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Maternal provision of non-sex-specific transformer messenger RNA in sex determination of the wasp *Asobara tabida*

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Abstract

In many insect species maternal provision of sex-specifically spliced messenger RNA (mRNA) of sex determination genes is an essential component of the sex determination mechanism. In haplodiploid Hymenoptera, maternal provision in combination with genomic imprinting has been shown for the parasitoid *Nasonia vitripennis*, known as maternal effect genomic imprinting sex determination (MEGISD). Here, we characterize the sex determination cascade of *Asobara tabida*, another hymenopteran parasitoid. We show the presence of the conserved sex determination genes *doublesex* (*dsx*), *transformer* (*tra*) and *transformer-2* (*tra2*) orthologues in *As*. *tabida*. Of these, *At-dsx* and *At-tra* are sex-specifically spliced, indicating a conserved function in sex determination. *At-tra* and *At-tra2* mRNA is maternally provided to embryos but, in contrast to most studied insects, *As. tabida* females transmit a non-sex-specific splice form of *At-tra* mRNA to the eggs. In this respect, *As. tabida* sex determination differs from the MEGISD mechanism. How the paternal genome can induce female development in the absence of maternal provision of sex-specifically spliced mRNA remains an open question. Our study reports a hitherto unknown variant of maternal effect sex determination and accentuates the diversity of insect sex determination mechanisms.

Keywords: maternal provision, hymenoptera, sex determination, transformer, doublesex, transformer-2.

Introduction

The genetic basis of developmental pathways is presumed to be well conserved owing to their functional necessity. One of these necessary functions is sex determination, a developmental process in almost all eukaryotes that leads to sexual differentiation of female and male traits. Despite its universality within the eukaryotic domain, sex determination comprises a wide variety of fast-evolving mechanisms. Sex determination pathways consist of a primary signal that starts a cascade of interacting genes. The signal is passed on through downstream genetic components towards the bottom switch that regulates sexual differentiation genes (Herpin & Schartl, 2015). The genes at the level of the bottom switch appear more conserved than the upstream signals, in line with Wilkins’ hypothesis that the cascade evolves from the bottom up (Wilkins, 1995). In insects, *doublesex* (*dsx*) has been identified in a range of insect species at the bottom of the sex determination cascade (Shukla & Nagaraju, 2010; Verhulst & van de Zande, 2015). It belongs to a group of DNA-binding motif (DM) encoding genes that are present amongst Metazoa and appear to play a role in sex determination of both invertebrates and vertebrates (Matson & Zarkower, 2012). *Dsx* is spliced into sex-specific variants that translate into male- or female-specific DSX proteins.

Sex-specific splicing of sex determination genes is a hallmark of insect sex determination. The gene upstream of *dsx*, controlling its splicing, is *transformer/feminizer* (*tra/fem*). It is not functionally conserved outside the insect class, and even within insects it is absent in Lepidoptera and basal lineages of Diptera (Geuverink
& Beukeboom, 2014; Kiuchi et al., 2014). Sex-specific tra messenger RNA (mRNA) is produced by alternative splicing. TRA belongs to a class of SR-type proteins that are rich in serine (S) and arginine (R) residues. For most insects an order-specific tra domain has been described, e.g., the hymenopteran (HYM) domain in Hymenoptera and the dipteran domain in Diptera (Verhulst et al., 2010b). The Ceratitis-Apis-Musca (CAM) domain is present in all female-specific splice variants of tra, excluding drosophilids, but absent from male-specific splice variants (Hediger et al., 2010). Only the female-specific splice form yields a functional protein. In addition to regulating dsx splicing, it governs splicing of premature tra mRNA into the female-specific form, thereby creating an auto-regulatory loop. The functional female TRA protein forms a complex with the Transformer-2 protein (TRA2) to direct female-specific splicing of dsx mRNA (Amrein et al., 1990; Hedley & Maniatis, 1991; Inoue et al., 1992). The structure of TRA2 is highly conserved and contains a RNA binding domain (RBD) flanked by two arginine-serine rich regions in all insects investigated thus far. Studies in various dipterans, the coleopteran Tribolium castaneum and the hymenopteran Apis mellifera have shown that TRA2 is necessary for female-specific tra splicing (Burghardt et al., 2005; Concha & Scott, 2009; Salvemini et al., 2009; Martin et al., 2011; Sarno et al., 2011; Nissen et al., 2012; Shukla & Pali, 2013). The activation/deactivation of tra and the tra-tra2-dsx signal-relaying pathway appears largely conserved in insects, but is governed by a large diversity in primary signals (Bopp et al., 2014).

