



HAL
open science

Evidence for an ichnovirus machinery in parasitoids of coleopteran larvae

Stéphanie Robin, Marc Ravallec, Marie Frayssinet, James Whitfield,
Véronique Jouan, Fabrice Legeai, Anne-Nathalie Volkoff

► **To cite this version:**

Stéphanie Robin, Marc Ravallec, Marie Frayssinet, James Whitfield, Véronique Jouan, et al.. Evidence for an ichnovirus machinery in parasitoids of coleopteran larvae. *Virus Research*, 2019, 263, pp.189-206. 10.1016/j.virusres.2019.02.001 . hal-02059774

HAL Id: hal-02059774

<https://hal.science/hal-02059774>

Submitted on 22 Oct 2021

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.



Distributed under a Creative Commons Attribution - NonCommercial 4.0 International License

Evidence for an ichnovirus machinery in parasitoids of coleopteran larvae

Stéphanie ROBIN^{1,2}, Marc RAVALLEC³, Marie FRAYSSINET³, James WHITFIELD⁴, Véronique JOUAN³, Fabrice LEGEAI^{1,2} and Anne-Nathalie VOLKOFF^{3*}

Affiliations

1. UMR 1349 INRA/Agrocampus Ouest/Université Rennes 1, Institut de Génétique, Environnement et Protection des Plantes (IGEPP), Le Rheu, France

2. Université Rennes 1, INRIA, CNRS, IRISA, F-35000 Rennes, France

3. DGIMI, INRA, University of Montpellier, Montpellier, France

3. Department of Entomology, University of Illinois, Urbana-Champaign, U.S.A.

* Corresponding author: anne-nathalie.volkoff@inra.fr

INTRODUCTION

Bathyplectes anurus and *B. curculionis* are morphologically similar and closely related ichneumonid wasps that parasitize larvae of the alfalfa weevil, *Hypera postica*, commonly found in alfalfa fields in the south of France. They are solitary parasitoids whose life cycle is synchronized with that of alfalfa weevils. *B. anurus* produces one generation per year and undergoes 2 diapause, one in the summer at the larval stage and the other following pupation in the winter at the pupal stage. The adult emerges from overwintered cocoons in the spring of the following year to oviposit into hosts. After the larva has consumed the *H. postica* larva, it emerges to spin a white-banded, dark brown cocoon, and enter diapause until the fall. On the other hand, some of the *B. curculionis* pupae issued from spring parasitism may develop until the adult stage leading to a second generation.

Bathyplectes spp. produce unusual particles in their ovaries that accumulate in the oviducts (Hesse et al., 1980). Interestingly, *Bathyplectes* spp. are classified in the subfamily Campopleginae that includes thousands of species that carry domesticated endogenous viruses from the *Polydnviridae* family. Polydnviruses are characterized by packaged genomes composed of several dsDNA circular molecules. They are reported from thousands of species from the families Ichneumonidae and Braconidae parasitizing lepidopteran larvae. Polydnviruses associated with ichneumonids and braconids differ in their morphology and genome, so they were classified into the genera Ichnovirus and Bracovirus, respectively. Polydnviruses illustrate an astonishing example of convergent evolution since the two “polydnvirus genera” result from two independent events of virus domestication. Bracoviruses result from the integration of a nudivirus (Bézier et al., 2009) whereas ichnoviruses derive from the domestication of a still unknown virus (Volkoff et al., 2010). In both cases, polydnviruses show a similar life cycle and are required for successful parasitism. The virus particles are produced in a specialized tissue from the female called the calyx. They are secreted and stored in the oviduct lumen, then injected into the insect host along with the parasitoid egg upon parasitization. The integrated polydnvirus genomes are dual in nature, and include regions that will be excised, circularized and encapsidated (the “packaged genome” that consists in dsDNA circular molecules or segments), and other regions directly descending from the viral ancestor, that are expressed in the calyx cells, are not encapsidated and are involved in the formation of the virus particles (the “viral machinery”). The viral machinery includes nudiviral genes in the case of bracoviruses, and genes with no similarity to any other known virus group in the case of ichnoviruses (see below). Conversely, the encapsidated segments carry almost no genes with homology to known viral genes (e.g. with predicted functions in viral DNA replication, transcription, or virion formation) but instead a number of genes that share homology with genes from insects or other eukaryotes, which are expressed in the parasitized insect host and involved in its physiological manipulation (Chen et al., 2011; Darboux et al., 2018; Desjardins et al., 2008; Espagne et al., 2004; Lapointe et al., 2007; Tanaka et al., 2007; Webb et al., 2006).

