

“The neuropeptide CCHamide 2 regulates diuresis in the Chagas’ disease vector *Rhodnius prolixus*”

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Summary statement: The neuropeptide RhoprCCHamide2 has a dual diuretic effect, enhancing the serotonin-induced secretion by Malpighian tubules, and inhibiting serotonin-induced absorption across the anterior midgut in *Rhodnius prolixus*.

List of abbreviations:

calcitonin-like diuretic hormone

CAP2b peptide-A: CAPA

central nervous system: CNS

CRF-like diuretic hormone: CRFDH

double strand RNA: dsRNA

G-protein coupled receptors: GPCRs

Serotonin: 5-hydroxytryptamine. 5HT

Abstract

Given that hematophagous insects ingest large quantities of blood in a single meal, they must undergo a rapid post-prandial diuresis in order to maintain homeostasis. In the kissing bug *Rhodnius prolixus* (Hemiptera: Reduviidae), the coordinated activity of the Malpighian tubules and anterior midgut maintains water and ion balance during the post-prandial diuresis. Three to four hours after the meal the diuretic process finishes, and the animal enters an antidiuretic state to ensure water conservation until the next blood intake. The diuretic and antidiuretic processes are tightly regulated by serotonin and neuropeptides in this insect. In the present work, we report that the neuropeptide precursor CCHamide 2 is involved in the regulation of the post-prandial diuresis in the kissing bug *R. prolixus*. Our results suggest a dual effect of *Rhopr*CCHamide2 peptide, enhancing the serotonin-induced secretion by Malpighian tubules, and inhibiting serotonin-induced absorption across the anterior midgut. To our knowledge, this is the first report of a hormone presenting opposite effects in the two osmoregulatory organs (i.e. midgut and Malpighian tubules) in insects, probably reflecting the importance of a well-tuned diuretic process in hematophagous insects during different moments after the blood meal.

1. Introduction

Hematophagous insects, including triatomines, take a large amount of blood in every meal, which can be equivalent to several fold their own body weight. A rapid post-prandial diuresis takes place in order to maintain the osmotic and ionic balance, and to recover mobility to escape from predators (Coast, 2009). *Trypanosoma cruzi*, the protozoan parasite that is the causative agent of Chagas' disease, is ingested by triatomines with the blood of an infected host. The parasite multiplies and differentiates to its infective form in the gut of the insect; when the infected triatomine takes a following blood meal it releases *T. cruzi* with its feces. The parasite enters the host through the wound of the bite or through intact mucosal membranes. Despite the efforts to prevent vectorial transmission of Chagas, it is still occurring in endemic regions of Latin America. Non-vectorial ways of transmission can also take place by blood transfusions, organ transplantation or transplacentally. Chagas is a severe neglected tropical disease which affects up to 6-7 million people worldwide (Rassi et al., 2010).

Given the relevance of triatomines excretion for Chagas' disease transmission and the convenience of *R. prolixus* as a model for physiological studies in insects (Ons, 2017), diuresis

in this species has been intensely explored since the pioneering experiments of Simon Maddrell (Maddrell, 1964; Maddrell and Gardiner, 1975; Maddrell and Gee, 1974). Water and ions from the blood meal are absorbed to the hemolymph through the anterior midgut. From the hemolymph the fluid is transferred to the lumen of the Malpighian tubules (reviewed in Coast, 2009). The upper (distal) segment of the tubule secretes a primary urine that is modified in the lower (proximal) segment to form urine which is expelled by the anus. Around 50% of the blood volume ingested is excreted during the first 3 h post feeding. Then, the insect enters an antidiuretic state that allows it to survive long periods without ingesting water or nutrients for up to several months (Cabello, 2001), until the following blood intake event (Quinlan et al., 1997). The transport processes must be precisely coordinated to ensure that the animal excretes the excess plasma fraction of the blood, without nutritional value, but at the same time conserves sufficient water and ions to survive long periods of water stress. Thus, the function of the excretory system, i.e. Malpighian tubules and the anterior midgut, is tightly regulated by a system of signals (e.g. hormones) that is not fully understood (Ons, 2017).

In *R. prolixus*, serotonin (5-hydroxytryptamine; 5HT) is a diuretic factor released into the hemolymph by the abdominal nerves (Orchard, 2006). 5HT triggers fluid uptake in the anterior midgut (Farmer et al., 1981), ion (Na^+ , K^+ and Cl^-) and water secretion in the distal part of the Malpighian tubules (Maddrell et al., 1971) and the reuptake of K^+ in the proximal part of the tubule (Maddrell et al., 1993). The neuropeptide corticotropin releasing factor-like diuretic hormone (CRF-DH) is a potent diuretic peptide (Te Brugge et al., 2009; Te Brugge et al., 2011), and CAP2b peptide-A (CAPA) presents strong anti-diuretic activity (Ianowski et al., 2010; Paluzzi and Orchard, 2006, 2010). Both neuropeptides act by regulating absorption from midgut and excretion from the Malpighian tubules. Other neuropeptides that have been associated with diuresis in *R. prolixus* are calcitonin-like diuretic hormone (CT-DH) (Te Brugge et al., 2009; Te Brugge et al., 2005; Zandawala et al., 2011; Zandawala et al., 2015) and allatotropin (Villalobos-Sambucaro et al., 2015).