Haplodiploid insects, comprising all Hymenoptera, Thysanoptera and several branches of Coleoptera and Hemiptera, are of special interest for sex determination research because they lack differentiated sex chromosomes. Males and females share all chromosomes but differ in ploidy level (males are haploid, females are diploid). Genetic studies of haplodiploid sex determination have focused on hymenopterans. Model organisms are the honey bee Ap. mellifera (Apoidae) and the parasitic wasp Nasonia vitripennis (Chalcidoidea). Information obtained from these species provides a framework for studies in other haplodiploid systems. Ap. mellifera has complementary sex determination (CSD) in which the allelic state of the complementary sex determiner (csd) locus, a paralogue of tra serves as the primary signal (Beye et al., 2003; Hasselmann et al., 2008). An individual that is homozygous or hemizygous at csd becomes male, whereas heterozygous individuals develop into females. A CSD-like mechanism has been inferred for over 60 species of Hymenoptera (van Wilgenburg et al., 2006; Heimpel & de Boer, 2008). The molecular details of CSD have only been elucidated in Ap. mellifera (Beye et al., 2003; Hasselmann et al., 2008; Gempe et al., 2009). N. vitripennis has no CSD, but sex determination is governed by maternal effects and genomic imprinting (MEGISD; Beukeboom & Kamping, 2006; Verhulst et al., 2010a). Female-specific Nvtra mRNA is maternally provided to initiate female-specific splicing of zygotic Nvtra transcripts, necessary for female development (Verhulst et al., 2010a). This constitutes the maternal effect element of the MEGISD mechanism. Zygotic transcription of Nvtra is hypothesized to be under the control of an activator gene, named womanizer (wom), that is silenced on the maternal complement, but active on the paternal complement in fertilized eggs (Verhulst et al., 2013). This constitutes the (maternal) genomic imprinting element of MEGISD. The identity of wom has not been elucidated yet, but presumably non-CSD sex determination in haplodiploids depends on a difference between the paternal and maternal genome set of which the genomic imprinting element of MEGISD is an example. Thus far, MEGISD has only been demonstrated for N. vitripennis and its phylogenetic distribution remains unclear.

Parasitoids of the Asobara genus (Braconidae) are a group of well-studied ichneumonoid wasps. They occur worldwide and use Drosophila larvae as hosts (Carton et al., 1986). CSD has been reported for numerous braconid species, yet there are also species in this group that lack CSD (van Wilgenburg et al., 2006; Asplen et al., 2009). Asobara tabida has tested negative for single-locus and multi-locus CSD through inbreeding crosses (Beukeboom et al., 2000; Ma et al., 2013). Sex determination in As. tabida could be similar to the MEGISD mechanism of N. vitripennis. A first step towards testing As. tabida for MEGISD is to elucidate its sex determination pathway in terms of genes and their regulation. Here, we investigate the presence of the sex determination genes dsx, tra2 and tra, and examine their role in As. tabida sexual development.

Results
Identification of key sex determination genes
Key sex determination genes were identified using translated BLAST (Altschul et al., 1997) against an As. tabida genomic assembly (Geuverink et al.; unpubl. data). Single homologues of tra, tra2 and dsx are present, but no paralogues (ie duplications) of tra were detected (Table 1).

Sex-specific splice forms of At-tra
Identification of tra splice variants in adult As. tabida by rapid amplification of cDNA ends PCR (RACE-PCR) and subsequent reverse-transcription PCRs (RT-PCRs) revealed a characteristic female-specific form (Fig. 1 and Supporting Information Fig. S1A). This splice variant (At-tra2) translates into a peptide containing all known
conserved TRA domains: the HYM domain, the CAM domain, an arginine-serine domain (RS domain) and a proline-rich region. It is diverged from Aculeata species (ants and bees) and *N. vitripennis* (Fig. S1B). Three male-specific isoforms were found (*At-traM1*, *At-traM2* and *At-traM3*), which contain exons that lead to different open reading frames (ORFs), all resulting in a truncated protein that only contains the HYM domain near the C-terminal end. The inclusion of male-specific exons is characteristic of the sex-specific splicing of *tra* and the CAM domain is typically absent in males (Sánchez, 2008; Verhulst et al., 2010b).

Two abundantly present non-sex-specific *At-tra* splice variants are referred to as *At-traNSS1* and *At-traNSS2* (Fig. 1). These two splice variants are similar, except for the last intron, resulting in a slightly longer ORF, retained in *At-traNSS2*. Both splice variants contain a putative alternative CAM domain, followed by a shortened RS-rich region compared to the one present in *At-traF*. The two CAM regions (75 bp each) of *At-traF* and *At-traNSS* show high similarity at the amino acid level (Fig. 2).