Ichnoviruses (IV) have so far been described in two ichneumonid subfamilies, the Campopleginae and the Banchinae. All IV fully described are carried by species of endoparasitoids of lepidopteran larvae. The IV particles reported from these subfamilies are surrounded by two unit membranes but differ in their morphology. Most campoplegine species produce IV particles that consist of a large fusiform nucleocapsid (Krell & Stoltz, 1980; Stoltz et al., 1981; Volkoff et al., 1995) whereas in the two studied Banchinae, multi-nucleocapsid virions were reported (Djoumad et al., 2013; Lapointe et al., 2007). Nucleocapsids from Banchinae resemble those from Campopleginae, but are smaller in size. A third morphological category of particles associated with campoplegine wasps corresponds to the virus-like particles (VLPs) reported from *Venturia canescens*, that have been proven to not be ichnoviruses but to result from a domestication of a nudivirus that occurred more recently, and functionally replaced the IV originally present in this lineage (Pichon et al., 2015). Lastly a fourth morphological category of virus particles carried by campoplegine wasps were reported in *Bathyplectes anurus* and *B. curculionis* (Hess et al., 1980; Stoltz et al., 1981). Interestingly, and in contrast to all the other wasp species carrying polydnviruses that parasitize lepidopteran larvae, these two species parasitize coleopteran larvae. *Bathyplectes* virus particle morphology is quite different from typical campoplegine IV particles. They consist of ovoid membrane particles that contain several small electron dense inclusions (Hess et al., 1980; Stoltz et al., 1981). As for the other examples, *Bathyplectes* particles are produced in the calyx. However, in absence of any genomic data regarding these species and the particles produced in their ovaries, it was still uncertain till now whether these particles were of viral nature and/or related to ichnoviruses.

Based on the absence of evidence that *Bathyplectes* spp. particles are actually polydnviruses, we focused in this work on *B. anurus* to address the question of their nature and origin. To identify genes potentially involved in the production of the particles, a transcriptomic analysis of the female reproductive tract, where the particles are produced, has been performed. Our results indicate that a number of IV genes are expressed in *B. anurus* ovaries, demonstrating that *B. anurus* atypical particles are indeed related to the ichnoviruses.

MATERIAL AND METHODS

Insect material

Hypera postica larvae were collected in alfalfa fields in different sites around Montpellier. The alfalfa weevil larvae were brought to the lab and kept at room temperature until formation of the *Bathyplectes* cocoons. In the fall, cocoons were maintained outdoors until next spring. At the end of the pupal stage, cocoons were dissected to isolate female pupae that were dissected in PBS to isolate the ovaries.

Alternatively, adult females were directly caught in the fields, then brought to the laboratory and dissected to collect their ovaries. Identity has been confirmed using COI barcoding. Briefly, genomic DNA was extracted from adults using Wizard® Genomic DNA Purification Kit (Promega) according to manufacturer instructions. Genomic DNA was used as a template for PCR amplification using COI specific primers (LCO1490: 5'- GGT CAA CAA ATC ATA AAG ATA TTG G -3' and HC02198: 5'- TAA ACT TCA GGG TGA CCA AAA AAT CA -3', as described in Folmer et al., 1994). PCR amplification products were sent for sequencing by Eurofins, and annotated subsequent to a Blastn similarity search against NCBI non redundant (nr) database.

Microscopy

Ovaries were dissected from old pupae and adults and were then fixed with 2% (v/v) glutaraldehyde in 0.1 M cacodylate buffer pH 7.4 for overnight at 4°C, rinsed 3 times for 10 mn in the same buffer then post-fixed with 2% (v/v) osmium tetroxide for 1 h at room temperature. Samples were dehydrated through an ethanol series and embedded in Embed 812 (EMS products). Semithin sections were stained with methylene blue and observed under a photonic microscope. Ultrathin sections contrasted with uranyl acetate and lead citrate were examined under an electron microscope Jeol 1200 EXII at 100 kV (MEA Platform, Université de Montpellier). Images were taken with an EMSIS Olympus Quemesa 11 Mpixels camera and analysed with Image J software (Rasband, 1997-2018).

RNAseq data generation and de novo transcriptome assembly

To obtain the ovary transcriptome, total RNA was extracted from the ovaries dissected from 60 *B. anurus* female pupae using the Qiagen RNeasy Mini Kit according to the manufacturer's protocol. PolyA-RNA-Seq Library construction and Illumina HiSeq 2000 sequencing (paired-end sequencing 2x100 bp) were performed by GATC Biotech AG company (GATC NG-7281 project).

Upon reception of the sequences, the following analyses were performed: (i) quality assessment using FastQC (<http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>), (ii) removal of sequencing adapters with Trimmomatic (Bolger et al., 2014); (iii) de novo transcript assembly with the Trinity suite version 2.2.0 (Haas et al 2013); (iv) calculation of transcript counts and fragments per kilobase per million (FPKM) using RSEM software (Li et al., 2011).

A total of 46,530 assembled transcripts (contigs) were obtained. The transcripts assembly obtained statistics were: a mean size of 990 bp, a median size of 470 bp, a N50 length of 1,942 bp, a L50 length of 6,588 bp and 42,46% of GC content.

For annotation, all 46,530 transcripts were used as a query for a BLASTx search (Altschul et al., 1997) in the 'National Center for Biotechnology Information' (NCBI) non-redundant (nr) database, considering all hits with an e-value<1E-08. Following BLAST search, we obtained 24,851 transcripts with "no hits" (53,4%). We also used BUSCO (Simão et al., 2015) to test for the presence of reference

genes in this transcriptome. Over the 1,658 Total BUSCO groups searched, we obtained 1,477 complete BUSCOs (87.6%), 1,063 complete and single-copy BUSCOs (64%), 414 complete and duplicated BUSCOs, 101 fragmented BUSCOs and 80 missing BUSCOs.

Finally, after filtering with FPKM ≥ 1 and isoform percentage (isopct) ≥ 15 , a total of 41,467 transcripts were kept for further analyses (list in Supplemental Table 1). A selected set of transcripts was manually analyzed to identify the open reading frames, then the predicted protein sequence was used in blastP similarities searches against NCBI nr protein database to assess amino acid identities between the *B. anurus* predicted protein and the best protein match.

