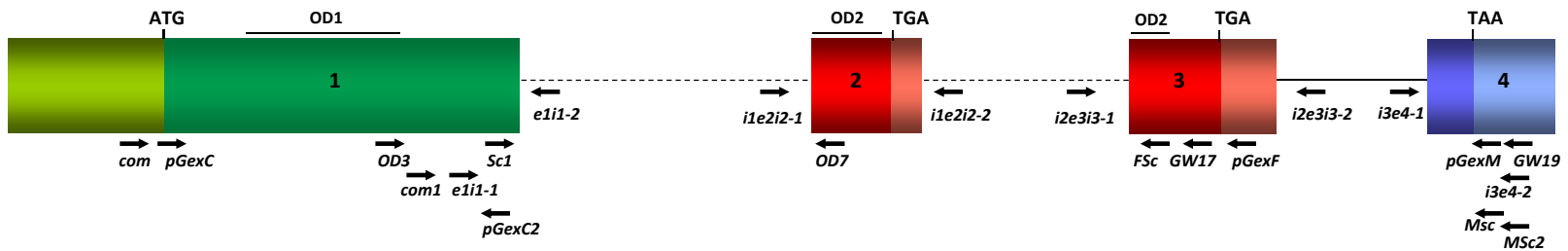
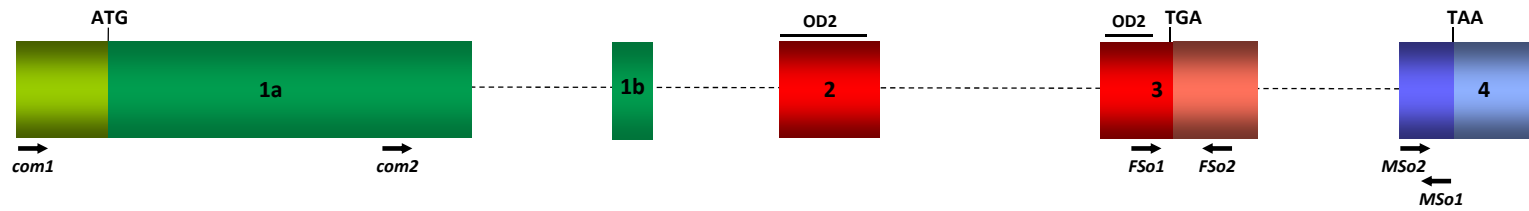
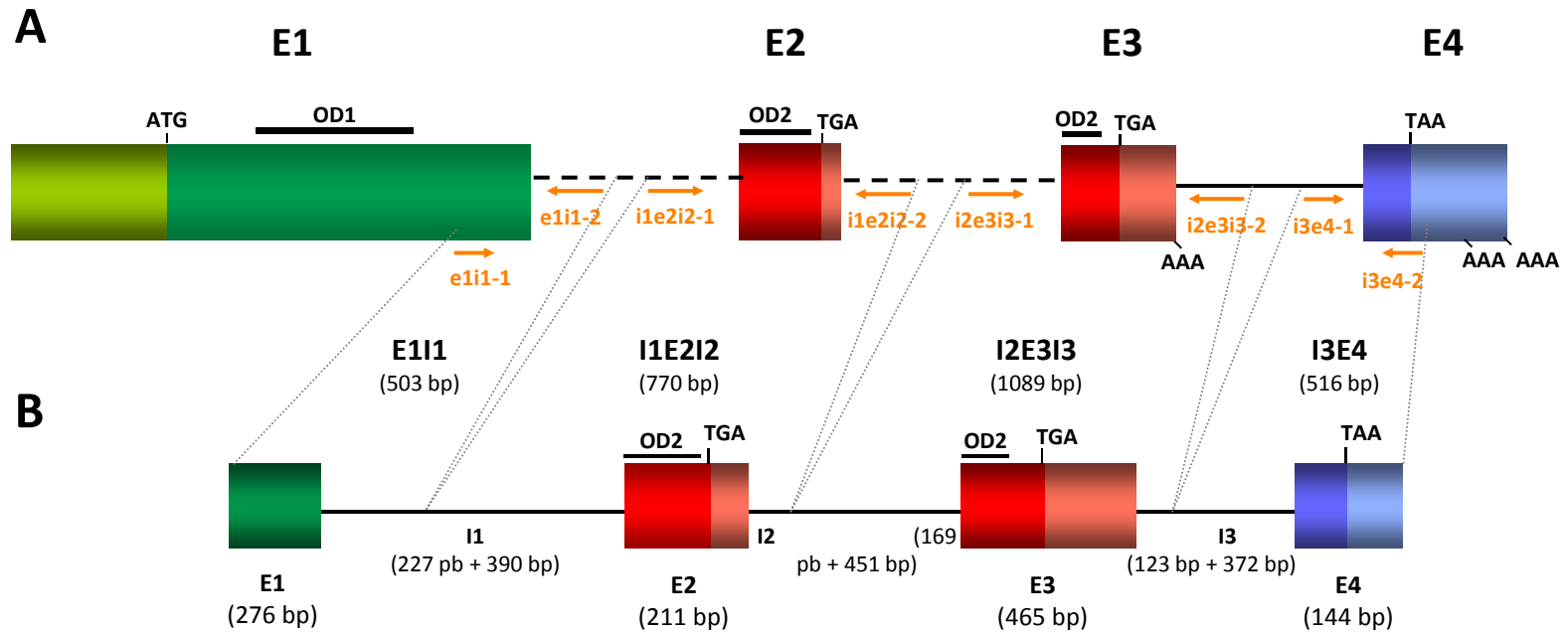
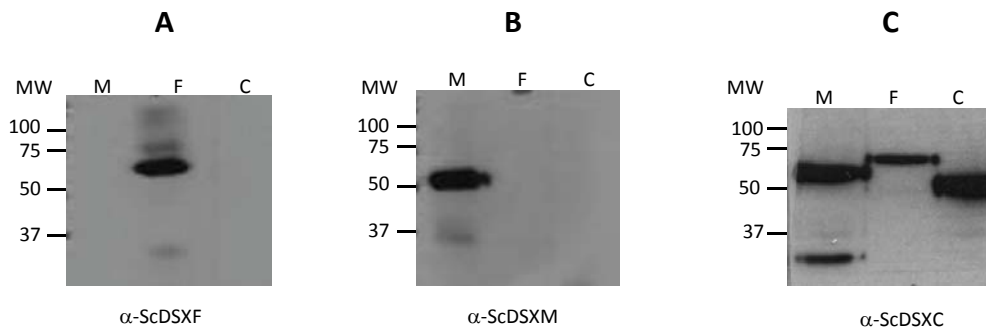


