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RESEARCH ARTICLE

Under-Expression of Chemosensory Genes in Domiciliary Bugs of the Chagas Disease Vector Triatoma brasiliensis

Axelle Marchant1,2, Florence Mougel1,2, Emmanuelle Jacquin-Joly3, Jane Costa4, Carlos Eduardo Almeida5,6, Myriam Harry1,2*

1 UMR Evolution, Génomes, Comportement, Ecologie, CNRS-IRD- Univ. Paris-Sud, Université Paris Saclay, Campus CNRS, Gif-sur-Yvette – France, 2 UFR Sciences, Université Paris Sud, Orsay, France, 3 INRA, UMR 1392, Institut d’Ecologie et des Sciences de l’Environnement de Paris, Route de Saint Cyr, Versailles, France, 4 Laboratório de Biodiversidade Entomológica; Instituto Oswaldo Cruz - Fiocruz; Rio de Janeiro; Brasil Instituto Oswaldo Cruz, Fiocruz – Brazil, 5 Universidade Estadual de Campinas (Uncamp), Campinas São Paulo – Brazil, 6 Universidade Federal da Paraíba (UFPB), Paraíba – Brazil

* myriam.harry@egce.cnrs-gif.fr, myriam.harry@u-psud.fr

Abstract

Background

In Latin America, the bloodsucking bugs Triatominae are vectors of Trypanosoma cruzi, the parasite that causes Chagas disease. Chemical elimination programs have been launched to control Chagas disease vectors. However, the disease persists because native vectors from sylvatic habitats are able to (re)colonize houses—a process called domiciliation. Triatoma brasiliensis is one example. Because the chemosensory system allows insects to interact with their environment and plays a key role in insect adaption, we conducted a descriptive and comparative study of the chemosensory transcriptome of T. brasiliensis samples from different ecotopes.

Methodology/Principal Finding

In a reference transcriptome built using de novo assembly, we found transcripts encoding 27 odorant-binding proteins (OBPs), 17 chemosensory proteins (CSPs), 3 odorant receptors (ORs), 5 transient receptor potential channel (TRPs), 1 sensory neuron membrane protein (SNMPs), 25 takeout proteins, 72 cytochrome P450s, 5 gluthatione S-transferases, and 49 cuticular proteins. Using protein phylogenies, we showed that most of the OBPs and CSPs for T. brasiliensis had well supported orthologs in the kissing bug Rhodnius prolixus. We also showed a higher number of these genes within the bloodsucking bugs and more generally within all Hemipterans compared to the other species in the super-order Paraneoptera. Using both DESeq2 and EdgeR software, we performed differential expression analyses between samples of T. brasiliensis, taking into account their environment (sylvatic, peridomiciliary and domiciliary) and sex. We also searched clusters of co-expressed contigs using HTSCluster. Among differentially expressed (DE) contigs, most were under-expressed in the chemosensory organs of the domiciliary bugs compared to
the other samples and in females compared to males. We clearly identified DE genes that play a role in the chemosensory system.

**Conclusion/Significance**

Chemosensory genes could be good candidates for genes that contribute to adaptation or plastic rearrangement to an anthropogenic system. The domiciliary environment probably includes less diversity of xenobiotics and probably has more stable abiotic parameters than do sylvatic and peridomiciliary environments. This could explain why both detoxification and cuticle protein genes are less expressed in domiciliary bugs. Understanding the molecular basis for how vectors adapt to human dwellings may reveal new tools to control disease vectors; for example, by disrupting chemical communication.

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**Author Summary**

In Latin America, bloodsucking bugs are vectors of *Trypanosoma cruzi*, the parasite that causes Chagas disease, which is one of the most important public health problems for rural human populations. Though chemical control campaigns have been effective against vectors, the disease persists because native vectors from natural habitats have been able to recolonize human habitations. This is the case of *Triatoma brasiliensis*. Its capacity to adapt to a new habitat could be linked to changes in the number and/or the expression of chemosensory system genes, particularly those encoding odorant-binding proteins (OBPs) and chemosensory proteins (CSPs), which are important for detecting odor stimuli. This study looks at the chemosensory system of Triatominae in an attempt to document the adaptation process and the domiciliation of disease vectors. We used RNAseq to annotate chemosensory genes and to evidence differential gene expression in *T. brasiliensis* samples from different habitats.

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**Introduction**

Chagas disease is a potentially fatal parasitic disease caused by *Trypanosoma cruzi*, an endemic kinetoplastida that has infected five million people in Latin America [1] and is transmitted by blood-sucking bugs (Hemiptera, Reduviidae, Triatominae). Chemical control campaigns against Chagas disease vectors have considerably reduced its prevalence in recent decades by eliminating populations of the most common vector species in human habitats. Vector transmission by *Triatoma infestans*, a non-native vector introduced from Bolivia, has been officially interrupted in Brazil [2] and the same achievement has been obtained for *Rhodnius prolixus* in parts of the Andean Pact and Central America [3,4]. But, there were some endemic states in Brazilian Northeastern where *T. infestans* has never reached, as it is the case of Paraiba (PB), Ceara (CE) and Rio Grande do Norte (RN) [5]. In this region, autochthonous vectors are present, including *T. brasiliensis*, that is the predominant species found inside domiciles. His involvement in the hyperendemic transmission foci of Chagas disease in RN is pointed out since Lucena's works in 1970 [6], that is before *T. infestans* elimination. However, since the strictly intradomiciliary *T. infestans* vector is eliminated, investment in vector control and surveillance has decreased in Brazil. Furthermore other triatomine specie—like *T. brasiliensis*—have been able to expand and colonize domiciliary and peridomiciliary environments from
sylvatic ones [5,7–10]. We have a critical need to understand how vectors adapt to human environments—a process called domiciliation—to control the spread of Chagas disease. The domiciliation process is considered as a gradual process that may have been happening to many species, and it was taken as one of the main scientific challenges for the next decades related to vector surveillance [4].

The insect chemosensory system plays a key role in ecological adaptation to new or changing hosts or habitats [11]. At the molecular level, chemical recognition depends on the activation of specific sets of genes, including genes encoding odorant-binding proteins (OBPs), chemosensory proteins (CSPs), olfactory receptors (ORs) and gustatory receptors (GRs) (reviewed in [12]). OBPs and CSPs are soluble, secreted proteins that appear to play a role in ligand binding and transport to membrane receptors. ORs and GRs recognize specific ligands and transform the chemical signal into an electrical signal that will be transmitted to the brain, leading to the insect response [13–15]. Insect OBPs [16], ORs [17] and GRs [18] evolve rapidly via gene duplication/loss events, in parallel with adaptation to new ecological niches. Changes in olfactory sensitivity can be driven by these gain and loss events but also by intragenic mutations [19] or variation in gene expression [20].

The insect odorant landscape also includes pheromones—some crucial for mating [21], as demonstrated for T. brasiliensis [22]. The expression of transport proteins of these specific odorants may therefore differ between sexes [23–28]. When their environment changes, organisms respond by tuning gene expression. Rapid response to a brief, stressful event can persist as a long-term adaptation to a selective pressure [29]. A change in gene expression is a major component of genetic modulation in phenotypic evolution [30]. New generations of sequencing have considerably expanded opportunities to explore transcriptomes of non-model organisms using RNA-seq. This revolutionary tool provides unprecedented precision in the measurement of transcript levels [31].

The aim of the present study was to detect differentially expressed genes that play a role in the domiciliation process and sexual behavior of T. brasiliensis bugs sampled in different ecotopes (sylvatic, peridomiciliary, domiciliary). We first evaluated the diversity of OBPs and CSPs through the analyses of a T. brasiliensis reference transcriptome [32] and compared this diversity within the super-order Paraneoptera by building protein phylogenetic trees. We then evaluated contigs that were significantly differentially expressed (DE) in different environmental conditions and searched for contig clusters that show similar expression patterns using HTSCluster. We evidenced genes significantly differentially expressed between sexes and ecotopes including genes belonging to the chemosensory system (especially OBP and CSP genes), genes encoding takeout proteins involved in adult feeding and male courtship behavior, or genes encoding for proteins involved in detoxification or in preventing toxins from penetrating the cuticle.

Materials and methods

Sampling, RNA extraction and sequencing

T. brasiliensis individuals were collected in March 2011 in Caicó city, Rio Grande do Norte, Brazil (from 06 23 12.6 to 06 41 58.0 S and 37 04 47.3 to 37 12 08.0 W; Table 1), within the Caatinga ecoregion [33]: i) domiciliary bugs were sampled in various localities (B, J, P, R, T, U) in the indoor spaces of homes where triatomines are generally found in the crevices of mud walls, in furniture and under beds; ii) peridomiciliary bugs was sampled in the D locality in areas outside and within approximately 100 m of homes, where domesticated animals sleep or are maintained, namely in our study in henhouses; and iii) sylvatic bugs were sampled in sylvatic areas (A, C) in the Environmental Conserved Area (ECA) of Caicó that is under the supervision of
military guards. The maximal linear distance is about 36 kms (between B and R, T, U), and the minimal linear distance is between A and C (about 1.5 km). Domiciliary and peridomiliary samples were collected in the daytime; sylvatic samples were collected at night but all were sacrificed at the same time. We obtained permission from house owners/residents to collect insects from all homes and properties.

For the domiciliary bugs, they were merged in a single sample named B-U. For all samples (B-U, D, A, C), only adults were used and separated according to sex. The heads were placed in RNAlater solution (Thermo Fisher Scientific) for RNA extractions. The body were placed in absolute ethanol for DNA extractions for population genetics studies and blood meal determination using molecular markers performed in [33]. For the all samples the nutritional status was determined as follows: if the molecular blood meal determination was not possible due to too little blood in its digestive tracts, the individual was considered as starved. For the sample A, 22% of the individuals were not starved, 44.5% for B-U, 80% for C and 41% for D. No major difference is notified between the nutritional status of males and females.

To target expressed chemosensory genes, we extracted RNA from the antennae and rostrum using the TRIzol Reagent kit (Invitrogen, Carlsbad, CA, USA). We pooled 4 to 15 individuals of the same sex and from the same sample to ensure there was enough RNA for sequencing and to measure average gene expression in a sample. We made technical replicates for samples with enough RNA (see details in Table 2). We sampled two biological replicates per sex for the sylvatic condition (SFA and SFC for females; SMA and SMC for males). Fourteen libraries were constructed using TruSeq RNA Kit 2010 from Illumina, and sequenced with the Illumina HiSeq 2000 method in single-reads of 100 bp on the LGC Genomics platform GmbH (Berlin, Germany).