RESULTS AND DISCUSSION

Bathyplectes virion morphogenesis resembles that of ichnoviruses

The *Bathyplectes* female ovary resembles that described in other campoplegine wasps (Figures 1A, 1B and 1C) with a marked calyx region at the junction between ovarioles and lateral oviducts. The calyx is spherical in shape and is constituted of a unicellular layer of large epithelial cells with a hypertrophied nucleus (Figure 1D). In the calyx lumen, a number of particles can be observed (Figure 1E). They are spherical in shape, with a 200 nm diameter and surrounded by two envelopes. In adult females, the particles contain small electron dense inclusions that appear punctiform or slightly elongated (Figure 1E).

Morphogenesis of *Bathyplectes* virus (BaV) particles occurs in the calyx cells, and generally corresponds to what was previously described by Hesse et al. (1980). Electron dense fibril-like structures are distributed within the calyx cell nuclei where BaV particles are formed. At the vicinity of these structures, probably virogenic stroma, a number of spherical vesicles can be observed (Figures 2A and 2B). These vesicles consist of single unit lipid bilayers of still unknown origin. In pupae, the vast majority of the vesicles appear to be empty (Figure 2A). Conversely, in the adults, they contain punctiform inclusions as described in Hesse et al. (1980) and BaV particles can be observed at the vicinity of the virogenic stroma and free in the nucleus (Figure 2B). The process of BaV particles formation is similar to what has been described for ichnoviruses. Indeed, in ichnoviruses, single enveloped particles are similarly assembled at the vicinity of virogenic stroma (Lapointe et al., 2007; Volkoff et al., 1995). Therefore, and as for the IVs, BaV particles envelopes are neoformed in the calyx cells nuclei and then filled with material probably originating from the fibril like material corresponding to a virogenic stroma. The origin of these envelopes remains unclear, as for IVs and BVs. Possibly they originate from the nuclear envelope as described for another type of enveloped dsDNA insect virus, the baculoviruses that acquire their envelopes from virus-induced intranuclear microvesicles (Crawford et al., 1985). Unfortunately, except for examples of nuclear envelopes found

in the vicinity of the nuclear envelope (Figure 2C), we did not succeed in clearly observing this event in *Bathyplectes* calyx cells. The enveloped BaV particles then bud through the nuclear envelope and reach the cell cytoplasm (Figure 2D), similarly to the process that occurs for ichnoviruses. The nuclear envelope remains intact and particles surrounded by two envelopes as can be observed within the cytoplasm (Figure 2D). As for IVs, this second envelope is lost during the migration of the particles within the cytoplasm towards the plasma membrane. Finally, the particles bud through the cell plasma membrane, which harbors numerous microvilli, and accumulate in the oviduct lumen (Figures 3A and 3B). Interestingly, we observed that in *B. anurus* diapausing pupae (Figure 3C), most of the released enveloped particles appeared empty, suggesting that somehow the calyx cells were already “induced” to produce the virus particles, even though assembly may be incomplete.

Therefore, despite morphology quite different from that of typical campoplegine ichnoviruses, the process by which *Bathyplectes* particles are formed, which includes synthesis of envelopes within the nuclei, migration from the nucleus to the oviduct lumen and acquisition of a second envelope during calyx cell budding, resembles what has been described for ichnoviruses.

A number of genes similar to IVSPER genes are highly transcribed in B. anurus ovaries

“Ichnovirus Structural Protein Encoding Regions” (IVSPERs) were first described in the campopleginae *H. didymator* (Volkoff et al., 2010) then in the banchine *Glypta fumiferanae* (Cusson et al., 2012). The IVSPER genes are specifically transcribed in the calyx tissue and 2/3rd of them encode proteins found associated with IV particles by mass spectrometry analyses. IVSPERs remain in the wasp genome and are not packaged within the IV particles. These regions hypothetically correspond to fingerprints of the ancestral ichnovirus which integrated into the ancestral wasp genome. Except for their involvement in the IV particle constitution, the precise function of all the IVSPER genes remains today unknown.

Following Blast search analyses, a total of 119 sequences matched with viruses, 80 (67%) matched with products of IVSPERs, 34 (29%) with products of IV genes, 4 (3%) with picornavirus gene products and 1 (1%) with an entomopoxvirus gene product (list in Supplemental Material 1). After manual curation, homologs corresponding to a total of 28 IVSPER genes were found in the *B. anurus* ovary transcriptome (Table 1; Supplemental Table 1). In *H. didymator* IVSPERs, a total of 24 “unknown” genes (U1 to U24) were described, as well as members of 6 families, named IVSP1 to IVSP4, p53 and p12 (Volkoff et al., 2010). Note that p12 and p53 genes were first described in the campoplegine *Campoletis sonorensis* (Deng et Webb, 1999; Deng et al., 2000). Homologs of 18 out of the 24 unknown *H. didymator* IVSPER genes were identified in *B. anurus*, as well as at least one homolog of IVSP1, IVSP2, IVSP3, IVSP4 (2 genes) and p53 gene families (Figure 4). However, no p12 gene homolog has been identified in *B. anurus* transcriptome by automatic annotation, maybe because they correspond to short sequences (about 100 aa) quite divergent among them (32 to 40%

amino acid identity between the p12 identified in *C. sonorensis*, *H. didymator* and *G. fumiferanae*; data not shown). We also identified in the *B. anurus* transcriptome sequences matching with N-gene family members. In *H. didymator*, the N-gene family includes genes present both in the IVSPERs and in the packaged viral segments. Members of this gene family were also identified in the IVSPER of the banchine *Glypta fumiferanae* (Cusson et al., 2012) although in Banchinae, N-genes are *a priori* absent from the viral segments. Finally, we also identified a homolog of the *G. fumiferanae* U28, which has for now not being identified in the campoplegine *H. didymator*.