The diuretic (5HT, CRF-like and CT-like) and antidiuretic (CAPA) factors described so far have the concordant actions on both components of the diuretic system (i.e. Malpighian tubules and anterior midgut). The diuretic factors stimulate ion transport in both organs, while the antidiuretic factors inhibit ion transport (Te Brugge et al., 2009; Te Brugge et al., 2005; Zandawala et al., 2011, Ianowski et al., 2010; Paluzzi and Orchard, 2006, 2010). Here we describe a neuropeptide, RhoprCCHamide2, with a fundamentally different physiological function since it has opposite effects on Malpighian tubules and anterior midgut.

CCHamide is a brain-gut neuropeptide precursor family conserved in insect genomes, where is usually represented by two paralogues named CCHamide1 and CCHamide2 (Hansen et al., 2011; Reiher et al., 2011). The physiological role of CCHamides has been studied in *Drosophila melanogaster*. *DromeCCHamide1* has been involved in alimentary behavior and sensorial perception of food (Farhan et al., 2013; Ida et al., 2012), whereas *DromeCCHamide2* seems to regulate the appetite (Ida et al 2012; Ren et al., 2015) and the coordination of growth with nutrition (Sano et al., 2015). *R. prolixus* genome (Mesquita et al., 2015) encodes both CCHamide 1 and CCHamide 2 paralogues. CCHamide2 is transcribed in two isoforms that give rise to identical mature peptides (Ons, 2017; Ons et al., 2011). Two Family A G-protein coupled receptors (GPCRs) for *RhoprCCHamide* were identified by database searches in the genomic sequence followed by phylogenetic analysis (Ons et al., 2016). However, no functional studies have been reported for this neuroendocrine system in *R. prolixus* to date.

Here, we report a role of *RhoprCCHamide2* in the post-prandial diuresis. Our results suggest a dual effect of *RhoprCCHamide2* on 5HT-stimulated diuresis, increasing the secretory effect of 5HT on Malpighian tubules, while blocking the effect of 5HT on the anterior midgut. Injections of double strand RNA (dsRNA) encoding a fragment of *RhoprCCHamide2* transcript resulted in a reduction in the amount of transcript detected and an increment in the urine volume produced during post-prandial diuresis in fourth instar *R. prolixus* nymphs. To our knowledge, this is the first report of a hormone presenting opposite effects in different osmoregulatory organs in insects.

2. Material and Methods

2.1 Insects

A colony of *R. prolixus* was maintained in our laboratory in a 12:12 hour light/dark period at 28 ± 2 °C. Insects were weekly fed on chickens, which were housed, cared, fed and handled in accordance with resolution 1047/2005 (Consejo Nacional de Investigaciones Científicas y Técnicas, CONICET) regarding the national reference ethical framework for biomedical research with laboratory, farm, and nature collected/wild animals. This framework is in accordance with international standard procedures. Biosecurity considerations agree with CONICET resolution 1619/2008, which is in accordance with the WHO Biosecurity Handbook (ISBN 92 4 354 6503).

2.2 RT-PCR:

The procedures performed for RT-PCR has been previously described (Sterkel et al 2012). Briefly, the complete central nervous system (CNS), anterior and posterior midgut, rectum and Malpighian tubules were microdissected from starved fifth instar *R. prolixus* nymphs (3 weeks after molt) under saline solution using a binocular microscope. The structures were separated and placed in a microtube containing Trizol® (Ambion, Sao Paulo, Brazil). Pools of five organs were used for RNA extractions, performed with Trizol according to the manufacturer's instructions. One µg of RNA from each sample was treated with DNaseI (Promega, Wisconsin, USA) and used to synthesize cDNA with the M-MLV Reverse Transcriptase kit (Promega). PCR amplifications of the specified transcripts were performed on triplicate in a 20 µL final volume (primers detailed in Table 1). *Rhopr*β-Actin was used as a positive control of the reaction. The program used in the amplifying reaction was 95°C for 5 min, and 30 cycles of 95°C for 30 sec; 50°C for 30 sec and 72°C for 30 sec. Three biological replicates were performed.

2.3 dsRNA synthesis:

For a detailed description on dsRNA synthesis see Wulff et al 2017. Briefly, a 270 bp fragment encoded in both isoforms of *Rhopr*CCHamide2 was PCR-amplified using Pegasus Taq Polymerase (Productos Bio-Lógicos, Argentina) and primers containing a fragment of T7 promoter sequence at 5' end (CCHaRNAiFw and CCHaRNAiRv, see primers sequences in Table 1). One µl of the PCR product was used for a secondary PCR using T7-promoter primer (T7 full, see primer sequence in Table 1). PCR product were used to generate *Rhopr*CCHa-dsRNAs by *in vitro* transcription using T7-RNA polymerase (Promega, USA) or the MEGAscript™ T7 kit (Ambion, São Paulo, Brazil), according to the manufacturer instructions. Reactions were performed at 37°C, overnight. The products of transcription were treated with DNase and RNaseA (Fermentas, USA). Subsequently a precipitation with AcNa 3M was performed. The precipitate was resuspended in saline solution. A 274 bp fragment from β-lactamase bacterial gene was PCR-amplified from the pGEM®-T vector with specific primers (ARNiAMPPrFw and ARNiAMPPrRv). This is an unspecific sequence that is absent from *R. prolixus* genome, and was used as a control dsRNA. PCR products were sequenced at Macrogen facility (Seoul; Korea) to corroborate the specificity of the fragment obtained. The formation of dsRNAs was confirmed by running a 2% agarose gel

and quantified from an image of the gel using the software ImageJ 1.32 (NIH, USA). The dsRNA was stored at -20°C until use.