The number of reads obtained for each sample, replicate and run is reported in the Table 2.

De novo assembly of the reference transcriptome
We assembled the reference transcriptome from datasets consisting of one chemosensory library of a sylvatic female sequenced via Illumina paired-end and of eight chemosensory libraries from the males and females of the four samples described above pooled and sequenced.

| Geographic index | Locality             | Environment | Geographic coord. (S/W) | Female NS/T(%) NS | Male NS/T(%) NS | Total pop NS/T(%) NS |
|------------------|----------------------|-------------|-------------------------|-------------------|-----------------|----------------------|
| B                | São João do Sabugi   | D           | 06 41 58.0 / 37 10 22.6 | 2/3 (66)          | 2/3 (66)        | 4/6 (66)             |
| J                | Caicó/downtown       | D           | 06 28 24.5 / 37 05 25.9 | 1/2 (50)          | 1/2 (50)        | 2/4 (50)             |
| P                | São Fernando         | D           | 06 23 12.6 / 37 12 08.0 | 0/1 (0)           | 0/1 (0)         | 0/1 (0)              |
| R                | Caicó/Sino           | D           | 06 32 30.6 / 37 04 47.3 | 0/1 (0)           | 0/1 (0)         | 0/1 (0)              |
| T                | São Fernando         | D           | 06 23 16.1 / 37 12 04.1 | 1/1 (100)         | 0/1 (0)         | 0/2 (0)              |
| U                | São Fernando         | D           | 06 23 16.1 / 37 12 04.1 | 0/1 (0)           | 0/2 (0)         | 0/3 (0)              |
| B-U              |                      | D           | 06 23 12.6 to 06 41 58.0 / 37 12 08.0 | 2/4 (50)          | 2/5 (40)        | 4/9 (44.5)           |
| D                | Caicó/Sino           | P           | 06 32 23.4 / 37 05 00.0 | 2/6 (33.5)        | 5/11 (45.5)     | 7/17 (41)            |
| A                | Caicó/EPA            | S           | 06 28 25.0 / 37 05 21.4 | 2/6 (25)          | 2/10 (20)       | 4/16 (22)            |
| C                | Caicó/EPA            | S           | 06 28 21.6 / 37 05 12.5 | 3/4 (75)          | 12/15 (80)      | 15/19 (80)           |

Geographic index, locality, environment (with D = domiciliary, P = peridomiliary, S = sylvatic) and geographic coordinates are provided; the number of not starved (NS) individuals / the total number of individuals is given per sex and per sample. The percentage of not starved individuals is in brackets.

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with 454 technology. We followed the procedure 10c published in a previous study [32] with the following modifications: we cleaned paired-ends using prinseq version 0.20.4 [34] and we added the step of selecting the longest isoform per transcript cluster (as defined in Trinity) from the Trinity output.

Transcriptome completeness was assessed using the CEGMA (Core Eukaryotic Genes Mapping Approach) pipeline that searches for the presence of sequences belonging to a set of ultra-conserved eukaryotic proteins [35].

Annotation

We look at contigs that encode for a set of proteins of interest (CSPs, OBPs, ORs, ionotropic receptors (IRs), gustatory receptors (GRs), transient receptor potential channels (TRPs), sensory neuron membrane proteins (SNMPs), takeout proteins, cytochrome P450, glutathione S-transferases, cuticular proteins) in the reference transcriptome. We queried insect amino acid sequences retrieved from GenBank against our reference transcriptome using Tblastn searches with an e-value threshold of $10^{-6}$. The selected contigs were aligned to the non-redundant protein database (Blastx with an e-value threshold of $10^{-6}$). Only contigs with at least one protein match from the families cited above were kept.

For the OBP and CSP protein families, contigs were translated and checked for the following: conservation of 6 (OBPs) and 4 (CSPs) cystein positions, the presence of $\alpha$ helices using PSIPRED [36], and the presence of a signal peptide using SignalP [37]. The OBP/CSP protein repertoires of T. brasiliensis were compared to those translated from genomes of several Para- neoptera: 27 OBPs and 19 CSPs from the triatome R. prolixus [12,38], 5 OBPs and 8 CSPs from the louse Pediculus humanus [39] and 19 OBPs and 13 CSPs from the pea aphid Acyrthosiphon pisum [40]. We added translated sequences from ESTs of two bugs from the Miridae family:

### Table 2. T. brasiliensis sample details and summary of RNAseq data.

| Sample name | Environment | Sex | No. of individuals | No. of adapter-filtered reads | No. of mapped reads |
|-------------|-------------|-----|--------------------|------------------------------|---------------------|
|             |             |     |                    | Run1 Run2 Total | Run1 Run2 Total | Percentage reads mapped/ total | Max counts (%) |
| DFB-U       | D           | F   | 4                  | 9,210,196 13,482,702 22,692,898 | 1,391,136 1,985,127 3,376,263 | 14.88 28.41 |
| DMB-U1      | D           | M   | 5                  | 13,945,801 29,820,509 87,001,857 | 4,198,630 9,667,151 24,653,737 | 30.41 38.81 |
| DMB-U2      | D           | M   | 5                  | 24,053,273 19,182,274 6,852,782 5,735,174 | 2,728,046 6,627,049 17,319,989 | 38.36 13.51 |
| PFD1        | P           | F   | 6                  | 7,024,781 15,993,588 45,152,589 | 2,728,046 6,627,049 17,319,989 | 38.36 13.51 |
| PFD2        | P           | F   | 6                  | 10,559,081 11,575,139 21,934,219 | 3,691,981 4,272,913 7,964,904 | 30.37 34.49 |
| PMD         | P           | M   | 11                 | 1,851,110 4,771,764 6,622,874 550,846 1,460,386 2,011,232 | 30.37 34.49 |
| SFA1        | S           | F   | 8                  | 5,122,662 20,488,218 48,421,974 | 1,849,122 7,924,973 16,626,180 | 34.34 22.21 |
| SFA2        | S           | F   | 8                  | 7,782,766 15,028,099 22,810,865 | 2,229,032 4,623,053 6,842,085 | 32.71 28.78 |
| SMA1        | S           | M   | 10                 | 25,231,786 33,195,444 58,427,230 | 9,460,295 1,285,816 10,746,111 | 28.87 |
| SMA2        | S           | M   | 10                 | 24,253,202 22,040,623 46,293,825 | 8,847,900 8,254,894 17,092,794 | 37.21 28.78 |
| SFC1        | S           | F   | 4                  | 31,123,710 40,633,951 71,757,661 94,201,052 | 5,794,452 7,943,048 13,737,499 | 17.94 20.88 |
| SFC2        | S           | F   | 4                  | 3,421,756 19,021,635 22,443,391 | 494,700 2,666,499 3,161,199 | 20.88 |
| SMC1        | S           | M   | 15                 | 13,953,748 21,062,918 34,016,666 46,892,268 | 4,876,329 8,285,962 13,162,292 | 40.91 46.26 |
| SMC2        | S           | M   | 15                 | 4,593,481 7,282,121 11,875,602 | 2,260,114 3,759,468 5,519,582 | 34.34 22.21 |

For sample names we used: the environment (D = domiciliary, P = peridomicular or S = sylvatic); the sex (M = male or F = female); and the geographic index (B-U, D, A, C). The number at the end of the sample names indicate technical replicate number (no technical replicate was performed for DFB-U and PMD). RNA was extracted from antennae and rostra, sequenced in Illumina single-reads and mapped on the reference transcriptome. Number of filtered reads and number of mapped reads per sample are indicated. The Max_counts represents the percentage of reads mapped in the most expressed contigs.

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13 OBP and 8 CSP sequences from *Adelphocoris lineolatus* [41–43] and 16 OBP and 12 CSP sequences from *Apolygus lucorum* [44–46]. Signal peptides were deleted before alignment using MAFFT version 7 [47] with the following options: E-INS-I with the BLOSUM62 scoring matrix and offset 0.1. We inspected the alignment by eye with BioEdit [48] and removed major gaps or sequences that were too short. We used ProtTest v3.2 [49] to predict the best-fit models for protein evolution. The LG model with estimated Gamma parameter was retained. The tree was built with PhyML v3.0 [50] with 100 bootstrap replicates and represented using iTOL web server [51].

**Mapping and counts**

Much less RNA was extracted from the PMD sample than from others, resulting in a poor quality cDNA library. Consequently, this sample was excluded from the differential expression analysis and clustering study. Reads from other samples were mapped to the reference transcriptome after removing sequence adapters using BWA with default options [52]. Though we selected only one isoform per “gene” (the isoform states were assigned by Trinity), isoforms remained in our reference transcriptome. To avoid a resulting bias in our count analysis, we excluded reads with multiple hits. Count tables of reads were performed for each sample using SAMtools [53]. To evaluate the variation between technical replicates and sequencing runs, we proceeded to an ACP based on normalized counts with a rlog function of DESseq2. The ACP revealed high similarity between runs and technical replicates (S1 Fig) allowing them to be pooled in the subsequent analyses.

**Differential expression analysis**

Two different statistical methods were used for differential expression analysis: DESeq2 package v. 1.6.3 [54] and EdgeR v. 3.8.5 [55]. For both packages, we filtered contigs with a low coverage using HTSfilter [56]. We used the DESeq normalization method and a threshold of five mapped reads on average. DESeq2 automatically evaluates normalization and dispersion but we turned off the independent filtering. We chose the RLE model for normalization and a robust estimation method to evaluate dispersion with EdgeR. In both cases, count data was modeled with a negative binomial distribution in a Generalized Linear Models (GLM) with two factors: environment and sex. For both methods, we controlled the factor "sex" when testing the factor "environment". We compared the differential expression for the three modalities (sylvatic, peridomiciliary, domiciliary) of the "environment" factor and for the two modalities (male, female) of the "sex" factor. Our two-factor model (sex and environment) allowed R packages to assess changes that would be due to one or the other factor despite the absence of biological replicates per sex for domiciliary and peridomiciliary conditions. We applied the Benjamini-Hochberg correction [57] for multiple tests. The contigs were considered to be differentially expressed (DE) when the Padj was below 0.05. We selected contigs that were differentially expressed with both the EdgeR and DESeq2 methods. These contigs were annotated using blastx (BLAST 2.2.29+) with the non-redundant protein database (version May 2015) and we selected only the best matches that had an e-value below 10^{-6}. The heatmap was built from chemosensory contig expression with DESeq2.