**A***Sciara coprophila dsx***B***Sciara ocellaris dsx*

**Figure S1** Location of the primers used in this work. The prefix-*dsx* has been omitted in the name of the primers.



**Figure S2** Construction of the *DScmg* mini-gene. For details, see Materials and methods. **(A)** Exons (boxes, E) and introns (lines) are not drawn to scale. The dotted lines for introns 1 and 2 indicate that their lengths remain unknown. The beginning and the end of the ORF are indicated by ATG and TGA or TAA, respectively. AAA stands for poly-A(+). Orange arrows indicate the location of the primers used. **(B)** The *DScmg* construct. The dotted lines from A to B indicate the regions of the whole primary transcript that is represented in *DScmg*, where the solid lines indicate now the intron sequences.



**Figure S3** Specificity of the anti-sera against the *Sciara* male and female DSX proteins. Western - blots of GST-ScDSXM (lane M), GST-ScDSXF (lane F) and GST-DSXC (lane C) probed with  $\alpha$ -ScDSXF serum **(A)**, with  $\alpha$ -ScDSXM serum **(B)** and with  $\alpha$ -ScDSXC serum **(C)**. To construct the GST-DSX fusion proteins, the procedure of Smith and Johnson [Smith DB, Johnson KS (1988) Single-step purification of polypeptides expressed in *Escherichia coli* as fusions with glutathione S-transferase. Gene 67:31–40] was followed with minor changes. To generate the GST-DSXF fusion, the whole ORF of *S. coprophila dsxF* was amplified from cDNA with primers pGexDxsC and pGexdsxF containing a restriction site for EcoRI and HindIII, respectively. To generate the GST-DSXM fusion, the whole ORF of *S. coprophila dsxM* was amplified from cDNA with primers pGexDxsC and pGexdsxM containing a restriction site for EcoRI and HindIII, respectively. To generate the GST-DSXC fusion, the fragment corresponding to the common N-terminal region of *S. coprophila dsx* was amplified from cDNA with primers pGexDxsC and pGexdsxC2 containing a restriction site for EcoRI and HindIII, respectively. The amplicons were cloned in pGEMT-easy (Promega) and sequenced. The DNA of the pGEMT-easy vectors was digested with EcoRI and HindIII and the fragments were ligated in frame into the pGex-B vector using the T4 DNA ligase (Roche). All the positive clones were sequenced to ascertain correct orientation.

