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Author(s)	Kato, Hiroto; Jochim, Ryan C.; Gomez, Eduardo A.; Uezato, Hiroshi; Mimori, Tatsuyuki; Korenaga, Masataka; Sakurai, Tatsuya; Katakura, Ken; Valenzuela, Jesus G.; Hashiguchi, Yoshihisa
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Analysis of salivary gland transcripts of the sand fly *Lutzomyia ayacuchensis*, a vector of Andean-type cutaneous leishmaniasis

Hiroto Kato^{a,*}, Ryan C. Jochim^b, Eduardo A. Gomez^c, Hiroshi Uezato^d, Tatsuyuki Mimori^e, Masataka Korenaga^f, Tatsuya Sakurai^a, Ken Katakura^a, Jesus G. Valenzuela^b, Yoshihisa Hashiguchi^{f,g,h}

^aLaboratory of Parasitology, Department of Disease Control, Graduate School of Veterinary Medicine, Hokkaido University, Japan

^bVector Molecular Biology Section, Laboratory of Malaria and Vector Research, National Institute of Allergy and Infectious Diseases, NIH, USA

^cPrograma de Control de Leishmaniasis, Servicio Nacional de Erradicacion de la Malaria (SNEM), Ministerio de Salud Publica, Ecuador

^dDepartment of Dermatology, Faculty of Medicine, University of the Ryukyus, Okinawa, Japan

^eDepartment of Microbiology, School of Health Sciences, Kumamoto University, Kumamoto, Japan

^fDepartment of Parasitology, Kochi Medical School, Kochi University, Kochi, Japan

^gPrometeo, Secretaria Nacional de Educacion Superior, Ciencia, Tecnologia e Innovacion (SENESCYT), Ecuador

^hUniversidad Central del Ecuador Centro de Biomedicina, Quito, Ecuador

*Corresponding author at: Laboratory of Parasitology, Department of Disease Control, Graduate School of Veterinary Medicine, Hokkaido University, North 18 West 9,

Kita-ku, Sapporo, Hokkaido, 060-0818, Japan.

Phone & Fax: +81-11-706-5196.

E-mail address: hkato@vetmed.hokudai.ac.jp

ABSTRACT

The saliva of blood sucking insects contains potent pharmacologically active components that assist them in counteracting the host hemostatic and inflammatory systems during blood feeding. In addition, sand fly salivary proteins affect host immunity and have the potential to be a vaccine against *Leishmania* infection. In the present study, the salivary gland transcripts of *Lutzomyia (Lu.) ayacuchensis*, a vector of cutaneous leishmaniasis in Ecuadorian and Peruvian Andes, were analyzed by sequencing randomly selected clones of the salivary gland cDNA library of this sand fly. This resulted in the identification of the most abundant transcripts coding for secreted proteins. These proteins were homologous to the salivary molecules present in other sand flies including the RGD-containing peptide, PpSP15/SL1 family protein, yellow-related protein, putative apyrase, antigen 5-related protein, D7 family protein, and 27 kDa salivary protein. Of note, homologues of maxadilan, an active vasodilator abundantly present in saliva of *Lu. longipalpis*, were not identified. This analysis is the first description of salivary proteins from a sand fly of the subgenus *Helcocyrtomyia* and from vector of cutaneous leishmaniasis in the New World. The present analysis will provide further insights into the evolution of salivary components in blood sucking arthropods.

Keywords: *Lutzomyia ayacuchensis*, Salivary gland, Transcript, Bioinformatics, cDNA library

1. Introduction

Phlebotomine sand flies are hematophagous insects of the family Psychodidae in the order Diptera, and approximately 80 species can transmit *Leishmania* protozoa, the causative agents of leishmaniasis (Munstermann, 2004; Kato et al., 2010a). During blood-feeding, sand flies inject saliva containing various physiologically active substances including anticoagulants, vasodilators, and inhibitors of platelet aggregation to facilitate successful acquisition of a blood meal (Ribeiro, 1995; Ribeiro and Francischetti, 2003; Valenzuela, 2005). The infection of mammalian hosts with *Leishmania* protozoa occurs during the blood feeding of an infected female sand fly where the parasites are co-inoculated into the hosts together with sand fly saliva (Rohousova and Volf, 2006; Oliveira et al., 2009). Sand fly saliva was shown to facilitate the transmission of *Leishmania* to mammalian hosts and to exacerbate the disease (Titus and Ribeiro, 1988; Theodos et al., 1991; Lima and Titus, 1996). Alternatively, cellular immune response to the salivary components protects the host from *Leishmania* infection (Belkaid et al., 1998, 2000; Kamhawi et al., 2000; Valenzuela et al., 2001; Gomes et al., 2008; Oliveira et al., 2008; Tavares et al., 2011). Humoral immunity to sand fly salivary components was shown in the case of *Leishmania braziliensis* to exacerbate infection (Oliveira et al., 2008). In addition, recent studies are showing that sand fly salivary proteins can be used as a specific marker of sand fly exposure and to use them to evaluate potential risks of *Leishmania* transmission (Teixeira et al., 2010; Vlkova et al., 2011). The profile of salivary components has been defined in 8 Old World *Phlebotomus* species; *Phlebotomus (P.) papatasi* [a vector of *Leishmania (Leishmania) major*] (Valenzuela et al., 2001), *P.*

ariasi [a vector of *L. (L.) infantum*] (Oliveira et al., 2006), *P. perniciosus* [a vector of *L. (L.) infantum*] (Anderson et al., 2006), *P. argentipes* [a vector of *L. (L.) donovani*] (Anderson et al., 2006), *P. duboscqi* [a vector of *L. (L.) major*] (Kato et al., 2006), *P. arabicus* [a vector of *L. (L.) tropica*] (Hostomská et al., 2009), *P. tobbi* [a vector of *L. (L.) infantum*] (Rohoušová et al., 2012), and *P. sergenti* [a vector of *L. (L.) tropica*] (Rohoušová et al., 2012). On the other hand, the salivary components of the New World *Lutzomyia* species have been analyzed only in *Lutzomyia (Lu.) longipalpis*, a vector of *L. (L.) infantum* [a synonym of *L. (L.) chagasi*] causing visceral leishmaniasis (Charlab et al., 1999; Valenzuela et al., 2004). To date, no information is available on the repertoire of salivary transcripts from vectors of the New World cutaneous leishmaniasis. In the present study, to obtain further insight into the salivary components of *Lutzomyia* species, the salivary gland transcriptome analysis was performed on *Lu. ayacuchensis*, which is a proven vector of *L. (L.) mexicana* (Takaoka et al., 1990; Kato et al., 2005, 2008) and *L. (Viannia) peruviana* (Caceres et al., 2004; Kato et al., 2008), causative agents of cutaneous leishmaniasis in Andean areas of Ecuador and Peru, respectively. This is the first report of salivary proteins from a sand fly of the subgenus *Helcocyrtomyia* and from vector of cutaneous leishmaniasis in the New World.

2. Materials and methods

2.1. *Lutzomyia ayacuchensis* salivary glands

Sand flies were captured using protected human bait at Huigra (2°20'S, 78°58'W; 1,200 m above sea level) in the Department of Chimborazo, Ecuador, where Andean-type cutaneous leishmaniasis caused by *L. (L.) mexicana* is endemic. The sand flies were dissected and identified at the species level based mainly on the morphology of their spermathecae (Young and Duncan, 1994). Salivary glands of *Lu. ayacuchensis* were dissected and transferred to tubes containing RNAlater (Ambion, Austin, TX) and kept at -20°C.

2.2. Construction of salivary gland cDNA library

Lu. ayacuchensis salivary gland mRNA was isolated from 38 pairs of salivary glands using the Micro FastTrack mRNA isolation kit (Invitrogen, San Diego, CA). The PCR-based cDNA library was prepared following the instructions for the SMART cDNA library construction kit (BD-Clontech, Palo Alto, CA) with some modifications (Valenzuela et al., 2004). The quality of the cDNA was checked by agarose gel electrophoresis and the absence of smaller fragments derived from degraded mRNA was confirmed. The obtained cDNA library was fractionated using a Chromaspin 1000 column (BD-Clontech) into small (approximately 400-800 bp), medium (approximately 800-1,200 bp) and large (>1,200 bp) transcripts based on their electrophoresis profiles on a 1.1% agarose gel. Pooled fractions were ligated into Lambda TriplEx2 vector (BD-Clontech) and packaged into lambda phage (Stratagene, La Jolla, CA).

2.3. *Sequence analysis of cDNA library*

Single isolated plaques were picked from the plate using sterile wooden sticks and placed into 50 µl of water. Amplification of cDNA was performed in a volume of 15 µl using a pair of primers, PT2F1 (5'-AAG TAC TCT AGC AAT TGT GAG C-3') and PT2R1 (5'-CTC TTC GCT ATT ACG CCA GCT G-3'), Premix Taq (Takara Bio, Shiga, Japan) and 3 µl of template DNA. After an initial denaturation at 75°C for 3 min and following 95°C for 4 min, PCR amplification was performed with 35 cycles of denaturation (95°C, 1 min), annealing (50°C, 1 min) and polymerization (72°C, 2 min). PCR products were cleaned using Multiscreen PCR cleaning plates (Millipore Corporation, Bedford, MA) and used as templates for cycle-sequencing kit (Applied Biosystems, Foster City, CA) with PT2F3 primer (5'-TCT CGG GAA GCG CGC CAT TGT-3'). Cycle-sequencing products were cleaned using sephadex and MultiScreen HV plates (Millipore Corporation), dried and stored at -20°C. Sequencing was performed on an ABI 3730xl DNA sequencer (Applied Biosystems).

2.4. *Bioinformatics*

Expressed sequence tags (ESTs) were trimmed of primer and vector sequences and clustered. The ESTs were grouped based on nucleotide homology of 95% identity over 100 residues using the BLASTn algorithm (Altschul et al., 1997). The assembly of the ESTs into transcript contigs was done using the CAP3 algorithm, generating a consensus sequence (Huang, 1992). Contigs and singletons (contig containing only one sequence) were compared using BLASTx or BLASTn (Altschul et al., 1997) of the non-redundant (NR) protein database of the National Center of Biological Information (NCBI), the gene ontology database (GO) (Ashburner et al.,

2000), and the Conserved Domains Database (CDD) that includes all Pfam (Bateman and Birney, 2000), SMART (Schultz et al., 1998) and COG protein domains in the NCBI (Marchler-Bauer et al., 2002). Additionally, contigs were compared using BLASTn (Altschul et al., 1997) to custom databases of mitochondrial (mit-pla) and rRNA (rrna) nucleotide sequences. Identification of putative secreted proteins was conducted using SignalP server (Bendtsen et al., 2004).

2.5. *T cell epitope prediction*

For the T cell epitope prediction, ProPred MHC Class-II Binding Peptide Prediction Server (Singh and Raghava, 2001) was utilized. HLA class II-binding peptides were searched on the 51 different HLA-DR alleles, and the promiscuous epitopes were selected from the *Lu. ayacuchensis* salivary protein sequences tested that were predicted to bind at least 20 alleles.

2.6. *Phylogenetic analysis*

The sequences that had homologies with secreted proteins by BLASTx analyses were aligned with CLUSTAL W software (Thompson et al., 1994) and examined using the program MEGA (Molecular Evolutionary Genetics Analysis) version 4.0 (Tamura et al., 2007). Phylogenetic trees by the neighbor-joining method were constructed with the distance algorithms available in the MEGA package. Bootstrap values were determined on 1,000 replicates of the data sets.