No alternative splicing of *At-tra2*

A single splice form of *tra2* was identified in *As. tabida* (Fig. 3). AT-TRA2 is highly conserved in its amino acid sequence and contains the characteristic RBD with a large number of flanking arginine and serine residues (Fig. S2A, B). Alternative splice forms were not detected in either sex or at different stages of development. Many insect species only transcribe a single splice form of *tra2* (Burghardt et al., 2005; Concha & Scott, 2009; Salvemini et al., 2009; Sarno et al., 2010; Schetelig et al., 2012; Liu et al., 2015). *Ap. mellifera* (Nissen et al., 2012) and *N. vitripennis* (Geuverink et al., 2017) do possess alternative splice variants of *tra2*, but these are present in both sexes and across all life stages.

Sex-specific splicing of *At-dsx*

The structure of DSX in *As. tabida* (AT-DSX), including the DM domain and the second oligomerization domain (OD2) domain, is conserved (Fig. S3A). AT-DSX clusters phylogenetically with other hymenopteran DSX orthologues (Fig. S3B). *At-dsx* is sex-specifically spliced into

![Figure 1](image_url) Exon-intron structure of the female-specific (F), male-specific (M) and non-sex-specific (NSS) splice variants of *transformer* (*tra*) in *Asobara tabida*. All splice variants are transcribed from one locus. White boxes represent the 5' and 3' untranslated regions, black boxes the coding sequence. Primer positions for quantitative real-time PCR are labelled qF (forward) and qR (reverse). Primers used to detect splice variation by reverse-transcription PCR are labelled rFF (forward) and rRR (reverse). Two different primer sets were used to test for sex-specific (SS) and NSS splicing. Incomplete intron lengths are marked by breaks in the line. CAM, Ceratitis-Apis-Musca.

<table>
<thead>
<tr>
<th>Gene</th>
<th>GenBank accession no.</th>
<th>Conservation (E-value compared to <em>Nasonia vitripennis</em> peptide sequence)</th>
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<tr>
<td>transformer</td>
<td>MF074329</td>
<td>2e-34</td>
</tr>
<tr>
<td>doublesex</td>
<td>MF074327</td>
<td>2e-37</td>
</tr>
<tr>
<td>transformer2</td>
<td>MF074326</td>
<td>4e-78</td>
</tr>
</tbody>
</table>

Table 1. Identified homologues of sex determination genes in *Asobara tabida*
one female-specific and one male-specific splice form (Fig. 4). The female-specific splice variant includes exon 4, which, upon translation, differs from the male-specific splice variant in yielding a shorter peptide containing a female-specific OD2 domain. The male-specific splice variant does not contain exon 4 and yields a male-specific OD2 domain in the resulting protein. The presence of sex-specific dsx splicing suggests functional conservation of the bottom of the sex determination cascade where dsx regulates sexual differentiation.

Sex-specific At-tra mRNA is not maternally provided

Developing embryos from both unfertilized (haploid) and fertilized (diploid) eggs, ranging from 0 to 144 h after oviposition, were collected to assess the expression of At-tra, At-tra2 and At-dsx. RT-PCRs were conducted on the samples to portray the pattern of At-tra and At-dsx splice variants at these time points. Mated females will produce a mixture of diploid fertilized eggs and haploid unfertilized eggs; thus, a certain number of haploid males (ratio of 0.38 overall) will be present in each ‘fertilized eggs’ labelled sample. At-traF and At-traM mRNA are absent in 0–2-h-old embryos as measured by quantitative real-time PCR (qPCR) amplification (Fig. 5A, measured together as At-traSS), indicating that the mother does not provide sex-specific tra (At-traSS) mRNA to her offspring. At 12–14 h of development At-traM expression appeared in haploid embryos (Figs 5A, 6A), indicating a zygotic origin. At this point, no splice variant can be detected by RT-PCR in diploid embryos from fertilized eggs (Fig. 6), and expression levels are equal to that of haploid embryos (Fig. 5). The RT-PCR splicing results vary in 12–14-h-old diploid embryos, where amplification covers a mixture of all four At-traSS splice variants (At-traF, At-traM1, At-traM2 and At-traM3). In contrast, the qPCR assay that amplifies the common region of the At-traSS splice variants is more sensitive. After the start of zygotic At-traSS transcription higher levels of At-traSS mRNA are present across developing diploid embryos compared to developing haploid embryos (Z = 2.48, P = 0.013).

