage WO has implications for the transmission of  
92 these genes, namely vertical transmission in the *Wolbachia* genome versus horizontal transfer of  
93 phage WO. The genes were proposed as candidate CI effectors due to the presence of one of the  
94 protein products in the spermathecae of infected female mosquitoes (Beckmann and Fallon 2013)  
95 and their absence in the *wAu Wolbachia* strain that lost CI function (Sutton, et al. 2014).  
96  
97 The *wMel* homologs of these genes are designated cytoplasmic incompatibility factors *cifA*  
98 (locus WD0631) and *cifB* (locus WD0632), with *cifA* always encoded directly upstream of *cifB*  
99 (LePage, et al. 2017). The gene set occurs in varying copy number across eleven total CI-  
100 inducing strains that correlates with CI levels. Core sequence changes of the two genes exhibit a  
101 pattern of codivergence and in turn closely match bidirectional incompatibility patterns between  
102 *Wolbachia* strains. Homologs of CifA and CifB protein sequences belong to four distinct  
103 phylogenetic types (designated Types I – IV) that do not correlate with various phylogenies of  
104 *Wolbachia* housekeeping genes or phage WO *gpW* (locus WD0640) (LePage, et al. 2017). The  
105 homologous sequences in *wPip* also cluster in Type I, though they are 66% and 76% different  
106 from *wMel*'s, respectively (Beckmann, et al. 2017). Hereinafter we use *cifA* and *cifB* to refer to  
107 these genes, unless specifically referring to analyses of the *wPip* homologs, *cidA* and *cidB*. *In*  
108 *vitro* functional analyses revealed that *cidB* can encode deubiquitylase activity, and *cidA* encodes  
109 a protein that binds CidB (Beckmann, et al. 2017). Mutating the catalytic residue in the  
110 deubiquitylating domain of CidB results in a loss of the CI-like function in transgenic flies  
111 (Beckmann, et al. 2017). Whether these genes have additional enzymatic or regulatory roles and  
112 which other residues are important for function remain open questions.

113

114 There are important considerations for the location, organization, and characterization of these  
115 genes. Whether or not *cifA* and *cifB* form a strict, toxin-antitoxin operon is debatable, and  
116 likewise has important implications for how gene expression is regulated by *Wolbachia* during  
117 host infection. Support for the operon hypothesis is based on weak transcription across the  
118 junction between *cidA* and *cidB*, inferred to be due to the presence of polycistronic mRNA  
119 (Beckmann and Fallon 2013; Beckmann, et al. 2017); an alternative explanation is transcriptional  
120 slippage. Quantitative transcription analyses and computational predictions of operon structure  
121 do not support the operon hypothesis (LePage, et al. 2017). Moreover and importantly,  
122 transgenic studies show that both *cifA* and *cifB* are required for induction of CI and thus cannot  
123 form a strict toxin (*cifB*) - antitoxin (*cifA*) system. As both genes encode CI function and can  
124 individually enhance *Wolbachia*-induced CI, and there is mixed evidence for classification as an  
125 operon, it does not appear that characterization as a strict toxin-antitoxin operon is warranted  
126 (LePage, et al. 2017). However, like toxin-antitoxin systems, CidA binds CidB *in vitro* and  
127 expression of *cidA* rescues temperature-sensitive growth inhibition induced by *cidB* expression  
128 in *Saccharomyces*, via an as-yet-unknown mechanism (Beckmann, et al. 2017).

129  
130 As it stands now, the genes remain largely unannotated with the exception of a few small  
131 domains. If other predicted protein domains occur in *cifA* and *cifB*, they would provide new  
132 hypotheses for the mechanism of CI. Finally, the sequence diversity and/or loss of *cif* genes  
133 across the *Wolbachia* tree may give insights into the selective conditions that maintain the *cif*  
134 genes versus those that do not. Exploration of *cif* gene regulation, expression, and function thus  
135 can provide a framework for more targeted investigations of *Wolbachia*-host interactions, and  
136 potentially inform the deployment of *Wolbachia*-based arthropod control.

137

## 138 **Materials and Methods**

### 139 **Expression**

140 For analysis of RNAseq data we used our published approach (Gutzwiller, et al. 2015). Briefly,  
141 fastq sequences for 1 day old male and female flies were mapped against the *Wolbachia wMel*  
142 reference genome (Ensembl Genomes Release 24,  
143 *Wolbachia\_endosymbiont\_of\_drosophila\_melanogaster.GCA\_000008025.1.24*) using bwa mem  
144 v. 0.7.5a with default parameters in paired-end mode. Mapped reads were sorted and converted  
145 to BAM format using samtools v0.1.19 after which BAM files were used as input to Bedtools  
146 (bedcov) to generate pileups and count coverage at each position. For expression correlations  
147 between genes, the raw RNAseq counts were divided by (gene length + 99), where 99  
148 corresponds to read length (100) – 1. Within a growth stage these values were multiplied by  $1e^6 /$   
149 (sum of values in stage) (Li and Dewey 2011). A pairwise distance between all genes was  
150 defined as  $(1 - R)$ , where the R is the Pearson correlation coefficient between the normalized  
151 expression values of two genes. Possible negative correlations would be “penalized” here,  
152 resulting in a larger distance. Distances were clustered using the Kitsch program of PHYLIP  
153 (Felsenstein 1989).

154

### 155 **Operon Prediction *in silico***

156 We used the dynamic profile of the transcriptome above to identify operons within the *wMel*  
157 genome using two different approaches. We used the program Rockhopper (McClure, et al.  
158 2013), using default parameters, in conjunction with the BAM files generated above to delineate  
159 likely operons across the entire genome. In addition, we took a fine-scale approach, focusing on

160 the junction between *cifA* and *cifB* (Fortino, et al. 2014), using the pileup files generated above  
161 and identifying drops in gene expression correlated to genomic position using a sliding window  
162 analysis.

163

#### 164 **Nucleic Acid Extractions and Quantitative PCR**

165 To identify *Wolbachia* gene expression in adult male and female *D. melanogaster*, RNA was  
166 extracted from individual, age-matched flies (1-3 days old, stock 145) using a modified Trizol  
167 extraction protocol. Briefly, 500 uL of Trizol was added to individual flies and samples  
168 homogenized using a pestle. After a 5-minute incubation at room temperature, a 12,000 rcf  
169 centrifugation (at 4C for 10 min) was followed by a chloroform extraction. Aqueous phase  
170 containing RNA was extracted a second time with phenol:chloroform before isopropanol  
171 precipitation of RNA. This RNA pellet was washed and resuspended in THE RNA Storage  
172 Solution (Ambion). To detect the number of *cifA* and *cifB* transcripts as well as RNA levels  
173 across the junction between *cifA* and *cifB*, we utilized the RNA extracted from these flies and the  
174 SensiFAST SYBER Hi-ROX One-step RT mix (Bioline) and the Applied Biosystems StepOne  
175 Real-time PCR system with the following primer sets: *cifAF*: ATAAAGGCGTTTCAGCAGGA,  
176 *cifAR*: TCAATGAGGCGCTTCTAGGT; *cifBF*: TACGGGAAGTTTCATGCACA,  
177 *cifBR*: TTGCCAGCCATCATTCAATAA; *cifA\_endF*:  
178 TCTGGTTCTCATAAGAAAAGAAGAATC, *cifB\_begR*: AACCATCAAGATCTCCATCCA.  
179 As a reference for transcription activity of the core *Wolbachia* genome, we utilized the  
180 *Wolbachia ftsZ* gene (Forward: TTTTGTTGTCGCAAATACCG; Reverse:  
181 AGCAAAGCGTTCACATTTCC). We designed primers to *ftsZ* because as a core protein  
182 involved in cell division, the quantities of *ftsZ* would better correlate with bacterial numbers and



183 activity. Reactions were performed in duplicate or triplicate in a 96-well plate and CT values  
184 generated by the machine, were used to calculate the relative amounts of *Wolbachia* using the  
185  $\Delta\Delta\text{Ct}$  (Livak) method.

186

### 187 **Correlated Cif Trees and Distance Matrices**

188 Quantifying congruence scores between the CifA and CifB trees was carried out with Matching  
189 Cluster (MC) and Robinson Foulds (RF) metrics using a custom python script previously  
190 described (Brooks, et al. 2016) and the TreeCmp program (Bogdanowicz, et al. 2012). MC  
191 weights topological congruency of trees, similar to the widely used RF metric. However, MC  
192 takes into account sections of subtree congruence and therefore is a more refined evaluation of  
193 small topological changes that affect incongruence. Significance in the MC and RF analyses was  
194 determined by the probability of 100,000 randomized bifurcating dendrogram topologies  
195 yielding equivalent or more congruent trees than the actual tree. Normalized scores were  
196 calculated as the MC and RF congruency score of the two topologies divided by the maximum  
197 congruency score obtained from random topologies. The number of trees that had an equivalent  
198 or better score than the actual tree was used to calculate the significance of observing that  
199 topology. Mantel tests were also performed on the CifA and CifB patristic distance matrices  
200 calculated in Geneious v8.1.9 (Kearse, et al. 2012). A custom Jupyter notebook (Pérez and  
201 Granger 2007) running python v3.5.2 (<http://python.org>) was written in the QIIME2 (Caporaso,  
202 et al. 2010) anaconda environment, and the Mantel test (Mantel 1967) utilized the scikit-bio  
203 v0.5.1 (scikit-bio.org) Mantel function run using scikit-bio distance matrix objects for each gene.  
204 The Mantel test was run with 100,000 permutations to calculate significance of the Pearson  
205 correlation coefficient between the two matrices using a two-sided correlation hypothesis.