3. Results and discussion

3.1. *Sequencing of Lutzomyia ayacuchensis salivary gland cDNA library*

Lu. ayacuchensis salivary gland cDNA library was constructed, and sequencing was performed on randomly selected 1,152 clones. As a result, 768 high-quality sequences were obtained. Three categories of expressed genes were derived from the manual annotation of the contigs: secreted, housekeeping and unknown. The putative secreted category comprised 45.7% of the clusters and 74.6% of the total sequences. The high ratio of transcripts encoding secreted proteins were also reported in other phlebotomine sand flies (Valenzuela et al., 2001; Oliveira et al., 2006; Anderson et al., 2006; Kato et al., 2006; Hostomská et al., 2009; Rohoušová et al., 2012). The housekeeping category had 35.0% of the clusters and 16.3% of the total sequences. Finally, the category of “unknowns” comprised 19.3% of the cluster and 9.1% of the sequences.

3.2. *Housekeeping genes*

The clusters of sequences attributed to housekeeping genes (94 clusters with 125 sequences in total) were further divided into 18 subgroups, according to their possible function (Table 1). The two largest subgroups were associated with “Energy production and conversion” (24 sequences in 20 clusters) and “Translation, ribosomal structure and biogenesis” (23 sequences in 19 clusters). Six sequences in 6 clusters, which represent conserved proteins with unknown function, were classified as “unknown conserved”. Other sequences were identified with homology to housekeeping genes and were associated with transport, metabolism, signal transduction,

and cell structure, among other potential activities.

3.3. Putative secreted proteins

The transcripts coding for secreted proteins were further analyzed using the BLASTx program for comparison to the NCBI non-redundant protein database. Table 2 lists clusters for the most abundant transcripts coding for the putative secreted salivary gland proteins from *Lu. ayacuchensis*. The table was arranged from the most abundant to the least abundant transcripts found in the cDNA library. The nomenclature for the transcripts on the cDNA library is the following: Lay = L*u.* a*yacuchensis*, S = salivary glands, and the number (ie: 45) denotes the contig number on the cDNA library where a contig is a cluster of identical transcripts. Many of the isolated transcripts code for proteins previously identified from the saliva of sand flies, *Lu. longipalpis* and *P. perniciosus*, including RGD-containing peptide, 14 kDa salivary protein, antigen 5-related protein, yellow-related protein and SL1-like protein (Table 2). Table 3 shows the classification of transcripts coding for putative secreted proteins in *Lu. ayacuchensis* salivary glands. Of the 573 transcripts associated with putative secreted proteins, the most abundant transcript (18.7%) had homology with that of RGD-containing peptide from salivary glands of *Lu. longipalpis*. The following abundant transcripts were SL1-like protein (14.3%) and 14 kDa salivary protein (12.4%), both of which belong to a family of PpSP15/SL1 originally identified as 15 kDa protein from *P. papatasi* saliva. Additional transcripts coding for secreted proteins include homologs to yellow-related protein (11.1%), putative apyrase (7.9%), D7-related salivary protein (7.3%), 27 kDa salivary protein (6.6%), antigen 5-related protein (6.5%), 16.4 kDa salivary protein (5.6%), and others (Table 3).

3.3.1. RGD-containing peptide

The most abundant sequences found in the *Lu. ayacuchensis* salivary gland transcriptome contain C-terminal RGD (Arg-Gly-Asp) sequence; a motif that has been shown to bind integrins such as $\alpha\beta3$ and $\alpha\beta5$ (Hynes, 1992). Ten transcripts of RGD-containing peptide (LayS38-LayS47) were identified in the cDNA library of *Lu. ayacuchensis* salivary glands. These *Lu. ayacuchensis* RGD-containing molecules have a predicted molecular mass of 5.3 kDa in the mature form and a calculated isoelectric point of 3.44 (Table 2). The only homologous protein has been identified in the salivary gland transcriptome of *Lu. longipalpis* (LuloRGD), and speculated to act as an inhibitor of platelet aggregation via its RGD motif; although, the function has not yet been characterized (Charlab et al., 1999). Alignment of the RGD-containing peptide showed a high level of homology among contigs, and an RGD-motif in the C-terminal was strictly conserved in all molecules (Fig. S1).

3.3.2. PpSP15/SL1 family

The PpSP15/SL1 family of proteins has been reported only in sand flies and the biological function during blood-feeding remains unknown. Interestingly, immunization of mice with PpSP15 protected against *Leishmania major* infection co-injected with *P. papatasi* saliva, suggesting that this family of protein is a vaccine candidate for *Leishmania* infection (Valenzuela et al., 2001). Two groups of molecules were identified from the *Lu. ayacuchensis* salivary gland cDNA library, SL-1-like proteins and 14 kDa salivary proteins (PpSP14-like protein), as members of the PpSP15/SL1 family. Twenty-five contigs (LayS48-LayS72) showed the highest

homology with SL1 protein from *Lu. longipalpis*, and six contigs (LayS32-LayS37) coding for a 14 kDa salivary protein were more homologous to the 14.6 kDa salivary protein from *P. perniciosus* (PpeSP09) (Table 2). Alignment of PpSP15/SL1 family showed a high level of homology among SL-1-like proteins and among 14 kDa salivary proteins (Figs. S2 and S3). When both groups of proteins from *Lu. ayacuchensis* were aligned with PpSP15/SL1 family proteins from other sand flies, only six cysteine residues and three other amino acids (P, F, and A) were conserved in the amino acid sequence of mature proteins (Fig. 1A), reflecting the divergence among PpSP15/SL1 family proteins in sand flies (Anderson et al., 2006). Since the proteins of this family are immunogenic and potential vaccines for *Leishmania* infection (Valenzuela et al., 2001), T cell epitopes were analyzed using ProPred MHC Class-II Binding Peptide Prediction Server. We identified two potential T cell epitopes, YRITKKHIE and IHHYYRCVV, in *Lu. ayacuchensis* SL-1-like proteins (Fig. S2), and two potential epitopes, IKNKAVDGS and FKYESAINSY, in 14 kDa salivary proteins (Fig. S3). A phylogenetic analysis of sand fly PpSP15/SL1 family proteins revealed that SL-1-like proteins and 14 kDa salivary proteins from *Lu. ayacuchensis* constructed separate clades (Fig. 1B).

3.3.3. Yellow-related protein

Yellow-related proteins are abundantly expressed in salivary glands of sand flies (Valenzuela et al., 2001; Oliveira et al., 2006; Anderson et al., 2006; Kato et al., 2006; Hostomská et al., 2009; Rohoušová et al., 2012). The proteins of this family are immunogenic and host antibody responses to this protein can be a potential marker for sand fly exposure (Teixeira et al., 2010; Vlková et al., 2011). Interestingly, prior

DNA vaccination of mice with PpSP44 coding for a 44 kDa yellow-related protein from *P. papatasi* saliva primed strong humoral immunity and exacerbated subsequent *L. major* infection in the presence of sand fly saliva (Oliveira et al., 2008). In contrast, a yellow-related protein from *Lu. longipalpis* saliva, LJM11, conferred protective cellular immunity in mice against *L. major* infection plus sand fly saliva. Other *Lu. longipalpis* yellow-related proteins, LJM111 and LJM17, were not protective, suggesting that structural features are a determinant for the host immunity against yellow-related proteins (Xu et al., 2011). Regarding the biological function, yellow-related proteins, LJM11, LJM111 and LJM17, were shown to act as high affinity binders of proinflammatory biogenic amines such as serotonin, catecholamines and histamine, suggesting that the proteins play a role for the reduction of inflammation during sand fly blood-feeding (Xu et al., 2011). In the *Lu. ayacuchensis* cDNA library, five contigs (LayS22-LayS24, LayS117 and LayS118) are putative yellow-related proteins, of which LayS117 was truncated in the 5' region. When these proteins were aligned with salivary yellow-related proteins from other sand fly species, four cysteine residues were conserved in the amino acid sequence of mature proteins (Fig. 2A and S4). In addition, an amino acid motif, T-x(52,63)-Y-Q-x(85,90)-[FY]-x(44,46)-F-x(54)-[IVL]-x(45,46)-[FY]-x-[TS]-D-x(13)-[NT]-x-[QHFL], recently identified in the ligand binding pocket of yellow-related proteins (Xu et al., 2011) were conserved in those from *Lu. ayacuchensis* (Fig. 2A), suggesting that these proteins work as anti-inflammatory agents in *Lu. ayacuchensis* saliva by binding biogenic amines. Two potential N-glycosylation sites were present in yellow-related proteins from *Lu. ayacuchensis*, but the positions of LayS118 were different from those of others (LayS22-LayS24) (Fig. 2A). T cell epitopes were

analyzed on the immunogenic proteins of this family, and we identified seven potential epitopes in LayS22-LayS24 (Fig. S4A) and 5 potential epitopes in LayS118 (Fig. S4B). A phylogenetic analysis of sand fly yellow-related proteins revealed that LayS22, LayS23 and LayS24 were closer related to LJM11 whereas LayS118 were closer related to LJM17 from *Lu. longipalpis* saliva (Fig. 2B). The result suggested that effect on the host immunity of LayS118 is different from those of LayS22, LayS23 and LayS24.

3.3.4. Apyrase

Apyrases are nucleoside triphosphate-diphosphohydrolases present in a variety of organisms. In the saliva of blood sucking arthropods, apyrases function to hydrolyze ADP in a Ca^{2+} -dependent manner and inhibit ADP-induced platelet aggregation to facilitate blood feeding (Ribeiro and Francischetti, 2003; Faudry et al., 2004). Apyrases identified in sand fly saliva belong to the *Cimex* apyrase family (Valenzuela et al., 2001; Hamasaki et al., 2009). Thirteen contigs (LayS8-LayS14 and LayS16-LayS21) were homologous to putative apyrase from *Lu. longipalpis* (LuloAPY). A multiple sequence alignment analysis together with LuloAPY confirmed the close relationship among putative apyrases of *Lu. ayacuchensis* (Fig. S5).

3.3.5. D7 family

D7 family proteins are abundantly expressed in salivary glands of blood-feeding Diptera such as mosquitoes, sand flies, black flies, and biting midges (James et al., 1991; Valenzuela et al., 2002; Campbell et al., 2005; Andersen et al., 2009). To date, the function of sand fly D7 proteins remains to be elucidated; however, several D7 family proteins have been functionally characterized in mosquitoes. Hamadarin from

Anopheles stephensi saliva was identified as a blood coagulation inhibitor affecting the activation of the plasma contact system (Isawa et al., 2002). Salivary D7 proteins from *Anopheles gambiae* and *Aedes aegypti* were characterized as binders of biogenic amines such as serotonin, histamine and norepinephrine (Calvo et al., 2006). Nine contigs (LayS95-LayS103) encoding a 26.6 kDa protein were homologous to the 27 kDa D7-related salivary protein from *P. argentipes* (PagSP10) and *P. perniciosus* (PpeSP04b). In a multiple sequence alignment analysis of D7 family proteins from sand flies, ten cysteine residues were strictly conserved in the amino acid sequence of mature proteins (Fig. 3A and S6). Alignment and phylogenetic analysis together with PpeSP04b showed that D7 family proteins of *Lu. ayacuchensis* had close relationships (Fig. 3B).

3.3.6. 27 kDa salivary protein

The protein family is also known as PpSP32-like family. Eleven contigs (LayS83-LayS93) encoding a 27 kDa protein were homologous to the 29.2 kDa salivary protein from *Lu. longipalpis* (Table 2). These transcripts are also present in the salivary glands from Old World sand flies such as *P. ariasi*, *P. duboscqi*, *P. arabicus*, *P. argentipes*, *P. papatasi*, *P. perniciosus*, *P. tobbi*, and *P. sergenti* (Valenzuela et al., 2001; Oliveira et al., 2006; Anderson et al., 2006; Kato et al., 2006; Hostomská et al., 2009; Rohoušová et al., 2012). To date, no homologues of these proteins have been reported in organisms other than sand flies and the biological function remains to be clarified. Although no conserved domains were found in the amino acid sequences, these proteins contain glycine-rich sequences in the middle region (amino acids 66-179 in LayS91) (Fig. S7).