2.4 RNAi mediated gene silencing of *RhoprCCHamide* in vivo:

Fourth instar *R. prolixus* nymphs (2 weeks after molt and starved since the last eclosion) were injected into the abdomen with 2 µl of dsRNA (1 µg/ µl, either dsCCHamide or control) diluted in *R. prolixus* saline solution (in mM: 129 NaCl, 8.6 KCl, 8.5 MgCl₂, 2 CaCl₂, 20 glucose, 10.2 NaHCO₃, 4.3 NaH₂PO₄, and 8.6 HEPES; pH=7) .

2.5 In vivo diuresis assay

Insects were weighed and individually differentiated by color marks with non-toxic acrylic paint in the posterior legs. All the animals from dsCCHa and control groups were mixed together in a single jar for feeding, to avoid potential differences on the blood meal conditions. The insects were allowed to feed for 15 min on an immobilized chicken. Those insects that did not feed to repletion (homogeneously distributed in both experimental groups) were discarded for the analysis. Once the feeding period was finished, the insects were weighed. The volume of blood ingested was estimated with the formula "final weight - initial weight". After this, the animals were individually placed in 1.5 ml microtubes previously weighed in a precision balance. Fifteen, 30, 45, 60, 90, 120, 150, 180 and 240 minutes after feeding each insect was changed to a new weighed microtube and the volume of excreted urine was estimated by subtracting the weight of the empty tube to the weight of the tube after the visit of the insect.

2.6 qRT-PCR

qRT-PCR was performed as described previously (Wulff et al 2018). Briefly, twenty-four hours after finished the *in vivo* diuresis assay, insects were dissected to obtain CNS, anterior midgut and Malpighian tubules separately. Five tissues/sample were pooled in a microtube containing Trizol reagent (Ambion, São Paulo, Brazil). cDNA was prepared as described above.

cDNA amplifications were performed for each sample in triplicate, in a 20 µl final volume (see primer sequences in Table 1). Gene expression levels were quantified using FastStart SYBR Green Master (Roche) in iQ single color in an Arial Mx Real-time PCR instrument (Applied Biosystems). The schedule used for the amplification reaction was: (i) 95°C for 5 min; (ii) 95°C for 30 sec; (iii) 50, 58 or 60°C (depending on the primers melting temperature) for 30 sec; (iv) steps (i) and (ii) were repeated for 40 cycles. A control without

a template was included in all batches. GAPDH and β - Actin were used as a reference genes; these genes were previously validated as stables in *R. prolixus* under different conditions (Majerowicz et al. 2011, Omondi et al. 2015).

2.7 Malpighian tubule secretion assay:

Malpighian tubules were isolated from fifth instar *R. prolixus* nymphs under saline solution using a binocular microscope. From each insect, two tubules were assigned to control group and the remaining two were assigned to the CCHamide2 group. Each tubule was placed into a 90 μ l droplet containing either saline solution (control group) or synthetic *RhoprCCHa-2* 1 μ M (GGCSAFGHSCFGGH-NH₂) (Genscript Corporation; Piscataway, New Jersey, USA) surrounded with mineral oil. The segment of the tubule proximal to the hindgut was wrapped to a pin held 2 mm away from the drop. The more distal portion of the tubule was exposed to the solution. A nick was carefully made with a fine forceps in the region of the tubule exposed to the mineral oil, in order to allow fluid secretion. After this period, 1 μ M serotonin was added to the medium in both groups to stimulate secretion (this is the 5HT concentration that generate the maximal rate of secretion by the Malpighian tubules; Te Brugge et al 2011). Secreted droplets were collected from the nicked segment of the tubule using a glass probe at 10 min intervals for 40 min after stimulation with serotonin. The secreted droplets were photographed using a microscope digital camera (MiniVid, LW Scientific, Lawrenceville, GA, USA) and the diameter measured offline with the software Image J 1.32 (NIH, USA). The volume of each drop of urine was calculated with the sphere equation ($V=4/3\pi r^3$). The cumulative volume secreted over 40 min was calculated.

2.8 Anterior midgut fluid transport assay:

The anterior midgut was microdissected from fifth instar nymphs 2 weeks after ecdysis and starved since eclosion under saline solution using a binocular microscope. The tissue was washed once for 5 min with gentle agitation to remove the remnants of blood. Subsequently, the posterior end was ligated with a silk thread and filled with 50 μ l of saline solution colored with bromophenol blue, in order to detect possible leaks. The anterior end was ligated with another strand of silk thread. The tissue was gently dried with an absorbent paper and weighed in a precision balance (model 1207 MP2, Sartorius, Göttingen, Germany). Finally, the preparation was incubated for 1 hour with either saline solution, 5HT 0.1 μ M in saline solution (this is the concentration of 5HT that more strongly stimulate the rate of absorption across the epithelium of the anterior midgut; Te Brugge et al 2009), synthetic *RhoprCCHa2* 0.1 μ M in saline solution, or 5HT 0.1 μ M plus *RhoprCCHa2* 0.1 μ M

in saline solution (Ianowski et al., 2010). The tissue was removed from the incubation medium, gently dried with absorbent paper and weighed. The difference "initial weight - final weight" / 60 min was evaluated as the rate of absorption of the anterior midgut.