206

## 207 **Genomes Used in Comparative Analyses**

208 In order to identify *cif* homologs across the *Wolbachia* genomes, we defined orthologs across  
209 existing, sequenced genomes using reciprocal best blastp. We included *Wolbachia* genomes  
210 across five Supergroups: monophyletic clades of *Wolbachia* based on housekeeping genes,  
211 denoted by uppercase letters (O'Neill, et al. 1992; Werren, et al. 1995). Supergroups A and B are  
212 the major arthropod infecting lineages, while C and D infect nematodes (Bandi, et al. 1998).  
213 Supergroup F *Wolbachia* infect a variety of hosts (Lo, et al. 2002). Included in this analysis were  
214 11 type A strains (*w*Ri, *w*Ana, *w*Suzi, *w*Ha, *w*Mel, *w*MelPop, *w*Au, *w*Rec, *w*Gmm, *w*Uni,  
215 *w*VitA), 10 type B strains (*w*PipJHB, *w*PipPel, *w*PipMol, *w*Bol1-b, *w*Bru, *w*CauB, *w*No, *w*Tpre,  
216 *w*AlbB, *w*Di), 2 type C strains (*w*Ov, *w*Oo), and one each type D (*w*Bm) and type F (*w*Cle). We  
217 included all genomic data available for each strain such that if multiple assemblies existed for  
218 each *Wolbachia* variant (such as in the case of *w*Uni) we included the union of all available  
219 contigs for that strain. *Wolbachia* orthologs were defined based on reciprocal best blast hits  
220 between amino acid sequences in *Wolbachia* genomes. An orthologous group of genes was  
221 defined by complete linkage such that all members of the group had to be the reciprocal best hit  
222 of all other members of the group. *w*Ana, *w*Gmm, *w*PipMol, *w*Bru, and *w*CauB were not used in  
223 subsequent analyses due to problematic assemblies. Information on strain phenotypes, hosts, and  
224 accession numbers can be found in Table 1.

225

## 226 **Cif Phylogenetics**

227 CifA and CifB protein sequences were identified using BLASTp searches of WOMelB WD0631  
228 (NCBI accession number AAS14330.1) and WD0632 (AAS14331.1), respectively. Homologs

229 were selected based on: 1)  $E \leq 10^{-30}$ , 2) query coverage greater than 70%, and 3) presence  
230 in fully sequenced *Wolbachia* genomes. All sequences were intact with the exception of a partial  
231 WOSuziC CifA (WP\_044471252.1) protein. The missing N-terminus was translated from the  
232 end of contig accession number CAOU02000024.1 and concatenated with partial protein  
233 WP\_044471252.1 for analyses, resulting in 100% amino acid identity to WORiC CifA  
234 (WP\_012673228.1). In addition, two previously identified sequences (LePage, et al. 2017),  
235 WOREcB CifB and WORiB CifB, were not available in NCBI's database and translated from  
236 nucleotide accession numbers JQAM01000018.1 and CP001391.1, respectively. The previously  
237 identified WOSol homologs (CifA: AGK87106 and CifB: AGK87078) (LePage, et al. 2017)  
238 were also included in our analyses. All protein sequences were aligned with the MUSCLE  
239 (Edgar 2004) plugin in Geneious Pro version 8.1.7 (Kearse, et al. 2012); the best models of  
240 evolution, according to corrected Akaike (Hurvich and Tsai 1993) information criteria, were  
241 estimated to be JTT-G using the ProtTest server (Abascal, et al. 2005); and phylogenetic trees  
242 were built using the MrBayes (Ronquist, et al. 2012) plugin in Geneious.

243

## 244 **Protein Structure**

245 All candidate CI gene protein sequences were assessed for the presence of domain structure  
246 using HHpred (<https://toolkit.tuebingen.mpg.de/hhpred/>) (Söding, et al. 2005)) with default  
247 parameters and the following databases: SCOPe95\_2.06, SCOPe70\_2.06, cdd\_04Jul16,  
248 pfamA\_30.0, smart\_04Jul16, COG\_04Jul16, KOG\_04\_Jul16, pfam\_04Jul16, and cd\_04Jul16.  
249 Schematics were created in inkscape (<https://inkscape.org/>), to show regions with significant  
250 structural hits, at a corrected p-value of  $p < 0.05$ . Modules were defined based on the presence of  
251 multiple highly significant hits within a region.

252

### 253 **Protein Conservation**

254 Protein conservation was determined with the Protein Residue Conservation Prediction tool  
255 (<http://compbio.cs.princeton.edu/conservation/index.html> (Capra and Singh 2007)), using  
256 aligned amino acid sequences, Shannon entropy scores, a window size of zero, and sequence  
257 weighting set to “false”. Conservation was subsequently plotted in R version 3.3.2, and module  
258 regions were delineated according to coordinates of the WOMelB modules within the alignment.  
259 CI gene conservation scores were calculated separately for Type I sequences, and for all types  
260 together. For CifB Type I sequences, the WOVitA4 ortholog was left out, due to the extended C-  
261 terminus of that protein. Conservation scores were also calculated for “control proteins”: Wsp  
262 (*Wolbachia* surface protein), known to be affected by frequent recombination events (Baldo, et  
263 al. 2005), and FtsZ, which is relatively unaffected by recombination (Baldo, et al. 2006b; Ros, et  
264 al. 2009). Variation in amino acid conservation between modules and non-module regions was  
265 assessed in R version 3.3.2 with a one-way ANOVA including “region” (either the unique  
266 module number, or “non-module”) as a fixed effect, and followed by Tukey Honest Significant  
267 Difference for post hoc testing.

268

### 269 **Cif Modules**

270 The WOMelB structural regions delineated by HHpred were used to search for the presence of  
271 Cifs or remnants of Cifs across the *Wolbachia* phylogeny. Amino acid sequences of the  
272 WOMelB modules were queried against complete genome sequences (Table 1) using tblastn.  
273 Any hit that was at least 50% of the length and 30% identity, or at least 90% of the length and  
274 20% identity of the WOMelB module was considered a positive match. Module presence was

275 plotted across a *Wolbachia* phylogeny constructed using the five Multi Locus Sequence Typing  
276 (MLST) genes defined by Baldo *et al.* (Baldo, et al. 2006b). Nucleotide sequences were aligned  
277 with MAFFT version 7.271 (Kato and Standley 2013), and concatenated prior to phylogenetic  
278 reconstruction with RAxML version 8.2.8 (Stamatakis 2014), the GTRGAMMA substitution  
279 model, and 1000 bootstrap replicates.

280

### 281 **Hidden Markov Model Searches**

282 To identify *cif* homologs in draft *Wolbachia* genome assemblies we used the program suite  
283 HMMER (Eddy 2011). We defined *cif* types based on our phylogenetic trees (Figure 4) and used  
284 aligned amino acids from these types as input to HMMBUILD, using default parameters. We  
285 then searched six *Wolbachia* WGS assemblies (NCBI project numbers PRJNA310358,  
286 PRJNA279175, PRJNA322628) using HMMSEARCH with  $-F3\ 1e-20$   $-cut\_nc$  and  $-domE\ 1e-$   
287 10. Regardless of thresholds used, or *cif* type of HMM, resulting hits did not differ.

288

### 289 **Results**

#### 290 ***cifA* and *cifB* are Not Co-transcribed or Co-regulated and Do Not Comprise an Operon in** 291 ***wMel***

292 To assess the operon hypothesis, we reasoned that genes which are co-transcribed and co-  
293 regulated will exhibit the following properties: similar total expression levels in whole animals  
294 and correlated gene expression across host development. We therefore utilized an existing  
295 RNAseq dataset for *Wolbachia* in *Drosophila melanogaster*, covering 24 life cycle stages and 3  
296 time samplings each for adult males and females (Gutzwiller, et al. 2015). We mapped reads to  
297 the existing *wMel* assembly (see methods), and calculated Pearson correlation coefficients for

298 normalized expression values for each pairwise comparison across host development. In adult  
299 males and females, *cifA* and *cifB* in *wMel* are not expressed at similar levels (Figure 1), with *cifA*  
300 expressed at significantly higher levels compared to *cifB* (eight-fold higher based on RPKM  
301 values across both genes).

302  
303 To further explore expression of the *cif* genes in *wMel* and assess whether or not polycistronic  
304 mRNA is produced, we performed a quantitative PCR analysis of gene expression from three-  
305 day old male and female flies (Figure 2). We observed transcripts covering the junction between  
306 *cifA* and *cifB*. However, transcripts covering this junction were much more similar to expression  
307 levels in *cifA*, while expression of *cifB* was nine-fold less. Therefore, as *cifA* and *cifB* are  
308 separated by only 76 bp, distinguishing between 3' UTRs from *cifA* and full *cifA-cifB* transcripts  
309 is not possible.

