

Article

Transduction of the vitellogenic signal of juvenile hormone by Methoprene-tolerant in the cockroach *Blattella germanica* (L.) (Dictyoptera, Blattellidae)

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Abstract

In adult females of the cockroach *Blattella germanica*, juvenile hormone (JH) promotes vitellogenin production. Depletion of Methoprene-tolerant (Met) mRNA levels with RNAi resulted in a clear reduction of vitellogenin expression in the fat body while basal oocyte growth was impaired. This demonstrates that Met is essential to transduce the vitellogenic signal of JH in this species. Interestingly, the expression of the transcription factor Kruppel homolog 1 (Kr-h1) was also reduced in Met-depleted specimens. This indicates that the JH signaling pathway promotes the transcription of Kr-h1 in adult fat body tissues, as occurs in the epidermis during nymphal development. Treatments with JH show that the expression of Met does not depend on JH, which suggests that Met is upstream the JH signaling pathway acting as JH receptor, as reported in other models and processes, especially in metamorphosis. JH treatments increased the transcription levels of vitellogenin and Kr-h1, which again suggests that Kr-h1 is a JH-dependent transcription factor in the fat body of adult females. The important roles of Met in nymphal development, as previously reported, and those reported herein in relation to reproduction, suggests that it can be an interesting target for the control of *B. germanica* in urban environments, using RNAi approaches.

Keywords German cockroach; *Blattella*; vitellogenesis; juvenile hormone; methoprene-tolerant.

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1 Introduction

In most insect species, especially in those phylogenetically more basal, vitellogenin production and oocyte growth is a JH-dependent process. This is the case, for example, of the cockroach *Blattella germanica*, in which a single vitellogenin has been characterized biochemically (Martin et al., 1995) and molecularly (Martin et al., 1998). In *B. germanica*, the pattern of vitellogenin production in the fat body of adult females (Martin et

al., 1995; Martin et al., 1998) coincides with the pattern of JH titer in the hemolymph (Treiblmayr et al., 2006). Moreover, JH treatment triggers a fast induction of vitellogenin expression *in vivo* (Comas et al., 1999) and *in vitro* (Comas et al., 2001). Nevertheless, nothing is known about the mechanisms of transduction of the vitellogenic signal of JH in this cockroach.

Recent studies have unveiled the identity of the bHLH-PAS protein Methoprene-tolerant (Met) as the JH receptor (Jindra et al., 2015b), especially in the context of insect metamorphosis (Jindra et al., 2015a; Jindra et al., 2013). However, the involvement of Met in the transduction of the vitellogenic signal of JH has been less documented. Among the hemimetabolous species where vitellogenin production is genuinely JH-dependent (Belles, 2005; Raikhel et al., 2004), the involvement of Met in vitellogenesis and oocyte maturation has been shown in the linden bug *Pyrrhocoris apterus* (Smykal et al., 2014), the migratory locust *Locusta migratoria* (Song et al., 2014) and the cockroach *Diploptera punctata* (Marchal et al., 2014). In holometabolous insects, the role of Met in reproductive processes has been shown in the fruitfly *Drosophila melanogaster*, where Met and germ cell-expressed (gce) mutants experienced retarded ovarian development and lower fecundity than wild type flies (Abdou et al., 2011; Wilson and Fabian, 1986). Similar results have been obtained in the mosquito *Aedes aegypti* after depleting Met mRNA levels by RNAi (Zou et al., 2013; Li et al., 2011). In the red flour beetle *Tribolium castaneum*, oogenesis is also impaired after Met depletion by RNAi (Parthasarathy et al., 2010). Notably, Met triggers vitellogenin expression in this beetle by acting upstream of insulin signaling; expression of the insulin-like peptide 2 in the brain and fat body requires JH and Met, and depletion of either the hormone or its receptor impairs vitellogenesis, but the effects can be counteracted with a bovine insulin treatment (Sheng et al., 2011).