Among all the obtained transcripts, the most highly transcribed one in the *B. anurus* calyx is a gene homolog to the *H. didymator* IVSPER gene U13 (Table 1; Supplemental Table 1). Note that this gene is absent from *G. fumiferanae* genome (Darboux et al., 2018). The *B. anurus* U13-like gene encodes a predicted protein which is similar in size with the *H. didymator* protein and with which it shares 44% identity (Table 1, Supplemental Figure 1). The second most transcribed is a long transcript matching in a short region with *H. didymator* IVSPER gene U20 which is also specific to this species. U20 encodes a very short protein sharing 48% amino acid identity with the *B. anurus* U8L predicted sequence (Table 1, Supplemental Figure 1). The two other most transcribed sequences in *B. anurus* ovaries with IVSPER similarities correspond to the genes U8 and IVSP4, for which homologs have been detected in both *H. didymator* and *G. fumiferanae*. Actually two genes belonging to the IVSP4 family have been detected in the *B. anurus* transcriptome, one more similar to *H. didymator* IVSP4-1, the other to *H. didymator* IVSP4-2 (Table 1, Supplemental Figure 1). Overall most of the *B. anurus* genes with similarities with IVSPER genes are highly transcribed in *B. anurus* ovaries, strongly suggesting that they correspond to functional and biologically active genes, therefore probably involved in *B. anurus* particles production.

Interestingly, we found in some cases contigs containing several IVSPER-like genes. This was the case of the contigs DN10347_c3_g1_i1, DN10385_c0_g1_i2, DN10351_c0_g1_i3 and DN10406_c0_g3_i3 which contained U19L and IVSP4L, IVSP3L, IVSP1L and U7L, IVSP2L and NgeneL, and U10L, U11L and U12L, respectively. Presence of multiple genes within the same contig suggests that they may have been (mis)assembled due to overlap of genes' UTRs. However, this succession of genes in the contigs matched with the order of their homologs in *H. didymator* IVSPERs (Figure 4), therefore suggesting some synteny between *B. anurus* IVSPER genes and *H. didymator* IVSPER genes and organization in clusters of the *B. anurus* IVSPER-like genes. A future sequencing of *B. anurus* genome would allow to characterize more precisely the IVSPER-like genes organization.

Altogether, the large number of IVSPER genes identified in the *B. anurus* ovary transcriptome, their high level of transcription, and the putative conserved organization in clusters indicates that an IV machinery is involved in the production of *B. anurus* particles, that could indeed be considered as IV particles.

***B. anurus* particles probably carry viral genomes with similarities to other campoplegine IVs**

Ichnoviruses carried by Campopleginae and Banchinae have both been sequenced, revealing quite surprising differences between the two. Campoplegine IV genomes include about 50 molecules generally ranging in size between 2 and 10 kb. They encode about 150 genes, including members of 6 gene families, such as the viral ankyrins (Vank), the cysteine-motif (Cys), the viral innexins (Vinx), or the “N-genes”. In campoplegine IVs, the most abundant gene family is the “repeat element” (rep) one that may include more than 30 genes (Tanaka et al., 2007, Dorémus et al., 2014). Conversely, banchine IV genomes are more fragmented and contain a completely different set of genes (Djournad et al., 2013). The most highly represented gene family in banchine IVs corresponds to the protein tyrosine phosphatase (PTP) genes, with 20 to 30 genes identified in the two sequenced genomes. The other conserved gene families include the NTPase-like gene, the BV-like and the MULE transposase domains encoding genes. The viral ankyrins represent the only gene family shared by both IV lineages (also present in bracoviruses, the polydnviruses carried by braconid wasps).

Bathyplectes particles morphology is quite atypical. Based on the literature, our observations in *B. anurus* and *B. curculionis*, BaV particles more closely resemble banchine IV than campoplegine IVs. However, the nature of the few genes identified in the *B. anurus* transcriptome with similarities with genes harbored by IV segments, thus putatively carried by packaged segments, strongly suggests that *Bathyplectes* viruses are more closely related to campoplegine than to banchine ichnoviruses. Except for viral ankyrins, no typical banchine IV gene was identified in the *B. anurus* transcriptome: indeed, no PTP or NTPase gene was found. On the other hand, a number of sequences corresponding to repeat element genes, which are characteristic of ichnoviruses associated with campoplegine wasps, were identified (Table 1; Supplemental Figure 1; Supplemental Table 1).

Regarding the levels of transcription, except for some repeat element genes (for instance contig DN7233_c1_g1_i3, FPKM = 1,984; contig DN9406_c3_g1_i3, FPKM = 1,103; contig DN9191_c0_g3_i1, FPKM = 1,026; Table 1), the *B. anurus* genes matching with IV segment genes were transcribed at lower level compared to those matching with IVSPER genes (Supplemental Table 1). This is expected as viral segment genes are genes transferred via the viral particles to the parasitoid host where they are expressed and involved in host physiology manipulation.