At 24–26 h At-traF splicing is evident in diploid embryos whereas At-traF is absent at all points in the development of haploid embryos (Fig. 6). The relative mRNA levels in haploid embryos consist solely of At-traM transcripts (Fig. 5A). The At-traSS expression (amplifying both At-traF and At-traM) in diploid embryos shows a similar pattern (Fig. 5A), but here the transcripts are composed mostly, but not exclusively, of At-traF mRNA. In both haploid and diploid embryos sex-specific zygotic tra expression peaks 48–52 h after oviposition (Fig. 5A).

Figure 2. Alignment of the putative Ceratitis-Apis-Musca domain of the Asobara tabida transformer female-specific (At-traF) and non-sex-specific (At-traSS) splice variants against hymenopteran, dipteran and coleopteran sequences. Amino acid sequences are shown with their relative conservation in greyscale (darker tones indicating higher conservation). The 11th amino acid is coded by an exon-spanning triplet and is indicative of the exclusion of male exons spliced out between exons A and B. The specific structure and number of exons A and B differ between species. In the gene structure of As. tabida the first 11 identical amino acids from At-traF and At-traSS are translated from the same exon 3, from the 12th amino acid onwards the At-traF sequence continues on exon 7 and the At-traSS sequence on exon 4.

Figure 3. Exon-intron structure of transformer-2 (tra2) in Asobara tabida. White boxes represent the 5’ and 3’ untranslated regions, the black boxes the coding sequence. The RNA binding domain is plotted as grey boxes on the exons. Primer positions for quantitative real-time PCR are labelled qF (forward) and qR (reverse). Incomplete intron lengths are marked by breaks in the line.
Expression of $\text{At-tra}^{\text{NSS}}$ variants does not only occur in adults but is also observed in embryos of all developmental stages and in both sexes (Figs 5B, 6). These variants are present in embryos less than 2 h of age, indicating that the mother provides these mRNAs to her eggs. The expression of the combined $\text{At-tra}^{\text{NSS}}$ variants follows a pattern similar to the $\text{At-tra}^{\text{SS}}$ expression in the later stages of development (Fig. 5B). The relative levels of $\text{At-tra}^{\text{NSS}}$ mRNA do not differ between female and male embryonic development [$F_{(1, 57)} = 1.2975, P = 0.26$].

Maternal provision of $\text{At-tra}2$

$\text{At-tra}2$ mRNA is maternally provided to embryos as detected with qPCRs (Fig. 5C). It remains present in all stages of both male and female development and shows no peak of mRNA levels. $\text{At-tra}2$ expression fluctuates more in males and overall has a higher level during male than female development [$F_{(1, 52)} = 19.592, P < 0.005$].

Expression of $\text{At-dsx}$ during development

Low $\text{At-dsx}$ mRNA levels measured by qPCR are visible in the earliest stages of development (Fig. 5D), indicating maternal provision. The third splice variant of $\text{At-dsx}$ has a slight alteration compared to $\text{At-dsx}^{\text{M}}$ (Fig. 4) and is only observed in some samples of both haploid and diploid embryos at the 12–14 h time point. This $\text{At-dsx}^{12\text{h}}$ transcript has a small 54-bp addition at the 5’ end of exon 5 causing a shortened ORF. At 12–14 h the $\text{At-dsx}^{12}$ splice variant is not yet present in diploid embryos. Only after sufficient $\text{At-tra}^{12}$ is present, $\text{At-dsx}$ transcription starts.
is spliced into the female mode at 24–26 h of development (Fig. 6).

After 12–14 h the haploid embryos exclusively display the male-specific splice variant of At-dsx (Fig. 6) and this splicing pattern continues in adult samples. In contrast, in diploid embryos and in adult females, a mixture of At-dsxF and At-dsxM is present in all stages after 12–14 h. This pattern of dsxM leakage in females matches that observed in Ap. mellifera and N. vitripennis, where the females have both splice variants (Verhulst et al., 2010a; Nissen et al., 2012). This is consistent with male development as the default state of the sex determination cascade.

Discussion

Conservation of the sex determination cascade in As. tabida

Orthologues of the key insect sex determination genes tra, tra2 and dsx are present in As. tabida. The sequence of At-tra is strongly diverged compared to other Hymenoptera, but its role in the sex determination cascade is evident from its sex-specific splicing patterns appearing at 12–14 h of development, followed by the activation of sex-specific splicing of At-dsx at 24–26 h. AT-TRA possesses all known TRA domains, including the HYM domain. This suggests that the HYM domain, previously documented in the Aculeata and N. vitripennis (Verhulst et al., 2010b; Fig. S1A), is conserved in all apocritan Hymenoptera. TRA2 distinctively lacks sex-specific isoforms and shows strong conservation of the RBD with flanking RS regions. The structure of DSX is similarly conserved with the presence of the OD2 domain. This suggests that the conservation of the transducing elements tra and dsx forms the start of the sexual differentiation process in the As. tabida sex determination cascade, even though At-tra regulation appears to deviate from the known insect mechanisms.