2.9 Anterior midgut contraction assay

Anterior midgut contraction assay has been previously described (Wulff et al 2018). Briefly, fifth instar *R. prolixus* nymphs (2-3 weeks after eclosion) were placed ventral surface down on a Petri dish covered with paraffin. The insects were fixed by melting a small part of the paraffin with a lighter and placing gently adjusting the animal until it solidifies. The dorsal cuticle was removed under saline solution, and the internal organs were exposed. The semi-intact preparation was equilibrated in 90 μ l saline solution for 20 min at room temperature ($25 \pm 2^\circ\text{C}$), replacing the fluid with fresh saline every 5 minutes. Anterior midgut contraction rate was measured by counting the number of contractions in 30 s. This procedure was repeated 6 times for each preparation, and the results of the 6 measurements were averaged. After this, the saline was removed and replaced with an equal volume of solution containing *RhoprCCHa2* at different concentrations (0.001, 0.01, 0.1, 1 and 10 μM). The anterior midgut rate was measured and expressed as % of the control (saline). Ten animals were analyzed for control and for each *RhoprCCHa-2* concentration.

3. Results

3.1 Expression pattern of *RhoprCCHamide2* and *CCHamide* GPCRs in tissues:

The expression pattern of *RhoprCCHamide2* and the two putative *RhoprCCHamide* GPCRs, encoded in the predicted transcripts RPRC00776 and RPRC000608 of the *R. prolixus* genomic sequence (www.vectorbase.org; RproC3 dataset), were determined using RT-PCR (Figure 1). The transcript encoding neuropeptide *RhoprCCHamide2* precursor was detected in the CNS, anterior midgut and Malpighian tubules, but not in posterior midgut nor in hindgut (Figure 1). Besides, a transcript encoding RPRC007766 was identified in PM and RPRC000608 transcript was PCR-amplified in AM, MT and PM (Figure 1).

3.2 *RhoprCCHamide2* regulates post-prandial diuresis:

The tissue-specific transcription of *RhoprCCHamide2* and its putative receptors suggested an involvement in the regulation of diuresis. In order to test this hypothesis, we performed an *in vivo* experiment using RNAi mediated gene silencing for *RhoprCCHamide2*. Unfed fourth instar *R. prolixus* nymphs were injected with control dsRNA (n=25) or dsRNA encoding a fragment of *RhoprCCHamide2* (dsCCHa group, n=44).

Seven days after the injections, control and dsCCHa insects were fed for 15 min. No significant differences in the weight of blood ingested were detected between control and dsCCHa groups (0.098 +/- 0.070 mg and 0.104 mg +/- 0.150 respectively).

dsCCHa-treated insects excreted significantly higher volumes of urine than the control group during the first 15 ($p < 0.001$), 30 ($p < 0.001$) and 45 ($p < 0.001$) minutes of post-prandial diuresis (Figure 2A). In the 60 min time point, no significant difference was detected between groups in the volume of urine excreted. Conversely, in the last time points evaluated the volume excreted was significantly lower for the treated group ($p < 0.001$ for 90, 120 and 240 min; $p < 0.01$ for 180 min. Two-way ANOVA with repeated measures, $n = 25-44$; Figure 2A).

In order to evaluate the net effect of *RhoprCCHamide2* silencing in the total volume excreted, we calculated the cumulative volume expelled by adding the volume excreted during every time point by each animal. We found that the cumulative volume was significantly higher for treated insects ($p < 0.01$ at 30 min; $p < 0.001$ at 45; 60; 90; 120; 180 and 240 min post feeding; Two-way ANOVA with repeated measures, $n = 25-44$; Figure 2B).

Twenty-four hours after finished the *in vivo* diuresis assay, *RhoprCCHamide2* transcription was evaluated by qRT-PCR in tissues from control and dsCCHa treated insects. When evaluated dsCCHa treated vs. control animals, we detected an 84 % decrement in the levels of transcript for *RhoprCCHamide* in the anterior midgut ($n = 5$, $p < 0.01$, Student's *t*-test), a 40 % of decrement in the CNS ($n = 5$, $p = 0.0951$) and a 30 % of decrement in the Malpighian tubules ($n = 5$, $p = 0.153$) (Figure 2C). Treated and control insects that were not dissected for qRT-PCR successfully molted to fifth instar, undergoing ecdysis around day 13 post-blood meal.

3.3 *RhoprCCHamide2* stimulates fluid secretion by Malpighian tubules:

We evaluated the activity of the neuropeptide *RhoprCCHamide2* in the secretory function of the Malpighian tubules from fifth instar *R. prolixus* nymphs using a secretion assay. Stimulation was achieved by the addition of 1 μM 5HT into the bathing droplet containing either saline solution (control group) or synthetic 1 μM *RhoprCCHa* (CCHa group).