Therefore, based on the presence of one of the most abundant and characteristic gene family of campoplegine IVs, we can conclude that *B. anurus* virus particles probably contain DNA molecules containing genes related to campoplegine IVs.

The genetic resemblances of BaV to campoplegine IVs, despite the host group of the wasps being Coleoptera, brings up the question of whether *Bathyplectes* are truly campoplegines, or something related at some level to campoplegines. Current taxon sampling in molecular phylogenetic and phylogenomic studies of Ichneumonidae do not allow a definitive answer to this question (either not

including *Bathyplectes*, or based on only a few genes that conflict in inferred phylogenetic relationships). Classifications based on morphology reveal the following:

Originally, all of the wasps in the "Ophioniformes" (including the current Campopleginae) belonged to the same subfamily, Ophioninae, one of only a half-dozen or so subfamilies of Ichneumonidae at the time). Townes, in his revisions of ichneumonids of many parts of the world (see especially Townes 1970), began to recognize many more, so that the classification started to converge to the current number of 39 subfamilies recognized. The definition of the Campopleginae (called Porizontinae by Townes) has been more or less stable for many years now, with only some controversy about whether 3 or 4 odd genera (not *Bathyplectes*) should be placed there or not.

The relationships within Campopleginae are another matter. Wahl (1991), based on comparative morphology of adults and larvae, recognized 5 "genus groups" within Campopleginae: 1) the *Bathyplectes* group, with 5 genera, was considered the most distant or early-diverging of these, sharing at least one character with the Ctenopelmatinae; 2) a *Gonotypus* group; 3) a *Nemeritis* group; 4) a *Menaka* group; and 5) a *Dusona* group, containing almost all the genera we normally think of (all those except *Bathyplectes* that have been surveyed for PDVs and VLPs). Wahl's classification would be definitely consistent with the idea that *Bathyplectes* might have different-looking PDVs than the others. As remarked above, molecular phylogenetic data neither strongly confirm nor reject the classification at this point, but there is certainly no evidence that *Bathyplectes* are not campoplegines, as the little molecular data (28S rDNA) available place *Bathyplectes* squarely within the Campopleginae (Quicke 2015).

CONCLUSION

The work conducted on the *B. anurus* pupal transcriptome therefore confirms that an ichnoviral machinery is highly expressed in the ovaries of this parasitoid of a coleopteran host, and therefore most probably involved in the production of BaV particles. Due to the lack of *Bathyplectes* laboratory colonies, we were not able to analyze the particles and their content in proteins and nucleic acids. However, our results suggest that the BaV particles contain proteins encoded by IVSPER genes and DNA molecules encoding genes such as viral ankyrins and repeat-element genes and are therefore related to campoplegine ichnoviruses. Deciphering the function of *Bathyplectes* IVSPER genes, which are involved in particles assembly, will allow us to better understand their atypical morphology whereas deciphering the function of the packaged BaV genes may allow to understand the unusual host range of the parasitoid producing them.

Acknowledgements. We thank the quarantine insect platform (PIQ), member of the Vectopole Sud network, for providing the infrastructure needed for insect maintenance. This work was in part supported by the Agence Nationale de la Recherche (ABC-PaPoGen, ref. ANR-12-ADAP-0001) and by the “Département Santé des Plantes et Environnement” from INRA.

The *B. anurus* transcriptomic dataset is available in the Sequence Read Archive (SRA) database under the accession number PRJNA508369. This Transcriptome Shotgun Assembly project has been deposited at DDBJ/EMBL/GenBank under the accession GHFB00000000. The version described in this paper is the first version, GHFB01000000.

References

- Andrews, S. FASTQC. A quality control tool for high throughput sequence data. <http://www.bioinformatics.babraham.ac.uk/projects/fastqc/>.
- Beliveau, C., Cohen, A., Stewart, D., Periquet, G., Djoumad, A., Kuhn, L., Stoltz, D., Boyle, B., Volkoff, A.N., Herniou, E.A., Drezen, J.M., Cusson, M., 2015. Genomic and Proteomic Analyses Indicate that Banchine and Campoplegine Polydnviruses Have Similar, if Not Identical, Viral Ancestors. *J. Virol.* 89, 8909-8921. DOI: 10.1128/JVI.01001-15.
- Bezier, A., Annaheim, M., Herbinière, J., Wetterwald, C., Gyapay, G., Samain, S., Wincker, P., Roditi, I., Heller, M., Belghazi, M., Pfister-Wilhem, R., Periquet, G., Dupuy, C., Huguët, E., Volkoff, A.N., Lanzrein, B., Drezen, J.M., 2009. Bracoviruses derive from an ancestral nudivirus. *Science* 323, 926. DOI: 10.1126/science.1166788.
- Bolger, A.M., Lohse, M., Usadel, B., 2014. Trimmomatic: a flexible trimmer for Illumina sequence data. *Bioinformatics* 30:2114–20. DOI: 10.1093/bioinformatics/btu170.
- Chen, Y.F., Gao, F., Ye, X.Q., Wei, S.J., Shi, M., Zheng, H.J., Chen, X.X., 2011. Deep sequencing of *Cotesia vestalis* bracovirus reveals the complexity of a polydnvirus genome. *Virology* 414, 42-50. doi: 10.1016/j.virol.2011.03.009.
- Crawford, A.M., Sheehan, C., 1985. Replication of *Oryctes* baculovirus in cell culture: Viral morphogenesis, infectivity and protein synthesis. *J. Gen. Virol.* 66, 529-539. DOI: 10.1099/0022-1317-66-3-529.
- Darboux, I., Cusson, M., Volkoff, A.N., 2019. The dual life of ichnoviruses. *Current Opinion in Insect Science* 32, 47-53. <https://doi.org/10.1016/j.cois.2018.10.007>.