310  
311 We next used two computational methods to test for a potential operon between *cifA* and *cifB*  
312 using our RNAseq analyses. After mapping reads to the *wMel* assembly, we used the resulting  
313 BAM files as input to Rockhopper (McClure, et al. 2013). The program was able to correctly  
314 identify known operons in *wMel* (such as the T4SS WD0004-WD0008 and the ribosomal protein  
315 operon) but it did not identify *cifA* and *cifB* as an operon. We also used a sliding-window  
316 approach, using pileup files generated as part of the mapping, to identify correlations between  
317 genomic position and gene expression drops in the RNAseq data, as in (Fortino, et al. 2014). The  
318 two open reading frames for *cifA* and *cifB* span positions 617223-618647 and 618723-622223,  
319 respectively. From positions 618600 to 618700, we observe a significant positive correlation  
320 between coverage and genomic location (Pearson Correlation = 0.99,  $p < 0.001$ ). However,

321 across the junction between *cifA* and *cifB* (position 618700), we saw a very large drop in gene  
322 expression in both males and females (from an average coverage of 4616 to 38 per position).  
323 This result suggests that *cifA* and *cifB* are not co-transcribed.

324  
325 Finally, we clustered the *wMel* *cif* genes based on their similarity in expression across  
326 *Drosophila* development (Supplemental Figure S1). *cifA* did not group with *cifB* in *wMel* (Figure  
327 3), suggesting that these two genes are not co-regulated. Indeed, the pattern of *cifA* expression  
328 differs strikingly from that of *cifB*. *cifB* is expressed during embryogenesis and generally down-  
329 regulated in pupae and adults, while *cifA* is highly expressed in adult males and females and late  
330 time points during embryogenesis (Figure 1). Curiously, the expression profile of *cifA* in flies  
331 during development is most closely correlated with the *wsp* locus WD1063 (Figure 3).

332

### 333 **New Protein Domain Predictions are Variable Across the Cif Phylogeny**

334 We recovered the four previously identified phylogenetic types (LePage, et al. 2017). Here, our  
335 analyses include additional strains that cause reproductive parasitism beyond CI  
336 (parthenogenesis and male-killing, Table 1), and the more divergent Type IV paralogs for *cifA*,  
337 so far identified in B-Supergroup *Wolbachia*. We recover a set of Type III alleles from *wUni*, a  
338 strain that induces parthenogenesis in the parasitoid wasp, *Muscidifurax uniraptor* (Stouthamer,  
339 et al. 1993). The *wBol1-b* strain, a male-killer that has retained CI capabilities (Hornett, et al.  
340 2008), has alleles belonging to both Type I and Type IV.

341

342 Homologs and predicted protein domains of CifA and CifB for all four phylogenetic types  
343 (LePage, et al. 2017) from *Wolbachia* strains that cause CI, parthenogenesis, male-killing, or no

344 reproductive phenotype were characterized by HHpred homology and domain structure  
345 prediction software (Söding, et al. 2005). Search parameters are described in the methods.  
346 Several new prominent protein domains (as determined by the presence of multiple highly  
347 significant structural predictions within a region), herein referred to as “modules”, were  
348 identified for each CifA and CifB protein sequence. In Table 2 we list the prominent module  
349 annotations identified across CifA and CifB Types. Multiple structural hits within a region can  
350 be explained by the homology of the significant domains predictions to each other.

351  
352 For CifA, three main modules were annotated (Figure 4A, Table 2). First, the most N-terminal  
353 module (ModA-1) in Type I, II and III variants shows homology to Catalase-rel ( $p = 0.001$ -  
354  $0.003$ ), which is predicted to catalyze the breakdown of hydrogen peroxide (Chelikani, et al.  
355 2004) (Type I) and protect the cell from toxic effects, or VirJ ( $p = 0.002$ - $0.003$ ), a bacterial  
356 virulence protein and component of T4SS secretion systems (Pantoja, et al. 2002) (Types II and  
357 III). The second CifA module in the central region (ModA-2) has homology to a caspase  
358 recruitment domain ( $p = 0.005$ - $0.009$ ), venom and toxin-related domains ( $p \leq 0.001$ ), and a  
359 thermal regulator protein ( $p = 0.002$ ). The very significant homology to a toxin is interesting,  
360 given that CifA was hypothesized to act as an antitoxin. Notably, CifA is required for and  
361 enhances the induction of CI (LePage, et al. 2017), which contradicts its proposed function as  
362 simply an antitoxin (Beckmann, et al. 2017). The last CifA module in the C-terminal region  
363 (ModA-3) has multiple strong hits to a STE-like transcription factor ( $p \leq 0.001$ ). There were  
364 additional annotations that emerged due to weak or singular matches. In Type IV variants, there  
365 is a separate N-terminal region that shares homology with a conserved eukaryotic family with  
366 potential methyltransferase activity, FAM86 ( $p = 0.003$ ). Most Type I alleles have C-terminal



367 homology to a nuclear cap-binding protein that binds RNA ( $p = 0.010 - 0.020$ ). WOHa1,  
368 WOBol1b, and WOSol have an additional N-terminal region containing a conserved domain of  
369 unknown function ( $p = <0.001 - 0.005$ ). Type IV genes have a yeast-like salt tolerance down-  
370 regulator domain NST1 ( $p = 0.003$ ). Lastly, WOVit4 and wUni lack the most N-terminal CifA  
371 homology region, ModA-1.  
372  
373 For CifB, three main modules were defined (Figure 4B, Table 2). The first (ModB-1) and second  
374 (ModB-2) most N-terminal regions both have matches to the PDDEXK nuclease family ( $p <$   
375  $0.001$ ), the HSDR\_N restriction enzyme ( $p = <0.001-0.010$ ), and domains of unknown function  
376 (DUF1052, DUF91). The third module, found only in the Type I C-terminus (ModB-3), has very  
377 strong homology to a number of ubiquitin-modification and peptidase domains ( $p < 0.001$ ), as  
378 well as YopJ, which in *Yersinia*, aids in infecting a eukaryotic host (Paquette, et al. 2012) ( $p =$   
379  $<0.001-0.020$ ). ModB-3 contains the catalytic residue associated with toxicity/CI function in  
380 CidB (Beckmann, et al. 2017). In addition to the annotated modules, all Type I alleles except  
381 WOBol1b and WORiB have a single hit to a conserved domain of unknown function in the N-  
382 terminus ( $p = 0.001 - 0.005$ ), and Type III alleles (except for wAlbB) have a region of homology  
383 to a methyltransferase domain (MTS) ( $p < 0.001$ ). Both Type II and III alleles have a single short  
384 hit in the N-terminus to a SecA regulator. WOVitA4 (Type 1) has an extended C-terminus not  
385 present in any other alleles, and within that extended C-terminus is an additional  
386 peptidase/YopT-like region, similar to ModB-3. CifB Type IV alleles (WOAlbB, WOPip2, and  
387 wBol1-b) were not included in the phylogenetic reconstruction, as they are highly divergent and  
388 not reciprocal blasts of WOMelB *cifB*. Despite their divergence, these Type IV CifB alleles have  
389 similar structures to Type II and III alleles: two PDDEXK-like modules, and no Ulp-1-like

390 module three (Supplemental Figure S3). Full structural schematics with exact coordinates and  
391 homology regions for each allele are available in the supplemental material (Supplemental  
392 Figures S2 and S3), as are all significant domain hits with associated p-values and extended  
393 descriptions (Supplemental Tables S1 and S2).

394

### 395 **CifA and CifB Codiverge**

396 Initial phylogenetic trees based on core amino acid sequences of Type I-III variants of CifA and  
397 CifB exhibited similar trees (LePage, et al. 2017). Here we statistically ground the inference of  
398 codivergence using the largest set of *Wolbachia* homologs to date. We quantified congruence  
399 between the CifA and CifB phylogenetic trees for Types I-III (Supplemental File S1) using  
400 Matching Cluster (MC) and Robinson–Foulds (RF) tree metrics (Bogdanowicz and Giaro 2013;  
401 Bogdanowicz, et al. 2012; Robinson and Foulds 1981), with normalized distances ranging from  
402 0.0 (complete congruence) to 1.0 (complete incongruence). Results show strong levels of  
403 congruence between CifA and CifB ( $p < 0.00001$  for both, normalized MC = 0.06 and  
404 normalized RF = 0.125). To further statistically validate the inference of codivergence, we  
405 measured the correlation between patristic distance matrices for CifA and CifB using the Mantel  
406 test (Mantel 1967). Results demonstrate a high degree of correlation between patristic distance  
407 matrices, and through permutation show that independent evolution of CifA and CifB is highly  
408 unlikely (Pearson correlation coefficient = 0.905,  $p = 0.00001$ ).