3.3.7. *Antigen 5-related protein*

This family of proteins belongs to the cysteine-rich secretory proteins (CRISPs) and is related to venom allergens in social wasps and ants (Lu et al., 1993; Hoffman, 1993; King and Spangfort, 2000). Transcripts coding for the members of this protein family have been identified in the salivary glands of blood sucking insects such as mosquitoes (Francischetti et al., 2002; Arcá et al., 2007), sand flies (Valenzuela et al., 2001; Oliveira et al., 2006; Anderson et al., 2006; Kato et al., 2006; Hostomská et al., 2009; Rohoušová et al., 2012) and triatomine bugs (Ribeiro et al., 2004; Santos et al., 2007; Assumpção et al., 2008; Kato et al., 2010b). Although the antigen 5 family of protein has been widely identified in blood-sucking arthropods, the function in their saliva has yet to be determined. Nine contigs (LayS73-LayS81) from *Lu. ayacuchensis* salivary glands were included in this family. A multiple sequence alignment analysis of antigen 5-related proteins with that of *Lu. longipalpis* revealed the close relationship among the proteins of *Lu. ayacuchensis* and strict conservation of 12 cysteine residues in mature forms (Fig. S8).

3.3.8. *16.4 kDa salivary protein*

Thirteen contigs (LayS120-LayS132) coded for 16.4 kDa protein containing a C-type lectin/C-type lectin-like domain (Table 2). This putative domain may function as a Ca²⁺-dependent carbohydrate-binding pocket involved in extracellular matrix organization, pathogen recognition and cell-to-cell interactions (Weis et al., 1998). Homologous proteins with molecular weight of 16.2-16.5 kDa have been identified from *Lu. longipalpis* saliva (Charlab et al., 1999; Valenzuela et al., 2004),

and they were similar to the previously described anticoagulant from *Lu. longipalpis* saliva (Charlab et al., 1999). A recombinant protein of mature LayS127 protein was expressed in *Escherichia coli*, and its activity on coagulation pathway was assessed; however, the protein inhibited neither intrinsic nor extrinsic coagulation pathways (data not shown). At present, the biological function of these proteins from *Lu. ayacuchensis* remains to be clarified. In a multiple sequence alignment analysis of *Lu. ayacuchensis* 16.4 kDa proteins together with *Lu. longipalpis* 16.5 kDa protein, three cysteine residues were strictly conserved in the amino acid sequence of mature proteins (Fig. S9).

3.3.9. 11.5 kDa salivary protein

Four contigs encoding 10.7-11.9 kDa proteins (LayS4-LayS7) were identified in the cDNA library of *Lu. ayacuchensis* salivary glands. The different size of these proteins was mainly resulted from the number of “SSDGSSG” repeat sequences with unknown function (Fig. S10). The only homologous protein has been identified in salivary glands of *Lu. longipalpis* (9 kDa salivary protein) with unknown function. The amino acid sequences of these proteins are rich in serine from the middle to the C-terminal regions (Fig. S10).

3.3.10. Other putative secreted proteins

Three contigs (LayS25-LayS27) coding for a 33.6 kDa protein had homology with a 34 kDa salivary protein from *P. ariasi*. Three contigs (LayS141-LayS143) coded for a 9.3 kDa protein. Three singletons (LayS109-LayS111) coding for a 15.9 kDa protein had homology with a 15.5 kDa salivary protein from *P. argentipes* with

unknown function. Two contigs (LayS2 and LayS3) coded for a 25.9 kDa protein homologous to allergen from *Culex quinquefasciatus* belonging to the sperm-coating protein (SCP) superfamily. Two singletons (LayS167 and LayS168) and one singleton (LayS153) coded for homologous proteins with a 32.4 kDa salivary protein and a 71 kDa salivary protein from *Lu. longipalpis*, respectively, although the sequence of LayS168 was truncated in the 5' region. A singleton (LayS147) coded for homologous protein with the 43.7 kDa salivary protein from *Lu. longipalpis*, a putative endonuclease, but the sequence was truncated in the 5' region. Singletons, LayS106 and LayS215, coded for homologous protein with the 27 kDa salivary protein from *P. ariasi* and trypsin inhibitor like cysteine rich domain containing protein from *Drosophila*, respectively.

4. Conclusions

The present study identified abundant salivary gland transcripts of *Lu. ayacuchensis*, a proven vector of *L. (L.) mexicana* (Takaoka et al., 1990; Kato et al., 2005, 2008) and *L. (V.) peruviana* (Caceres et al., 2004; Kato et al., 2008) causative agents of cutaneous leishmaniasis in Andean areas of Ecuador and Peru, respectively. The relatively divergent transcripts resulting in the generation of a variety of contigs noted for each component probably reflects population of the sand flies used in this study; that is, our cDNA library was constructed from field-captured *Lu. ayacuchensis* while most studies prepared the cDNA libraries from colonized insects. To date, the salivary components of the New World *Lutzomyia* species have been analyzed only in *Lu. longipalpis* (Charlab et al., 1999; Valenzuela et al., 2004), a subgenus *Lutzomyia* species, transmitting *L. (L.) infantum*, a causative agent of visceral leishmaniasis (Young and Duncan, 1994). On the other hand, *Lu. ayacuchensis* is a vector species of cutaneous leishmaniasis and belongs to the subgenus *Helcocyrtomyia* (Young and Duncan, 1994). Therefore, the present analysis is the first description of salivary proteins of a sand fly in the subgenus *Helcocyrtomyia* and a vector of cutaneous leishmaniasis in the New World.

In the present analysis, transcripts homologous to maxadilan, an active vasodilator abundantly present in saliva of *Lu. longipalpis*, were not identified. Maxadilan was originally isolated from saliva of *Lu. longipalpis* (Lerner et al., 1991), and its homologue was reported from *Lu. neivai* (Aires et al., 2005). Conversely, maxadilan-related proteins have never been identified in Old World *Phlebotomus* species (Valenzuela et al., 2001; Oliveira et al., 2006; Anderson et al., 2006; Kato et al.,

2006; Hostomská et al., 2009). *Phlebotomus* sand flies except for *P. duboscqi* lack adenosine deaminase (ADA) that hydrolyze adenosine and adenosine monophosphate (AMP) (Oliveira et al., 2006; Anderson et al., 2006; Kato et al., 2006; Hostomská et al., 2009), but contain large amounts of adenosine and AMP, very active vasodilators, in their saliva (Ribeiro et al., 1999; Katz et al., 2000; Ribeiro and Modi, 2001). On the other hand, *Lu. longipalpis* has ADA (Charlab et al., 1999, 2000; Valenzuela et al., 2004) and lacks adenosine and AMP in the saliva (Ribeiro et al., 1989). Therefore, with an exception, salivary vasodilators of sand flies are considered to be adenosine and AMP in *Phlebotomus* species and maxadilan in *Lutzomyia* species. Unexpectedly, neither ADA nor maxadilan were identified in *Lu. ayacuchensis*, which is similar to *Phlebotomus* species, suggesting that salivary vasodilators of this species may be adenosine and AMP. Further analysis of small molecules in the saliva of *Lu. ayacuchensis* will elucidate this issue.

In conclusion, the most abundant proteins of *Lu. ayacuchensis* saliva were identified in this study. These results will provide further insights into the evolution of salivary components in blood sucking arthropods. In addition, the cDNAs and future recombinant proteins prepared from these transcripts will result in the discovery of vaccine candidates and markers of sand fly exposure as well as novel pharmacologically active compounds.

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References

- Aires, J.M., Chociay, M.F., Nascimento, M.M., Figueiredo, J.F., Roselino, A.M., 2005. Maxadilan (MAX) - Salivary protein of *Lutzomyia longipalpis*: Detection of antibodies anti-MAX in American tegumentar leishmaniasis (ATL), and genetic and protein expression of MAX in *Lutzomyia neivai*. An. Bras. Dermatol. 80, S333-338.
- Altschul, S.F., Madden, T.L., Schäffer, A.A., Zhang, J., Zhang, Z., Miller, W., Lipman, D.J., 1997. Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Res. 25, 3389-4002.
- Andersen, J.F., Pham, V.M., Meng, Z., Champagne, D.E., Ribeiro, J.M.C., 2009. Insight into the sialome of the Black Fly, *Simulium vittatum*. J. Proteome Res. 8, 1474-1488.
- Anderson, J.M., Oliveira, F., Kamhawi, S., Mans, B.J., Reynoso, D., Seitz, A.E., Lawyer, P., Garfield, M., Pham, M., Valenzuela, J.G., 2006. Comparative salivary gland transcriptomics of sandfly vectors of visceral leishmaniasis. BMC Genomics. 7, 52.
- Arcà, B., Lombardo, F., Francischetti, I.M.B., Pham, V.M., Mestres-Simon, M., Andersen, J.F., Ribeiro, J.M.C., 2007. An insight into the sialome of the adult female mosquito *Aedes albopictus*. Insect Biochem. Mol. Biol. 37, 107-127.
- Ashburner, M., Ball, C.A., Blake, J.A., Botstein, D., Butler, H., Cherry, J.M., Davis, A.P., Dolinski, K., Dwight, S.S., Eppig, J.T., Harris, M.A., Hill, D.P., Issel-Tarver, L., Kasarskis, A., Lewis, S., Matese, J.C., Richardson, J.E., Ringwald, M., Rubin, G.M., Sherlock, G., 2000. Gene ontology: tool for the unification of biology. The

- Gene Ontology Consortium. Nat. Genet. 25, 25-29.
- Assumpção, T.C., Francischetti, I.M.B., Andersen, J.F., Schwarz, A., Santana, J.M., Ribeiro, J.M.C., 2008. An insight into the sialome of the blood-sucking bug *Triatoma infestans*, a vector of Chagas' disease. Insect Biochem. Mol. Biol. 38, 213-232.
- Bateman, A., Birney, E., 2000. Searching databases to find protein domain organization. Adv. Protein Chem. 54, 137-157.
- Belkaid, Y., Kamhawi, S., Modi, G., Valenzuela, J., Noben-Trauth, N., Rowton, E., Ribeiro, J., Sacks, D.L., 1998. Development of a natural model of cutaneous leishmaniasis: powerful effects of vector saliva and saliva preexposure on the long-term outcome of *Leishmania major* infection in the mouse ear dermis. J. Exp. Med. 188, 1941-1953.
- Belkaid, Y., Valenzuela, J.G., Kamhawi, S., Rowton, E., Sacks, D.L., Ribeiro, J.M.C., 2000. Delayed-type hypersensitivity to *Phlebotomus papatasi* sand fly bite: An adaptive response induced by the fly? Proc. Natl. Acad. Sci. USA. 97, 6704-6709.
- Bendtsen, J.D., Nielsen, H., von Heijne, G., Brunak, S., 2004. Improved prediction of signal peptides: SignalP 3.0. J. Mol. Biol. 340, 783-795.
- Caceres, A.G., Villaseca, P., Dujardin, J.C., Bañuls, A.L., Inga, R., Lopez, M., Arana, M., Le Ray, D., Arevalo, J., 2004. Epidemiology of Andean cutaneous leishmaniasis: incrimination of *Lutzomyia ayacuchensis* (Diptera: psychodidae) as a vector of *Leishmania* in geographically isolated, upland valleys of Peru. Am. J. Trop. Med. Hyg. 70, 607-612.
- Calvo, E., Mans, B.J., Andersen, J.F., Ribeiro, J.M.C., 2006. Function and evolution of a mosquito salivary protein family. J. Biol. Chem. 281, 1935-1942.