Deng, L., Webb, B.A., 1999. Cloning and expression of a gene encoding a *Campoletis sonorensis* polydnavirus structural protein. *Arch. Insect Biochem. Physiol.* 40, 30-40. DOI: 10.1002/(SICI)1520-6327(1999)40:1<30::AID-ARCH4>3.0.CO;2-Y.

Deng, L., Stoltz, D.B., Webb, B.A., 2000. A gene encoding a polydnavirus structural polypeptide is not encapsidated. *Virology* 269, 440-450. <https://doi.org/10.1006/viro.2000.0248>.

Desjardins, C.A., Gundersen-Rindal, D.E., Hostetler, J.B., Tallon, L.J., Fadrosch, D.W., Fuester, R.W., Pedroni, M.J., Haas, B.J., Schatz, M.C., Jones, K.M., Crabtree, J., Forberger, H., Nene, V., 2008. Comparative genomics of mutualistic viruses of *Glyptapanteles* parasitic wasps. *Genome Biol.* 9, R183. doi: 10.1186/gb-2008-9-12-r183.

Djoumad, A., Stoltz, D., Béliveau, C., Boyle, B., Kuhn, L., Cusson, M., 2013. Ultrastructural and genomic characterization of a second banchine polydnavirus confirms the existence of shared features within this ichnovirus lineage. *J Gen Virol.* 94, 1888-95. doi: 10.1099/vir.0.052506-0.

Dorémus, T., Cousserans, F., Gyapay, G., Jouan, V., Milano, P., Wajnberg, E., Darboux, I., Cònsoli, F.L., Volkoff, A.N., 2014. Extensive transcription analysis of the *Hyposoter didymator* Ichnovirus genome in permissive and non-permissive Lepidoptera host species. *PLOS One* 9(8), e104072. doi:10.1371/journal.pone.0104072.

Espagne, E., Dupuy, C., Huguet, E., Cattolico, L., Provost, B., Martins, N., Poirié, M., Periquet, G., Drezen, J.M., 2004. Genome sequence of a polydnavirus: insights into symbiotic virus evolution. *Science* 306, 286–289. DOI: 10.1126/science.1103066.

Folmer, O., Black, M., Hoeh, W., Lutz, R., Vrijenhoek, R., 1994. DNA primers for amplification of mitochondrial cytochrome c oxidase subunit I from diverse metazoan invertebrates. *Molecular Marine Biology and Biotechnology* 3, 294–299.

Haas, B.J., Papanicolaou, A., Yassour, M., Grabherr, M., Blood, P.D., Bowden, J., Couger, M.B., Eccles, D., Li, B., Lieber, M., MacManes, M.D., Ott, M., Orvis, J., Pochet, N., Strozzi, F., Weeks, N., Westerman, R., William, T., Dewey, C.N., Henschel, R., LeDuc, R.D., Friedman, N., Regev, A., 2013. De novo transcript sequence reconstruction from RNA-seq using the Trinity platform for reference generation and analysis. *Nat Protoc.* 8, 1494–512. DOI: 10.1038/nprot.2013.084.

Hess, R.T., Poinar, Jr., G.O., Etzel, L., Merritt, C.C., 1980. Calyx particle morphology of *Bathyplectes anurus* and *B. curculionis* (Hymenoptera: Ichneumonidae). *Acta zool. (Stockh.)* 61(2): 111–116. DOI: 10.1111/j.1463-6395.1980.tb01297.x}.

Krell, P.J., Stoltz, D.B., 1980. Virus-like particles in the ovary of an ichneumonid wasp: Purification and preliminary characterization. *Virology* 101, 408-418. [https://doi.org/10.1016/0042-6822\(80\)90454-7](https://doi.org/10.1016/0042-6822(80)90454-7).

Lapointe, R., Tanaka, K., Barney, W.E., Whitfield, J.B., Banks, J.C., Beliveau, C., Stoltz, D., Webb, B.A., Cusson, M., 2007. Genomic and morphological features of a banchine polydnavirus: comparison with bracoviruses and ichnoviruses. *J. Virol.* 81, 6491-6501. DOI: 10.1128/JVI.02702-06.

Li, B., Dewey, C.N., 2011. RSEM: accurate transcript quantification from RNA-Seq data with or without a reference genome. *BMC Bioinformatics* 12, 323. DOI: 10.1186/1471-2105-12-323.

Pichon, A., Bezier, A., Urbach, S., Aury, J.M., Jouan, V., Ravallec, M., Guy, J., Cousserans, F., Theze, J., Gauthier, J., Demetere, E., Schmieder, S., Wurmser, F., Sibut, V., Poirie, M., Colinet, D., Da Silva, C., Couloux, A., Barbe, V., Drezen, J.M., Volkoff, A.N., 2015. Recurrent DNA virus domestication leading to different parasite virulence strategies. *Sci. Adv.* 1(10):e1501150. DOI : 10.1126/sciadv.1501150.