409

### 410 **Cif Proteins Evolve Rapidly**

411 Amino acid sequence conservation across the full length of the Cif proteins was determined and  
412 compared to *Wolbachia* amino acid sequences of genes that either have signatures of

413 recombination and directional selection (Wsp, *Wolbachia* surface protein) or have not undergone  
414 extensive recombination and directional selection (FtsZ, cell division protein). Wsp protein  
415 sequences exhibit considerable divergence (mean conservation = 0.85), with very few sites in a  
416 row being completely conserved (Figure 5A). In contrast, FtsZ is relatively conserved (mean  
417 conservation = 0.94), and most of the divergence is clustered at the C-terminus (Figure 5B).  
418 Mean conservation for the Cif protein sequences were lower than Wsp - 0.83 for Type I CifA  
419 alleles (Figure 5C) and 0.82 for Type I CifB alleles (Figure 5E, Table 3). When all Cif alleles  
420 were considered, mean conservation was even further reduced - 0.58 for CifA (Figure 5D) and  
421 0.43 for CifB (Figure 5F). The lower average conservation of CifB genes is in part due to the  
422 many insertions and deletions in the alignment, and the missing C-terminal deubiquitylase  
423 region, ModB-3, of the Type II and III alleles. Thus, several CifB proteins apparently lack this  
424 activity, and whether these variants cause CI remains to be determined. Importantly, although the  
425 CifB proteins are highly divergent, the catalytic residue (red dot in Figures 5E and 5F) in the  
426 deubiquitylating module of CifB is unique to and completely conserved for the Type I alleles.  
427 The Cif proteins have extensive amounts of diversity, with completely conserved amino acids  
428 distributed across the length of the protein, and not confined to any particular regions (Figure  
429 5C-F, Supplemental Tables S3-S6). There were significant differences in the level of  
430 conservation between modules and non-module regions for the Type I alignments of both CifA  
431 ( $F_{3,495} = 11.75$ ,  $p = 0.0021$ ) and CifB ( $F_{3,1195} = 11.75$ ,  $p = 1.38e-07$ ) (Table 3). The only module  
432 that had significantly higher conservation than the non-module regions of the alignment was  
433 ModB-1 ( $p = 0.0173$ ). The *w*Mel strain contains the (P)D-(D/E)XK motif (blue dots in Figures  
434 5E and 5F) (Kosinski, et al. 2005), but it is less than 80% conserved across strains despite the  
435 higher average conservation of this module. In contrast, ModA-3 and ModB-3 are significantly

436 less conserved than the non-module regions of the corresponding proteins (CifA,  $p = 0.0400$ ;  
437 CifB,  $p = 0.0001$ ).

438

### 439 **Cif Module Presence Generally Predicts Reproductive Phenotype**

440 We used the *wMel* predicted Cif modules as a seed to search for the presence of homologous  
441 modules across *Wolbachia* genome sequences using tblastn (Figure 6). In strains with more  
442 divergent Cif Types, we report modules that were expected based on the HHpred results, but not  
443 recovered with tblastn due to sequence divergence from WOMelB. For example, the WOSuziC  
444 and WORiC ModA-1 (Catalase-rel in *wMel* and other Type I, VirJ in Type II and III) was not  
445 recovered. Additionally, we recover homologous modules outside of the annotated *cif* open  
446 reading frames, such as the chromosomal region with a ModB-3 (Ulp-1-like) region in *wNo*. The  
447 high number of modules in *wSuzi* and *wRi* are due to the presence of a duplicated set of Type I  
448 *cifs*. All arthropod-infecting strains, with the exception of *wAu* (a non-CI inducing strain),  
449 contained at least one recovered module. This includes the bed-bug mutualist *wCle*, found in  
450 Supergroup-F, and two strains that have lost CI abilities, *wUni* and *wTpre*. Importantly, all  
451 strains that are known to be capable of inducing or rescuing CI have four or more recovered  
452 modules, though they do not necessarily have ModB-3, which contains the catalytic residue  
453 implicated in CI function (Beckmann, et al. 2017). The non-CI strains have fewer recovered  
454 modules: ModB-1 in *wTpre*, ModB-1 and -2 in *wUni*, ModA-3 in *wCle*. and no modules in *wAu*  
455 and the nematode-infecting strains. *wUni* is a unique case, where we identified *cif* alleles in the  
456 genome, but recovered relatively few modules. The CifA modules are either missing (Figure 4A)  
457 or divergent enough from WOMelB that they were not considered a positive match. The two N-  
458 terminal *wUni* CifB modules, ModB-1 and ModB-2, are relatively more conserved, and the

459 ModB-3 is missing due to the truncated C-terminus present in all non-Type I CifB alleles (Figure  
460 4B). *wAlbB* and *wNo*, both CI-inducing strains with Type III and IV alleles, have fewer  
461 recovered modules, but this is congruent with the more divergent nature of those Cif types. We  
462 recovered many modules in *wSuzi*, which is a strain not known to induce CI (Cattel, et al. 2016;  
463 Hamm, et al. 2014). This discrepancy between *cif* presence and absence of a reproductive  
464 phenotype might be explained by the disrupted Type II *cifA* in *wSuzi*. The split WOSuziC  
465 sequenced was concatenated to allow for a more robust phylogenetic reconstruction (Figure 4),  
466 but it is in fact disrupted by a transposase (Conner, et al. 2017). However, having a functional set  
467 of Type I *cif* alleles appears to be sufficient for CI-induction in other strains (Beckmann, et al.  
468 2017; LePage, et al. 2017), so it is not clear how inactivation of the Type II alleles here may  
469 affect the final CI phenotype. Strain *wDi*, infecting the Asian citrus psyllid *Diaphorina citri*, has  
470 no identified reproductive phenotype, but only contains a single module: ModB-1.

471  
472 The lack of evidence for homologous *cif* genes in the nematode-infecting *Wolbachia* agrees with  
473 previous findings (LePage, et al. 2017) that CI-function is restricted to the A+B-Supergroup  
474 clade (likely due to WO phage activity), and the absence of WO phages for the nematode-  
475 infecting strains (Gavotte, et al. 2007). The loss of CI within the A and B Supergroups is likely a  
476 derived trait due to the rapid evolution of prophage WO (Ishmael, et al. 2009; Kent, et al.  
477 2011b), and relaxed selection after transition to a new reproductive phenotype. The low number  
478 of modules identified in such strains is consistent with gene degradation and loss.

479  
480 To further explore the conservation of the *cif* genes across the sequenced *Wolbachia*, and to  
481 uncover diversity that may be present in other genomes, we searched the WGS databases for

482 recently sequenced genomic scaffolds from *Wolbachia* infecting the *Nomada* bees (*wNleu*, *wNla*,  
483 *wNpa*, *wNfe*) (Gerth and Bleidorn 2016), *Drosophila inocompta* (*wInc\_Cu*)(Wallau, et al. 2016),  
484 and *Laodelphax striatellus* (*wStri*) (GenBank Accession Number NZ\_LRUH00000000.1) using  
485 HMMER. Only for *wStri* do we have direct evidence of CI induction (Noda, et al. 2001) yet the  
486 *wStri* and *wInc\_Cu* WGS projects each contain only one *cif* locus, with distant homology to *cifA*  
487 (~25% identify across 60% of the *wMel* protein). Based on HHpred analyses, the *wStri* homolog  
488 (WP\_063631193.1) contains none of the domain modules associated with *cifA*. The *wInc\_Cu*  
489 homolog (WP\_070356873.1) contains three modules: an N-terminal Catalase-rel domain and an  
490 internal Ectatomin domain, followed by the STE like transcriptional factor domain. Because  
491 these are incomplete genome projects, it is possible that other *cif* homologs have been missed  
492 due to the current sequencing coverage. Alternatively, it is possible that other, as yet  
493 undiscovered, mechanisms of reproductive manipulation exist in these strains. In contrast, the  
494 *Nomada*-associated *Wolbachia* contain a large repertoire of *cif* homologs, including Type I, II,  
495 III, IV and several homologs with variations on the Type IV domain architecture for *cifA*  
496 (Supplemental Figure S4). The *Nomada Wolbachia* all harbor Type II *cifB* homologs and each of  
497 the strains harbors either duplicates of this *cifB* type or novel domain architectures for *cifB*  
498 including an N-terminal Oleosin domain and a C-terminal Ulp-1 domain (Supplemental Figure  
499 S4).

500

## 501 **Discussion**

502 We explored three key features of *cif* evolution: (i) the toxin-antitoxin operon hypothesis, (ii)  
503 potential enzymatic and regulatory functions across the *cifA* and *cifB* phylogenies, and (iii) the  
504 conservation and diversity of *cif* genes across strains with different host-manipulation

505 phenotypes. We provide multiple lines of evidence that *cifA* and *cifB* do not comprise an operon  
506 in *wMel*, including quantifications of transcription and *in silico* operon predictors. Moreover,  
507 expression of *cifA* and *cifB* across host development are not correlated with each other. In fact,  
508 *cifB* expression does not significantly correlate with any other *Wolbachia* locus. Combined with  
509 the drastic drop off in expression across the short junction between *cifA* and *cifB*, and negative  
510 results from the operon prediction software, we conclude that *cifA* and *cifB* are not co-transcribed  
511 or co-regulated as an operon in *wMel*, the *Wolbachia* strain currently used in mosquito control  
512 programs. While we think it unlikely that the *cif* genes are regulated and transcribed in  
513 drastically different ways across closely related *cif* Types, more detailed analyses from a variety  
514 of strains would be beneficial for developing a comprehensive understanding of the factors  
515 regulating expression of these genes. It is especially interesting that synteny has generally been  
516 maintained across prophage WO regions, despite the high level of recombination and  
517 rearrangements in prophage WO and *Wolbachia* genomes (Baldo, et al. 2006a; Ellegaard, et al.  
518 2013; Kent, et al. 2011a). It is not clear if there is an advantage (and what the advantage may be)  
519 to maintaining syntenic orientation of these two genes; perhaps this feature can be attributed to  
520 their location within prophage WO and/or functions associated with the ability of *cifA* and *cifB* to  
521 act synergistically to induce CI (LePage, et al. 2017). Since type IV secretion system genes and  
522 their predicted effectors are scattered across the *Wolbachia* genome (Rice, et al. 2017; Wu, et al.  
523 2004) gene products involved in *Wolbachia*-host interactions can function together even when  
524 the genes encoding them are not syntenic. We conclude that *cifA* and *cifB* do not comprise an  
525 operon, and do not act strictly as a toxin-antitoxin system due to the requirement of both proteins  
526 for the induction of CI in the insect host. Determining how *cifA* and *cifB* expression is regulated  
527 in the insect host will greatly benefit vector control programs that use *Wolbachia*-mediated CI.