**Table S1 Sequence of primers.**

Primer	Sequence
<i>dsxOD3</i>	5' TGGARAARTGYCGMYTRACNGCSGAYCG 3'
<i>dsxOD7</i>	5' GTATCACATACATNARNGGC 3'
<i>dsxSccom</i>	5' GGTCAGAACATAAGCGAAGTG 3'
<i>dsxSc1</i>	5' ATCGTCGGGATTCCTTACG 3'
<i>dsxMSc</i>	5' TGTA <sup>T</sup> CTTCTAGGTAAACGCAG 3'
<i>dsxM2Sc</i>	5' CACTCATGGCTTTTATCATAAT 3'
<i>dsxFSc</i>	5' GTCCGTTCCACAATTGACATG 3'
<i>GW17</i>	5' TCGTGTTATCATCCCCGTTTGGTATCG 3'
<i>GW19</i>	5' TCAATCCATCGCATTGCTTAATTAC 3'
<i>dsxcom1</i>	5' CGTCACCGTCATTGACACCTGATCAG 3'
<i>e1i1-1</i>	5' ATAAGAAT <b>GCGGCCG</b> CGTCATTGACACCTGATCAG 3'
<i>e1i1-2</i>	5' GCTCTAGATGCTAATCACGACACAGACG 3'
<i>i1e2i2-1</i>	5' GCTCTAGATGAAAGAAGGAAATCCTAAGTC 3'
<i>i1e2i2-2</i>	5' TGCACT <b>G</b> CAGGTTTTAGGACCAGGATGAGC 3'
<i>i2e3i3-1</i>	5' TGCACT <b>G</b> CAGTTCTGACTGTACTTTTGTAGC 3'
<i>i2e3i3-2</i>	5' CCCT <b>G</b> AGGTCTCGATCAAGGATGTCTG 3'
<i>i3e4-1</i>	5' CCCT <b>G</b> AGAATCAATACGATACTGAGCATC 3'
<i>i3e4-2</i>	5' GGG <b>T</b> ACCTAAATTCATCCATCGCATTG 3'
<i>pGexdsxC</i>	5' <b>GGAATTC</b> GAAATGGTCTCTAATGATATATCTG 3'
<i>PGexdsxC2</i>	5' <b>CCAAGCTT</b> GTCAGCCAGGCTTATAATGAGTATCC 3'
<i>pGexdsxF</i>	5' <b>CCAAGCTT</b> GGTCCGTTCCACAATTGACATG 3'
<i>pGexdsxM</i>	5' <b>CCAAGCTT</b> GTGTACTTCTAGGTAAACGCAG 3'
<i>DsxSo1</i>	5' TATGCTCATCATCTCACAATAG 3'
<i>dsxMSo</i>	5' TGTA <sup>T</sup> ACTATAGTTGTAGAGTGC 3'
<i>dsxFSo</i>	5' CAACAACCTCAACATATACGAC 3'
<i>rp49.1</i>	5' ATCCGCCACCAGTCGGATC 3'
<i>rp49.2</i>	5' TGGCGCGCTCGACAATCTC 3'
<i>rpl10.1</i>	5' GAGTGCATCCATTCCACGT 3'
<i>rpl10.2</i>	5' GTATTTGACGTTGCAACCGT 3'
<i>yp2Dm1</i>	5' GTCGTTGAGGCCACCATGC 3'
<i>yp2Dm2</i>	5' GGAGTGGTTCGCTCGCATG 3'
<i>M13 Forward</i>	5' GTAAAACGACGGCCAG 3'
<i>M13 Reverse</i>	5' CAGGAAACAGCTATGAC 3'
<i>Oligo d(T)</i>	5' TGC CAC GCT CGA CTA GTA CGT <sub>N22</sub> 3'
<i>T30</i>	5' T <sub>N30</sub> 3'
<i>AnchorT</i>	5' GCCACGCGTCTGACTAGTACGT <sub>N22</sub> 3'
<i>Anchor</i>	5' GCCACGCGTCTGACTAGTACG 3'

The highlighted black bases indicate the restriction sites used in the construction of the *DScmg* mini-gen and GST fusion proteins of *S. coprophila*.