In the present work, we have studied the effects of Met depletion by RNA interference (RNAi) in vitellogenesis and basal oocyte development in the German cockroach, *B. germanica*. The German cockroach is a widespread and serious urban pest, as it produces a number of proteins that can trigger allergic episodes that correlate with asthma development, and early exposure leads to increased sensitization and asthma severity (Dillon et al., 2015; Rosenstreich et al., 1997; Gore and Schal, 2007). Moreover, *B. germanica* is a potential vector of pathogenic and antibiotic-resistant microorganisms (Cloarec et al., 1992; Jalil et al., 2012; Zurek and Schal, 2004). Chemical insecticides are the most used tools for controlling cockroach populations in human habitats, although there are evidences showing that apartments treated with chemical pesticides and untreated apartments may support equal cockroach populations (Koehler et al., 1987; Schal and Hamilton, 1990). This illustrates the need to reexamine the current treatments that rely on insecticides and explore other alternatives. RNAi has been considered as an interesting approach for pest control (Katoch et al., 2013; Scott et al., 2013), also in human environments (Zhu et al., 2016). The German cockroach has been proven to be especially sensitive to RNAi (Belles, 2010), and previous reports have shown that Met is crucial to regulate postembryonic development in this species (Lozano and Belles, 2014). The present report describes that RNAi depletion of Met impairs vitellogenesis and oocyte growth in *B. germanica*, which reinforces the interest of Met as a target for controlling this urban pest using RNAi strategies.

2 Materials and Methods

2.1 Insects

Specimens of *B. germanica* were obtained from a colony reared on dry dog food (Panlab 125C3) and water in the dark at $30 \pm 1^\circ\text{C}$ and 60-70% relative humidity. Virgin females were used for the study of gene expression levels during the first gonadotrophic cycle, except in the case of day 8, when mated females on the first day of oothecal transport were used. Abdominal fat bodies were dissected under saline solution from carbon dioxide-anesthetized animals. After dissection, tissues were immediately frozen in liquid nitrogen and stored at -80°C.

2.2 RNA extraction, cDNA synthesis and real-time PCR analyses

The expression levels of the different genes studied were measured using quantitative real-time PCR (qRT-PCR) using cDNA prepared from abdominal fat body as previously described (Maestro et al., 2009). Briefly, fat body tissue adhered to the abdominal sternites was dissected out, and 1 µg of total RNA was used for reverse transcription. The absence of genomic contamination was confirmed using a control without reverse transcription. cDNA amplifications of Met, vitellogenin, Kruppel homolog 1 (Kr-h1) and Actin 5C were performed in triplicate, in a 20 µl final volume, using the primers detailed in Table 1 (Lozano and Belles, 2014, Suren-Castillo et al., 2012; Lozano and Belles, 2011). cDNA levels were quantified using iQ SYBR Green supermix (Bio-Rad) in an iQ cycler and iQ single color detection system (Bio-Rad), as previously described (Ons et al., 2015). Real-time data was collected through the iQ5 optical system software v.2.0 (BioRad).

2.3 RNA interference

RNAi *in vivo* in females of *B. germanica* was performed as previously described (Maestro and Belles, 2006, Ciudad et al., 2006). For Met RNAi, the 458 bp dsRNA fragment (dsMet) described by Lozano and Belles (2014) was used. Primers to prepare the corresponding dsRNA are indicated in Table 1. In all experiments, a heterologous 307-bp fragment from the polyhedrin of *Autographa californica* nucleopolyhedrovirus (dsMock) was used as control (Lozano and Belles, 2014). A dose of 2 µg of dsRNA diluted in sterile saline was injected into the abdomen of freshly emerged adult females, and a second 2-µg dose was injected three days later. Effects were examined on day 5 of adult stage.

Table 1 Primers used to detect transcript levels by qPCR in *Blattella germanica* tissues and to prepare the dsRNA for RNAi experiments on Met. Gene abbreviations: *Met* (*Methoprene-tolerant*), *vg* (vitellogenin), *Kr-h1* (Kruppel homolog 1).