- Campbell, C.L., Vandyke, K.A., Letchworth, G.J., Drolet, B.S., Hanekamp, T., Wilson, W.C., 2005. Midgut and salivary gland transcriptomes of the arbovirus vector *Culicoides sonorensis* (Diptera: Ceratopogonidae). *Insect Mol. Biol.* 14, 121-136.
- Charlab, R., Rowton, E.D., Ribeiro, J.M.C., 2000. The salivary adenosine deaminase from the sand fly *Lutzomyia longipalpis*. *Exp. Parasitol.* 95, 45-53.
- Charlab, R., Valenzuela, J.G., Rowton, E.D., Ribeiro, J.M.C., 1999. Toward an understanding of the biochemical and pharmacological complexity of the saliva of a hematophagous sand fly *Lutzomyia longipalpis*. *Proc. Natl. Acad. Sci. USA.* 96, 15155-15160.
- Faudry, E., Rocha, P.S., Vernet, T., Lozzi, S.P., Teixeira, A.R., 2004. Kinetics of expression of the salivary apyrases in *Triatoma infestans*. *Insect Biochem. Mol. Biol.* 34, 1051-1058.
- Francischetti, I.M.B., Valenzuela, J.G., Pham, V.M., Garfield, M.K., Ribeiro, J.M.C., 2002. Toward a catalog for the transcripts and proteins (sialome) from the salivary gland of the malaria vector *Anopheles gambiae*. *J. Exp. Biol.* 205, 2429-2451.
- Gomes, R., Teixeira, C., Teixeira, M.J., Oliveira, F., Menezes, M.J., Silva, C., de Oliveira, C.I., Miranda, J.C., Elnaiem, D.E., Kamhawi, S., Valenzuela, J.G., Brodskyn, C.I., 2008. Immunity to a salivary protein of a sand fly vector protects against the fatal outcome of visceral leishmaniasis in a hamster model. *Proc. Natl. Acad. Sci. USA.* 105, 7845-7850.
- Hamasaki, R., Kato, H., Terayama, Y., Iwata, H., Valenzuela, J.G., 2009. Functional characterization of a salivary apyrase from the sand fly, *Phlebotomus duboscqi*, a vector of *Leishmania major*. *J. Insect. Physiol.* 55, 1044-1049.
- Hoffman, D.R., 1993. Allergens in Hymenoptera venom. XXV: The amino acid

- sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity. *J. Allergy Clin. Immunol.* 92, 707-716.
- Hostomská, J., Volfová, V., Mu, J., Garfield, M., Rohousová, I., Volf, P., Valenzuela, J.G., Jochim, R.C., 2009. Analysis of salivary transcripts and antigens of the sand fly *Phlebotomus arabicus*. *BMC Genomics.* 10, 282.
- Huang, X., 1992. A contig assembly program based on sensitive detection of fragment overlaps. *Genomics.* 14, 18-25.
- Hynes, R.O., 1992. Integrins: versatility, modulation, and signaling in cell adhesion. *Cell.* 69, 11-25.
- Isawa, H., Yuda, M., Orito, Y., Chinzei, Y., 2002. A mosquito salivary protein inhibits activation of the plasma contact system by binding to factor XII and high molecular weight kininogen. *J. Biol. Chem.* 277, 27651-27658.
- James, A.A., Blackmer, K., Marinotti, O., Ghosn, C.R., Racioppi, J.V., 1991. Isolation and characterization of the gene expressing the major salivary gland protein of the female mosquito, *Aedes aegypti*. *Mol. Biochem. Parasitol.* 44, 245-253.
- Kamhawi, S., Belkaid, Y., Modi, G., Rowton, E., Sacks, D., 2000. Protection against cutaneous leishmaniasis resulting from bites of uninfected sand flies. *Science.* 290, 1351-1354.
- Kato, H., Anderson, J.M., Kamhawi, S., Oliveira, F., Lawyer, P.G., Pham, V.M., Sangare, C.S., Samake, S., Sissoko, I., Garfield, M., Sigutova, L., Volf, P., Doumbia, S., Valenzuela, J.G., 2006. High degree of conservancy among secreted salivary gland proteins from two geographically distant *Phlebotomus duboscqi* sandflies populations (Mali and Kenya). *BMC Genomics.* 7, 226.
- Kato, H., Cáceres, A.G., Gomez, E.A., Mimori, T., Uezato, H., Marco, J.D., Barroso,

- P.A., Iwata, H., Hashiguchi, Y., 2008. Molecular mass screening to incriminate sand fly vectors of Andean-type cutaneous leishmaniasis in Ecuador and Peru. *Am. J. Trop. Med. Hyg.* 79, 719-721.
- Kato, H., Gomez, E.A., Cáceres, A.G., Uezato, H., Mimori, T., Hashiguchi, Y., 2010a. Molecular epidemiology for vector research on leishmaniasis. *Int. J Environ. Res. Public Health.* 7, 814-826.
- Kato, H., Jochim, R.C., Gomez, E.A., Sakoda, R., Iwata, H., Valenzuela, J.G., Hashiguchi, Y., 2010b. A repertoire of the dominant transcripts from the salivary glands of the blood-sucking bug, *Triatoma dimidiata*, a vector of Chagas disease. *Infect. Genet. Evol.* 10, 184-191.
- Kato, H., Uezato, H., Katakura, K., Calvopiña, M., Marco, J.D., Barroso, P.A., Gomez, E.A., Mimori, T., Korenaga, M., Iwata, H., Nonaka, S., Hashiguchi, Y., 2005. Detection and identification of *Leishmania* species within naturally infected sand flies in the andean areas of Ecuador by a polymerase chain reaction. *Am J Trop Med Hyg.* 72, 87-93.
- Katz, O., Waitumbi, J.N., Zer, R., Warburg, A., 2000. Adenosine, AMP, and protein phosphatase activity in sandfly saliva. *Am. J. Trop. Med. Hyg.* 62, 145-150.
- King, T.P., Spangfort, M.D., 2000. Structure and biology of stinging insect venom allergens. *Int. Arch. Allergy Immunol.* 123, 99-106.
- Lerner, E.A., Ribeiro, J.M.C., Nelson, R.J., Lerner, M.R., 1991. Isolation of maxadilan, a potent vasodilatory peptide from the salivary glands of the sand fly *Lutzomyia longipalpis*. *J. Biol. Chem.* 266, 11234-11236.
- Lima, H.C., Titus, R.G., 1996. Effects of sand fly vector saliva on development of cutaneous lesions and the immune response to *Leishmania braziliensis* in BALB/c

- mice. *Infect. Immun.* 64, 5442-5445.
- Lu, X., Deadman, J.J., Williams, J.A., Kakkar, V.V., Rahman, S., 1993. Synthetic RGD peptides derived from the adhesive domains of snake-venom proteins: evaluation as inhibitors of platelet aggregation. *Biochem. J.* 296, 21-24.
- Marchler-Bauer, A., Panchenko, A.R., Ariel, N., Bryant, S.H., 2002. Comparison of sequence and structure alignments for protein domains. *Proteins.* 48, 439-446.
- Munstermann, L.E., 2005. Phlebotomine sand flies, the Psychodidae. Marquardt, W.C., Black, W.C., Freier, J.E., Hagedorn, H.H., Hemingway, J., Higgs, S., James, A.A., Kondratieff, B., Moore, C.G., eds. *In: Biology of Disease Vectors.* Second edition. Elsevier, San Diego CA, 141-151.
- Oliveira, F., Jochim, R.C., Valenzuela, J.G., Kamhawi, S., 2009. Sand flies, *Leishmania*, and transcriptome-borne solutions. *Parasitol. Int.* 58, 1-5.
- Oliveira, F., Kamhawi, S., Seitz, A.E., Pham, V.M., Guigal, P.M., Fischer, L., Ward, J., Valenzuela, J.G., 2006. From transcriptome to immunome: identification of DTH inducing proteins from a *Phlebotomus ariasi* salivary gland cDNA library. *Vaccine.* 24, 374-390.
- Oliveira, F., Lawyer, P.G., Kamhawi, S., Valenzuela, J.G., 2008. Immunity to distinct sand fly salivary proteins primes the anti-*Leishmania* immune response towards protection or exacerbation of disease. *PLoS Negl. Trop. Dis.* 2, e226.
- Ribeiro, J.M.C., Andersen, J., Silva-Neto, M.A., Pham, V.M., Garfield, M.K., Valenzuela, J.G., 2004. Exploring the sialome of the blood-sucking bug *Rhodnius prolixus*. *Insect Biochem. Mol. Biol.* 34, 61-79.
- Ribeiro, J.M.C., Francischetti, I.M.B., 2003. Role of arthropod saliva in blood feeding: sialome and post-sialome perspectives. *Annu. Rev. Entomol.* 48, 73-88.

- Ribeiro, J.M.C., Katz, O., Pannell, L.K., Waitumbi, J., Warburg, A., 1999. Salivary glands of the sand fly *Phlebotomus papatasi* contain pharmacologically active amounts of adenosine and 5'-AMP. *J. Exp. Biol.* 202, 1551-1559.
- Ribeiro, J.M.C., Modi, G., 2001. The salivary adenosine/AMP content of *Phlebotomus argentipes* Annandale and Brunetti, the main vector of human kala-azar. *J. Parasitol.* 87, 915-917.
- Ribeiro, J.M.C., Vachereau, A., Modi, G.B., Tesh, R.B., 1989. A novel vasodilatory peptide from the salivary glands of the sand fly *Lutzomyia longipalpis*. *Science.* 243, 212-214.
- Ribeiro, J.M.C., 1995. Blood-feeding arthropods: live syringes or invertebrate pharmacologists? *Infect. Agents.* 4, 143-152.
- Rohoušová, I., Subrahmanyam, S., Volfová, V., Mu, J., Volf, P., Valenzuela, J.G., Jochim, R.C., 2012. Salivary gland transcriptomes and proteomes of *Phlebotomus tobbi* and *Phlebotomus sergenti*, vectors of leishmaniasis. *PLoS Negl. Trop. Dis.* 6, e1660.
- Rohoušová, I., Volf, P., 2006. Sand fly saliva: effects on host immune response and *Leishmania* transmission. *Folia Parasitol.* 53, 161-171.
- Santos, A., Ribeiro, J.M.C., Lehane, M.J., Gontijo, N.F., Veloso, A.B., Sant'Anna, M.R., Nascimento Araujo, R., Grisard, E.C., Pereira, M.H., 2007. The sialotranscriptome of the blood-sucking bug *Triatoma brasiliensis* (Hemiptera, Triatominae). *Insect Biochem. Mol. Biol.* 37, 702-712.
- Schultz, J., Milpetz, F., Bork, P., Ponting, C.P., 1998. SMART, a simple modular architecture research tool: identification of signaling domains. *Proc. Natl. Acad. Sci. USA.* 95, 5857-5864.

- Singh, H., Raghava, G.P., 2001. ProPred: prediction of HLA-DR binding sites. *Bioinformatics*. 17, 1236-1237.
- Takaoka, H., Gomez, E.A., Alexander, J.B., Hashiguchi, Y., 1990. Natural infections with *Leishmania* promastigotes in *Lutzomyia ayacuchensis* (Diptera: Psychodidae) in an Andean focus of Ecuador. *J. Med. Entomol.* 27, 701-702.
- Tamura, K., Dudley, J., Nei, M., Kumar, S., 2007. MEGA4: Molecular Evolutionary Genetics Analysis (MEGA) software version 4.0. *Mol. Biol. Evol.* 24, 1596-1599.
- Tavares, N.M., Silva, R.A., Costa, D.J., Pitombo, M.A., Fukutani, K.F., Miranda, J.C., Valenzuela, J.G., Barral, A., de Oliveira, C.I., Barral-Netto, M., Brodskyn, C., 2011. *Lutzomyia longipalpis* saliva or salivary protein LJM19 protects against *Leishmania braziliensis* and the saliva of its vector, *Lutzomyia intermedia*. *PLoS Negl. Trop. Dis.* 5, e1169.
- Teixeira, C., Gomes, R., Collin, N., Reynoso, D., Jochim, R., Oliveira, F., Seitz, A., Elnaiem, D.E., Caldas, A., de Souza, A.P., Brodskyn, C.I., de Oliveira, C.I., Mendonca, I., Costa, C.H., Volf, P., Barral, A., Kamhawi, S., Valenzuela, J.G., 2010. Discovery of markers of exposure specific to bites of *Lutzomyia longipalpis*, the vector of *Leishmania infantum chagasi* in Latin America. *PLoS Negl. Trop. Dis.* 4, e638.
- Theodos, C.M., Ribeiro, J.M.C., Titus, R.G., 1991. Analysis of enhancing effect of sand fly saliva on *Leishmania* infection in mice. *Infect. Immun.* 59, 1592-1598.
- Thompson, J.D., Higgins, D.G., Gibson, T.J., 1994. CLUSTAL W: improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. *Nucleic Acids Res.* 22, 4673-4680.