528  
529 Despite the conservation of gene order, Cif proteins showed extensive amounts of divergence  
530 and differences in domain structure as previously reported (LePage, et al. 2017). Here, the levels  
531 of amino acid conservation in the Cifs are lower than FtsZ and Wsp, the latter of which is known  
532 to recombine and be subject to directional selection. The conservation of the catalytic residue in  
533 the C-terminal deubiquitylase domain is an important feature of CidB (Beckmann, et al. 2017).  
534 However, only Type I of the four identified Types has this domain. Additionally, strains known  
535 to induce CI, such as *wAlbB* and *wNo* have no Type I alleles, implying that the Ulp-1 region  
536 may not be essential for inducing CI. The complete, functional capacity of Types I-IV has yet to  
537 be explored *in vivo*, but is a promising direction for understanding the evolution of *Wolbachia*-  
538 host associations.

539  
540 Based on what is known about *Wolbachia* biology, some of the protein domains may be  
541 especially good candidates for further study and *in vivo* functional characterization. Predicted  
542 PDDEXK-like domains are present in all four CifB types. Given the predicted interaction of  
543 these domains with DNA (Kosinski, et al. 2005), and the presence of these domains across CifB  
544 proteins, determining if and how these regions interact with host (*Wolbachia* or insect) DNA,  
545 and whether or not they contribute to CI function would be useful in understanding the consistent  
546 presence of this module. Another good candidate for further exploration is the predicted  
547 methyltransferase domain in several Type III CifB proteins, as *Wolbachia* infection has been  
548 linked to changes in host genome methylation in several insects (LePage, et al. 2014; Negri, et al.  
549 2009; Ye, et al. 2013), though knockout of *Drosophila* methyltransferases does not alter CI  
550 levels (LePage, et al. 2014). Likewise, the antioxidant catalase domain is noteworthy as these



551 domains decompose hydrogen peroxide into water and oxygen and thus protect cells from its  
552 toxic effects, which are present in *Wolbachia*-infected spermatocytes (Brennan, et al. 2012).  
553  
554 *Wolbachia* strains that have lost CI have a strong signature of *cif* gene degradation and loss. The  
555 two parthenogenesis-inducing strains (*wTpre* and *wUni*) appear to be at different places in this  
556 process of gene loss, with divergent Cif amino acid sequences recovered for *wUni*, but only one  
557 PDDEXK module identified in *wTpre*. There are several explanations for this. *wUni* is likely a  
558 more recent transition to parthenogenesis, as it is closely related to a CI strain (*wVitA*) (Baldo, et  
559 al. 2006b; Newton, et al. 2016). In comparison, *wTpre* is part of a unique clade of *Wolbachia* that  
560 all induce parthenogenesis in *Trichogramma* wasps (Rousset, et al. 1992; Schilthuizen and  
561 Stouthamer 1997; Werren, et al. 1995). This strain has lost its WO phage association and only  
562 has relics of WO phage genes (Gavotte, et al. 2007; Lindsey, et al. 2016). Additionally, the two  
563 strains that independently transitioned to the parthenogenesis phenotype have evolved separate  
564 mechanisms for doing so (Gottlieb, et al. 2002; Stouthamer and Kazmer 1994). Differences in  
565 time since transition to the parthenogenesis phenotype, phage WO associations, and mechanisms  
566 of parthenogenesis induction likely all play a role in the rate of *cif* gene degradation.  
567  
568 Based on our analyses, we propose three avenues of research on the function of the Cif proteins.  
569 First, functional confirmation of the newly annotated modules will be important to understanding  
570 how these genes function enzymatically. In total, we predict six modules in the Cif protein  
571 sequence homologs, with varying degrees of confidence (Supplemental Tables S1 and S2  
572 Tables). For some of these modules, straightforward experiments can be designed in model  
573 systems (such as *Saccharomyces*) to determine if their predicted function is correct, as has been

574 done for CidB (Beckmann, et al. 2017) and countless other bacterial effectors (Archuleta, et al.  
575 2011; Kramer, et al. 2007; Siggers and Lesser 2008). Second, necessity and importance of these  
576 modules to the CI phenotype can be assessed in the *Drosophila* model, where the induction of  
577 the phenotype and rescue is straightforward (LePage, et al. 2017). Finally, we suggest that  
578 although the discovery of these genes is fundamental, it is clear from this analysis that we have  
579 not comprehensively evaluated or identified the mechanisms behind CI and other reproductive  
580 manipulations. The gene characterization analyses described here reveal new and relevant  
581 annotations, substantial unknown sequence regions across all of the phylogenetic types, missing  
582 deubiquitylase domains in particular CI strains, and a coevolving, phylogenetic relationship  
583 across the Cif trees. Importantly, the locus and mechanism behind rescuing CI are still unknown,  
584 as is the exact mechanism by which all Cif proteins induce CI. Therefore, the recent discovery of  
585 these genes, and the gene characterization analyses described here, pave the most comprehensive  
586 road to date for investigating key mechanisms of the *Wolbachia*-host symbiosis.

587

## 588 **Acknowledgments**

589 This work was supported by the National Science Foundation (DEB 1501227 to A.R.I.L., IOS  
590 1456545 to I.L.G.N., and IOS 1456778 to S.R.B); the United States Department of Agriculture  
591 (NIFA 2016-67011-24778 to A.R.I.L.); the National Institutes of Health (R21 HD086833 and  
592 R01 AI132581 to S.R.B.); and Robert and Peggy van den Bosch Memorial Scholarships to  
593 A.R.I.L. We thank J. Dylan Shropshire for feedback on an earlier draft of the manuscript.

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836

837

838 **Tables**

839 **Table 1. Strains used in comparative analyses of *cifA* and *cifB*.**

Supergroup	Strain	Host	Reproductive Phenotypes <sup>a</sup>	Accession Number
A	wMel	<i>Drosophila melanogaster</i>	CI	NC_002978.6
	wMelPop	<i>Drosophila melanogaster</i>	CI	AQQE00000000.1
	wRec	<i>Drosophila recens</i>	CI	NZ_JQAM00000000.1
	wAu	<i>Drosophila simulans</i>	None	LK055284.1
	wHa	<i>Drosophila simulans</i>	CI	NC_021089.1
	wRi	<i>Drosophila simulans</i>	CI	NC_012416.1
	wSuzi	<i>Drosophila suzukii</i>	None	NZ_CAOU00000000.2
	wUni	<i>Muscidifurax uniraptor</i>	PI	NZ_ACFP00000000.1
wVitA	<i>Nasonia vitripennis</i>	CI	NZ_MUJM00000000.1	
B	wAlbB	<i>Aedes albopictus</i>	CI	CAGB00000000.1
	wNo	<i>Drosophila simulans</i>	CI	NC_021084.1
	wDi	<i>Diaphorina citri</i>	Undetermined	NZ_KB223540.1
	wTpre	<i>Trichogramma pretiosum</i>	PI	CM003641.1
	wVitB	<i>Nasonia vitripennis</i>	CI	AERW00000000.1
	wBol1-b	<i>Hypolimnas bolina</i>	CI, MK	NZ_CAOH00000000.1
	wPipJHB	<i>Culex quinquefasciatus</i>	CI	ABZA00000000.1
wPipPel	<i>Culex pipiens</i>	CI	NC_010981.1	
C	wOo	<i>Onchocerca ochengi</i>	OM	NC_018267.1
	wOv	<i>Onchocerca volvulus</i>	OM	NZ_HG810405.1
D	wBm	<i>Brugia malayi</i>	OM	NC_006833.1
F	wCle	<i>Cimex lectularius</i>	OM	NZ_AP013028.1

840 <sup>a</sup>Reproductive phenotypes include: CI) cytoplasmic incompatibility, PI) parthenogenesis-  
841 inducing, MK) male-killing, OM) obligate mutualism, None) no phenotype discovered after  
842 assessment, and Undetermined) phenotype was not assayed.