As expected, the stimulation of the tubules with 5HT activated fluid secretion; the secretion rate with 1 μM serotonin in the bath was 12.05 nl/min (Figure 3). Our results showed that synthetic *RhoprCCHamide* stimulated secretion in 5HT-activated tubules, generating a secretion rate of 18.29 nl/min (Figure 3). This represents a significant increase

of 1.52 fold in the secretion rate ($p < 0.001$; Figure 3). Furthermore, the accumulated secreted volume was significant higher for *RhoprCCHamide2* incubated tubules at 30 min ($p < 0.05$) and 40 min ($p < 0.01$) after stimulation with 5HT (Two-ways ANOVA; $n = 37; 47$). Synthetic *RhoprCCHa* was not able to induce fluid secretion in non-stimulated tubules during 40 min incubations (data not shown).

3.4 *RhoprCCHamide2* regulates fluid transport by *R. prolixus* anterior midgut:

Treatment with serotonin (0.1 μM) stimulated fluid transport by the anterior midgut of fifth instar *R. prolixus* nymphs from the lumen into the bath ($n = 8-10$; $p < 0.05$, One-way ANOVA and Tukey-Kramer contrasts) (Figure 4). The transport rate was 76.0 ± 9.6 nl/min, in agreement with a previous report (Ianowski et al., 2010). Exposing the tissue to synthetic *RhoprCCHa2* (1 μM in bathing saline solution) had no effect on the fluid transport rate ($n=11$) (Figure 4). However, *RhoprCCHamide2* significantly reduced the stimulatory effect of serotonin on anterior midgut ($n=11$; $p < 0.05$, One-way ANOVA and Tukey-Kramer contrasts) (Figure 4). Even though the fluid transport is higher in the group treated with 5HT+synthetic *RhoprCCHamide2* respect to saline and *RhoprCCHamide2* groups, the differences were not statistically significant in our analysis (Figure 4). Finally, *RhoprCCHamide* had no effect on the contractility of the anterior midgut at concentrations of 0.001 to 10 μM (data not shown).

4. Discussion

In this work we demonstrate that CCHamide2, a scarcely studied neuroendocrine peptide in insects, possess a role in the regulation of 5HT-stimulated excretory organs in *R. prolixus*. Furthermore, RNAi-mediated gene silencing of *RhoprCCHamide2* alters the time course and intensity of the post-prandial diuresis, suggesting that it may play a role on osmoregulation after feeding.

Like most insect neuropeptides, the transcript of *RhoprCCHamide2* was detected in the CNS. We also found this transcript in the anterior midgut, suggesting that it is a brain-gut neuropeptide such as *DromeCCHamide* and *BommoCCHamide* (Reiher et al., 2011; Roller et al., 2008). *RhoprCCHamide2* transcript was also detected in Malpighian tubules. Even though the Malpighian tubules are not a common site of neuropeptide precursor expression, *RhoprFGLamide* was also found in this structure (Zandawala et al., 2012). Our finding may suggest that *RhoprCCHamide* could regulate Malpighian tubules function in an autocrine or paracrine way. Furthermore, the transcripts of the putative GPCRs for *RhoprCCHamide* were

found in the posterior midgut (RPRC007766) and in the anterior midgut, posterior midgut and Malpighian tubules (RPRC000608), also pointing to a possible role in feeding related events, diuresis, and/or excretion.

Through the silencing of *RhoprCCHamide2* expression by means of RNAi, we determined a biphasic modulation of diuresis over time. An initial increase in the diuresis during the first 45 min compared to controls, followed by a reduction respect to controls towards the end of the diuretic process. Despite this temporal modulation, dsCCHamide-treated insects excreted a higher accumulated volume after completion of diuresis (Figure 2 B), indicating a net anti-diuretic role for this neuropeptide. However, given that the reduction in gene expression was more robust in anterior midgut than in CNS and Malpighian tubules (Figure 2C), we cannot rule out that the net antidiuretic effect and/or the temporal modulation are mainly related to the role of *RhoprCCHamide2* in the anterior midgut than in other structures. Animals that were treated with dsCCHamide2 were able to feed and molt normally. Thus, in the experimental conditions the effects of dsCCHamide2 on diuresis do not deleteriously compromise homeostasis. However, this regulation could be important for the animal to survive in particular stressful situations, such as for example starvation for long periods.

In vitro tests demonstrated that *RhoprCCHamide* has an effect on both the 5HT-stimulated Malpighian tubules and in the 5HT-stimulated anterior midgut, albeit with opposite effects. Treatment with *RhoprCCHamide* triggered an increase in fluid secretion across the distal segment of the Malpighian tubules when they were stimulated with 5HT, but inhibited 5HT-stimulated fluid transport from the midgut lumen into the hemolymph. Although other reports of peptides with diuretic or antidiuretic activity have been described in *R. prolixus*, the effects were always concordant (i.e. stimulation or inhibition) in both Malpighian tubules and anterior midgut (Janowski et al., 2010; Paluzzi and Orchard, 2006; Paluzzi et al., 2008; Te Brugge et al., 2009; Te Brugge et al., 2011). Here, we report a stimulatory effect of *RhoprCCHamide* (1 μ M) on 5HT-treated Malpighian tubules, with a significant increase in the secretion rate. This stimulatory effect is lower than the observed for *RhoprCRF-DH*, which has a strong secretory-enhancing effect in non-stimulated tubules (Te Brugge et al., 2011). Moreover, *RhoprCTDH* caused a small stimulatory effect in the rate of secretion of Malpighian tubules, and an additive effect when acting in conjunct with 5HT (Te Brugge et al., 2005). In the case of *RhoprCCHamide*, the enhancing effect in the secretory activity of the Malpighian tubules was observed only when they were previously stimulated with 5HT. On the other hand, we observed that *RhoprCCHamide* has an inhibitory effect on