- Titus, R.G., Ribeiro, J.M.C., 1988. Salivary gland lysates from the sand fly *Lutzomyia longipalpis* enhance *Leishmania* infectivity. *Science*. 239, 1306-1308.
- Valenzuela, J.G., 2005. Blood-Feeding Arthropod Salivary Glands and Saliva. Marquardt, W.C., Black, W.C., Freier, J.E., Hagedorn, H.H., Hemingway, J., Higgs, S., James, A.A., Kondratieff, B., Moore, C.G., eds. *In: Biology of Disease Vectors*. Second edition. Elsevier, San Diego CA, 377-386.
- Valenzuela, J.G., Belkaid, Y., Garfield, M.K., Mendez, S., Kamhawi, S., Rowton, E.D., Sacks, D.L., Ribeiro, J.M.C., 2001. Toward a defined anti-*Leishmania* vaccine targeting vector antigens: characterization of a protective salivary protein. *J. Exp. Med.* 194, 331-342.
- Valenzuela, J.G., Charlab, R., Gonzalez, E.C., de Miranda-Santos, I.K., Marinotti, O., Francischetti, I.M.B., Ribeiro, J.M.C., 2002. The D7 family of salivary proteins in blood sucking diptera. *Insect Mol. Biol.* 11, 149-155.
- Valenzuela, J.G., Garfield, M., Rowton, E.D., Pham, V.M., 2004. Identification of the most abundant secreted proteins from the salivary glands of the sand fly *Lutzomyia longipalpis*, vector of *Leishmania chagasi*. *J. Exp. Biol.* 207, 3717-3729.
- Vlkova, M., Rohousova, I., Drahotka, J., Stanneck, D., Kruedewagen, E.M., Mencke, N., Otranto, D., Volf, P., 2011. Canine antibody response to *Phlebotomus perniciosus* bites negatively correlates with the risk of *Leishmania infantum* transmission. *PLoS Negl. Trop. Dis.* 5, e1344.
- Weis, W.I., Taylor, M.E., Drickamer, K., 1998. The C-type lectin superfamily in the immune system. *Immunol. Rev.* 163, 19-34.
- Xu, X., Oliveira, F., Chang, B.W., Collin, N., Gomes, R., Teixeira, C., Reynoso, D., My Pham, V., Elnaiem, D.E., Kamhawi, S., Ribeiro, J.M.C., Valenzuela, J.G., Andersen,

J.F., 2011. Structure and function of a "yellow" protein from saliva of the sand fly *Lutzomyia longipalpis* that confers protective immunity against *Leishmania major* infection. J. Biol. Chem. 286, 32383-32393.

Young, D.G., Duncan, M.A., 1994. Guide to the Identification and Geographic Distribution of *Lutzomyia* Sand Flies in Mexico, the West Indies, Central and South America (Diptera: Psychodidae), Memoirs of the American Entomological Institute, 54, Associated Publishers—American Entomological Institute, Gainesville, FL.

Figure legends

Fig. 1. (A) Sequence alignment of PpSP15/SL1 family proteins from *Lutzomyia* (*Lu.*) *ayacuchensis* (LayS36, LayS37, LayS58, LayS59, LayS66, LayS68, LayS71, and LayS72) together with those from *Phlebotomus* (*P.*) *arabicus* (Pab), *P. argentipes* (Pag), *P. ariasi* (Par), *P. duboscqi* (Pdu), *P. papatasi* (Pp), *P. perniciosus* (Ppe), and *Lu. longipalpis* (Lulo). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site. (B) Phylogenetic tree analysis of amino acid sequences of PpSP15/SL1 family proteins from sand flies. Accession numbers are in parentheses and node values indicate branch support.

Fig. 2. (A) Sequence alignment of yellow-related proteins from *Lu. ayacuchensis* (LayS22, LayS23, LayS24, and LayS118) together with those from *P. arabicus* (Pab), *P. argentipes* (Pag), *P. ariasi* (Par), *P. duboscqi* (Pdu), *P. papatasi* (Pp), *P. perniciosus* (Ppe), and *Lu. longipalpis* (LJM). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site. Closed circles show conserved amino acids contained in the ligand binding pocket of yellow-related protein family. Potential N-glycosylation sites of *Lu. ayacuchensis* yellow-related proteins are boxed. (B) Phylogenetic tree

analysis of amino acid sequences of yellow-related proteins from sand flies.

Accession numbers are in parentheses and node values indicate branch support.

Fig. 3. (A) Sequence alignment of D7 family proteins from *Lu. ayacuchensis* (LayS101, LayS102, and LayS103) together with those from *P. arabicus* (Pab), *P. argentipes* (Pag), *P. ariasi* (Par), *P. duboscqi* (Pdu), *P. papatasi* (Pp), *P. perniciosus* (Ppe), and *Lu. longipalpis* (Lulo). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site. (B) Phylogenetic tree analysis of amino acid sequences of D7 family proteins from sand flies. Accession numbers are in parentheses and node values indicate branch support.

Legends for supplemental figures

Fig. S1. Sequence alignment of RGD-containing peptides from *Lutzomyia* (*Lu.*) *ayacuchensis* (LayS) together with that from *Lu. longipalpis* (LuloRGD).

Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site.

Fig. S2. Sequence alignment of SL1-like proteins from *Lu. ayacuchensis* (LayS) together with that from *Lu. longipalpis* (LuloSL1). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site. The bold line over amino acids denotes potential T cell epitopes as searched by using ProPred MHC Class-II Binding Peptide Prediction Server.

Fig. S3. Sequence alignment of 14 kDa salivary proteins from *Lu. ayacuchensis* (LayS) together with *P. perniciosus* 14 kDa salivary protein (PpeSP09). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site. The bold line over amino acids denotes potential T cell epitopes as searched by using ProPred MHC

Class-II Binding Peptide Prediction Server.

Fig. S4. Sequence alignment of yellow-related proteins from *Lu. ayacuchensis*, LayS22-LayS24 (A) and LayS118 (B), together with that of *Lu. longipalpis*, LJM11 (A) and LJM17(B), respectively. Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site. The bold line over amino acids denotes potential T cell epitopes as searched by using ProPred MHC Class-II Binding Peptide Prediction Server.

Fig. S5. Sequence alignment of putative apyrases from *Lu. ayacuchensis* (LayS) together with that from *Lu. longipalpis* (LuloAPY). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. An arrowhead indicates the predicted signal peptide cleavage site.

Fig. S6. Sequence alignment of D7 family proteins from *Lu. ayacuchensis* (LayS) together with that from *P. perniciosus* (PpeSP04b). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site.

Fig. S7. Sequence alignment of 27 kDa salivary proteins from *Lu. ayacuchensis* (LayS) together with *Lu. longipalpis* 29.2 kDa salivary protein (Lulo 29.2kDa). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. An arrowhead indicates the predicted signal peptide cleavage site.

Fig. S8. Sequence alignment of antigen 5-related proteins from *Lu. ayacuchensis* (LayS) together with that of *Lu. longipalpis* (Lulo Ag5). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site.

Fig. S9. Sequence alignment of 16.4 kDa proteins from *Lu. ayacuchensis* (LayS) together with *Lu. longipalpis* salivary 16.5 kDa protein (Lulo 16.5kDa). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment. Asterisks at the top of the amino acids denote conserved cysteine residues, and an arrowhead indicates the predicted signal peptide cleavage site.

Fig. S10. Sequence alignment of 11.5 kDa proteins from *Lu. ayacuchensis* (LayS) together with *Lu. longipalpis* salivary 9 kDa protein (Lulo 9kDa). Black-shaded amino acids represent identical amino acids and gray-shaded amino acids represent conserved amino acids. Dashes indicate gaps introduced for maximal alignment.

An arrowhead indicates the predicted signal peptide cleavage site.