843



844 **Table 2. Predicted structural modules of Cif proteins.**

Protein	Module <sup>a</sup>	Size Range (AA)	Homology
CifA	ModA-1 ●	24-55	<ul style="list-style-type: none"> <li>Catalase-rel, decomposes hydrogen peroxide into water and oxygen</li> <li>VirJ, bacterial virulence protein and component of T4SS secretion systems</li> </ul>
	ModA-2 ●	99-152	<ul style="list-style-type: none"> <li>DUF3243, DUF603, domains of unknown function</li> <li>CARD_MDA5_r1, Caspase activation and recruitment domain</li> <li>Ectatomin, toxic component of ant venom</li> <li>Ldr, type I toxin-antitoxin system</li> <li>IstR, lineage-specific thermal regulator protein</li> </ul>
	ModA-3 ●	47-68	<ul style="list-style-type: none"> <li>STE, STE-like transcription factor</li> </ul>
CifB	ModB-1 ●	97-127	<ul style="list-style-type: none"> <li>PDDEXK, PD-(D/E)XK nuclease superfamily</li> <li>DUF91, Domain of Unknown Function</li> <li>HSDR_N, type I restriction enzyme R protein N terminus</li> </ul>
	ModB-2 ●	122-155	<ul style="list-style-type: none"> <li>PDDEXK, PD-(D/E)XK nuclease superfamily</li> <li>DUF1052, domain of unknown function</li> <li>HSDR_N, type I restriction enzyme R protein N terminus</li> </ul>
	ModB-3 <sup>b</sup> ○	277	<ul style="list-style-type: none"> <li>RE_XamI, XamI restriction endonuclease</li> </ul>
			<ul style="list-style-type: none"> <li>Ulp-1, ubiquitin-like proteases</li> <li>SUMO, small ubiquitin-related modifier</li> <li>YopJ, Serine/Threonine acetyltransferase (<i>Yersinia</i>)</li> <li>Ssel, deubiquitylase</li> <li>SidE, Dot/Icm substrate protein</li> </ul>

845 <sup>a</sup>Colors next to modules are used throughout the text

846 <sup>b</sup>Only present in Type I

847

848

849 **Table 3. Average amino acid conservation of Cifs and modules.**

<b>Protein</b>	<b>Region<sup>a</sup></b>	<b>Type I</b>	<b>All</b>
CifA	ModA-1	0.94	0.70
	ModA-2	0.82	0.55
	ModA-3	0.77	0.53
	CifA	0.83	0.58
CifB	ModB-1	0.89	0.71
	ModB-2	0.85	0.62
	ModB-3 <sup>b</sup>	0.77	0.39
	CifB	0.82	0.43

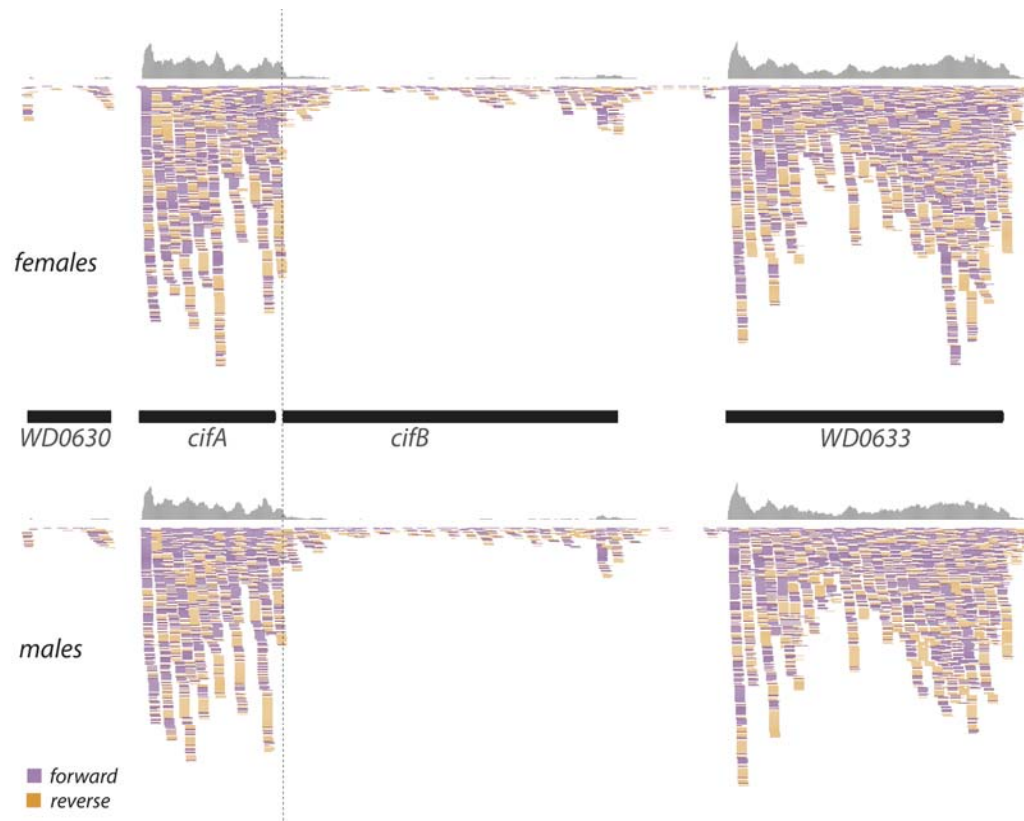
850 <sup>a</sup>Module number defined in Table 2

851 <sup>b</sup>Only present in Type I

852

853 **Figures**

854 **Figure 1**



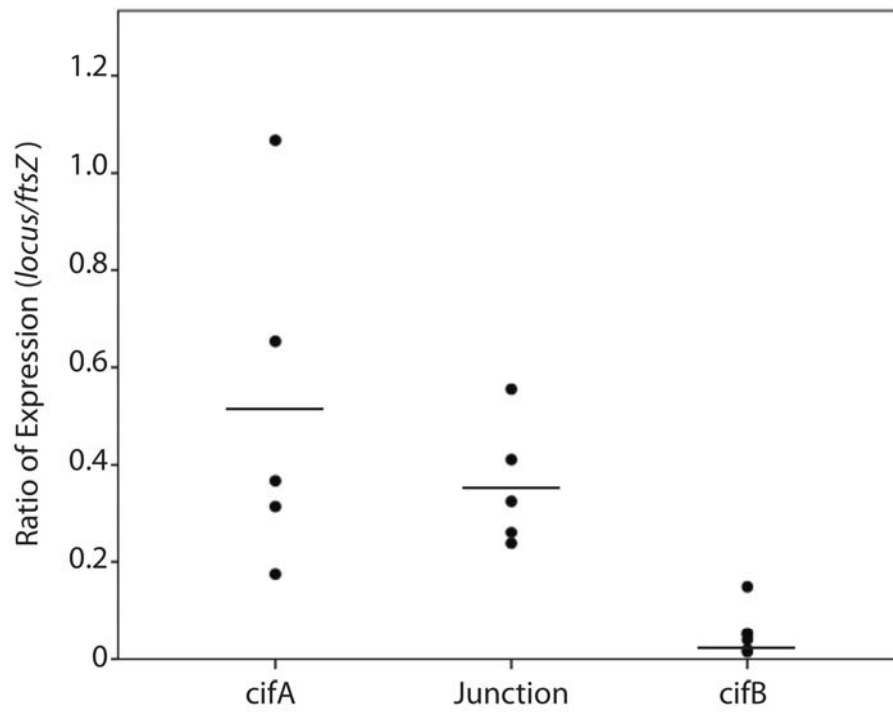
855  
856

857 **Figure 2**

(A)

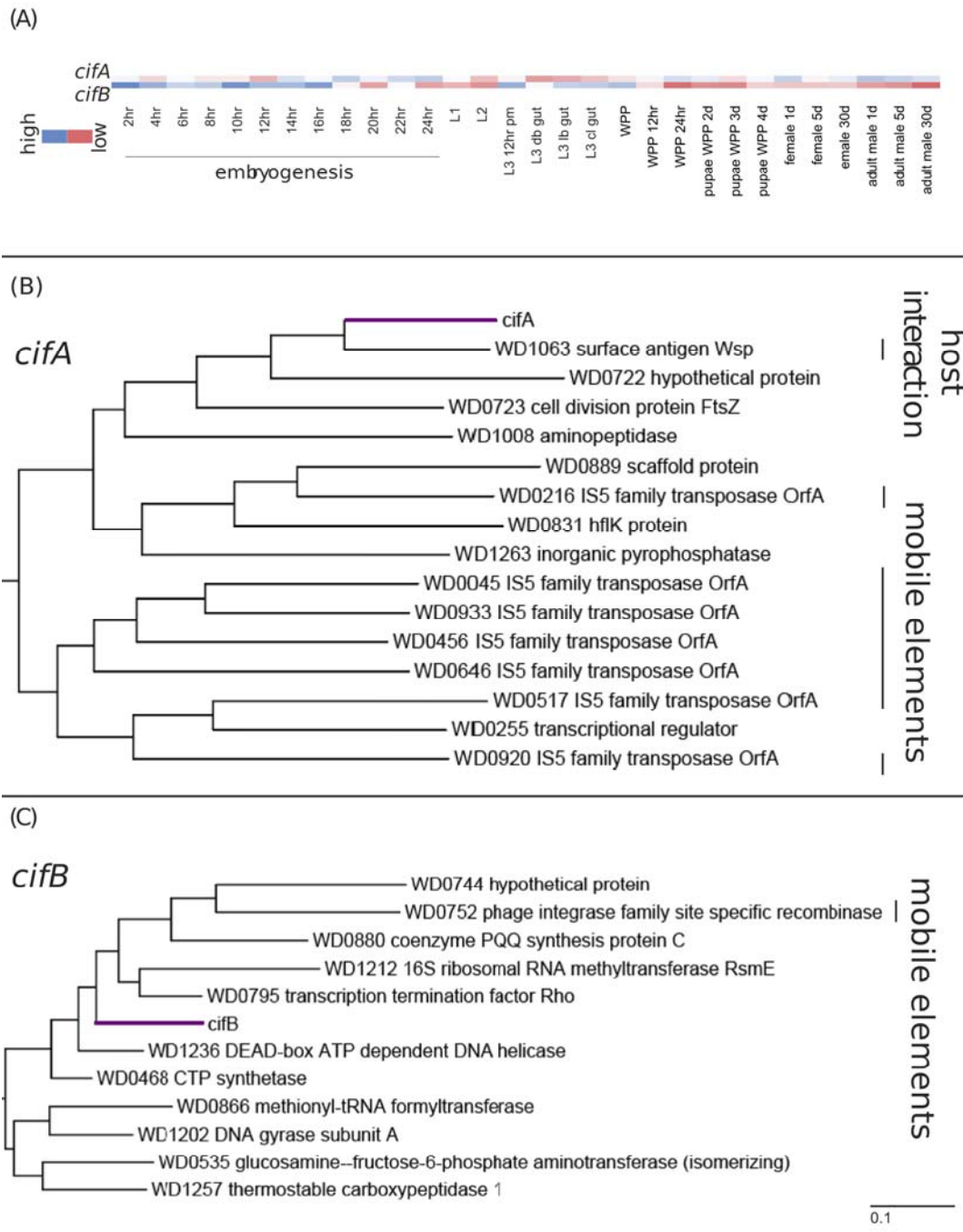


(B)