**Gene clustering based on transcriptomic data**

Clusters of co-expressed contigs were searched using HTSCluster [58]. This R package implements a Poisson mixture model to cluster expression observations. Despite the use of TMM normalization, HTSCluster is sensitive to library size. The sample DFB-U was excluded from the analysis because of the lack of a technical replicate for this sample otherwise there would
have been one quarter fewer reads mapped than other samples for which technical replicates were collapsed. The count table was first filtered to remove contigs with a normalized average below 5. We selected the slope heuristic DDSE method.

Results

Reference transcriptome

We selected only the biggest isoforms from Trinity "genes" using the assembly 10c workflow established by [32], and obtained a reference transcriptome of 48,290 contigs with an N50 of around 1,160 bp and a total length of 56,014,905 bp. The transcriptome appeared to be quite complete, with a CEGMA value of 94.35%. Males and females sampled from several samples were pooled to generate the 454 sequencing data so that the reference transcriptome represented all environmental conditions and sexes.

Annotation in reference transcriptome

We obtained 25 and 16 contigs annotated as CSPs and OBPs (S1 Table) in the T. brasiliensis transcriptome. All CSP deduced proteins showed α helices, a signal peptide and four aligned cysteins (except for TbraCSP16). OBP proteins were less conserved. Nevertheless, the majority showed α helices, a signal peptide, and six aligned cysteins. All OBP and CSP contigs presented mapped reads in all samples (except for TbraOBP12 in the SMC sample), suggesting they are expressed in both sexes and under all environmental conditions.

Some R. prolixus proteins, have no tangible orthologs deduced from the T. brasiliensis chemosensory transcriptome (= RproCSP6, RproCSP9, RproCSP18, RproOBP5, RproOBP7, RproOBP8, RproOBP15, RproOBP16, RproOBP19, RproOBP25; Fig 1a and 1b). In the same way, no R. prolixus orthologs were found for two T. brasiliensis deduced proteins (= TbraOBP5 and TbraOBP7; Fig 1a and 1b). However, most of the OBPs and CSPs from T. brasiliensis have well supported orthologs deduced from the R. prolixus genome (for examples, several orthology relationships could be observed in CSP tree: RproCSP1 and TbraCSP1; RproCSP16 and TbraCSP16; RproCSP17 and TbraCSP6). Several OBPs and CSPs of T. brasiliensis are grouped with a single R. prolixus protein (for example, TbraOBP23 and TbraOBP24 were clustered with RproOBP24, see clades joined with a brace in Fig 1a and 1b). These proteins could be paralogs that arose from gene duplication specific to T. brasiliensis. In other cases, several transcripts of T. brasiliensis are grouped with several deduced proteins of R. prolixus (for example, TbraCSP3 and 4 were close to RproCSP3 and 4, two paralogs of R. prolixus). These proteins could be orthologs that arose from gene duplication in recent common ancestry of Triatominae. In such hypothesis (paralogy), each contig is supposed to represent a specific gene. However, as the T. brasiliensis chemosensory transcriptome was built from RNA pooled from several individuals, these proteins could also be encoded by allelic variants or isoforms from the same gene. Under these allelic or isoform hypothesis, all clustered contigs derive from the same gene. Therefore, the numbers of OBP/CSP genes expressed in antennae and rostra vary from 25 to 19 OBPs and 16 to 14 CSPs, depending on the hypothesis (paralogs versus alleles/isoforms). Hereafter, with the aim to limit overestimation of OBP/CSP gene numbers based on RNAseq database, we will only reference the lower and more stringent estimate of gene numbers (allelic/isoform hypothesis).

Because some OBP/CSP genes may not be expressed in selected tissues or stage used for samples, we can have underestimated the number of these gene in species from which only RNA data was available (T. brasiliensis, A. lucorum and A. lineolutus) compared to species from which genomic data was used (R. prolixus, A. pisum and P. humanus). Despite this underestimation, a higher number of OBPs and CSPs can be observed in the phylogeny of bloodsucking bugs (see pink blocks, Fig 1a and 1b) and more generally in Hemiptera (purple empty
block, Fig 1a and 1b) compared to the other species of Paraneoptera. Enlarged genomic sample of Paraneoptera species would be required to validate this preliminary observation to infer genome evolution scenarios. Only 3 contigs encoding for odorant receptors (ORs), could be annotated comprising one Co-odorant receptor (Co-OR; S2 Table). Except Co-OR, ORs are poorly expressed compared to other chemosensory genes. Consequently, too few reads are sequenced from ORs transcripts to be de novo assembled explaining the low number of contigs annotated as ORs. Probably for the same reason, we didn't found any ionotropic receptors (IRs) and gustatory receptors (GRs). We also annotated contigs that encode for the following proteins: transient receptor potential channels (TRPs) indispensable for the perception of the environment (n = 5); sensory neuron membrane proteins (SNMPs) potentially involved in detection of pheromones (n = 1); takeout proteins involved in the integration of processes related to circadian rhythm, in feeding-relevant activities and in male courtship behavior (n = 25); proteins involved in protection against toxin penetration or in detoxification-like cuticle proteins (n = 49); cytochrome P450s (n = 72); and glutathione S-transferases (n = 5) (S2 Table).

**Sequencing, mapping and counts**

The sequencing depth varied a lot between samples: from 22,692,898 (DFB-U) to 94,201,052 reads (SFC), excluding the cDNA library of the PMD sample (Table 2). The library size (total...
number of mapped reads) which depends both on sequencing depth and on the percentage of mapped reads, also varied between samples. For example, only 14.88% of DFB-U reads were mapped compared to 40.91% of SMC. Overall, the library size included between 3,376,263 and 27,848,905 mapped reads.

Most of the mapped reads were captured by very few genes, which is quite common in RNAseq analysis. The maximum percent of reads mapped to a single contig varied from 13.51% (PFD) to 46.26% (SMC) (Table 2). The most expressed contig was the same in all samples except DFB-U. It was associated by blast with a putative uncharacterized protein (gi:133916482) of the immune-related transcriptome of *Thermobia domestica* [59].

**Differential expression analysis**

We used both DESeq2 and EdgeR software, which differ in dispersion estimation methods (see Fig 2 for DESeq2). For both software, dispersion decreases when expression increases, which is typical for RNAseq data among biological replicates. We used a two-factor general linear model (GLM) with both packages, allowing differential analysis despite the lack of biological replicates for some conditions. DESeq2 and EdgeR presented similar *p*-value distributions for all but the comparison between the sylvatic and peridomiciliary habitats. The peak was close to 0, corresponding to differentially expressed contigs between modalities and a uniform distribution for larger *p*-values, indicating a good fit to models generated by both types of software (Fig 3). However, the number of DE contigs differed between the two types of software. To increase the reliability of our results, we selected contigs in which we found DE with both EdgeR and DESeq2 (Table 3). We found numerous DE contigs (n = 148) between males and females (Table 3). More DE contigs (n = 3875) were found between peridomiciliary and domiciliary samples than between sylvatic and domiciliary samples (n = 29) and between sylvatic

![Fig 2. Dispersion estimates from DESeq2 and gene count measures between samples.](doi:10.1371/journal.pntd.0005067.g002)
and peridomiciliary samples (n = 29). Among DE contigs, most were over-expressed in the chemosensory organs of the peridomiciliary bugs, while they were mainly under-expressed in those of the domiciliary bugs.

Annotation of differentially expressed genes

We were only able to annotate 50% of the DE contigs with the non-redundant proteins database. Three CSPs (CSP14, 15 and 16) and one OBP (OBP4) were differentially expressed between sexes, and all were over-expressed in males. A significant proportion of OBP and CSP contigs were differentially expressed between environments, particularly in the
peridomiciliary-domiciliary comparison (S2 Table). Most were under-expressed in the domiciliary samples. However, no expression difference was observed for contigs annotated as ORs. We used a heatmap to compare chemosensory contig expression (Fig 4), revealing two distinct groups: one merged sylvatic and peridomiciliary samples and the other merged domiciliary samples plus the sylvatic SFC sample. The similarity between gene expression in domiciliary samples and this peculiar sylvatic sample could explain why few DE contigs were detected in the sylvatic versus domiciliary comparison.

Among differentially expressed contigs, we also found contigs that encode TRPs (n = 3), SNMP (n = 1), takeout proteins (n = 16), cytochrome P450s (n = 38), glutathione S-transferases (n = 3) and cuticle proteins (n = 22) (S2 Table). These genes were under-expressed in females compared to males and in domiciliary samples compared to peridomiciliary and sylvatic ones. However, some cuticle proteins were over-expressed in peridomiciliary samples compared to sylvatic ones.

Gene Clustering

We selected the slope heuristic DDSE methods from HTSCluster to estimate the number of clusters because BIC and ICL did not converge. We detected 24 clusters containing 28 to 14,385 contigs per cluster. Most contigs were reliably classified in a cluster with a maximum conditional probability close to 1 (Fig 5a). The quality of this classification, however, varied between clusters (Fig 5b). For example, only 21.65% of the contigs were classified in cluster 15 with a maximum conditional probability greater than 0.9, while 91.35% of contigs were classified in cluster 5 with the same probability. Clustering results agreed globally with results obtained from the differential expression study. For example, clusters 12 and 14 were made up primarily of contigs that were under-expressed in the domiciliary environment (Fig 6). Most contigs belonging to clusters 12 and 14 were significantly under-expressed in domiciliary/sylvatic or domiciliary/peridomiciliary comparisons with both DESeq2 and EdgeR.