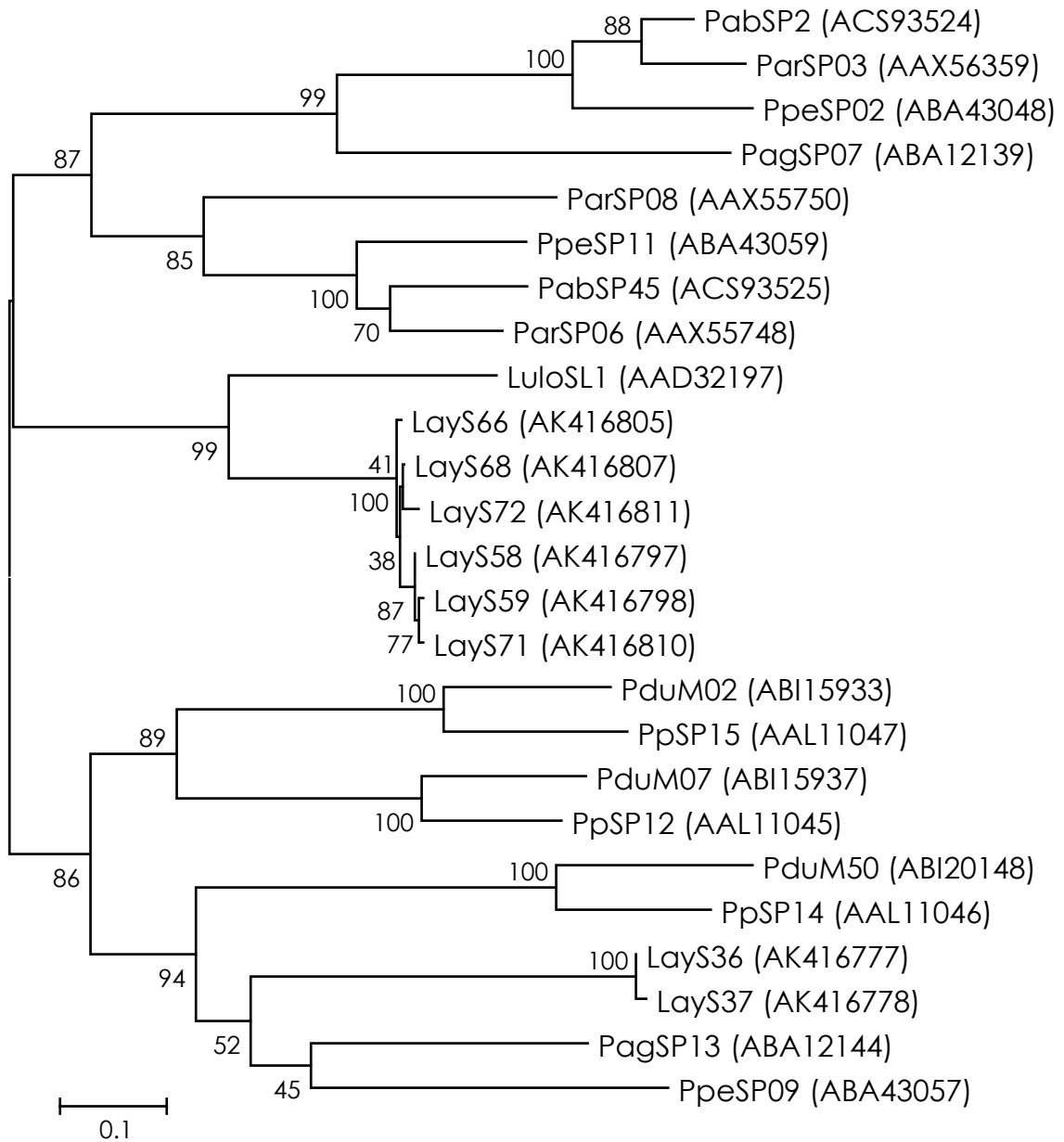


Fig. 1B

LayS22	M	LFLLVFTGILFQGILGVEITQG	KWRO	LYGDVTPGT	NPDTN	PIAFAHADADGHK	FLT	PRKFKPKIPTLA	VDTEKNPGVSGKRS	90						
LayS23	M	LFLLVFTGILFQGILGVEITQG	KWRO	LYGDVTPGT	NPDTN	PIAFAHADADGHK	FLT	PRKFKPKIPTLA	VDTEKNPGVSGKRS	90						
LayS24	M	LFLLVFTGILFQGILGVEITQG	KWRO	LYGDVTPGT	NPDTN	PIAFAHADADGHK	FLT	PRKFKPKIPTLA	VDTEKNPGVSGKRS	90						
LayS118	M	FFLCFFVFLSQGHIGAYVEIG	SWSN	TFEGLDTRK	KPRNN	PIAFAHADPEGYK	FIS	PRRLPQVPYVMA	LNTVMHPGVVERA	90						
LJM17	M	FFVFLAIVLFGQIGHAYVEIG	SLRN	TFEGLDTRD	NPKFN	PIGLAVDPEGYR	FIA	PRRKPVPYVVA	LNMVMNPGFVERA	90						
LJM111	M	LFFFLYTFGLVQTFGVEIKQG	KWNK	LYEGDTSN	NPDDN	LIAFAYDPESQK	FLT	PRKYPETMYTVA	VDTEKNSFESGDT	90						
LJM11	M	VEFISIFTLVLVFGQTLGAD-TQG	KWQK	LYNNVTPGS	NPDDN	SIAFAYDAEGEK	FLA	PRKLPVRVYVVA	VDTKNSLGVKGGKS	89						
PabSP26	M	IFLCLFAVVSFHGAFAYHVERE	AWKN	TYEGIDQAS	NIENT	PIAFAHADAISSK	FIT	PRRYPQVPITLTL	LDTSKHPE---RSP	87						
PagSP04	M	WFLFLLSTIFVQGLGYHVERE	AWRN	TFEGVNPS	NVLHS	PIGFAYDAETQK	FVA	PRRYPQVPHTLTL	IERKKHP---RSP	87						
ParSP04	M	IFLCLFAAVSIOGALASQIERE	AWKN	IYEGIDQGS	NIENS	PIAFAHADAAASK	FIT	PRIN-QVPTLTL	FDSIKYPG---GSP	87						
ParSP04b	M	IFEMGLIAVVSIOGALAYHVERE	AWKN	TYEGIDQAS	NIENS	PIAFAHADAISSK	IIA	PRRYPQVPITLTL	LDTSKHPE---RSP	86						
PduM10	M	FILSVLALASFOHVFCDVERA	AWRN	SFVDTREGT	NPEVD	PIGVTHDAKTK	YFG	PRLYPNIPYVVA	IDTNRKNSSEIRSP	90						
PduM35	M	LILTVLAFSLQVALSDDVGRLE	EWSE	DIVGVRSV	DSSNI	PIGVAYDAASKM	FFG	PRKVASVPIVVA	LSTRSYNSAEIRRD	90						
PpSP42	M	LILCVLSFSLQVALSDDVGRLE	EWSE	KLVGVRPNA	DSSNI	PIGVAYDAASKM	FFG	PRIYSRVPIVVA	LSTRSYNSAEIRPN	90						
PpSP44	M	FFLSVIALASFOHVFCDVERE	AWRN	TFEVDKGT	KPGDV	PIGVTHDAKTK	YFG	PRRYSNIPYVVA	IDTNRNRSSEIRSP	90						
PpeSP03	M	IFLCLIAVVSIOGVALYIERE	AWKN	SFEGIDPAS	SVKNS	PIGFADDAASK	FIT	PRLN-PVPIVVA	LDTTKHPE---GSP	86						
PpeSP03b	M	IFLCLIAVVSIOGVVGFHVERE	AWKN	SYEGVDPAL	NIDNI	PIGFVDAINKK	FIA	PRRSPQIPVITLTL	LDTTKHPE---RSP	87						
LayS22	P	---LLN	ESGHKSGNELT	SYQPID	CRRLW	VDVGSV	YRSRGAQDYP	PSHRPAVVA	DIKPNYPE	VRHHFPVRLVE-KPTYFGGF	176					
LayS23	P	---LLN	ESGHKSGKELT	SYQPID	CRRLW	VDVGSV	YRSRGAQDYP	PSHRPAVVA	DIKPNYPE	VRHHFPVRLVE-KPTYFGGF	176					
LayS24	P	---LLN	ESGHKSGKELT	SYQPID	CRRLW	VDVGSV	YRSRGAQDYP	PSHRPAVVA	DIKPNYPE	VRHHFPVRLVE-KPTYFGGF	176					
LayS118	P	---KLS	ETGQ-SSKDLV	SYQPID	CRRLW	VDVGSV	YSGDDAGKYK	TQKPAIVV	DIKDHYPE	GRYELPDSVAS-KPTSEGGF	175					
LJM17	P	SEFEKFK	ENGE-GKKDLV	SYQPID	CRRLW	LDVGSV	YTGDDAQYPKG	KPTLVA	DIKDHYPE	HRFEIPDDLSYS-SQVEFGGF	176					
LJM111	P	---LLG	ESGHETGKELT	SYQPID	CRRLW	VDVGSV	RNSDGTGEGE	PHNPTVA	DIKANYPE	IRYTFPDNSIE-KPTFLCGF	178					
LJM11	P	---LLN	ESGHKTGKELT	SYQPID	CRRLW	VDVGSV	YRSRGAQDYP	PSHRPAVVA	DIKPNYPE	VRYYFPVRLVE-KPTYFGGF	175					
PabSP26	P	---LS	EPG---SDDL	SYQPID	CRRLW	VDVGSV	YKG-DEQKYP	PKNSAAVVA	DIKDNYPE	GRYEIPRKISG-NPLGFGGF	178					
PagSP04	P	---LS	EPG---SSKDL	SYQPID	CRRLW	LDVGSV	YKE-GQPKYR	KQNPAAVVA	DIKDNYPE	DRYELPAEVVK-NPLSFGCF	160					
ParSP04	P	---LS	EPG---SDNI	SYQPID	CRRLW	VDVGSV	YKG-DEQKYP	PKKNPAVVA	DIKDNYPE	DRYEIPINIAG-NPLGFGGF	167					
ParSP04b	P	---LE	EPG---SDKL	SYQPID	CRRLW	VDVGSV	YKG-DEQKYP	PKKNPAVVA	DIKDNYPE	DRYEIPINIAG-NQIGFGGF	168					
PduM10	P	---FS	ENSQ-GGKEFT	SYQPID	CRRLW	LDVGSV	YKK-NGEYPT	KNPEVVA	DIKDNYPE	HRYLEKGDVAR-TPLGFGGF	173					
PduM35	P	---LD	ESGK-SKKPLT	SYQPID	CRRLW	LDVGSV	VKA-ERKTYPT	KNPAVVA	DIKDPYPE	HRYELTGAAD-TPLGYCGF	173					
PpSP42	P	---LD	ESGK-SKQPLT	SYQPID	CRRLW	LDVGSV	NEA-ERKTYPT	IKKNSVVA	DIKDNYPE	HRYELTGEAGK-NPLGYCGF	173					
PpSP44	P	---FS	ENSQ-SGKEFT	SYQPID	CRRLW	LDVGSV	YKK-NGEYPT	KNPEVVA	DIKDNYPE	HRYLEKGDVAR-NPLGFGGF	173					
PpeSP03	P	---LS	EPG---SDKL	SYQPID	CRRLW	VDVGSV	YKG-DEQKYP	PKNSAAVVA	DIKDNYPE	DRYEIPNNVAG-NPLGFGGF	167					
PpeSP03b	P	---LS	EPG---SDKL	SYQPID	CRRLW	ADVGRV	YKG-DEQKYP	QNNAVVA	DIKDNYPE	HRYEIPSKIAGSNTIPFGGF	169					
LayS22	A	DVYNPTGDCS	---EYVY	TNLSNA	FIVD	HKNOQ	SNVTD	AKA	---RPSTFDHQG	-KQYTYKAG	FGITLGRD	KDGR	IRPAYYL	260		
LayS23	A	DVYNPTGDCS	---EYVY	TNLSNA	FIVD	HKNOQ	SNVTD	AKA	---RPSTFDHQG	-KQYTYKAG	FGITLGRD	KDGR	IRPAYYL	260		
LayS24	A	DVYNPTGDCS	---EYVY	TNLSNA	FIVD	HKNOQ	SNVTD	AKA	---RPSTFDHQG	-KQYTYKAG	FGITLGRD	KDGR	IRPAYYL	260		
LayS118	A	DVINTKGDCT	---EYVY	TNLEENT	IIVD	QTSKD	WKFSD	BKP	---KESKFSHLR	-EQATYKVG	FGITLGRD	KDGR	IRPAYYL	259		
LJM17	A	DVINTKGDCT	---EYVY	TNLDNS	IIVD	ETQK	WKFSD	BKP	---KESKFSHLR	-EQATYKVG	FGITLGRD	KDGR	IRPAYYL	263		
LJM111	A	DVVKPD-ECS	---EYVY	TNLTNA	IIVD	HKNKD	SNVQDS	BGP	---KKSFKDHDG	-QYQYEAQ	FGITLGRD	NEGR	IRPAYYL	259		
LJM11	A	DVANPKGDCS	---EYVY	TNLRGA	FIVD	HKKQD	SNVTHP	BKA	---RPTKFDYGG	-KEYEFKAG	FGITLGRD	SEGR	IRPAYYL	259		
PabSP26	A	DVYNPTGECG	---KTEVY	TNLEENT	IIVD	QEKD	WKSISHG	BKP	---HDSVLTHNG	-KEHKYKVG	FGITLGRD	PEGR	IRPAYYL	252		
PagSP04	A	DVINPKGCG	---DTEVY	TNLEENT	IIVD	KKKA	WKSISHD	BKP	---KDVNIVL	DGGKYSYKVG	FGITLGRD	REATGR	IRPAYYL	255		
ParSP04	A	DVINPKGCG	---KTEVY	TNLEDNT	IIVD	QEKD	WKSISHG	BKP	---HESILIHNG	-VDHILKLE	FGITLGRD	SEGR	IRPAYYL	251		
ParSP04b	A	DVINPKGCG	---KTEVY	TNLEDNT	IIVD	QEKD	WKSISHG	BKP	---HESFNHNG	-AQYKYKAG	FGITLGRD	PEGR	IRPAYYL	252		
PduM10	A	DVILNPNKCA	TSDE-EYVY	TNIDNA	IIVD	MKNRN	WKLIND	BKP	---PGKSVFNHKG	-EYYSVIG	FGITLGRD	KDGR	IRPAYYL	261		
PduM35	A	DVYNPKK-CGK	NDKPYVVA	ANVENS	IIVD	KKSD	WVLKDD	BKP	---GVSTYHNG	-KEHELKTE	FGITLGRD	RNKEGR	IRPAYYL	260		
PpSP42	A	DVYNPKR-CSD	KNKPYVVA	ANVENS	IIVD	KKGE	WLSKDD	BKP	---GVTTFTLNG	-KEHKFAG	FGITLGRD	RNKEGR	IRPAYYL	260		
PpSP44	A	DVILNPNKCA	KSDE-EYVY	TNIDNA	IIVD	MKNRN	WKFIND	BKP	---PGKSVFNHKG	-EQYSIAG	FGITLGRD	RNKEGR	IRPAYYL	261		
PpeSP03	A	DVYNPKGCG	---KTEVY	TNLEDNT	IIVD	QEKD	WKSISHD	BKP	---HESILTHNG	-AQHILKLE	FGITLGRD	PEGR	IRPAYYL	251		
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LayS22	AGS	TKVYS	NTKELKQ	NKKNPELLNCRGKLN	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSNTRFV	G	DISV	350	
LayS23	AGS	TKVYS	NTKELKQ	NKKNPELLNCRGKLN	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSNTRFV	G	DISV	350	
LayS24	AGS	TKVYS	NTKELKQ	NKKNPELLNCRGKLN	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSNTRFV	G	DISV	350	
LayS118	AGS	TKVYS	NTKELKQ	GGSLNPTLHCDRGPHTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	VQTE	-LKPENTDV	LYSARFV	G	DISV	348	
LJM17	AGS	TKVYS	NTKELKQ	NGQLNPQLHCDRGRKTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	VNME	-LKPENTDV	LYSARFV	G	DISV	352	
LJM111	VAS	TKVYS	NTKELKQ	GSKVNAVYLEDRGEST	AA	GLVYDPKTRV	FEA	BSNTROV	SCW	TOET	-LKNKIDV	LYHNADF	G	DISV	348	
LJM11	AGS	TKVYS	NTKELKQ	GSKVNAVYLEDRGEST	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSARFV	G	DISV	349	
PabSP26	AGS	TKVYS	NTKELKQ	GAKFDPVRI	CDRGRHTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSARFV	G	DISV	341
PagSP04	AGS	TKVYS	NTKELKQ	GAKFDPVRI	CDRGRHTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSARFV	G	DISV	344
ParSP04	AGS	TKVYS	NTKELKQ	GAKFDPVRI	CDRGRHTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSARFV	G	DISV	340
ParSP04b	AGS	TKVYS	NTKELKQ	GAKFDPVRI	CDRGRHTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSARFV	G	DISV	341
PduM10	AGS	TKVYS	NTKELKQ	VKSLKPTLLCBRGYKTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	IQKD	-LKPENGVV	LYTNAFV	G	DISV	350	
PduM35	AGS	TKVYS	NTKELKQ	GSKLVKPLICDRGRYKTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	IKKE	-LKPENGVV	LYSSAKL	EA	DMV	349	
PpSP42	AGS	TKVYS	NTKELKQ	GSKLVKPLICDRGRYKTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	IKKE	-LKPENGVV	LYANPNF	G	DMV	349	
PpSP44	AGS	TKVYS	NTKELKQ	GASLKERLLCBRGYKTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	IQKE	-LKPENGVV	LYTNAFV	G	DISV	350	
PpeSP03	AGS	TKVYS	NTKELKQ	AGQIETPLCBRGYKTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKS	-LKNPNIDV	LYHSPDF	G	DISV	340	
PpeSP03b	AGS	TKVYS	NTKELKQ	GAKFDPVRI	CDRGRHTA	AA	ALAYDPKTRV	FEA	BSNTROV	SCW	TQKMP	IRMOHTDV	LYSARFV	G	DISV	342
LayS22	DSKGLWFM	NGEPPVKN	SQKFK	---FDYPRYR	LN	-DTQAAIAGTN	-CEIKPR	-----							400	
LayS23	DSKGLWFM	NGEPPVKN	SQKFK	---FDYPRYR	LN	-DTQAAIAGTN	-CEIKPR	-----							400	
LayS24	DSKGLWFM	NGEPPVKN	SQKFK	---FDYPRYR	LN	-DTQAAIAGTN	-CEIKPR	-----							400	
LayS118	DKKGLWFM	NGEPPVKN	SQKFK	---K-LKFYDR	KIR	MR	-NTYNVLPYSK	-CNEDYKGG	QGI	FV					405	
LJM17	DSKGLWFM	NGEPPVKN	SQKFK	---K-LKFYDR	KIR	MR	-NTYNVLPYSK	-CNEDYKGG	QGI	FV					412	
LJM111	DSQDNLWFL	NGEPPVKN	SQKFK	---FTKPRYQ	FK	-NIQEA	IAGTK	-CEKNL							397	
LJM11	DSKGLWFM	NGEPPVKN	SQKFK	---YDFPRYR	MRI	-DTQEA	IAGTA	-CDMA							399	
PabSP26	DSESLWFL	NGEPPVKN	SQKFK	---FDKPHIR	MR	-DTEKS	IRTR	-CEVKPIKPP	----						393	
PagSP04	DSNSTLWFM	NGEPPVKN	SQKFK	---NNEFYK	PQIR	LY	-DTRKS	IRTR	-CDVNG	NKP	----				398	
ParSP04	DSESLWFL	NGEPPVKN	SQKFK	---SDKPHIR	IS	-DTEKA	IRGTR	-CEVKA							388	
ParSP04b	DSDSLWFL	NGEPPVKN	SQKFK	---FDKPHIR	MR	-DTKNS	IRTR	-CEVKPIKPP	----						393	
PduM10	DADSLWFM	NAHPPTKI	PKLE	---FDKQIR	MK	-PTHRA	IRNLP	-CEMRKA							399	
PduM35	DSKGLWFM	NGEPPVKN	SQKFK	---YEDPHIR	MK	-KTKKA	IRGTR	-CEVKA							395	
PpSP42	DSKGLWFM	NGEPPVKN	SQKFK	---YDVPQIR	MK	-KTKKA	IRGTR	-CEVKA							394	
PpSP44	DADSLWFM	NAHPPTKI	PKLE	---FDKQIR	MY	-PTHRA	IRNLP	-CEMRKA							400	
PpeSP03	DSESLWFL	NGEPPVKN	SQKFK	---FDKPHIR	IS	-DTEKS	IRGTR	-CEVKA							388	
PpeSP03b	DSESLWFL	NGEPPVKN	SQKFK	---FDKPHIR	MR	-DTAKA	IRTR	-CEVKPRK	----						393	