Quicke, D.L.J., 2015. *The Braconid and Ichneumonid Parasitoid Wasps: Biology, Systematics, Evolution and Ecology.* Wiley Blackwell, Chichester, Sussex. 681 pp. ISBN: 978-1-118-90705-4.

Rasband, W.S., ImageJ, U. S. National Institutes of Health, Bethesda, Maryland, USA, <https://imagej.nih.gov/ij/>, 1997-2018.

Simão, F.A., Waterhouse, R.M., Ioannidis, P., Kriventseva, E.V., 2015. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. *Genome Anal.* 31, 9–10. <https://doi.org/10.1093/bioinformatics/btv351>.

Stoltz, D.B., 1981. A putative baculovirus in the ichneumonid parasitoid, *Mesoleius tenthredinis*. *Can J Microbiol.* 27, 116-122. <https://doi.org/10.1139/m81-018>.

Tanaka, K., Lapointe, R., Barney, W.E., Makkay, A.M., Stoltz, D., Cusson, M., Webb, B.A., 2007. Shared and species-specific features among ichnovirus genomes. *Virology* 363, 26-35. DOI: 10.1016/j.virol.2006.11.034.

Townes, H.K., 1970. The Genera of Ichneumonidae, Part 3. Banchinae, Scolobatinae and Porizontinae. *Memoirs of the American Entomological Institute* 13, 1-307.

Volkoff, A.N., Jouan, V., Urbach, S., Samain, S., Bergoin, M., Wincker, P., Demetere, E., Cousserans, F., Provost, B., Coulibaly, F., Legeai, F., Béliveau, C., Cusson, M., Gyapay G. Drezen, J.M., 2010. Analysis of virion structural components reveals vestiges of the ancestral ichnovirus genome. *PLoS Pathog.* 6:e1000923. doi: [10.1371/journal.ppat.1000923].

Volkoff, A.N., Ravallec, M., Bossy, J.P., Cerutti, P., Rocher, J., Cerutti, M., Devauchelle, G., 1995. The replication of *Hyposoter didymator* polydnavirus: Cytopathology of the calyx cells in the parasitoid. *Biology of the Cell* 83, 1–13. [https://doi.org/10.1016/0248-4900\(96\)89926-6](https://doi.org/10.1016/0248-4900(96)89926-6)

Wahl, D.B., 1991. The status of *Rhimphoctona*, with special reference to the higher categories within Campopleginae and the relationships of the subfamily (Hymenoptera: Ichneumonidae). Transactions of the American Entomological Society 117, 193-213.

Webb, B.A., Strand, M.R., Dickey, S.E., Beck, M.H., Hilgarth, R.S., Barney, W.E., Kadash, K., Kroemer, J.A., Lindstrom, K.G., Rattanadechakul, W., Shelby, K.S., Thoetkiattikul, H., Turnbull, M.W., Witherell, R.A., 2006. Polydnavirus genomes reflect their dual roles as mutualists and pathogens. Virology 347, 160-174. DOI: 10.1016/j.virol.2005.11.010.

Figure legends

Figure 1. *Bathyplectes* ovaries and virus particles. **A.** View of the *B. anurus* ovary at the diapausing pupal stage. **B.** View of the *B. curculionis* ovary at the adult stage. **C.** Detail on the *B. curculionis* calyx region at the adult stage. For A, B and C, arrow indicates the calyx. **D.** Semi-thin transverse section of the calyx region in a diapausing *B. anurus* pupa, stained with methylene blue, showing the layer of calyx cells containing large nuclei. **E.** Transmission electronic microscopy (TEM) observation of a section of the oviduct lumen in a *B. curculionis* adult female. Spherical enveloped particles containing punctiform inclusions (probably nucleocapsids) can be observed.

Figure 2. *Bathyplectes* particles formation within the calyx cells nuclei. **A.** TEM view of the calyx of *B. anurus* at the diapausing pupal stage. Electron dense fibril-like structure (probably virogenic stroma) is surrounded by spherical envelopes apparently empty (black arrow). Occasionally some contain electron dense material (white arrow). At this stage it is difficult to determine whether the envelopes are migrating towards the virogenic stroma or coming from the virogenic stroma. **B.** TEM view of the calyx of *B. curculionis* at the adult stage. Close to the virogenic stroma, numerous enveloped particles containing punctiform inclusions (probably nucleocapsids) can be observed. **C.** Detail of the calyx of *B. anurus* at the diapausing pupal stage showing envelopes at the vicinity of the nuclear envelope (NE). **D.** Detail showing particles in an older diapausing pupa. Although the majority of them appear empty, some begin to contain the characteristic punctiform inclusions observed in adults (arrows). **E.** Detail of the calyx of *B. curculionis* at the adult stage showing particles budding from the nucleus to the cytoplasm through the nuclear envelope (NE). One particle is budding (white arrow) whereas another can be observed within the cytoplasm surrounded by two envelopes (black arrow), suggesting that the particles may acquire transiently a second envelope originating from the nuclear envelope.