Primer set	Forward primer (5'-3')	Reverse primer (5'-3')	Reference sequence
RNAi			
<i>Met</i>	GCAAATTGTATCCTTCATCTGC	TGACAGACTCGCGCTTATG	HG965209
qRT-PCR			
<i>Met</i>	CTGTTGGGACATCAGCAGAA	GGCAGGTGATGGAGTGAACT	HG965209
<i>vg</i>	CTGGGCATTGACAACACAAACAT	TTGAAGAGCTGCTGGAGAGTTG	AJ005115
<i>Kr-h1</i>	GCGAGTATTGCAGCAAATCA	GGGACGTTCTTCGTATGGA	HE575250
<i>Actin 5c</i>	AGCTTCCTGATGGTCAGGTGA	TGTCGGCAATTCCAGGGTACATGGT	AJ862721

2.4 Juvenile hormone treatments

JH treatments were performed to assess that Met expression is not JH-dependent. A dose of 10 µg of JH III (Sigma) diluted in analytical grade acetone at a concentration of 10 µg/µl was topically applied on the abdominal tergites of freshly emerged or 2-day-old adult females, to which wings had been cut. Controls were equivalently treated with acetone. Dissections for mRNA measurements were carried out 24 h later.

3 Results

3.1 Expression profiles of vitellogenin and Met

Transcript levels of vitellogenin and Met were measured in the fat body of adult females throughout the first reproductive cycle. Vitellogenin mRNA levels followed a pattern which paralleled that of circulating JH (Treiblmayr et al., 2006), showing low levels at the beginning of the cycle, a peak at day 6, and a subsequent

rapid decline (Fig. 1A). Conversely, mRNA levels of Met did not show significant changes through the reproductive cycle (Fig. 1A).

3.2 RNAi depletion of Met reduces vitellogenin expression

In order to study the role of Met in vitellogenesis, Met mRNA levels were depleted using systemic RNAi. A dose of 2 µg of dsMet was injected into the abdomen of freshly emerged adult females, and the treatment was repeated at adult day 3. Females equivalently treated with dsMock were used as controls. Met mRNA levels were examined in the fat body of dsMet-treated females on day 5, and results showed that they were 67% lower as average in comparison with dsMock-treated controls (Fig. 1B). Moreover, vitellogenin mRNA levels showed 53% reduction as average in the dsMet-treated group compared with the dsMock-treated controls. This was concomitant with a dramatic reduction of the basal oocyte length (Fig. 1B). Interestingly, mRNA levels of Kr-h1 were also reduced (55% as average) in Met-depleted specimens (Fig. 1B).