Interestingly, clustering results may also provide more subtleties. For example, DE analysis revealed very few contigs that were over-expressed in females and in domiciliary samples. Nevertheless, clustering analysis revealed that contigs in clusters 3 and 20 showed higher expression in sylvatic females compared to all other samples (Fig 3). Similarly, contigs in clusters 1, 5, 7, 13 and 23 showed higher expression in the domiciliary sample than in the sylvatic/peridomiciliary samples (Fig 3). This apparent discrepancy may have arisen because over expression

| Condition comparisons | DESeq2 | EdgeR | Found in both DESeq2 and EdgeR |
|-----------------------|--------|-------|--------------------------------|
|                       | +      | -     | total | +      | -     | total | genes of interest |
| M/F                   | 148    | 4     | 152   | 1537   | 636   | 2173   | 144    | 4     | 148 |
|                       |        |       |       | +      | -     | total | 2 CSPs; 1 OBPs; 3 TOs; 3 P450s; 14 CPs |
| S/P                   | 5      | 26    | 31    | 20     | 383   | 403    | 3      | 26    | 29  |
|                       |        |       |       | +      | -     | total | 2 CPs |
| D/S                   | 11     | 292   | 303   | 2      | 30    | 32     | 2      | 27    | 29  |
|                       |        |       |       | +      | -     | total | 3 OBPs; 4 P450s |
| D/P                   | 19     | 4062  | 4081  | 427    | 5756  | 7183   | 16     | 3859  | 3875 |
|                       |        |       |       | +      | -     | total | 13 CSPs; 17 OBPs; 14 TOs; 3 TRPs; 1 SNMP; 16 CPs; 3 GSTs; 37 P450s |

Results are indicated for DESeq2 and EdgeR. We selected contigs that both packages identified as differentially expressed. “+” indicates number of over-expressed contigs in the first modality listed in each condition comparison (example, 148 contigs are found as over-expressed in males compared to females using DESeq2). “-” indicates the number of under-expressed contigs. We annotated differentially expressed contigs found in both DESeq2 and EdgeR and we indicated the number of transcripts encoding odorant-binding proteins (OBPs), chemosensory proteins (CSPs), takeout proteins (TOs), transient receptor potential channels (TRPs), sensory neuron membrane protein (SNMP), cuticular proteins (CPs), glutathione S-transferases (GSTs) and Cytochrome P450 (P450s). D = domiciliary, P = peridomiciliary and S = sylvatic; M = male and F = female.

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was too slight to be detected in the DE study. Joint analysis of several contigs with similar expression patterns would help to detect if this were the case. However, contigs with similar patterns of DE between modalities may be split into several clusters based on estimates of their expression pattern distribution. For example, this was the case for *TbraOBP23* and *TbraOBP24*,

**Fig 4.** Heatmaps showing the sample distance of the expression data of differentially expressed OBP/CSP contigs (DESeq2).

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which have very similar sequences (grouped with *Rhodnius prolixus* OBP24 in the phylogenetic tree) and are both over-expressed in the peridomestic sample compared to the domiciliary sample. They were, however, allocated to clusters 10 and 19, respectively. Similar conclusions can be drawn for *TbraCSP3* and *TbraCSP4*.

Unfortunately, we were not able to test gene ontology enrichment of the cluster because of the low proportion of the transcriptome annotated (*T. brasiliensis* is quite distant from *R. prolixus* for which a reference genome is available).

**Discussion**

In Brazil, *T. brasiliensis* is the main concern for re-emerging hyperendemic foci of Chagas disease in semi-arid zones because this vector is found in a variety of ecotopes, namely g sylvatic, peridomestic and domestic ones. In this last environment *T. brasiliensis* is included in a restrict list of Brazilian native domiciliated species, along with *P. megistus*, *T. pseudomaculata* and *T. sordida* [5]. Odor stimuli are important in Chagas disease vectors and because there are remarkable distinctions between ecotopes it is expected that their capacity to adapt to a new habitat is linked to changes in chemosensory system genes.

**Reference transcriptome, CSP/OBP annotation**

We estimated at least 19 OBP and 14 CSP genes from the *T. brasiliensis* reference transcriptome. Compared to annotated genes in the *R. prolixus* genome (27 OBPs and 19 CSPs) [38], about 85% of the potential gene repertoire was retrieved from *T. brasiliensis* chemosensory transcriptome. Annotation of *T. brasiliensis* OBP/CSP genes might be incomplete because the transcriptome was performed from antennae and rostrum while some OBPs and CSPs could be specifically expressed in other tissues. Therefore the total number of CSP and OBP genes occurring in the *T. brasiliensis* genome is likely higher than reported here. Interestingly, two *T. brasiliensis* OBPs have no orthologs in the *R. prolixus* genome. As they are clustered with OBPs

**Fig 5.** Histogram (a) of maximum conditional probabilities of cluster membership for all genes and (b) Boxplots of maximum conditional probabilities that genes assigned to each cluster (HTSCluster) are actually a member of that cluster. doi:10.1371/journal.pntd.0005067.g005
from other species \((A. lucorum\) and \(P. humanus\)), these copies could have been lost secondarily in \(R. prolixus\).

Our results confirm the hypothesis that bloodsucking bugs have more \(OBP\) and \(CSP\) genes than other Paraneoptera, especially \(A. pisum\) (19 \(OBPs\) and 13 \(CSPs\)) and \(P. humanus\) (5 \(OBPs\) and 8 \(CSPs\)). How specialized a species is could be linked to how many \(OBP\) and \(CSP\) genes it has. The insect chemosensory genes are known to have evolved rapidly via gene duplication or loss events, in parallel with adaptation to new ecological niches \([15–17,60,61]\). The stable environment that results from a host-dependent lifestyle could explain why \(A. pisum\) and \(P. humanus\) have fewer \(OBP\) and \(CSP\) genes \([39,40]\). Two hypotheses might explain the \(OBP\) and \(CSP\) expansions in Chagas disease vectors that may be related to i) recruitment for a derived function, and more specifically in relation to hematophagy or ii) new chemosensory functions selected in response to environmental change. Striking similarities between \(OBPs\) and heme-binding proteins—like the occurrence of a signal peptide, six cysteins and a conserved \(PBP\_\text{GOBP}\) domain \([12]\)—support the hypothesis that \(OBP\) and \(CSP\) gene expansion is an
adaptation to hematophagia. Some OBPs could have a derived function in providing protection from oxidative stress by binding the heme from digested blood hemoglobin, like heme-binding proteins [62]. Moreover, some CSPs share an OS-D domain—a chemical characteristic of lipocalins—with proteins encoded by genes found in the salivary transcriptome of another bloodsucking bug, *Triatoma matogrossensis*. Lipocalins are a class of proteins secreted in the saliva of bloodsucking bugs. They serve primarily as carriers of small ligands, and are used to disarm the host hemostatic machinery [63]. Some CSPs may play a similar role [12]. Further studies are needed to explore such derived functions of olfactory/chemosensory proteins in bloodsucking bugs.

In Chagas disease vectors, gene expansion could also reflect a process of selecting new chemosensory functions, providing an evolutionary advantage to individuals able to recognize various odor stimuli. Indeed, Triatominae are associated with diverse habitats, namely vertebrate nests or burrows in sylvatic habitats found in trees, palms, bromeliads or rocks, cracks and crevices in anthropogenic habitats such as corrals, chicken coops or human dwellings. The Triatominae feed on a broad range of vertebrate hosts; 1150 vertebrate host species have been described [64]. For feeding sources detected for *T. brasiliensis* in Caico [33], a species of sylvatic rodent (*Kerodon rupestris*) was prevalent in conserved sylvatic area whereas synantropic (*Galea spixii*) or domestic animals (*Capra hircus* and *Gallus gallus*) were prevalent for anthropogenic systems (peridomestic and domiciliary environments). Thus, the diversity of OBPs and CSPs could be explained as adaptation in blood-sucking insects that live in a putative diversity of ecological niches.

**Differential gene expression**

To maximize support for our results, we selected contigs that the EdgeR and DESeq2 techniques both identified as differentially expressed. Recent studies suggest that EdgeR and DESeq2 R packages are the best statistical methods for normalization and differential expression analysis of multi-factored experiments without a reference genome [58,59,65,66]. They are currently the only methods able to maintain a reasonable false-positive rate without decreasing the power of differentially expressed gene detection. They are stable under different sequencing depths. However, DESeq2 and EdgeR did not provide the same results with our dataset. EdegR found more differentially expressed contigs than did DESeq2. Moreover, EdgeR found a higher log2-fold change than did DESeq2. Nevertheless, RNAseq is a recent technology and statistical research into how best to use differential expression analysis software with this kind of data is ongoing.

Recently, a gene clustering methodology based on transcriptomic data has been developed to highlight co-expressed contigs (HTSCluster, [58]). We found similar results using differential expression analysis and the HTSCluster gene clustering methodology. Furthermore, gene clustering provides additional detail about the dynamics of gene expression, especially for chemosensory contigs. We were able to annotate OBP or CSP contigs with very similar sequences to different clusters that reflect different expression patterns, suggesting they represent recent paralogs or isoforms rather than allelic variants. This could support the idea that these sequences play a role in different functions, for instance they could target different odorant molecules.

**Differential expression between sexes**

We found 148 contigs to be differentially expressed between males and females. These were probably genes involved in sex-specific behavior or sexual dimorphism.

One OBP and three CSPs were all over-expressed in males. Authors proposed that only male *T. brasiliensis* are attracted by sexual signals [22]. OBPs and CSPs that are over-expressed
in males in our study could be involved in this kind of sexually dimorphic behavior. Previous studies of *A. lucorum* and *A. lineolatus*, two species that were included in the phylogenetic tree, showed that most of the OBP s and CSP s are over-expressed in female *A. lucorum* antennae. [45,46] while OBP or CSP over-expression may occur in either males or females in *A. lineolatus* [41–43]. This suggests that expression and function of these proteins vary within Hemiptera.

Three contigs annotated as *takeout* were also over-expressed in males. *Takeout* genes have been shown to affect male courtship [67] and sexual dimorphism in locomotor activity, modulating the circulating juvenile hormone level in *Drosophila melanogaster* [68]. Locomotor activity also varies between sexes in *T. infestans*, where females disperse more than males both by walking [69] and flying [70]. In contrast, dispersal activity seems to be higher in male than in female *T. brasiliensis*: more males than females could be collected when using a flashlight to capture dispersing individuals [71]. Thus, differential courtship or sexual locomotor activity between sexes could explain the over-expression of *takeout* genes observed in *T. brasiliensis*.

We also detected differences between sexes in expression of contigs involved in insecticide resistance, e.g. genes encoding P450 s and cuticle proteins. The *cytochrome P450* gene family is implicated in several functions other than detoxification. For example, in *D. melanogaster*, a *cytochrome P450* (*cyp4d21*) named *sxe1* is differentially expressed between males and females and identified as a circadian-regulated gene involved in male courtship and mating success [72]. Differences in the ratio of cuticular proteins have also been found in the thoracic cuticle of male and female crickets (*Schistocerca gregaria* and *Locusta migratoria*). This difference has been linked to the specific mechanical ability of females to stretch intersegmental membranes [73]. Likewise, six genes that encode cuticular proteins were differentially expressed between the two sexes of *Anopheles gambiae*, which is probably linked to the sex-specific hematophagous behavior in this species [74].