the anterior midgut, by reducing fluid transport rate across the anterior midgut previously stimulated with 5HT, in a similar way to the effect reported for *Rhopr*CAPA (Ianowski et al., 2010).

The physiological function of *Rhopr*CCHamide is still to be determined. However, we can hypothesize from its mode of action that could be involved in hemolymph homeostasis during post-prandial diuresis. In contrast with diuretic and antidiuretic signals described to date, which stimulate or block, respectively, both the Malpighian tubules and the anterior midgut, *Rhopr*CCHamide has opposite effects on the tubules and anterior midgut. Also, it is interesting to note that the decrease in fluid transport rate in the anterior midgut stimulated with 5HT and treated with *Rhopr*CCHamide2 is near double of the effect of *Rhopr*CCHamide observed in the stimulated Malpighian tubules (see Figures 3 and 4). Thus, it would uncouple the function of those organs by simultaneously slowing midgut fluid absorption and stimulating Malpighian tubules secretion. This would necessarily result in a decrease in the hemolymph volume. Moreover, *Rhopr*CCHamide2 does not have an effect on the excretory organs when applied alone, but rather has an effect only on stimulated organs. We propose that *Rhopr*CCHamide2 may function during post-prandial diuresis to modulate the Malpighian tubule and anterior midgut fluid transport rate to maintain hemolymph volume and composition homeostasis. Such a regulatory mechanism is necessary because the rate of fluid transport across the midgut is dependent on the Na^+ concentration in the blood meal plasma (Farmer et al., 1981). As a result, blood meals with high Na^+ content, such as avian blood, would trigger faster fluid transport across the midgut than blood meals with low Na^+ , such as amphibian hosts. In contrast, the Malpighian tubules seem to have a more constant secretion rate that is not dependent on Na^+ content of the hemolymph. Tubules exposed to Na^+ concentrations ranging from 98 to 137 mM displayed the same secretion rate after 5HT stimulation (Ianowski et al., 2004). Thus, the fluid transport rate of the midgut does not match that of the Malpighian tubules by default, but rather must be modulated to ensure that amount of fluid absorbed matches that secreted to avoid large fluctuations in hemolymph volume and composition.

Given that *T. cruzi* is transmitted to humans during the post-prandial diuresis of triatomine insects, a detailed understanding of neuroendocrine regulation of diuresis could provide target candidates for new-generation management strategies (Audsley and Down, 2015; Verlinden et al., 2014). This is specially urgent for triatomines, given the high level of pyrethroid resistance registered in domiciliary populations of *Triatoma infestans* (Capriotti et al., 2014; Fabro et al., 2012; Picollo et al., 2005; Sierra et al., 2016), which is a challenge for

the control of Chagas' disease transmission. Pseudopeptides and non-peptidic mimetics could be modeled in order to interfere with *RhoprCCHamide2* function. This kind of molecules has been already assayed in with success in *R. prolixus* for other neuropeptide family (Lange et al., 2016). Hence, our finding of a new member of the hormonal system that regulate diuresis in this species is relevant for basic and applied entomology.

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Tables

Table 1: Sequences of primers

Primer Name	Sequence 5' → 3'	Melting (°C)	Amplicon length (bp)	PCR efficiency (%)	Use
CCHaRNAiFw	TAATACGACTCACTATAGGGCGGCTC TGTAGATCGTTCTCT	58	270	ND	dsRNA synthesis
CCHaRNAiRv	TAATACGACTCACTATAGGGCCTTTG AAAGCGGCTCCAT	58			
CCHaRpFwd	TACGATCCAGGGACACCAT	58	99	80	qPCR
CCHaRpRv	CATGGACGGTGAGCAGTAAG	58			
rCCHa7766RpFw	CAGAGAATGCTATCACAGTCATACC	57	90	ND	RT-PCR
rCCHa7766RpRv	GACGAGGAATATCACAGCGAATAC	57			
rCCHa608RpFw	TAAGCAACGTAGAAGAATACACAC	54	90	ND	RT-PCR
rCCHa608RpRv	ACACCGACTAGGAACATCAC	56			
ARNiAMPFw	TAATACGACTCACTATAGGGCCAGTG CTGCAATGATAC	53	274	ND	Control dsRNA synthesis
ARNiAMPRv	TAATACGACTCACTATAGGGGAGCTG AATGAAGCCATAC	53			
<i>Rhopr</i> β-ActinFw	ACACCCAGTTTTGCTTACGG	58	300	ND	RT-PCR
<i>Rhopr</i> β-ActinRv	GTTCGGCTGTGGTGATGA	57			
<i>Rhopr</i> GAPDHFw	GACTGGCATGGCATTACAGATT	60	182	102.5	qPCR
<i>Rhopr</i> GAPDHRv	CCCCATTAAAGTCCGATGACACC	60			
<i>Rhopr</i> ActinFw	ATCTGTTGGAAGGTGGACAG	58	125	102.3	qPCR
<i>Rhopr</i> ActinRv	CCATGTACCCAGGTATTGCT	58			
T7 full	ATAGAATTCTCTCTAGAAGCTTAATA CGACTCACTATAGGG	61	---	ND	dsRNA synthesis