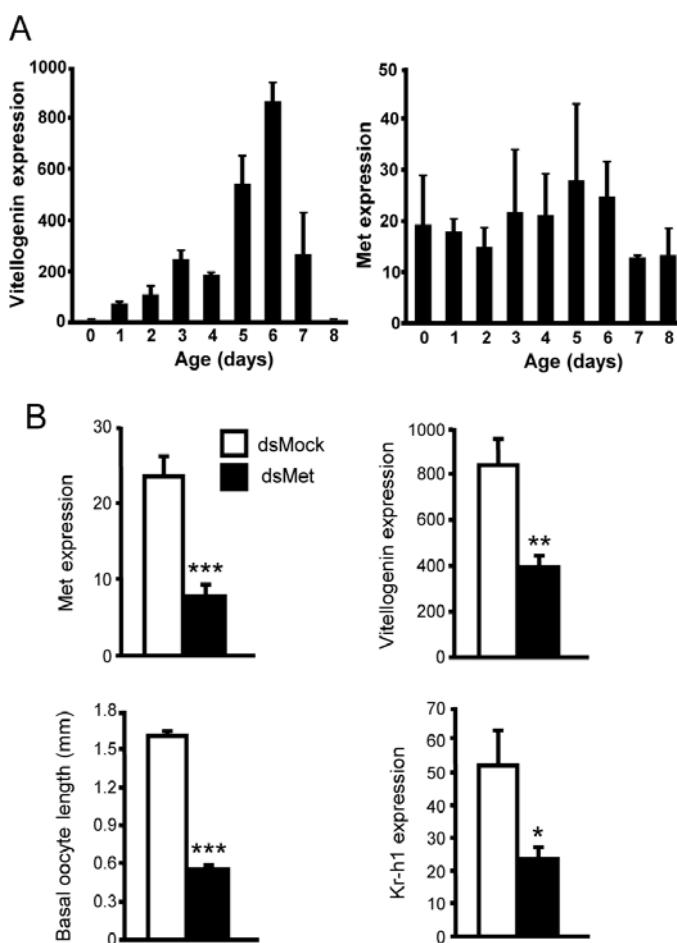


Fig. 1 Expression of vitellogenin and Methoprene-tolerant (Met) during the reproductive cycle of *Blattella germanica* and effect of RNAi treatment. A. Expression pattern of vitellogenin and Met in the fat body of adult females throughout the first reproductive cycle ($n = 3$); day 8 is the first day of ootheca transport. B. Effect of Met depletion in the fat body of adult females. Freshly ecdised adult females were injected with dsMet or dsMock (Control) at days 0 and 3; fat body mRNA levels of Met, vitellogenin and Kr-h1, and basal oocyte length were measured at adult day 5 ($n = 10-11$ for mRNA measurements, and $n = 16-19$ for basal oocyte length). Results are expressed as the mean \pm S.E. Gene expression is represented as copies of the given transcript per copy of Actin 5C in the case of vitellogenin, and copies per 1000 copies of Actin 5C for Met and Kr-h1 transcripts. Asterisks represent significant differences between control and dsMet (Student's *t* test, * $P < 0.05$; ** $P < 0.001$; *** $P < 0.0001$).

3.3 JH treatment does not affect Met expression

We aimed at assessing that Met is at the top of the JH signaling pathway in the regulation of vitellogenesis, as it is in the regulation in metamorphosis, and whose expression is not JH-dependent. Thus, we treated freshly emerged adult females with 10 µg of JH III and we quantified the expression of Met 24 h later. JH treatment did not affect Met expression, as expected (Fig. 2A). Conversely, it produced a dramatic increase of vitellogenin expression in fat body, and a more modest, although statistically significant, increase of Kr-h1 mRNA levels. When we carried out the same JH treatment but in 2 day old adult females, Met was again unaffected, whereas vitellogenin mRNA levels tended to increase and Kr-h1 mRNA levels significantly increased (Fig. 2B).