**Table S2** Insect species and GenBank accession numbers for the DSX sequences analyzed in the present work.

DSX	Taxa	Protein Acc#	
		<i>Female-specific</i>	<i>Male-specific</i>
<b>DIPTERA</b>			
<b>Calliphoridae</b>			
1.	<i>Lucilia cuprina</i>	ADG37649	ADG37648
<b>Culicidae</b>			
2.	<i>Aedes aegypti</i>	ABD96571	ABD96573
3.	<i>Anopheles gambiae</i>	AAX48939	AAX48940
<b>Drosophilidae</b>			
4.	<i>Drosophila erecta</i>	XP_001979242	XP_001979242
5.	<i>Drosophila melanogaster</i>	NP_731198	NP_731197
6.	<i>Drosophila persimilis</i>	XP_002013146	XP_002013146
7.	<i>Drosophila pseudoobscura</i>	XP_003736648	XP_001359020
8.	<i>Drosophila sechellia</i>	XP_002038750	XP_002038750
9.	<i>Drosophila simulans</i>	XP_002102542	XP_002102542
10.	<i>Drosophila yakuba</i>	XP_002086778	XP_002086778
<b>Muscidae</b>			
11.	<i>Musca domestica</i>	AAR23812	AAR23813
<b>Phoridae</b>			
12.	<i>Megaselia scalaris</i>	AF283695_1	AF283696_1
<b>Sciaridae</b>			
13.	<i>Sciara coprophila</i>	HG934386	HG934387
<b>Tephritidae</b>			
14.	<i>Anastrepha obliqua</i>	AAY25166	AAY25167
15.	<i>Bactrocera oleae</i>	CAD67986	CAD67987
16.	<i>Ceratitis capitata</i>	AAN63598	AAN63597
<b>HYMENOPTERA</b>			
<b>Apidae</b>			
17.	<i>Apis mellifera</i>	ABV55180	ABV55178
<b>Pteromalidae</b>			
18.	<i>Nasonia vitripennis</i>	ACJ65508	ACJ65511
<b>LEPIDOPTERA</b>			
<b>Bombycidae</b>			
19.	<i>Bombyx mori</i>	BAB13471	BAB13472
<b>Saturniidae</b>			
20.	<i>Antheraea assama</i>	ADL40848	ADL40846
<b>COLEOPTERA</b>			
<b>Tenebrionidae</b>			
21.	<i>Tribolium castaneum</i>	AFQ62106	AFQ62105
<b>DIPLOSTRACA</b>			
<b>Daphniidae</b>			
22.	<i>Daphnia magna</i>	BAJ78307	BAJ78307

Table S3 Comparison of DSX proteins in insects: nº of amino acids (degree of similarity = identical plus conserved amino acids)

Species	DSXF	DSXM	N-terminal region	OD1 domain	OD1-OD2		C-terminal region	C-terminal region
					Intermediate region	OD2 domain	DSXF	DSXM
<i>Sciara</i>	273	221	41	46	111	61	14	23
<i>Anophelex</i>	241 (0,43)	283 (0,29)	37 (0,21)	46 (0,78)	82 (0,23)	61 (0,50)	15 (0,42)	72 (0,16)
<i>Aedex</i>	278 (0,38)	548 (0,33)	34 (0,17)	46 (0,78)	123 (0,24)	60 (0,50)	15 (0,42)	300 (0,12)
<i>Ceratitit</i>	315 (0,44)	394 (0,38)	40 (0,42)	46 (0,80)	152 (0,22)	62 (0,54)	15 (0,57)	109 (0,12)
<i>Bactrocera</i>	321 (0,45)	400 (0,38)	40 (0,42)	46 (0,80)	158 (0,23)	62 (0,54)	15 (0,64)	109 (0,12)
<i>Anastrepha</i>	317 (0,45)	396 (0,38)	40 (0,42)	46 (0,80)	154 (0,22)	62 (0,54)	15 (0,64)	109 (0,08)
<i>Drosophila</i>	427 (0,43)	549 (0,38)	40 (0,40)	46 (0,80)	264 (0,24)	62 (0,50)	15 (0,64)	152 (0,12)
<i>Musca</i>	397 (0,46)	527 (0,39)	42 (0,41)	46 (0,82)	232 (0,28)	62 (0,50)	15 (0,57)	160 (0,08)
<i>Lucilia</i>	396 (0,44)	532 (0,38)	42 (0,41)	46 (0,80)	231 (0,25)	62 (0,50)	15 (0,57)	166 (0,08)
<i>Megaselia</i>	310 (0,41)	573 (0,40)	37 (0,37)	46 (0,80)	151 (0,25)	61 (0,47)	15 (0,50)	293 (0,20)
<i>Bombyx</i>	264 (0,39)	266 (0,33)	31 (0,16)	46 (0,78)	91 (0,35)	62 (0,49)	34 (0,42)	51 (0,04)
<i>Antheraea</i>	265 (0,43)	279 (0,33)	31 (0,06)	46 (0,80)	92 (0,35)	62 (0,54)	34 (0,42)	63 (0,16)
<i>Apis</i>	277 (0,24)	336 (0,23)	59 (0,14)	45 (0,60)	101 (0,14)	49 (0,32)	23 (0,07)	87 (0,12)
<i>Nasonia</i>	235 (0,23)	224 (0,18)	30 (0,16)	45 (0,53)	100 (0,17)	47 (0,23)	13 (0,07)	5 (-)
<i>Tribolium</i>	227(0,44)	322(0,30)	25(0,24)	46(0,76)	84(0,29)	61(0,52)	11(0,36)	125(0,27)