Regulation of female-specific tra and dsx splicing

From the 24 h developmental stage onwards, a peak of female-specific At-tra mRNA levels appears in diploid embryos and At-tra is spliced into the female mode. In haploid embryos from unfertilized eggs, At-traSS expression peaks around 48 h (Fig. 5A) but the male splice variant is already detectable from 12 h onwards (Fig. 6). It has to be noted that expression patterns in diploid embryo samples are not restricted to one sex, because of the experimentally unavoidable inclusion of haploid male embryos. Mated females under our experimental set-up produce mixed broods of 38% haploid male and 62% diploid female embryos. Downstream of At-tra, At-dsx is spliced into sex-specific variants, consistent with its conserved role in insect sex determination. Initially, At-dsx mRNA seems to be spliced into the male mode in both diploid and haploid embryos at 12–14 h of development.
At this time point both At-tra<sup>NSS</sup> and At-tra2 mRNA are already present as a result of the maternal provision, but apparently not capable of regulating At-dsx splicing in the absence of At-tra<sup>F</sup>. Female At-tra splicing is clearly present at 24–26 h, which coincides with At-dsx switching to female-specific splicing in diploid embryos. As At-dsx is not spliced into the female-specific variant before At-tra<sup>F</sup> is present, it appears that, as in all other studied insects, AT-TRA regulates At-dsx splicing.

At-tra<sup>NSS</sup> mRNA is present in early embryos, similar to its early expression in Ap. mellifera (Nissen et al., 2012) and N. vitripennis (Geuverink et al., 2017). A potential complex with the female-specific TRA protein, as demonstrated in Drosophila melanogaster (Amrein et al., 1994), can however only be formed at a later stage in development, when At-tra<sup>F</sup> is actively transcribed in the zygote. Non-sex-specific At-tra<sup>NSS</sup> is present prior to zygotic transcription and is most likely maternally provided, but it is not yet known whether AT-TRA<sup>NSS</sup> products form a complex with AT-TRA2, or if only AT-TRA<sup>F</sup> is involved in this interaction in As. tabida.

Functionality of alternative tra splice variants

The alternative CAM domain and the arginine-serine rich region of AT-TRA<sup>NSS</sup> are shorter than those of AT-TRA<sup>F</sup> and there is no proline-rich region. In Drosophila melanogaster, the proline-rich region appears not to be directly interacting with the spliceosome (Sciabica & Hertel, 2006), suggesting that AT-TRA<sup>NSS</sup> may share some aspects of TRA<sup>F</sup> function. It is unknown whether At-tra<sup>NSS</sup> splice variants in As. tabida have a similar function in starting auto-regulation as female-specific tra in other species. Additionally, non-sex-specific patterning and high expression in each developmental stage may indicate a role in overall development of the embryo.

Possibility of MEGISD in As. tabida

The absence of maternally provided female-specific At-tra<sup>F</sup> would be the key difference between the MEGISD system of N. vitripennis and a possible MEGISD-like system in As. tabida. The function of the abundant maternal provision of non-sex-specific tra mRNA and the putative duplicate CAM domain in this splice variant are currently unclear, and further study is required to determine their role in the functioning of sex determination in As. tabida. Functional studies of the At-tra<sup>NSS</sup> splice variant may provide the next important clue regarding the underlying sex determination mechanism, which deviates from thus far identified mechanisms (Fig. 7).

The default zygotic state of tra in every hymenopteran species is ‘OFF’, leading to male development (Fig. 7, left pane of each box). Maternal products are supplied to the egg, whether fertilized or not. Consequently, it is impossible that these maternal products are the sole feminizing elements as this would also direct the development of unfertilized haploid eggs into the female mode. A paternal factor, such as the paternal genome or other paternally provided epigenetic marks (eg
microRNAs), is a necessary element in the feminization of the fertilized egg, in combination with the supplied maternal products. The mechanisms of this interaction appear different for each hymenopteran species tested thus far. Therefore, early differential splicing of haploid and diploid zygotic At-tra transcripts depends on a paternal factor. As CSD has been refuted as the primary signal in *As. tabida* it is tempting to speculate that a paternal factor, only available in diploid zygotes, would enable female-specific splicing of zygotic At-tra transcripts by non-sex-specific AT-TRA. This model (Fig. 7) resembles both the start of the *Ap. mellifera* sex determination cascade where csd initiates the female-specific splicing of *fem* (tra), and the start of *N. vitripennis* sex determination, where the paternal *wom* gene initiates zygotic *Nvtra* expression. *As. tabida* does not determine sex by a CSD mechanism and the absence of a tra parologue is consistent with a non-CSD system. The mechanism of *As. tabida* could be similar to *N. vitripennis*, but without maternal provision of female-specific tra mRNA. These conclusions are consistent with the fast evolution of sex determination mechanisms and their underlying cascade of genes, even within insect orders.