Figures

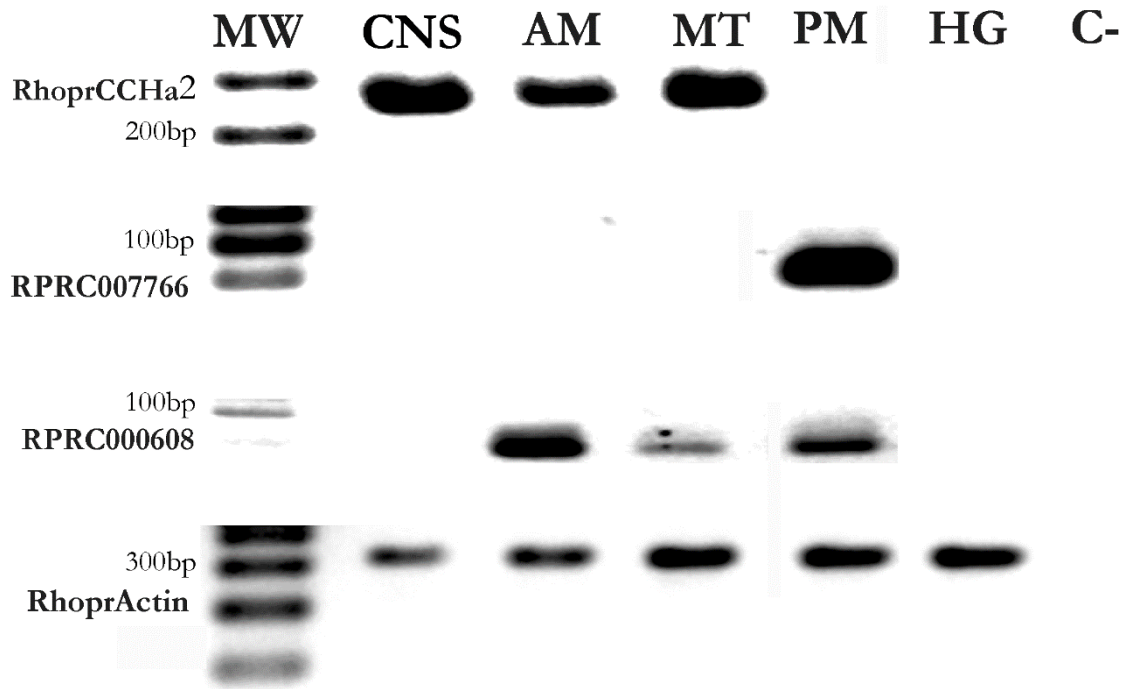


Figure 1: Transcripts encoding *RhoprCCHamide* and its GPCRs (RPRC00776 and RPRC000608) were PCR-amplified in different tissues of *R. prolixus*. MW: molecular weight marker, CNS: central nervous system, AM: anterior midgut, MT: Malpighian tubules, PM: posterior midgut, HG: hindgut and (C-): negative control without template was assayed for each primer pair. *RhoprActin* transcript was PCR-amplified from every tissue as a positive control to test the quality of the cDNAs. An agarose gel image representative of the three biological replicates performed is showed.