Fig. 2A

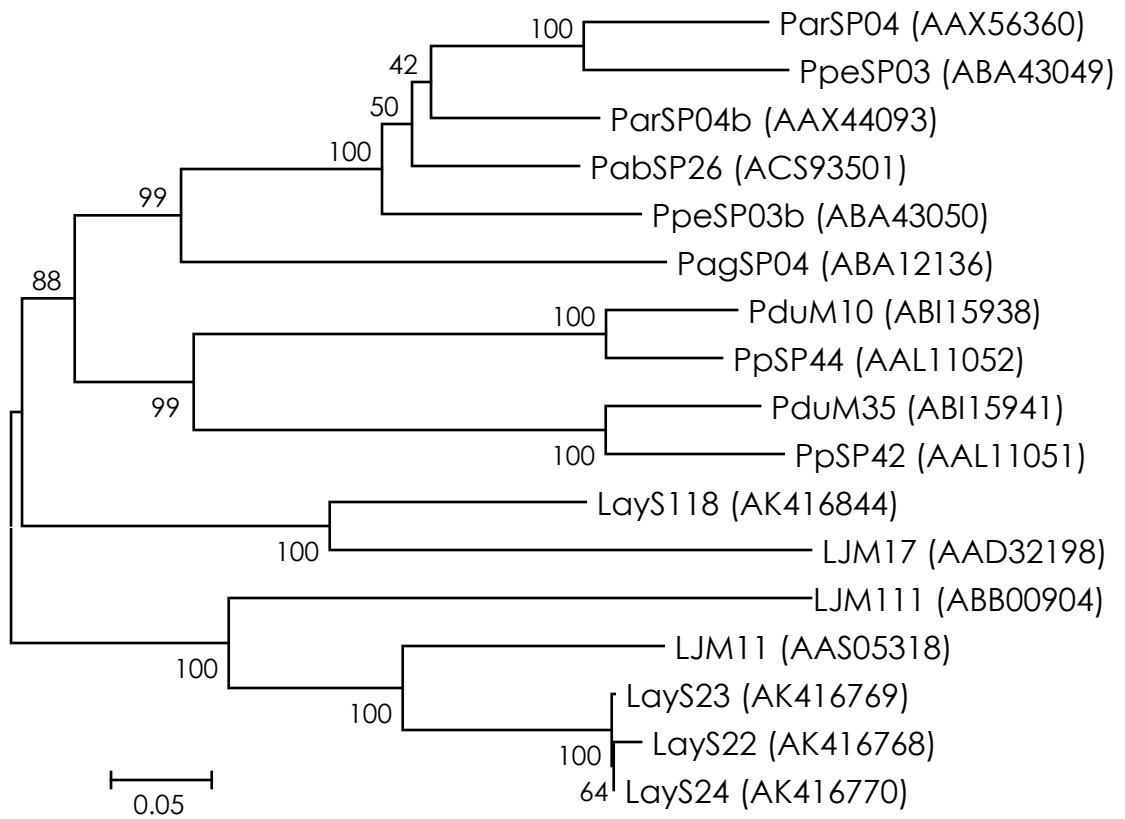


Fig. 2B

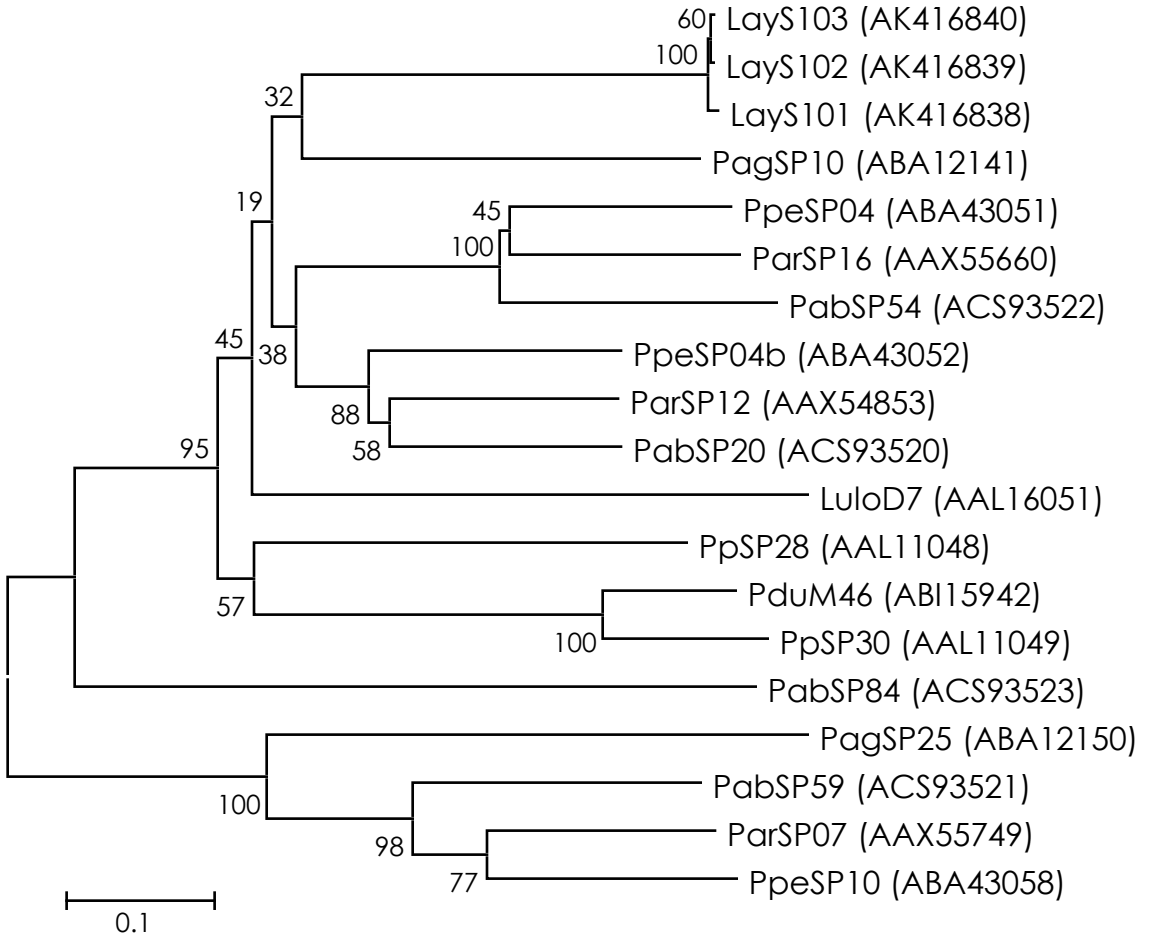


Fig. 3B

Table 1. Functional classification of housekeeping genes expressed in *Lutzomyia ayacuchensis* salivary glands