Experimental procedures

Insect culturing

The highly inbred TMS strain (Ma et al., 2013), which originates from strains SOS (Sospel, France) and Italy (Pisa, Italy), was used as genomic source material and in subsequent experiments. The wasps were cultured on second-instar *D. melanogaster* host larvae (72 h of development) at 20 °C under constant light.

Orthologue identification

Orthologues of sex determination genes were identified using translated BLAST (Altschul et al., 1997) against an *As. tabida* genomic assembly (Geuverink et al.; unpubl. data). DXS and TRA protein sequences of *Ap. mellifera* (ABW99105, NP_001128300) and *N. vitripennis* (ACJ65507, NP_001128299) and the TRA2 sequence of *Ap. mellifera* (NP_001252514) were used as queries. Prior to availability of the genomic assembly, a small fragment of *transformer* was detected in an *As. tabida* expressed sequence tag data set (Kremer et al., 2012) using translated BLAST. This fragment was used for initial primer development.

RNA extraction, cDNA synthesis and splice-variant detection

Adult females and males were individually collected 24–48 h after their emergence from the *D. melanogaster* pupae. RNA extraction was performed according to the manufacturer’s protocol with Trizol (Invitrogen, Carlsbad, CA, USA). RACE-PCRs were notably only performed on adult individuals and alternative transcription start sites could be present in early stages of development. For 3’RACE, reverse transcription of RNA was conducted with a RevertAID™ H Minus First Strand cDNA Synthesis Kit (Fermentas, Hanover, MD, USA) using 25 μM 3’RACE adapter (5’-GCCAGCACAGAATTATAGCACTTATTAGGT12 VN-3) from a FirstChoice RLM-RACE kit (Ambion, Austin, TX, USA). For 5’RACE, RNA was processed according to the manufacturer’s instructions (FirstChoice RLM-RACE kit), whereas reverse transcription was conducted with the RevertAID™ H Minus First Strand cDNA Synthesis Kit (Fermentas). To assess the At-tra splice variants present in adult males and females 5’RACE-PCR was performed with outer primer Attra5RACEout (5'-CCATTCTGAAATGATCGATGC-3') and inner primer Attra5RACEin (5’-CTTGGAGACTTGGTTACTCCT-3') under PCR conditions of 94 °C for 3 min, 35 cycles of 94 °C for 30 s, 58 °C for 30 s and 72 °C for 2 min, concluded by a final extension of 10 min at 72 °C. Outer primer Attra3RACEout (5’-AGGAGCGAGTCTGGAAACCT-3') and inner primer Attra3RACEin (5’-CGGAGACGCTGACATCTAAGCAGA-3') were used in 3’RACE-PCR at an annealing temperature of 55 °C and otherwise identical conditions. 5’RACE-PCR of At-dsx was performed with outer primer Atdsx5RACEout (5’-ATCATTCTGTCTCATCTGC-3') and inner primer Atdsx3RACEin (5’-CGGTATTTGCAATATCTCTTGTCTGC-3') under PCR conditions of 94 °C for 3 min, 40 cycles of 94 °C for 30 s, 56 °C for 30 s and 72 °C for 60 s, concluded by a final extension of 7 min at 72 °C. Outer primer Atdsx3RACEout (5’-GGGACAAGAGATATTGCA-3') and inner primer Atdsx3RACEin (5’-CATTTTCTACGGAGTATGGA-3') were used in 3’RACE-PCR with an extension time of 2 min and otherwise identical conditions. 5’RACE-PCR of At-tra2 did not yield any fragments after various attempts and was eliminated from the tests. RNAseq isoforms and the genomic contig yielded a putative tra2 homologue including the 5’ untranslated region (5’UTR; Table 1). 3’RACE-PCR of At-tra2 was performed with outer primer Attra23RACEout (5’-AGGGAGCAGTCTATTCTCCTAGG-3') and inner primers Attra23RACEin1/Attra23RACEin2 (5’-TAGGATCTCAATGTCATCAAGAAGG-3’/5’-TCATGTGCAAAGACTGGGAG-3') under PCR conditions of 94 °C for 3 min, 40 cycles of 94 °C for 30 s, 56 °C for 30 s and 72 °C for 60 s, concluded by a final extension of 7 min at 72 °C.