**Differential expression between environments: under-expression of contigs in domiciliary bugs**

Our study revealed numerous differentially expressed genes in the transcriptomes of bugs sampled in different environments. This could either be explained by genetic adaptation to an anthropogenic system or by a phenotypic plasticity due to changes in gene expression induced by local environmental conditions. Whatever the mechanism, as the peridomestic environment is human-modified, and because it is commonly assumed that the direction of re-colonization of homes after insecticide spraying is likely to be from peridomestic to domiciliary environments [75], we expected more similar phenotypes in the domiciliary and peridomestic samples (e.g. under- or over-expression of the same set of genes). But, our comparison of peridomestic against domiciliary samples revealed much more differentially expressed contigs than did a comparison of sylvatic against domiciliary or peridomestic samples. However, our results are congruent with the population genetics and eco-epidemiologic data previously obtained on *T. brasiliensis* populations evidencing that i) the sylvatic and domiciliary cycles are genetically connected, ii) the co-occurrence of two *T. cruzi* strains in sylvatic *T. brasiliensis* population that is also consistent with a link between sylvatic and domiciliary cycles, and iii) the preponderance of *G. spixii* in the *T. brasiliensis* feeding source in peridomestic areas revealing that this rodent is no longer only sylvatic but become a highly synantropic animal [33].

Although domiciliary individuals were sampled in different localities, which could have resulted in expression variability, a difference in gene expression is nevertheless observed, most DE genes were under-expressed in this environment compared to the others, probably reflecting a less variable and more predictable biotope (abiotic and biotic conditions). A single sylvatic sample is probably responsible for the low number of DE genes detected between sylvatic
Expression of chemosensory genes

Contigs annotated as OBPs and CSPs followed the general trend of under-expression in the domiciliary samples. Poor biotic diversity probably led to lower diversity of odorant stimuli in the domiciliary environment than in others. This reduction of stimuli could explain the under-expression of chemosensory genes in domiciliary bugs. Furthermore, several studies have linked chemosensory gene expression to feeding status. In the fly *Glossina morsitans*, transcription of CSP genes was related to host searching behavior [76]. A recent study of bloodsucking bugs [77] revealed that, in *R. prolixus*, some odorant and ionotropic coreceptor genes are less expressed after a blood feeding. Similar results were previously found in *An. gambiae* [78].

Concerning the *T. brasiliensis* samples, their nutritional status was somewhat similar except the sylvatic sample (C) that was the less starved. Thus, the nutritional status of the bugs when they were sacrificed is not the most likely factor to explain the differential expression of the OBP/CPS genes in the domiciliary sample, but it cannot be entirely discarded.

Expression of *takeout* gene families

*Takeout* genes are also expressed in chemosensory organs and have been proposed to be associated with chemo sensory perception in both taste and olfactory systems [79]. Takeout proteins link temporal cycle and feeding status information that are involved in the circadian cycle. They are involved in feeding-related metabolism and behavior [67,80] and in the regulation of locomotor activity during foraging [68]. Seven contigs were described as belonging to the *takeout* gene family in a transcriptome study of the digestive tract of *R. prolixus* [81], but until now no *takeout* genes had been annotated in *Triatoma*. We found a high number of *takeout* genes in *T. brasiliensis* that were differentially expressed according to the environments. The nocturnal activity pattern displayed by adult triatomine bugs is described as generally bimodal with the first peak just after dusk associated with host-seeking activities and the second at dawn, with the search of an appropriate daytime shelter [82–84]. Some authors correlate host searching induced by the nutritional status of the bug with the dispersion process that may lead Chagas disease vectors to colonize domiciliary habitats [71,85,86]. Because the nutritional status of the domiciliary sample is similar to that of two others samples (peridomiciliar and sylvatic A), a lower foraging activity is again more likely, linked to the higher host availability in domiciliary habitats.

Expression of genes encoding Sensory Neuron Membrane Proteins and Transient Receptor Potential channels

The sensory neuron membrane proteins (SNMPs) were recently suggested to play a significant role in insect chemoreception. Insect SNMPs are two transmembrane domain-containing proteins in olfactory neurons of antennae and localized in dendrite membranes. They were first identified in the pheromone-sensitive hairs of the wild silk moth *Antheraea polyphemus* [87] and tobacco hornmoth *Manduca sexta* [88,89], and now are described in various insect orders namely including Lepidoptera, Coleoptera, Hymenoptera and Diptera [90] and recently Orthoptera [91]. Several functions of insect SNMPs in odorant detection have been predicted (reviewed in [90]) including interactions with pheromone binding protein (PBP)-pheromone complexes, OBP/odorant complexes, OR proteins. Moreover, it was demonstrated in drosophila, that SNMPs regulates sexual and social aggregation behaviours [92,93]. Transient Receptor
Potential (TRP) superfamily of ion channels is essential for the perception of environment. In insects, TRPs are involved in phototransduction, thermosensation, vision, hygrosensation, mechanosensation and also in chemosensation, including taste and olfaction [94,95]. By their function, TRPs have an important impact on insect behaviour [96]. A recent study suggested that a TRP belonging to vanilloid receptors family (TRPVs) could be involved in the high sensitivity to heat in *R. prolixus* which uses these capacities to perceive warm-blooded hosts [97]. In *T. brasiliensis*, the unique SNMP annotated and three out the five TRP contigs annotated were over-expressed in peridomiciliary samples. By way of explanation, in henhouses, we can mention that, in *T. brasiliensis* and more strikingly in *T. pseudomaculata*, very strong triatomine aggregation is observed in their shelters (C. Almeida personal communication). One can assume that henhouses where host density is high compared to other habitats there is a higher sensory interference, so bugs produce aggregation pheromones in higher quantity in their shelters to better find them after their blood meal. This could results in SNMP over-expression in the peridomestic sample. Moreover, the average body temperature of chickens is 40–42°C, compared to the 37°C of mammal vertebrates. This higher temperature of chicken hosts could explain the TRP over expression in relation to a higher exposition to heat.

### Expression of genes involved in insecticide resistance

Regular insecticide spraying campaigns in Brazil have been used against triatomin bugs after the 1970s [98]. Although, all *T. brasiliensis* tested until now have been highly susceptible to deltamethrin, an alpha-cyano-substituted pyrethroid insecticide [99], insecticide resistance has been demonstrated for some Chagas disease vectors, including *T. infestans* [100–102]. We found DE genes involved in the insecticide resistance process, including genes encoding cytochrome P450s, gluthatione S-transferases and cuticle proteins. Accordingly, several studies of cytochrome P450s have revealed over-expression in field populations of insects that are resistant to insecticide [103–108]. Cytochrome P450 genes are involved in detoxification. They catalyze various reactions, e.g. mono-oxygenation [106,107]. The role of gluthatione S-transferases in detoxification is less understood. Several studies showed that they are linked to insecticide resistance and are over-expressed in pyrethroid-resistant insect populations [106,109–111].

Insecticide resistance could also come from an increased ability to prevent toxins from penetrating the cuticle. Thus, changes in cuticle conformation or thickness could increase insecticide resistance [106,112,113]. For example, over-transcription in a resistant strain of *An. gambiae* has suggested that the cuticle plays a role in response to selection pressures resulting from insecticide treatments [114]. In our study, cytochrome P450s, gluthatione S-transferases and cuticular proteins were all under-expressed in domiciliary bugs, which should be the most exposed to insecticide treatment. However, the domiciliary individuals were sampled in houses that had not been sprayed with insecticide for three years. Over-expression of these same genes in sylvatic and peridomiciliary bugs could reflect the involvement of detoxification enzymes in a large range of xenobiotics, including some that may differ according to the habitat [106]. In addition to their role in insecticide resistance, cuticle proteins also play a role in the response to environmental stresses [115]. The domiciliary environment probably has lower xenobiotic diversity and more stable abiotic parameters than do sylvatic and peridomiciliary environments. This could explain why both detoxification and cuticle protein genes were less expressed in domiciliary bugs.

### Conclusion

Our aim was to better understand the domiciliation process in *T. brasiliensis*. We focused on the chemosensory transcriptome because chemosensory genes are implicated in adaptation to
changing environments. In the absence of a reference genome for *T. brasiliensis*, we used the methods of Marchant *et al.* [32] to build a reference transcriptome. RNAseq is a recent technology, so differential expression analysis software is still not optimized. Therefore, to generate results with strong support, we selected congruent results from two different programs: EdgeR and DESeq2. We then processed an independent clustering analysis based on the same expression pattern data. We characterized numerous DE transcripts from bugs of different environments and of different sexes. The domiciliary sample showed different expression profiles than those of sylvatic and peridomestic samples. Since few samples from domiciliary and peridomestic samples were analyzed, it is difficult to generalize our conclusions, but this study has identified new questions that need to be answered to understand the domiciliation process.

Focusing on specific gene families, we highlighted the link between the environment from which a bug originates and expression of chemosensory genes (OBPs, CSPs), detoxification, cuticle protein and takeout genes. These are good candidate genes for playing a role in adaptation or in plastic rearrangement in response to environmental changes, which could include anthropic pressure. To generalize our results, we plan to develop specific primers for these candidate genes to evaluate their expression by qPCR on a wide range of domiciliary, peridomestic and sylvatic samples of *T. brasiliensis*. Further studies are also needed to understand the function of genes highlighted by our analysis and to propose scenarios of molecular evolution of multigenic gene families (paralogs, isoforms, allelic variants) that will require new data, especially genomics. Understanding the molecular basis of vector adaptation to human dwellings creates the potential to develop new tools for disease vector control, such as disrupting chemical communication.