858  
859

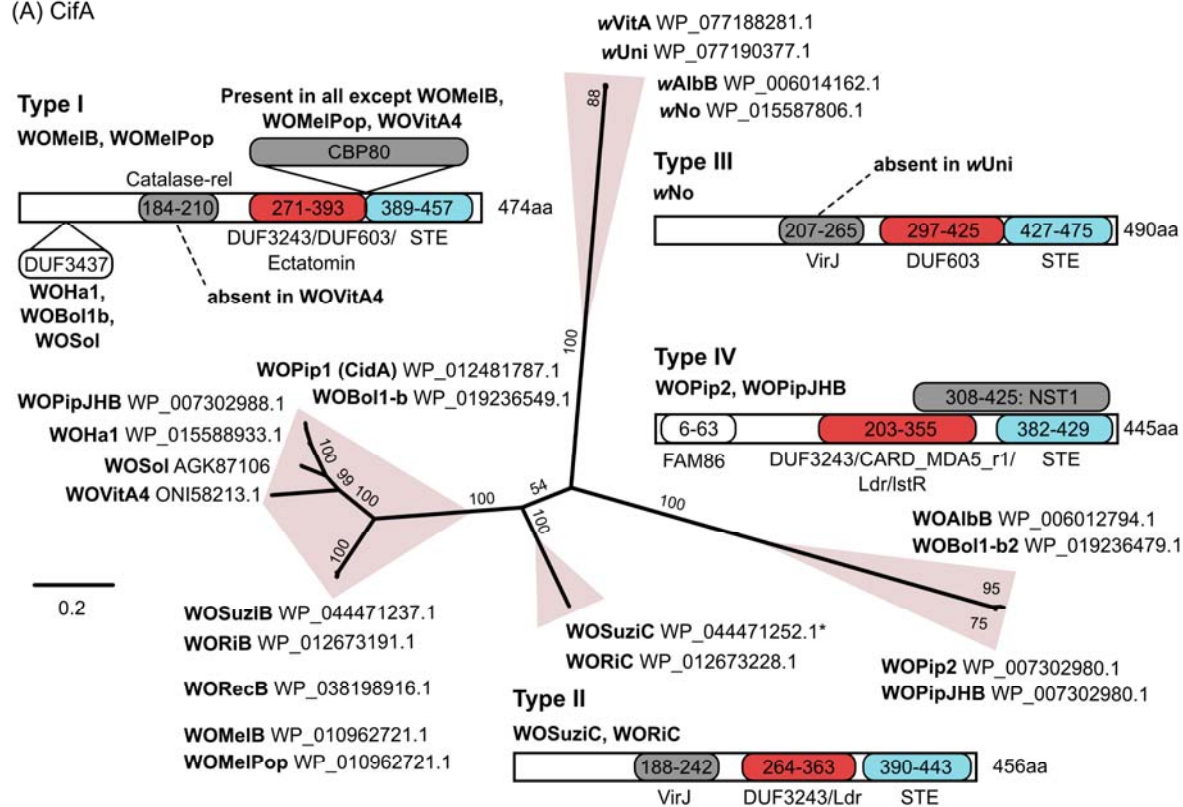
860 **Figure 3**



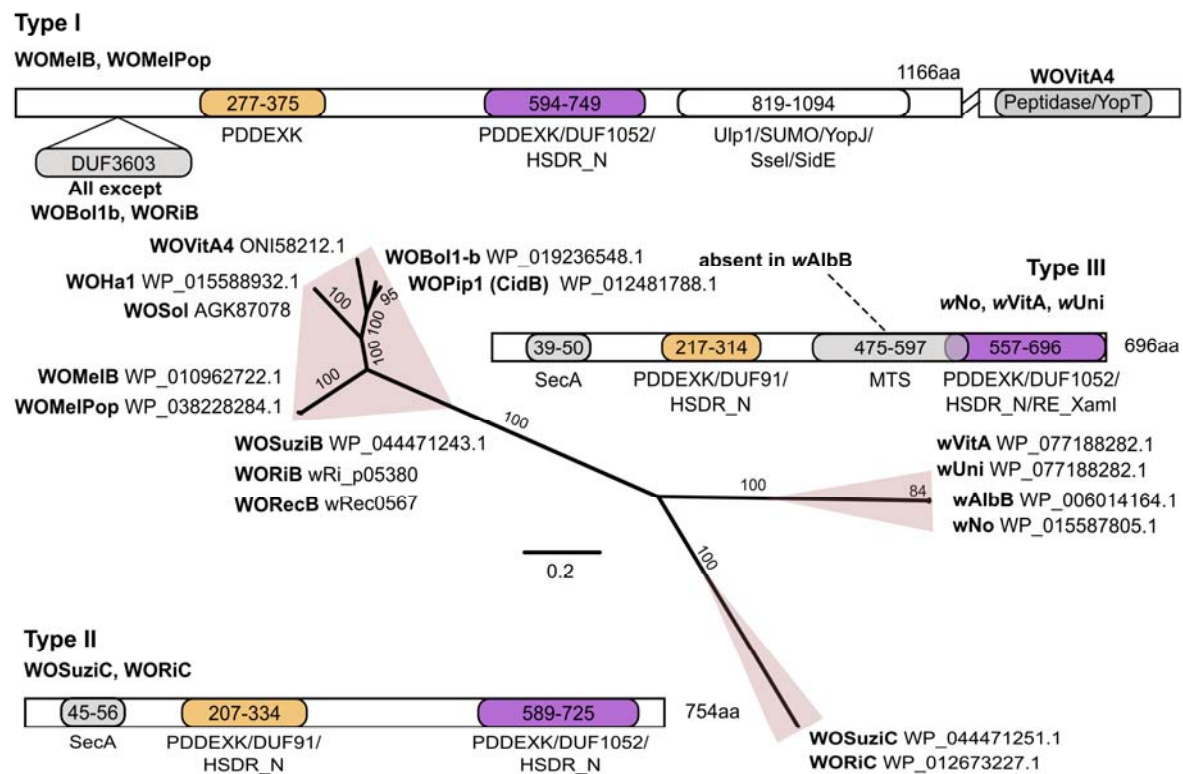
861  
862

863 **Figure 4**

(A) CifA



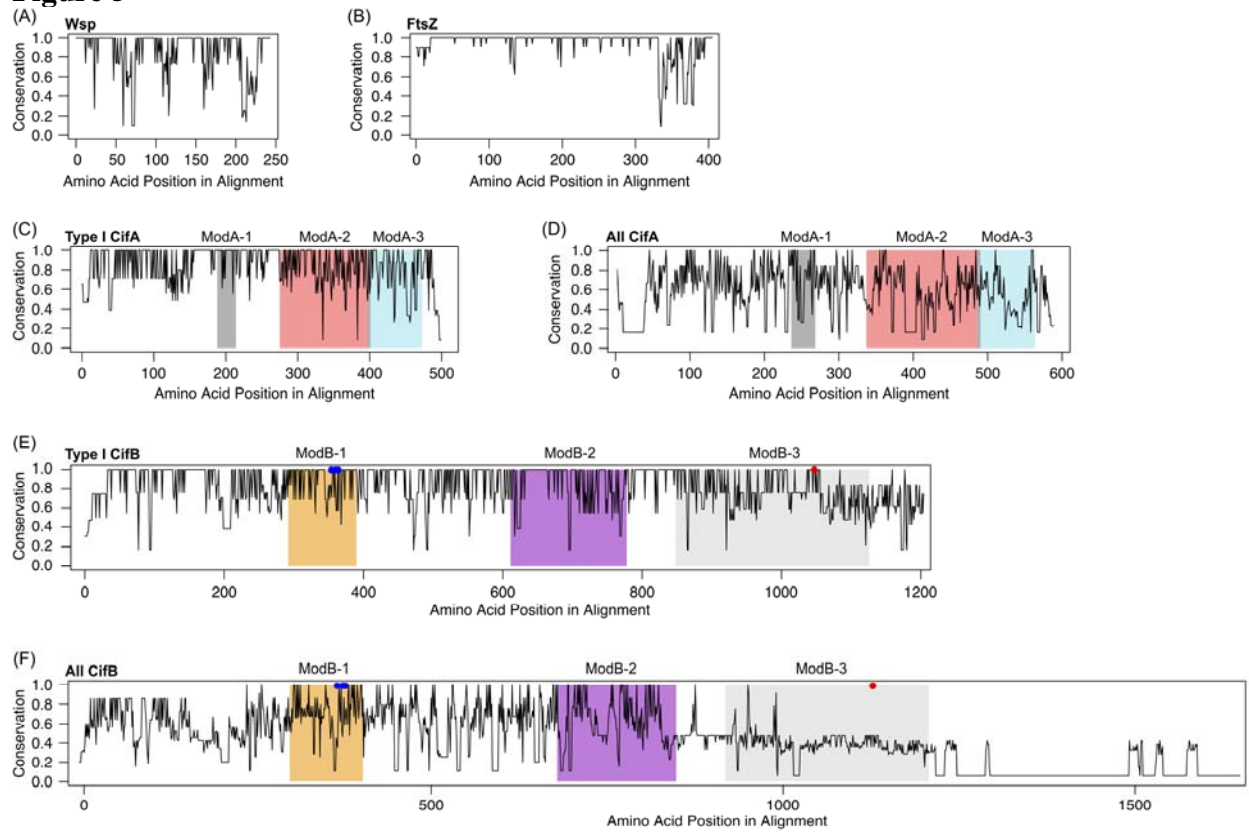
(B) CifB



864

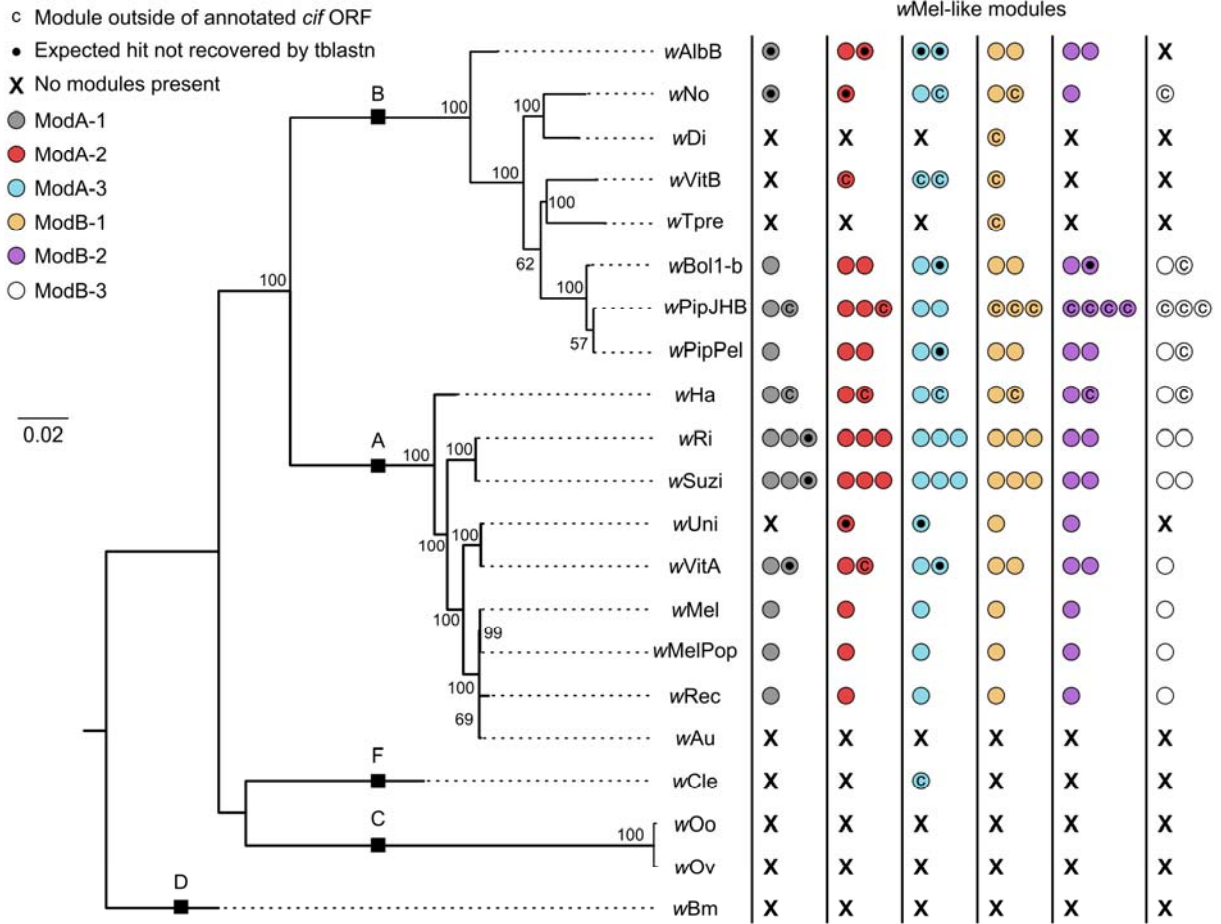
865

## Figure 5



866  
867

868 **Figure 6**



869



870 **Figure legends**

871 **Fig 1. RNASeq analysis of *cifA* and *cifB* gene expression in whole adult, 1 day old female**  
872 **and male *Drosophila melanogaster* flies.** Raw reads were mapped to the *wMel* assembly (using  
873 *bwa*) and coverage visualized using the Integrated Genomics Viewer (v2.3.77). The start of the  
874 *cifB* open reading frame is denoted by a vertical, dotted line.

875

876 **Fig 2. Relative expression ratio of *cifA*, the junction between *cifA/cifB*, and *cifB* to *ftsZ*.**

877 Expression of both genes and their junction was quantified using qRT-PCR, and normalized to  
878 *Wolbachia ftsZ* gene expression. *cifB* gene expression is significantly less than that of the  
879 junction ( $t= 3.220$ ,  $df=16$ ,  $p=0.005$ ) and less than *cifA* ( $t=-3.840$ ,  $df=17$ ,  $p=0.001$ ).

880

881 **Fig 3. Gene expression of *cifA* and *cifB* during *Drosophila melanogaster* development. A)**

882 Heatmap representation of normalized transcripts per kilobase million (TPM) for both *cifA* and  
883 *cifB* during *Drosophila melanogaster* development. *cifB* is highly expressed during  
884 embryogenesis and downregulated after pupation while *cifA* is more highly expressed in adults  
885 and pupae. Clustering of *Wolbachia* loci based on expression across fly development illustrates  
886 correlated expression profiles between *wMel* loci and *cifA* (B) or *cifB* (C). Mobile elements and  
887 loci involved in host interaction (*wsp*) are indicated with vertical lines on the right side of the  
888 figure.

889

890 **Fig 4. Phylogenetic relationships and representative predicted protein structure of Cif**  
891 **protein types. A) CifA and B) CifB.** Alleles are in bold next to their corresponding accession  
892 number, and pink shapes around branches designate monophyletic “types”. Representative

893 structures are shown for each type, with the length of the protein indicated at the C-terminus.  