RT-PCRs to confirm the splicing variation of each gene were performed with primers AttraF (5’-AAACATGCTTGAAGAATCGAGGA-3’) and AttraSSR (5’-CTGTAGTGGAGTCAGGCAGAAC-3’) for *Attra*, primers AtdsxfrontF (5’-CTCCACCCTGTCAATGCTG-3’) and AtdsxbackR (5’-GTAGAGCTCAGCCTTCTCAG-3’) for *At-dsx* and primers Attra2frontF (5’-CCAACAGAAGACTCCGCA-3’) and Attra2exon4R (5’-CCTTCAACCTTCTCTTATCATCC-3’) for *Attra*2. All RACE-PCR and RT-PCR products were purified using a GeneJET Gel Extraction Kit (Fermentas) and subsequently ligated into a pGEM-T vector (Promega, Madison, WI, USA). Ligation reactions were used to transform competent JM-109 *Escherichia coli* (Promega). Colony-PCR was conducted with pGEM-T promoters (5’-GATATTGAAGCTGGGAG-3’ and 5’-GGGAAACAGCTATGACCA TG-3’) under PCR conditions of 94 °C for 3 min, 30 cycles of 94 °C for 30 s, 55 °C for 30 s and 72 °C for 2 min, concluded by a final extension of 7 min at 72 °C. Both strands were sequenced on an ABI 3730XL capillary sequencer (Applied Biosystems, Foster City, CA, USA) and fragments were aligned to one another and to the assembled genomic contigs to inspect the splicing variation. The exon-intron structure of the genes was visualized with EXON-INTRON GRAPHIC MAKER (http://wormweb.org/exonintron). Alignments of TRA,
TRA-CAM, TRA-2 and DSX were produced with Geneious8 (Biomatters Ltd, Auckland, New Zealand) and gene trees were constructed using a Maximum Likelihood algorithm in MEGA7 (Kumar et al., 2016) based on Jones-Taylor-Thornton (JTT) (Jones et al., 1992) and Le & Gascuel (2008) models. Transcript sequences were deposited in GenBank (accession numbers: MF074326–MF074334).

**Embryo collection for At-tra expression and splice variation**

Hosts containing TMS strain wasps in the pupal stage were placed individually in tubes to prevent females from mating. A batch of mated females was collected from mass culture bottles. Groups of three virgin or mated females were allowed to parasitize hosts for 2 h to train host detection. Following this pretreatment they were kept for 2 days at 12 °C and provided with honey for feeding. Next, each group of wasps was provided with 30 hosts for 2 h every third day, alternated with a period of 2 days with honey-feeding instead of hosts. This allowed for collection of embryos of life stages up to 24–26 h. As differences in development and chances of encapsulation by the host increase in later developmental stages of the hosts, the wasps were allowed more time to parasitize during the collection points of 48–52 h (4 h), 72–76 h (4 h) and 120–144 h (24 h). Petri dishes containing parasitized hosts were kept under constant light at 20 °C. After the allotted development time the Petri dishes were rinsed with water and the host larvae collected and stored crushed in TriZol at −80 °C. A subset of wasps from each group and time point was left to develop into adults. This set was used to verify the virgin state of the unmated females, as they only produce male offspring, and to measure the progeny sex ratio of the mated female. The sex ratio was on average 0.38 (proportion male). Of each group and time point, six tubes with 10 parasitized larvae each were used for RNA extraction, as described for adult tissue above. All total RNA was used for cDNA synthesis, as only a small proportion of the total RNA extracted was of parasitoid wasp origin. Reverse-transcription was performed with a mixture of 1:6 random oligo-dT : random hexamers from the RevertAid™ H Minus First Strand cDNA Synthesis Kit (Fermentas). Controls of unparasitized *D. melanogaster* larvae of similar age groups were included.

**qPCR**

For qPCR both embryological and adult samples were diluted 1:50. 5 μl diluted cDNA was combined with 10 μl PerfeCTa SYBR Green Fast Mix (Quanta BioSciences, Gaithersburg, Maryland, USA) and 200 nM of primers. Two different primer sets were used to differentiate between the At-tra splice variants: AttraSSqF (5′-GAACGTGAAGACTGAGGTTGAG-3′) plus AttraSSqR (5′-CTTGACCTCCCGTCATGCCT-3′); and AttraNSSqF (5′-GAAGAGAAGGGAAGGCTCG-3′) plus AttraNSSqR (5′-GAAGGTTGGATGAATAAGG-3′). The first set measures the expression of both female-specific and male-specific splice variants, combined noted as SS (sex-specific). The latter set amplifies the non-sex-specific (NSS) splice variants of *transformer* in *As. tabida*, which were measured combined as their amino acid sequence shows very strong similarity. The primer set for At-dsx, consisting of AtdsxqF (5′-TTCAGCAATGTAACATCGGTTG-3′) and AtdsxqR (5′-TACAGAATTGCTCCAGAAGTTTGAC-3′), amplified all splice variants. Primers Attra2qF (5′-TAACCGCAAGAGCACATA-CAC-3′) and Attra2qR (5′-GAGCTTTCTCTACCGCTG-3′) were used to amplify the single mRNA transcript of At-tra.2. Elongation factor 1 alpha (EF1α) was used as the reference gene with primers EF1αF (5′-TACCGGTCAGGTATTTGTC-3′) and EF1αR (5′-GGCACAGATTGCAGATGCTG-3′). All primer sets were cloned, according to the protocol above, to confirm the sequence identity of the amplicon. Negative control samples of unparasitized *D. melanogaster* larvae were tested under the same qPCR conditions and did not show any amplification after 45 cycles.