**Supporting Information**

**S1 Fig.** ACP based on normalized counts with the rlog function of DESeq2.

(TIF)

**S2 Fig.** Diagnostic plots provided by the *capushe* package for the DDSE approach of HTSCluster.

(TIF)

**S1 Table.** Blast annotation of CSPs and OBPs, and information about differential expression status. Results of Blast: For all contigs that matched with a CSP or an OBP from the non-redundant protein database, we indicate the ID of this protein (Blast NR ID) and its denomination (Annotation). For each match, we provide the percentage of identity (%ident), the score and the e-value. Each contig that matches with an OBP or CSP was translated and the corresponding protein analyzed by checking for the number of conserved cysteins, the presence of peptide signal and the number of α-helices. For each contig annotated as OBP or CSP, we indicated in which comparison both DESeq2 and EdgeR found it to be differentially expressed. D = domiciliary, P = peridomestic and S = sylvatic; M = male and F = female. The log2fold and the adjusted *p*-value for both packages are provided, as well as the cluster number allocated by HTSCluster.

(DOCX)

**S2 Table.** Blast annotation of ORs, TRPs, SNMPs, takeout, cytochrome P450, glutathione S-transferase and cuticular proteins and information about differential expression status. Results of Blast: For all contigs that matched with a protein of interest in the non-redundant protein database, we indicate the protein ID (Blast NR ID) and its denomination (Annotation). For each match, we provide the percentage of identity (%ident), the score and the e-value. For each contig, we indicate in which comparison both DESeq2 and EdgeR found it to be
differentially expressed. D = domiciliary, P = peridomiciliary and S = sylvatic; M = male and F = female. The log2fold and the adjusted p-value for both packages are provided, as well as the cluster number allocated by HTSCluster.

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Author Contributions

Conceived and designed the experiments: MH.

Performed the experiments: AM EJJ.

Analyzed the data: AM FM MH.

Contributed reagents/materials/analysis tools: JC CEA.

Wrote the paper: AM FM CAE MH.

References

1. World Health Organization. Weekly epidemiological record. 2015; 90: 33–44.

2. Ferreira I de LM, Silva TPT e. Eliminação da transmissão da doença de Chagas pelo Triatoma infestans no Brasil: um fato histórico. Rev Soc Bras Med Trop. 2006; 39: 507–509.

3. Abad-Franch F, Diotaiuti L, Gurgel-Gonçalves R, Gürtler RE, Abad-Franch F, Diotaiuti L, et al. Certifying the interruption of Chagas disease transmission by native vectors: cui bono? Mem Inst Oswaldo Cruz. 2013; 108: 251–254. doi: 10.1590/0074-0276108022013022 PMID: 23579810

4. Schofield CJ, Diotaiuti L, Dujardin JP. The process of domestication in triatominae. Mem Inst Oswaldo Cruz. 1999; 94: 375–378. doi: 10.1590/S0074-02761999000700073 PMID: 10677759

5. Costa J, Almeida CE, Dotson EM, Lins A, Vinhaes M, Silveira AC, et al. The epidemiologic importance of Triatoma brasiliensis as a Chagas disease vector in Brazil: a revision of domiciliary captures during 1993–1999. Mem Inst Oswaldo Cruz. 2003; 98: 443–449. doi: 10.1590/S0074-02762003000400002 PMID: 12937751

6. Lucena de D. Estudo sobre a doença de Chagas no Nordeste do Brasil. Rev Bras Malariol E Doencas Trop. 1970; 22: 3–174.

7. Almeida CE, Pacheco RS, Haag K, Dupas S, Dotson EM, Costa J. Inferring from the Cyt B Gene the Triatoma brasiliensis Neiva, 1911 (Hemiptera: Reduviidae: Triatominae) Genetic Structure and Domiciliary Infestation in the State of Paraíba, Brazil. Am J Trop Med Hyg. 2008; 78: 791–802. PMID: 18458315

8. Borges ÉC, Dujardin J-P, Schofield CJ, Romanha AJ, Diotaiuti L. Dynamics between sylvatic, peridomestic and domiciliary populations of Triatoma brasiliensis (Hemiptera: Reduviidae) in Ceará State, Northeastern Brazil. Acta Trop. 2005; 93: 119–126. doi: 10.1016/j.actatropica.2004.10.002 PMID: 15589804

9. Costa J. The synanthropic process of Chagas disease vectors in Brazil, with special attention to Triatoma brasiliensis Neiva, 1911 (Hemiptera, Reduviidae, Triatominae) population, genetical, ecological, and epidemiological aspects. Mem Inst Oswaldo Cruz. 1999; 94: 239–241. doi: 10.1590/S0074-02761999000700038
10. Costa J, de Almeida JR, Britto C, Duarte R, Marchon-Silva V, Pacheco R da S. Ecotopes, natural infection and trophic resources of Triatoma brasiliensis (Hemiptera, Reduviidae, Triatominae). Mem Inst Oswaldo Cruz. 1998; 93: 7–13.

11. Benton R. Multigene Family Evolution: Perspectives from Insect Chemoreceptors. Trends Ecol Evol. 2015; 30: 590–600. doi: 10.1016/j.tree.2015.07.009 PMID: 26411616

12. Mesquita RD, Vionette-Amaral RJ, Lowenberger C, Rivera-Pomar R, Monteiro FA, Minx P, et al. Genome of Rhodnius prolixus, an insect vector of Chagas disease, reveals unique adaptations to hematophagy and parasite infection. Proc Natl Acad Sci. 2015; 20150622 6. doi: 10.1073/pnas.1506261112 PMID: 26627243

13. Bohbot JD, Pitts RJ. The narrowing olfactory landscape of insect odorant receptors. Chem Ecol. 2015; 3: 39. doi: 10.3389/fevo.2015.00039

14. Jacquin-Joly E, Merlin C. Insect Olfactory Receptors: Contributions of Molecular Biology to Chemical Ecology. J Chem Ecol. 2004; 30: 2359–2397. doi: 10.1007/s10886-004-7941-3 PMID: 15724962

15. Sánchez-Gracia A, Vieira FG, Rozas J. Molecular evolution of the major chemosensory gene families in insects. Heredity. 2009; 103: 208–216. doi: 10.1038/hdy.2009.55 PMID: 19436326

16. Vieira FG, Sánchez-Gracia A, Rozas J. Comparative genomic analysis of the odorant-binding protein family in 12 Drosophila genomes: purifying selection and birth-and-death evolution. Genome Biol. 2007; 8: R235. doi: 10.1186/gb-2007-8-11-r235 PMID: 18039354

17. Guo S, Kim J. Molecular evolution of Drosophila odorant receptor genes. Mol Biol Evol. 2007; 24: 1198–1207. doi: 10.1093/molbev/msm038 PMID: 17331958

18. Engsontia P, Sangket U, Chotigeat W, Satasok C. Molecular Evolution of the Odorant and Gustatory Receptor Genes in Lepidopteran Insects: Implications for Their Adaptation and Speciation. J Mol Evol. 2014; 79; 21–39. doi: 10.1007/s00239-014-9633-0 PMID: 25038840

19. Krieger J, von Nickisch-Rosenegk E, Mameli M, Pelosi P, Breer H. Binding proteins from the antennae of Bombyx mori. Insect Biochem Mol Biol. 1996; 26: 297–304. doi: 10.1016/0965-1748(95)00096-8 PMID: 8900598

20. Krieger J, Raming K, Breer H. Cloning of genomic and complementary DNA encoding insect pheromone binding proteins: evidence for microdiversity. Biochem Biophys Acta—Gene Struct Expr. 1991; 1088: 277–284. doi: 10.1016/0167-4781(91)90064-S

21. Vogt RG, Prestwich GD, Lerner MR. Olfactory and gustatory receptor subfamilies associate with distinct classes of olfactory receptor neurons in insects. J Neurobiol. 1991; 22: 74–84. doi: 10.1002/neu.480220108 PMID: 2010751

22. Vogt RG. Pheromone binding and inactivation by moth antennae. Nature. 1981; 293: 161–163. doi: 10.1038/293161a0 PMID: 18074618

23. Lopez-Maury L, Marguerat S, Bähler J. Tuning gene expression to changing environments: from rapid responses to evolutionary adaptation. Nat Rev Genet. 2008; 9: 583–593. doi: 10.1038/nrg2398 PMID: 18951982

24. Holloway AK, Lawniczak MKN, Mezey JG, Begun DJ, Jones CD. Adaptive Gene Expression Divergence Inferred from Population Genomics. PLoS Genet. 2007; 3: e187. doi: 10.1371/journal.pgen.0030187 PMID: 17967066

25. Wang Z, Gerstein M, Snyder M. RNA-Seq: a revolutionary tool for transcriptomics. Nat Rev Genet. 2009; 10: 57–63. doi: 10.1038/nr82494 PMID: 19015660
32. Marchant A, Mougel F, Almeida C, Jacquin-Joly E, Costa J, Harry M. De novo transcriptome assembly for a non-model species, the blood-sucking bug Triatoma brasiliensis, a vector of Chagas disease. Genetica. 2015; 143: 225–239. doi: 10.1007/s10709-014-9790-5 PMID: 25233990

33. Almeida CE, Faucher L, Lavina M, Costa J, Harry M. Molecular Individual-Based Approach on Triatoma brasiliensis: Inferences on Triatome Foci, Trypanosoma cruzi Natural Infection Prevalence, Parasite Diversity and Feeding Sources. PLOS Negl Trop Dis. 2016; 10: e0004447. doi: 10.1371/journal.pntd.0004447 PMID: 26891047

34. Schmieder R, Edwards R. Quality control and preprocessing of metagenomic datasets. Bioinformatics. 2011; 27: 863–864. doi: 10.1093/bioinformatics/btr26 PMID: 21278185

35. Parra G, Bradnam K, Korel I. CEGMA: a pipeline to accurately annotate core genes in eukaryotic genomes. Bioinformatics. 2007; 23: 1061–1067. doi: 10.1093/bioinformatics/btm071 PMID: 17323020

36. McGuinness LJ, Bryson K, Jones DT. The PSIPRED protein structure prediction server. Bioinformatics. 2000; 16: 404–405. doi: 10.1093/bioinformatics/16.4.404 PMID: 10869041

37. Petersen TN, Brunak S, von Heijne G, Nielsen H. SignalP 4.0: discriminating signal peptides from transmembrane regions. Nat Methods. 2011; 8: 785–786. doi: 10.1038/nmeth.1701 PMID: 21959131

38. Marchant A, Mougel F, Mendonça V, Quartier M, Jacquin-Joly E, da Rosa JA, et al. Comparing de novo and reference-based transcriptome assembly strategies by applying them to the blood-sucking bug Rhodnius prolixus. Insect Biochem Mol Biol. 2016; 69: 25–33. doi: 10.1016/j.ibmb.2015.05.009 PMID: 26005117