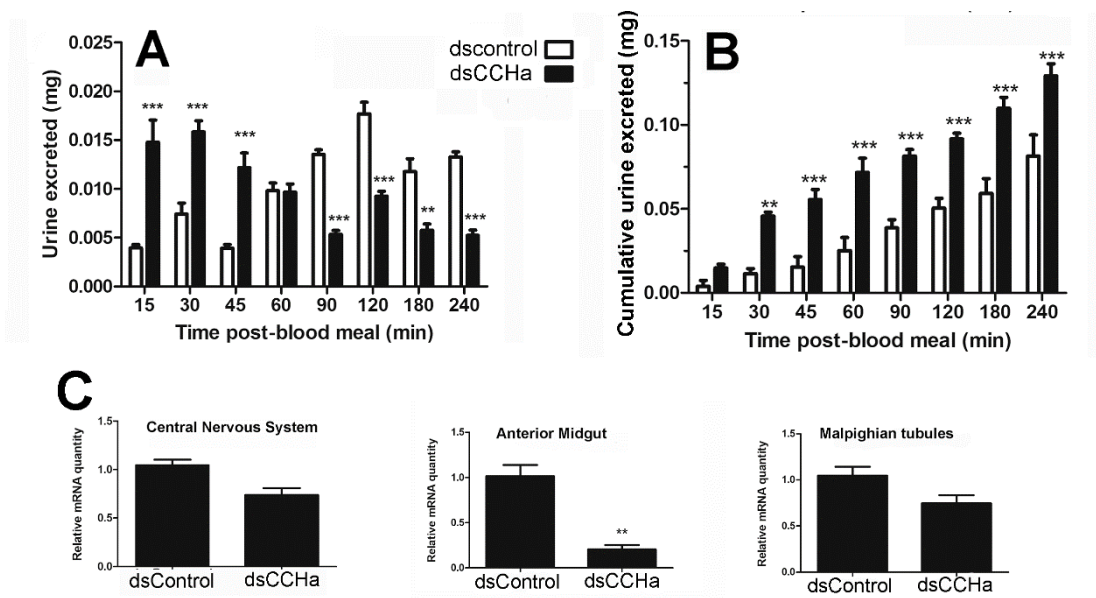


Figure 2: dsCCHA injection stimulates urine excretion by *R. prolixus*. A) Milligrams of urine excreted at different time points post-blood intake in dsControl (n=25) and dsCCHA (n=44) injected insects. Each data represents the mean \pm standard error. Two-way ANOVA with repeated measures, Tukey test was used for post-hoc comparisons. *=p<0.05; **=p<0.01; ***=p<0.001. B) Cumulative volume excreted for the dsControl (n=25) and dsCCHA (n=44) groups. Each data represents the mean \pm standard error. Two-way ANOVA with repeated measures, Tukey test was used for post-hoc comparisons. **=p<0.01, ***=p<0.001. C) Effect of dsCCHA injection on the mRNA levels of *RboprCCHamide2* in the Anterior Midgut, Central Nervous System and Malpighian tubules (n=5). **=p <0.01 Student's t-test.

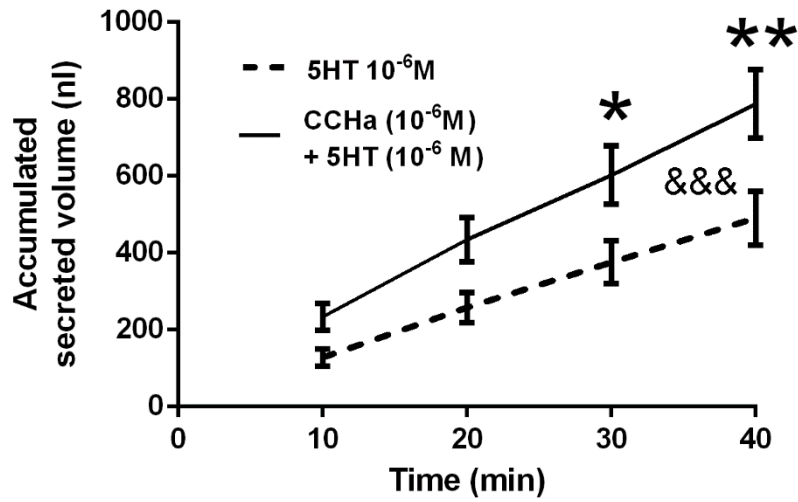


Figure 3: Malpighian tubules secretion volume at different times after stimulation with serotonin (1 μ M) in tubules incubated in saline solution (n=47) or synthetic *Rhopr*CCHa (1 μ M) (n=37). *= $p < 0.05$; **= $p < 0.01$. Two-ways ANOVA with repeated measures followed by Bonferroni's contrasts. Secretion rate slopes in both experimental groups are significant different (&&&= $p < 0.001$, linear regression analysis).

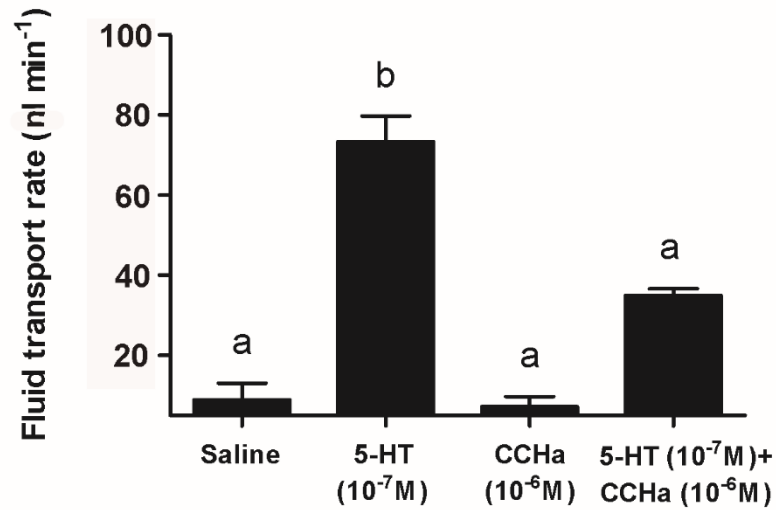


Figure 4: Effect of *RhoprCCHamide* on the fluid transport rate in the anterior midgut of 5th instar *R. prolixus*. The tissue was incubated with either saline (n=8), serotonin 0.1 μ M (n=10), *RhoprCCHa2* 1 μ M (n=11) and serotonin 0.1 μ M + *RhoprCCHa2* 0.1 μ M (n=11). Different letters indicate significant differences (One-way ANOVA, Tukey-Kramer contrasts, $p < 0.05$).