Type of transcripts	Cluster	%	Sequence	%
Energy production and conversion	20	21.3	24	19.2
Translation, ribosomal structure and biogenesis	19	20.2	23	18.4
General function prediction only	9	9.6	10	8.0
Signal transduction mechanisms	8	8.5	8	6.4
Posttranslational modification, protein turnover, chaperones	7	7.4	14	11.2
Lipid transport and metabolism	5	5.3	5	4.0
Amino acid transport and metabolism	4	4.3	4	3.2
Chromatin structure and dynamics	2	2.1	2	1.6
Inorganic ion transport and metabolism	2	2.1	2	1.6
Intracellular trafficking, secretion, and vesicular transport	2	2.1	3	2.4
RNA processing and modification	2	2.1	2	1.6
Secondary metabolites biosynthesis, transport and catabolism	2	2.1	2	1.6
Transcription	2	2.1	14	11.2
Carbohydrate transport and metabolism	1	1.1	3	2.4
Cell cycle control, cell division, chromosome partitioning	1	1.1	1	0.8
Cell wall/membrane/envelope biogenesis	1	1.1	1	0.8
Defense mechanisms	1	1.1	1	0.8
Unknown conserved	6	6.4	6	4.8
Total	94	100.0	125	100.0

Table 2. Most abundant salivary gland transcripts from *Lutzomyia ayacuchensis*

Cluster	Sequence name	No. of seq in cluster	Mature Mw (kDa)	pI	Best match to NR protein database				Accession No.
					Accession No.	Organism	E value	% identity	
LayS45	RGD-containing peptide	90	5.3	3.44	AAD32196	<i>Lu. longipalpis</i>	3E-07	47	AK416785
LayS37	14 kDa salivary protein	58	14.1	8.21	ABA43057	<i>P. perniciosus</i>	6E-39	50	AK416778
LayS81	antigen 5-related protein	24	28.5	9.08	AAD32191	<i>Lu. longipalpis</i>	1E-135	80	AK416820
LayS24	yellow-related protein	23	43.5	9.37	AAS05318	<i>Lu. longipalpis</i>	0	78	AK416770
LayS59	SL1-like protein	19	13.8	8.22	AAD32197	<i>Lu. longipalpis</i>	1E-51	64	AK416798
LayS91	27 kDa salivary protein	17	27.2	10.14	AAS16906	<i>Lu. longipalpis</i>	2E-92	59	AK416828
LayS117*	yellow related-protein	16			AAD32198	<i>Lu. longipalpis</i>	4E-77	66	AB744655
LayS118	yellow related-protein	14	43.8	8.05	AAD32198	<i>Lu. longipalpis</i>	1E-164	67	AK416844
LayS127	16.4 kDa salivary protein	11	16.4	8.05	ABB00903	<i>Lu. longipalpis</i>	1E-29	39	AK416852
LayS21	putative apyrase	11	35.7	9.19	AAD33513	<i>Lu. longipalpis</i>	1E-123	65	AK416767
LayS142	9.3 kDa protein	10	9.3	4.22	XP_001238639	<i>Eimeria tenella</i>	0.012	44	AK416859
LayS103	D7-related salivary protein	9	26.6	8.81	ABA43052	<i>P. perniciosus</i>	7E-86	59	AK416840
LayS36	14 kDa salivary protein	9	14.1	8.21	ABA43057	<i>P. perniciosus</i>	2E-39	50	AK416777
LayS6	11.5 kDa salivary protein	8	11.5	6.67	AAS16919	<i>Lu. longipalpis</i>	2E-07	33	AK416753
LayS102	D7-related salivary protein	8	26.6	8.81	ABA43052	<i>P. perniciosus</i>	7E-86	59	AK416839
LayS19	putative apyrase	8	35.8	9.09	AAD33513	<i>Lu. longipalpis</i>	1E-127	65	AK416765
LayS58	SL1-like protein	8	13.8	8.22	AAD32197	<i>Lu. longipalpis</i>	1E-51	64	AK416797
LayS68	SL1-like protein	8	13.9	8.61	AAD32197	<i>Lu. longipalpis</i>	7E-52	64	AK416807
LayS90	27 kDa salivary protein	8	26.6	10.08	AAS16906	<i>Lu. longipalpis</i>	1E-90	58	AK416827
LayS101	D7-related salivary protein	7	26.6	8.81	ABA43052	<i>P. perniciosus</i>	2E-86	59	AK416838
LayS66	SL1-like protein	6	13.9	8.61	AAD32197	<i>Lu. longipalpis</i>	1E-51	64	AK416805
LayS20	putative apyrase	6	35.5	9.00	AAD33513	<i>Lu. longipalpis</i>	1E-128	65	AK416766
LayS22	yellow-related protein	6	43.4	9.39	AAS05318	<i>Lu. longipalpis</i>	1E-125	75	AK416768
LayS17	putative apyrase	5	35.5	9.11	AAD33513	<i>Lu. longipalpis</i>	1E-128	65	AK416763
LayS18	putative apyrase	5	36.0	9.46	AAD33513	<i>Lu. longipalpis</i>	1E-128	65	AK416764
LayS23	yellow-related protein	5	43.5	9.37	AAS05318	<i>Lu. longipalpis</i>	0	78	AK416769
LayS26	33.6 kDa salivary protein	5	33.7	8.95	AAx55751	<i>P. ariasi</i>	6E-91	53	AK416772
LayS44	RGD-containing peptide	5	5.3	3.47	AAD32196	<i>Lu. longipalpis</i>	8E-07	46	AK416784
LayS71	SL1-like protein	5	13.8	8.22	AAD32197	<i>Lu. longipalpis</i>	2E-50	64	AK416810
LayS72	SL1-like protein	5	13.8	8.43	AAD32197	<i>Lu. longipalpis</i>	3E-51	64	AK416811
LayS100	D7-related salivary protein	4	26.6	8.61	ABA43052	<i>P. perniciosus</i>	4E-86	59	AK416837
LayS131	16.4 kDa salivary protein	4	16.4	8.32	ABB00903	<i>Lu. longipalpis</i>	7E-26	39	AK416856
LayS3	allergen-related protein	4	26.0	5.68	XP_001865175	<i>Culex quinquefasciatus</i>	8E-31	35	AK416750
LayS64	SL1-like protein	4	13.9	8.61	AAD32197	<i>Lu. longipalpis</i>	5E-48	59	AK416803
LayS97	D7-related salivary protein	4	26.6	8.81	ABA43052	<i>P. perniciosus</i>	2E-86	59	AK416834
LayS128	16.4 kDa salivary protein	3	16.4	8.05	ABB00903	<i>Lu. longipalpis</i>	1E-29	39	AK416853
LayS129	16.4 kDa salivary protein	3	16.4	7.69	ABB00903	<i>Lu. longipalpis</i>	2E-29	40	AK416854
LayS16	putative apyrase	3	36.6	9.34	AAD33513	<i>Lu. longipalpis</i>	1E-125	64	AK416762
LayS27	33.6 kDa salivary protein	3	33.7	8.69	AAx55751	<i>P. ariasi</i>	1E-90	52	AK416773
LayS46	RGD-containing peptide	3	5.3	3.44	AAD32196	<i>Lu. longipalpis</i>	1E-07	49	AK416786
LayS47	RGD-containing peptide	3	5.3	3.44	AAD32196	<i>Lu. longipalpis</i>	2E-07	47	AK416787
LayS70	SL1-like protein	3	13.9	7.98	AAD32197	<i>Lu. longipalpis</i>	5E-51	64	AK416809
LayS77	antigen 5-related protein	3	28.6	9.21	AAD32191	<i>Lu. longipalpis</i>	1E-135	80	AK416816
LayS89	27 kDa salivary protein	3	26.6	10.08	AAS16906	<i>Lu. longipalpis</i>	5E-90	58	AK416826
LayS98	D7-related salivary protein	3	26.6	8.81	ABA43052	<i>P. perniciosus</i>	3E-86	59	AK416835
LayS130	16.4 kDa salivary protein	2	16.4	8.05	ABB00903	<i>Lu. longipalpis</i>	2E-29	40	AK416855
LayS132	16.4 kDa salivary protein	2	16.4	8.05	ABB00903	<i>Lu. longipalpis</i>	2E-29	40	AK416857
LayS2	allergen-related protein	2	26.0	5.46	XP_001865175	<i>Culex quinquefasciatus</i>	5E-30	34	AK416749
LayS60	SL1-like protein	2	13.9	7.98	AAD32197	<i>Lu. longipalpis</i>	7E-51	64	AK416799
LayS61	SL1-like protein	2	13.8	8.22	AAD32197	<i>Lu. longipalpis</i>	1E-51	65	AK416800
LayS62	SL1-like protein	2	13.8	8.52	AAD32197	<i>Lu. longipalpis</i>	6E-51	64	AK416801
LayS63	SL1-like protein	2	13.8	8.23	AAD32197	<i>Lu. longipalpis</i>	1E-51	64	AK416802
LayS65	SL1-like protein	2	13.8	7.98	AAD32197	<i>Lu. longipalpis</i>	1E-51	64	AK416804
LayS67	SL1-like protein	2	13.8	8.35	AAD32197	<i>Lu. longipalpis</i>	1E-50	64	AK416806
LayS69	SL1-like protein	2	13.9	8.22	AAD32197	<i>Lu. longipalpis</i>	4E-51	64	AK416808
LayS7	11.5 kDa salivary protein	2	10.8	8.36	AAS16919	<i>Lu. longipalpis</i>	2E-07	34	AK416754
LayS78	antigen 5-related protein	2	28.4	9.16	AAD32191	<i>Lu. longipalpis</i>	1E-133	80	AK416817
LayS79	antigen 5-related protein	2	28.4	9.08	AAD32191	<i>Lu. longipalpis</i>	1E-135	80	AK416818
LayS80	antigen 5-related protein	2	28.5	9.01	AAD32191	<i>Lu. longipalpis</i>	1E-135	80	AK416819
LayS92	27 kDa salivary protein	2	27.3	10.14	AAS16906	<i>Lu. longipalpis</i>	9E-91	58	AK416829
LayS93	27 kDa salivary protein	2	27.2	10.14	AAS16906	<i>Lu. longipalpis</i>	1E-91	58	AK416830
LayS95	D7-related salivary protein	2	26.6	8.81	ABA43052	<i>P. perniciosus</i>	5E-86	59	AK416832
LayS96	D7-related salivary protein	2	26.6	8.81	ABA43052	<i>P. perniciosus</i>	1E-85	58	AK416833
LayS99	D7-related salivary protein	2	26.6	8.81	ABA43052	<i>P. perniciosus</i>	6E-86	59	AK416836

*truncated in the 5' region

Table 3. Classification of transcripts coding for putative secreted proteins in *Lutzomyia ayacuchensis* salivary glands

	Cluster	Sequence	% sequence
RGD-containing peptide	10	107	18.7
SL1-like protein	25	82	14.3
14 kDa salivary protein	6	71	12.4
yellow-related protein	5	64	11.1
putative apyrase	13	45	7.9
D7-related salivary protein	9	42	7.3
27 kDa salivary protein	11	38	6.6
antigen 5-related protein	9	37	6.5
16.4 kDa salivary protein	13	32	5.6
9.3 kDa protein	3	16	2.8
11.5 kDa salivary protein	4	12	2.1
33.6 kDa salivary protein	3	9	1.6
allergen-related protein	2	6	1.0
Others	9	12	2.1
Total	122	573	100.0