39. Kirkness EF, Haas BJ, Sun W, Braig HR, Perotti MA, Clark JM, et al. Genome sequences of the human body louse and its primary endosymbiont provide insights into the permanent parasitic lifestyle. Proc Natl Acad Sci. 2010; 107: 12168–12173. doi: 10.1073/pnas.1003379107 PMID: 20566863

40. Zhou J-J, Vieira FG, He X-L, Smadja C, Liu R, Rozas J, et al. Genome annotation and comparative analyses of the odorant-binding proteins and chemosensory proteins in the pea aphid Acyrthosiphon pisum. Insect Mol Biol. 2010; 19: 113–122. doi: 10.1111/j.1365-2583.2009.00919.x PMID: 20482644

41. Gu S-H, Wang S-Y, Zhang X-Y, Ji P, Liu J-T, Wang G-R, et al. Functional Characterizations of Chemosensory Proteins of the Alfalfa Plant Bug Adelphocoris lineolatus Indicate Their Involvement in Host Recognition. PLoS ONE. 2012; 7: doi: 10.1371/journal.pone.0042871 PMID: 22900060

42. Gu S-H, Wang S-P, Zhang X-Y, Wu K-M, Guo Y-Y, Zhou J-J, et al. Identification and tissue distribution of odorant binding protein genes in the lucerne plant bug Adelphocoris lineolatus (Goeze). Insect Biochem Mol Biol. 2011; 41: 254–263. doi: 10.1016/j.ibmb.2011.01.002 PMID: 21232599

43. Sun L, Zhou J-J, Gu S-H, Xiao H-J, Guo Y-Y, Liu Z-W, et al. Chemosensillum immunolocalization and ligand specificity of chemosensory proteins in the alfalfa plant bug Adelphocoris lineolatus (Goeze). Sci Rep. 2015; 5: doi: 10.1038/srep08073 PMID: 25627422

44. Hua J-F, Zhang S, Cui J-J, Wang D-J, Wang C-Y, Luo J-Y, et al. Functional characterizations of one odorant binding protein and three chemosensory proteins from Apolygus lucorum (Meyer-Dur) (Hemiptera: Miridae) legs. J Insect Physiol. 2013; 59: 690–696. doi: 10.1016/j.jinsphys.2013.04.013 PMID: 23665333

45. Hua J-F, Zhang S, Cui J-J, Wang D-J, Wang C-Y, Luo J-Y, et al. Identification and Binding Characterization of Three Odorant Binding Proteins and One Chemosensory Protein from Apolygus lucorum (Meyer-Dur). J Chem Ecol. 2012; 38: 1163–1170. doi: 10.1007/s10886-012-0178-7 PMID: 23053914

46. Ji P, Gu S-H, Liu J-T, Zhu X-Q, Guo Y-Y, Zhou J-J, et al. Identification and expression profile analysis of odorant-binding protein genes in Apolygus lucorum (Hemiptera: Miridae). Appl Entomol Zool. 2013; 48: 301–311. doi: 10.1007/s13355-013-0188-0

47. Katoh K, Misawa K, Kuma K, Miyata T. MAFFT: a novel method for rapid multiple sequence alignment based on fast Fourier transform. Nucleic Acids Res. 2002; 30: 3059–3066. doi: 10.1093/nar/ gkf436 PMID: 12136088

48. Hall TA. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic acids symposium series. 1999. pp. 95–98.

49. Darriba D, Taboada GL, Doallo R, Posada D. ProtTest 3: fast selection of best-fit models of protein evolution. Bioinformatics. 2011; 27: 1164–1165. doi: 10.1093/bioinformatics/btr088 PMID: 21335321

50. Guindon S, Dufayard J-F, Lefort V, Anisimova M, Hordijk W, Gascuel O. New Algorithms and Methods to Estimate Maximum-Likelihood Phylogenies: Assessing the Performance of PhyML 3.0. Syst Biol. 2010; 59: 307–321. doi: 10.1093/sysbio/sys010 PMID: 20525638

51. Letunic I, Bork P. Interactive Tree Of Life (ITOL): an online tool for phylogenetic tree display and annotation. Bioinformatics. 2007; 23: 127–128. doi: 10.1093/bioinformatics/btl552 PMID: 17050570
52. Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics. 2009; 25: 1754–1760. doi: 10.1093/bioinformatics/btp324 PMID: 19451168

53. Li H, Handsaker B, Wysoker A, Fennell T, Ruan J, Homer N, et al. The Sequence Alignment/Map format and SAMtools. Bioinformatics. 2009; 25: 2078–2079. doi: 10.1093/bioinformatics/btp352 PMID: 19505943

54. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biol. 2014; 15. doi: 10.1186/s13059-014-0550-8 PMID: 25516281

55. McCarthy DJ, Chen Y, Smyth GK. Differential expression analysis of multifactor RNA-Seq experiments with respect to biological variation. Nucleic Acids Res. 2012; 40: 4288–4297. doi: 10.1093/nar/gks042 PMID: 22287627

56. Rau A, Gallopin M, Ceulemans G, Jaffrézic F. Data-based filtering for replicated high-throughput transcriptome sequencing experiments. Bioinformatics. 2013; 29: 2146–2152. doi: 10.1093/bioinformatics/btt350 PMID: 23821648

57. Benjamini Y, Hochberg Y. Controlling the False Discovery Rate: A Practical and Powerful Approach to Multiple Testing. J R Stat Soc Ser B Methodol. 1995; 57: 289–300.

58. Rau A, Maugis-Rabusseau C, Martin-Magniette M-L, Ceulemans G. Co-expression analysis of high-throughput transcriptome sequencing data with Poisson mixture models. Bioinformatics. 2015; 31: 1420–1427. doi: 10.1093/bioinformatics/btv242 PMID: 25563332

59. Altmiciek B, Vilcinskas A. Identification of immune-related genes from an apterygote insect, the fire-brat Thermobia domestica. Insect Biochem Mol Biol. 2007; 37: 726–731. doi: 10.1016/j.ibmb.2007.03.012 PMID: 17550828

60. Kondrashov FA. Gene duplication as a mechanism of genomic adaptation to a changing environment. Proc R Soc Lond B Biol Sci. 2012; 279: 5048–5057. doi: 10.1098/rspb.2012.1108 PMID: 22977152

61. Vieira FG, Rozas J. Comparative Genomics of the Odorant-Binding and Chemosensory Protein Gene Families across the Arthropoda: Origin and Evolutionary History of the Chemosensory System. Genome Biol Evol. 2011; 3: 476–490. doi: 10.1093/gbe/evr100 PMID: 21527792

62. Dansa-Petrès M, Ribeiro JMC, Atella GC, Masuda H, Oliveira PL. Antioxidant Role of Rhodnius prolixus Heme-binding Protein Protection Against Heme-Induced Lipid Peroxidation. J Biol Chem. 1995; 270: 10893–10896. doi: 10.1074/jbc.270.18.10893 PMID: 7738029

63. Ribeiro JM., Andersen J, Silva-Neto MA., Pham V., Garfield M., Valenzuela J. Exploring the sialome of the blood-sucking bug Rhodnius prolixus. Insect Biochem Mol Biol. 2004; 34: 61–79. doi: 10.1016/j.ibmb.2003.09.004 PMID: 14976983

64. Patterson BD. Accumulating Knowledge on the Dimensions of Biodiversity: Systematic Perspectives on Neotropical Mammals. Biodivers Lett. 1994; 2: 79–86. doi: 10.2307/2999761

65. Dillies M-A, Rau A, Aubert J, Hennequet-Antier C, Jeanmougin M, Servant N, et al. A comprehensive evaluation of normalization methods for Illumina high-throughput sequencing data analysis. Brief Bioinform. 2013; 14: 671–683. doi: 10.1093/bib/bbs046 PMID: 22988256

66. Zhang ZH, Jhaveri DJ, Marshall VM, Bauer DC, Edson J, Narayanan RK, et al. A Comparative Study of Techniques for Differential Expression Analysis on RNA-Seq Data. PLoS ONE. 2014; 9: e103207. doi: 10.1371/journal.pone.0103207 PMID: 25119138

67. Sarov-Blat L, So WV, Liu L, Rosbash M. The Drosophila takeout Gene Is a Novel Molecular Link between Circadian Rhythms and Feeding Behavior. Cell. 2000; 101: 647–656. doi: 10.1016/S0092-8674(00)80876-4 PMID: 10892651

68. Meunier N, Belgacem YH, Martin J-R. Regulation of feeding behaviour and locomotor activity by takeout in Drosophila. J Exp Biol. 2007; 210: 1424–1434. doi: 10.1242/jeb.02755 PMID: 17401125

69. Abrahao LB, Gorla DE, Catalá SS. Dispersal of Triatoma infestans and other Triatominae species in the arid Chaco of Argentina: Flying, walking or passive carriage? The importance of walking females. Mem Inst Oswaldo Cruz. 2011; 106: 232–239. doi: 10.1590/S0074-02762011000200019 PMID: 21537686

70. Minoli SA, Lazzari CR. Take-off activity and orientation of triatomines (Heteroptera: Reduviidae) in relation to the presence of artificial lights. Acta Trop. 2006; 97: 324–330. doi: 10.1016/j.actatropica.2005.12.005 PMID: 16460653

71. Sarquis O, Carvalho-Costa FA, Oliveira LS, Duarte R, D Andrea PS, de Oliveira TG, et al. Ecology of Triatoma brasiliensis in northeastern Brazil: seasonal distribution, feeding resources, and Trypanosoma cruzi infection in a sylvatic population. J Vector Ecol J Soc Vector Ecol. 2010; 35: 385–394. doi: 10.1111/j.1948-7134.2010.00097.x PMID: 21175946
72. Fuji S, Toyama A, Amrein H. A Male-Specific Fatty Acid ω-Hydroxylase, SXE1, Is Necessary for Efficient Male Mating in Drosophila melanogaster. Genetics. 2008; 180: 179–190. doi: 10.1534/genetics.108.089177 PMID: 18716335

73. Andersen SO. Amino acid sequence studies on endocuticular proteins from the desert locust, Schistocerca gregaria. Insect Biochem Mol Biol. 1998; 28: 421–434. doi: 10.1016/S0965-1748(98)00028-9 PMID: 9692242