Raw data were base-line corrected using LinRegPCR 11.0 (Ramakers et al., 2003). Relative mRNA levels were determined by dividing At-tra2, At-traNSS, At-traSS and At-dsx N0 (starting concentration) values by At-EF1α N0. As EF1α has stable expression in adults, assessing expression in early embryo stages is not possible. Thus, different time points were not compared and raw expression levels of each gene closely monitored to avoid biases due to reference gene use. At-tra2, At-traNSS and At-dsx were tested in a general linear model with categorical factors fertilization and time point. A Kruskal–Wallis test was used to compare the relative mRNA levels of At-traSS between fertilized and unfertilized eggs sorted by time point. Relative mRNA levels of At-traNSS across development differences between females and males were compared with a Mann–Whitney U-test in **STATISTICA** 7 (StatSoft Inc, Tulsa, OK, USA).

**Splice variant presence during development**

RT-PCRs with primers AttraRTF (5′-TCTTCTGTCAGATCATA-GATCC-3′) and AttraRTR (5′-TTCTCAACCTCATGCTTCAC-3′) were performed on embryo and adult cDNA samples under PCR conditions of 94 °C for 3 min, 45 cycles of 94 °C for 30 s, 54 °C for 30 s and 72 °C for 2 min, concluded by a final extension of 7 min at 72 °C. The non-sex-specific At-tra transcripts were amplified with the same primers used in the qPCR: AttraNSSF (5′-GAAGAGAAGGGAAGGCTCG-3′) and AttraNSSR (5′-GAAGGTTGGATGAATAAGG-3′). Reactions were performed under PCR conditions of 94 °C for 3 min, 45 cycles of 95 °C for 30 s, 58 °C for 30 s and 72 °C for 30 s, concluded by a final extension of 7 min at 72 °C. At-dsx splicing was amplified using AtdsxRTF (5′-GAAGCAATTCTGTAGG-3′) and AtdsxRT (5′-CCGGTGAATTCTTGTAGT-3′) under PCR conditions of 94 °C for 3 min, 40 cycles of 94 °C for 30 s, 55 °C for 30 s, 72 °C for 1 min, concluded by a final extension of 7 min at 72 °C. Products were run on a 1.5% agarose gel with ethidium bromide.

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References


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**Supporting Information**

Additional Supporting Information may be found in the online version of this article at the publisher’s web-site:

Figure S1. (A) Alignment of *transformer* (TRA) female-specific amino acid sequences. Conservation of sites is shown in greyscale with darker tones indicating higher conservation. (B) Gene tree of female-specific TRA using the maximum likelihood method under Jones-Taylor-Thornton model with incorporation of amino acid frequencies from the data set (JTT-f) (Jones et al. 1992). All sites of the alignment are used to infer the gene tree. Bootstrap values (1000 replicates) are shown on the branches. The scale bar shows the number of substitutions per site.

Figure S2. (A) Alignment of *transformer-2* (TRA2) amino acid sequences. Conservation of sites is shown in greyscale with darker tones indicating higher conservation. (B) Gene tree of TRA2 using the maximum likelihood method based on the Le & Gascuel (2008) model. All sites of the alignment are used to infer the gene tree. Bootstrap values (1000 replicates) are shown on the branches. The scale bar shows the number of substitutions per site.

Figure S3. (A) Alignment of *doublesex* (DSX) female-specific amino acid sequences. Conservation of sites is shown in grey scale with darker tones indicating higher conservation. (B) Gene tree of DSX using the maximum likelihood method based on the Jones-Taylor-Thornton (JTT) matrix-based model (Jones et al., 1992). All sites of the alignment are used to infer the gene tree. Bootstrap values (1000 replicates) are shown on the branches. The scale bar shows the number of substitutions per site.