894 Variations in within-type structure are shown. If an allele is not listed as a representative, and  
895 significant structural variations are not indicated, then only the exact coordinates of the structural  
896 regions differed by a few amino acids. All HHpred structural predictions are significant at a  
897 corrected p-value of  $< 0.05$ , and listed in order of ascending p-value for regions with multiple  
898 structural hits. Allele names use the previously described naming convention with a WO prefix  
899 referring to particular phage haplotype, and the *w* prefix indicating a phage-like island (LePage,  
900 et al. 2017). The N-terminus of WOSuziC (\*) was translated from the end of another contig and  
901 concatenated to get the full-length protein (see methods). WOMelB and WOMelPop are identical  
902 at the amino acid level, as are WOPipJHB and WOPip2.

903

904 **Fig 5. Protein conservation, as determined by Shannon entropy scores.** A) Wsp (*Wolbachia*  
905 surface protein), B) Cell division protein FtsZ, C) Type I CifA, D) All CifA, E) Type I CifB  
906 alleles except for WOVitA4, F) All CifB alleles. Red dots in E and F indicate the ModB-3  
907 catalytic residue (Beckmann, et al. 2017), unique to and completely conserved for Type I alleles.  
908 Blue dots in E and F represent the (P)D-(D/E)XK motif (Kosinski, et al. 2005) present in *w*Mel.  
909 We found no (P)D-(D/E)XK putative catalytic motif in the second PDDEXK-like module of  
910 CifB.

911

912 **Fig 6. Presence of *w*Mel-like Cif modules across the *Wolbachia* phylogeny.** The WOMelB  
913 module sequences were used to query available *Wolbachia* genomes to look for the presence of  
914 Cif-like regions beyond those within the annotated Cifs (Figure 4). Colored dots correspond to  
915 the structural regions delimited by HHpred, shown in Figure 4, and listed in Table 2. A "C"

916 within a dot indicates the presence of a module outside of annotated *cif* open reading frames  
917 (Figure 4 and Supplemental Figures S2 and S3). The black dot indicates a module annotated by  
918 HHpred, but not identified by tblastn due to divergence from the WOMelB module. Black boxes  
919 labeled with uppercase letters indicate branches leading to *Wolbachia* Supergroups. Dotted lines  
920 on the phylogeny lead to taxon names and are not included in the branch length.