74. Togawa T, Dunn WA, Emmons AC, Nagao J, Willis JH. Developmental expression patterns of cuticular protein genes with the R&RC Consensus from Anopheles gambiae. Insect Biochem Mol Biol. 2008; 38: 508–519. doi: 10.1016/j.ibmb.2007.12.008 PMID: 18405829

75. Diotaialii L, Filho F, FO, Cameiro FCF, Dias JCP, Pires HHR, et al. Operational aspects of Triatoma brasiliensis control. Cad Saúde Pública. 2000; 16: S61–S67. doi: 10.1590/S0102-311X20000000800006

76. Liu R, He X, Lehane S, Lehane M, Hertz-Fowler C, Berriman M, et al. Expression of chemosensory proteins in the tsetse fly Glossina morsitans morsitans is related to female host-seeking behaviour. Insect Mol Biol. 2012; 21: 41–48. doi: 10.1111/j.1365-2583.2011.01114.x PMID: 22074189

77. Latorre Estivalis JM, Omondi BA, DeSouza O, Oliveira IHR, Ignell R, Lorenzo MG. Molecular basis of peripheral olfactory plasticity in Rhodnius prolixus, a Chagas disease vector. Chem Ecol. 2015; 3: 74. doi: 10.3389/fevo.2015.00074

78. Rinker DC, Pitts RJ, Zhou X, Suh E, Rokas A, Zwiebel LJ. Blood meal-induced changes to antennal transcriptome profiles reveal shifts in odor sensitivities in Anopheles gambiae. Proc Natl Acad Sci. 2013; 110: 8260–8265. doi: 10.1073/pnas.1302562110 PMID: 23630291

79. Fujikawa K, Seno K, Ozaki M. A novel Takeout-like protein expressed in the taste and olfactory organs of the blowfly, Phormia regina. FEBS J. 2006; 273: 4311–4321. doi: 10.1111/j.1742-4658.2006.05422.x PMID: 16930135

80. So WV, Sarov-Blat L, Kotarski CK, McDonald MJ, Allada R, Rosbash M. takeout, a novel Drosophila peripheral olfactory plasticity in Rhodnius prolixus, a Chagas disease vector. Mol Cell Biol. 2000; 20: 6935–6944. PMID: 10958689

81. Ribeiro JMC, Genta FA, Sorgine MHF, Logullo R, Mesquita RD, Paiva-Silva GO, et al. An Insight into the Transcriptome of the Digestive Tract of the Bloodsucking Bug, Rhodnius prolixus. PLoS Negl Trop Dis. 2014; 8: e2594. doi: 10.1371/journal.pntd.0002594 PMID: 24416461

82. Lazzari CR. Circadian organization of locomotion activity in the haematophagous bug Triatoma infestans. J Insect Physiol. 1992; 38: 895–903. doi: 10.1016/0022-1910(92)90101-I

83. Lorenzo MG, Lazzari CR. Activity pattern in relation to refuge exploitation and feeding in Triatoma infestans (Hemiptera: Reduviidae). Acta Trop. 1998; 70: 163–170. doi: 10.1016/S0001-706X(98)00025-4 PMID: 9698262

84. Settembrini BP. Circadian Rhythms of Locomotor Activity in Triatoma Infestans (Hemiptera: Reduviidae). J Med Entomol. 1984; 21: 204–212. doi: 10.1093/jmedent/21.2.204 PMID: 6374148

85. Lehane MJ, Schofield CJ. Flight initiation in Triatoma infestans (Klug) (Hemiptera: Reduviidae). J Insect Physiol. 1982; 72: 497–510. doi: 10.1017S0007485300013687

86. Schofield CJ. Nutritional status of domestic populations of Triatoma infestans. Trans R Soc Trop Med Hyg. 1984; 78: 770–778. doi: 10.1046/j.1365-3104.80.09197-2 PMID: 7010698

87. Rogers ME, Sun M, Lerner MR, Vogt RG. Snmp-1, a Novel Membrane Protein of Olfactory Neurons of the Silk Moth Antheraea polyphemus with Homology to the CD36 Family of Membrane Proteins. J Biol Chem. 1997; 272: 14792–14799. doi: 10.1074/jbc.272.23.14792 PMID: 9169446

88. Robertson HM, Martos R, Sears CR, Todres EZ, Walden KKO, Nardi JB. Diversity of odourant binding proteins revealed by an expressed sequence tag project on male Manduca sexta moth antennae. Insect Mol Biol. 1999; 8: 508–519. doi: 10.1046/j.1365-2583.1999.00146.x PMID: 10620045

89. Rogers ME, Krieger J, Vogt RG. Antennal SNMPs (sensory neuron membrane proteins) of lepidoptera define a unique family of invertebrate CD36-like proteins. J Neurobiol. 2001; 49: 47–61. doi: 10.1002/neu.1056 PMID: 11536197

90. Gu SH, Yang R-N, Guo M-B, Wang G-R, Wu K-M, Guo Y-Y, et al. Molecular identification and differential expression of sensory neuron membrane proteins in the antennae of the black cutworm moth Agrotis ipsilon. J Insect Physiol. 2013; 59: 430–443. doi: 10.1016/j.jinsphys.2013.02.003 PMID: 23454276

91. Jiang X, Pregitzer P, Grosse-Wilde E, Breer H, Krieger J. Identification and Characterization of Two “Sensory Neuron Membrane Proteins” (SNMPs) of the Desert Locust, Schistocerca gregaria (Orthoptera: Acrididae). J Insect Sci. 2016; 16: 33. doi: 10.1093/jisesa/iew015 PMID: 27012870

92. Benton R, Vannice KS, Vosshall LB. An essential role for a CD36-related receptor in pheromone detection in Drosophila. Nature. 2007; 450: 289–293. doi: 10.1038/nature06328 PMID: 17943085
93. Jin X, Ha TS, Smith DP. SNMP is a signaling component required for pheromone sensitivity in Drosophila. Proc Natl Acad Sci. 2008; 105: 10996–11001. doi: 10.1073/pnas.0803309105 PMID: 18653762

94. Calixto JB, Kassuya CAL, André E, Ferreira J. Contribution of natural products to the discovery of the transient receptor potential (TRP) channels family and their functions. Pharmacol Ther. 2005; 106: 179–208. doi: 10.1016/j.pharmthera.2004.11.008 PMID: 15866319

95. Clapham DE. TRP channels as cellular sensors. Nature. 2003; 426: 517–524. doi: 10.1038/nature02196 PMID: 14654832

96. Fowler MA, Montell C. Drosophila TRP channels and animal behavior. Life Sci. 2013; 92: 394–403. doi: 10.1016/j.lfs.2012.07.029 PMID: 22877650

97. Zermoglio PF, Latorre-Estivalis JM, Crespo JE, Lorenzo MG, Lazzari CR. Thermo sensation and the TRPV channel in Rhodnius prolixus. J Insect Physiol. 2015; 81: 145–156. doi: 10.1016/j.jinsphys.2015.07.014 PMID: 26225467

98. Dias JCP, Silveira AC, Schofield CJ. The impact of Chagas disease control in Latin America: a review. Mem Inst Oswaldo Cruz. 2002; 97: 603–612. doi: 10.1590/S0074-02762000500002 PMID: 12219120

99. Pessoa GCD, Trevizani NAB, Dias LS, Bezerra de CM, Melo de BV, Diotaiuti L, et al. Toxicological profile of deltamethrin in Triatoma brasiliensis (Hemiptera: Reduviidae) in State of Ceará, Northeastern Brazil. Rev Soc Bras Med Trop. 2015; 48: 39–43. doi: 10.1590/0037-8682-0010-2015 PMID: 25860462

100. González Audino P, Vassena C, Barrios S, Zerba E, Picollo MI. Role of enhanced detoxication in a deltamethrin-resistant population of Triatoma infestans (Hemiptera, Reduviidae) from Argentina. Mem Inst Oswaldo Cruz. 2004; 99: 335–339. doi: 10.1590/S0074-0276200400000018 PMID: 15273811

101. Mougabure-Cueto G, Picollo MI. Insecticide resistance in vector Chagas disease: Evolution, mechanisms and management. Acta Trop. 2015; 149: 70–85. doi: 10.1016/j.actatropica.2015.05.014 PMID: 26003952

102. Orihuela PLS, Vassena CV, Zerba EN, Picollo MI. Relative Contribution of Monooxygenase and Esterase to Pyrethroid Resistance in Triatoma infestans (Hemiptera: Reduviidae) from Argentina and Bolivia. J Med Entomol. 2008; 45: 887–892. doi: 10.1093/jmedent/45.1.887 PMID: 18310111

103. Cariño FA, Koener JF, Plapp FW Jr., Feyereisen R. Constitutive overexpression of the cytochrome P450 gene CYP6A1 in a house fly strain with metabolic resistance to insecticides. Insect Biochem Mol Biol. 1994; 24: 411–418. doi: 10.1016/0965-1748(94)90034-5 PMID: 8025560

104. Boonseupsakul S, Luempromthai E, Rongnorpun P. Characterization of Anopheles minimus CYP6A4A3 expressed in a recombinant baculovirus system. Arch Insect Biochem Physiol. 2008; 69: 13–21. doi: 10.1002/arch.20248 PMID: 18615616

105. Vontas J, Small G, Hemingway J. Glutathione S-transferases as antioxidant defence agents confer pyrethroid resistance in Nilaparvata lugens. Biochim Biophys Acta. 2001; 14: 35–46. doi: 10.1016/1674-2133(00)00212-8 PMID: 11514537
113. Lin Y, Jin T, Zeng L, Lu Y. Cuticular penetration of β-cypermethrin in insecticide-susceptible and resistant strains of Bactrocera dorsalis. Pestic Biochem Physiol. 2012; 103: 189–193. doi: 10.1016/j.pestbp.2012.05.002

114. David J-P, Faucon F, Chandor-Proust A, Poupardin R, Riaz M, Bonin A, et al. Comparative analysis of response to selection with three insecticides in the dengue mosquito Aedes aegypti using mRNA sequencing. BMC Genomics. 2014; 15: 174. doi: 10.1186/1471-2164-15-174 PMID: 24593293

115. Zhang J, Goyer C, Pelletier Y. Environmental stresses induce the expression of putative glycine-rich insect cuticular protein genes in adult Leptinotarsa decemlineata (Say). Insect Mol Biol. 2008; 17: 209–216. doi: 10.1111/j.1365-2583.2008.00796.x PMID: 18477239