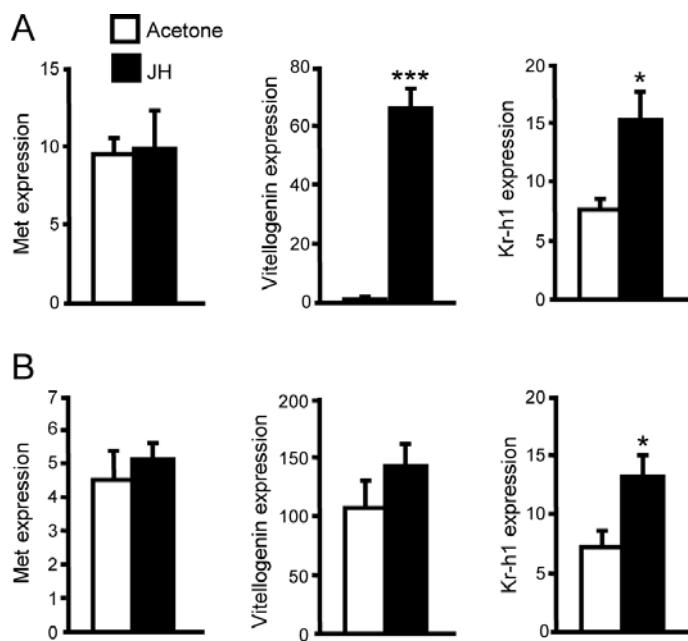


Fig. 2 Effects of exogenous juvenile hormone (JH) treatments on Methoprene-tolerant (Met) expression in *Blattella germanica*. Effects of treatment (10 µg of JH III or acetone) carried out on freshly ecdised adult females and examined on day 1 on fat body tissues (n = 6). B. Effects of treatment (same dose and control) carried out on day 2 adult females and examined on day 3 on fat body tissues (n = 6). Results are expressed as the mean ± S.E. Gene expression is represented as copies of the given transcript per copy of Actin 5C in the case of vitellogenin, and copies per 1000 copies of Actin 5C for Met and Kr-h1 transcripts. Asterisks represent significant differences (Student's t test, *P<0.05; ***P<0.000).

4 Discussion

The pattern of vitellogenin transcription in the fat body of adult female *B. germanica* during the first reproductive cycle is similar to that obtained previously using semi-quantitative methods (Martin et al., 1998) and parallels the pattern of vitellogenin in terms of protein (Martin et al., 1995). These patterns are also coincident with that of JH titer in the hemolymph (Treiblmayr et al., 2006), which is not surprising, as vitellogenin expression in *B. germanica* is strictly JH-dependent (Comas et al., 1999; Comas et al., 2001).

Although the pattern of Met expression in the fat body do not correlate with that of vitellogenin expression, depletion of Met mRNA levels resulted in a clear reduction of vitellogenin expression in the fat body and of basal oocyte length. Interestingly, Kr-h1 expression was also reduced, which indicates that the JH signaling pathway promotes its transcription in adult fat body tissues, as occurs in nymphal epidermis in the context of nymphal development and metamorphosis (Lozano and Belles, 2011). Intriguingly, Met depletion in *P.*

apterus (Smykal et al., 2014) and *L. migratoria* (Song et al., 2014) resulted in relatively higher reductions of vitellogenin and Kr-h1 mRNA levels, as if vitellogenin and Kr-h1 expression were less sensitive to Met in *B. germanica*. In any case, the results suggest that Met is necessary to transduce the vitellogenic signal of JH in *B. germanica*. This is in agreement with other reports based on hemimetabolism (Marchal et al., 2014, Smykal et al., 2014, Song et al., 2014) and holometabolism (Abdou et al., 2011; Li et al., 2011; Wilson and Fabian, 1986; Zou et al., 2013) species. Thus, the function of Met as initial transductor of JH in relation to vitellogenesis and oocyte development, in general, appears conserved from cockroaches to flies.

The treatments with exogenous JH show that the expression of Met does not depend on JH, which suggests, as expected, that Met is upstream the JH signaling pathway acting as JH receptor, as shown in other models and processes, especially in the regulation of metamorphosis (Jindra et al., 2015a; Jindra et al., 2013). The increase of vitellogenin transcription after the JH treatment is not surprising as this has been previously reported (Comas et al., 1999; Comas et al., 2001) in *B. germanica*, and serves here as a positive control to show that the treatment was efficient, especially when JH was administered on freshly emerged females. The lower effect in the treatment on 2-day-old females is probably due to the high levels of vitellogenin transcription that occur at this age (Fig. 1A), which can be hardly increased even with exogenous JH. Interestingly, mRNA levels of Kr-h1 significantly increased after JH treatment at the two ages assayed. This again suggests that Kr-h1 is a JH-dependent transcription factor in the fat body of adult females.

A previous report had shown that RNAi of Met induces precocious metamorphosis, triggering the formation of non-viable miniature adults (Lozano and Belles, 2011). The present results demonstrate that Met depletion impairs vitellogenesis and basal oocyte growth. Thus, RNAi of Met affects nymphal development as well as adult reproduction, which makes it a potential target for German cockroach control using RNAi strategies.

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