Figure 3. Exit of *Bathyplectes* particles from the calyx cells. **A.** TEM view of the *B. curculionis* calyx at the adult stage. Numerous particles are present in the cytoplasm (white arrow) and some can be observed in the **microvilli** (Mv) of the calyx cell (black arrow), by which they bud towards the oviduct lumen acquiring a second outer envelope. **B.** TEM view of the *B. curculionis* calyx at the adult stage. BaV particles exit from the calyx cell at the plasma membrane harboring abundant microvilli (black arrows) and accumulate in the oviduct lumen. **C.** TEM view of the *B. anurus* calyx at the diapausing pupal stage. The cytoplasm is filled with vesicles (Ves). In the cytoplasm as well as in the oviduct lumen, vesicles containing electron dense material can be observed (arrows) that may correspond to “immature” particles. Mv: plasma membrane microvilli.

Figure 4. IVSPER genes in *Bathyplectes anurus* ovary transcriptome. Schematic representation of the IVSPER genes identified in *B. anurus*. They are indicated in the upper part of an alignment with the IVSPERs published for the campoplegine wasp *Hyposoter didymator* (Darboux et al., 2018). Directions for *B. anurus* genes were intentionally not indicated as the orientation of one gene relative to the others in *B. anurus* genome is not known. Dashed red lines indicate clusters of genes that were detected in a single *B. anurus* contig.

Table 1. List of selected *Bathyplectes anurus* transcripts displaying similarities with ichnovirus genes. For each transcript, are indicated the ID, the length, the obtained FPKM value, the corresponding gene name, the amino acid sequence of the predicted protein, the size of the predicted protein. For each predicted *B. anurus* protein are indicated details concerning the best hit obtained following BlastP similarity search (against nr NCBI database): the e-value, the NCBI ID, whether it is encoded by an IVSPER or a packaged IV segment, its name, the parasitoid species, the protein size and the amino acids identity with the *B. anurus* protein.

Supplemental Table 1. List of the transcripts in the *Bathyplectes anurus* ovary transcriptome.

Supplemental Material 1. Analysis and list of *Bathyplectes anurus* transcripts matching with virus sequences.

Supplemental Figure 1. Alignment of selected *Bathyplectes anurus* predicted proteins (Ba_U13L, Ba_U20L, Ba_U8L, Ba_IVSP4L, Ba_rep1L, Ba_Rep2L, Ba_Rep3L and Ba_VankyrinL) with known ichnovirus proteins using CLUSTAL O(1.2.4) multiple sequence alignment software (<https://www.ebi.ac.uk/Tools/msa/clustalo/>).

Table

1:

Bathypectes anurus transcript_id	length (nt)	FPKM	Gene name	Predicted protein	Predicted protein size (aa)	BlastP e-value	BlastP_I D	IVSPER/segment	Name	Species	Protein size (aa)	Amino acids identity
DN10347_c3_g4_i1	589	7,646.28	Ba_IVSP_U13L	>Ba_U13L_aa MSFVSAILNEIFFNGKEKYAGDNPFLDALPIFNCPLLYARMLNEHW NSGEPSPFKPKTLFTAEGITVSVPEGDNFRPVKRHASMPIERP YLLQEIKDVHTYGRREIMNAESHGSEDDAKAEDGEDEDEMLLSIFGNL DEGMDDVDQDS	147	1,E-20	ADI40471 .1	IVSPER	U13	<i>Hyposoter didymator</i>	152	52/115 (45%)
DN8671_c0_g1_i1	6,494	4,533.64	Ba_IVSP_U20L	>Ba_U20L_aa MEERKASRLRVISRRPYNQKNSEAIVQTALKIHARLEAMPIDEPLS PDLRAVTHCDQCQSVR	45 (partial?)	3,E-04	ADI40485 .1	IVSPER	U20	<i>Hyposoter didymator</i>	70	26/54 (48%)
DN9501_c0_g1_i1	1,290	4,247.41	Ba_IVSP_U8L	>Ba_IVSP_U8L_aa MSRDTNTGRRNRRKASSERSKGVGKMLTPIDELLRSLIAKTINERQ QWADIVLDSVQPVYTSDTFTYINKKTGDEVLYA	79	2,E-14	ADI40466 .1	IVSPER	U8	<i>Hyposoter didymator</i>	77	37/75 (49%)
DN10347_c3_g1_i1	5,107	1,100.42	Ba_IVSP_4L-1	>Ba_IVSP4L_aa MTPCSMIRSKQC VSLNTVSVPCVPLKHPKMIKFSSKTYFDISFVHT GRKVYTVEEALRTVRTVSWATASIDKVKKEILKALSAWKFPTRKS RNMFDLAFRFGLOHFYRYLCICEDNKLLYDETYFDDLYDYLGESG YLSGQVQQLSSEMICETLAFIRDHSSIDATCSANKKEAEQERTKM KEFRERDFVTLFKMKSFIDDDSVAGSDP ADPVVTTNP AEAKNVIVS FISCLLSSESQVNHSLDFFSKQWLSEIYKGCYQFTSVEAFCMFFN NVSVYQFSDRVMFYMPDPREKFRRLVIRETCLSGTGDPADCAP EDPDCKCDMIRLISGVDIVENGSNLEVEALASKKLNRPMSAIRM CPTGDAIMSIRGNLKTISEILCKNKEQSDGAYWSDGATVSDDDAS TDVDDIRLSCRVKKRAAKRRKRGLI	437	2,E-132	ADI40475 .1	IVSPER	IVSP4-1	<i>Hyposoter didymator</i>	446	201/396 (51%)
DN10347_c3_g1_i2	6,099	332.45	Ba_IVSP_U19L	>Ba_U19L_aa_partial MVHHFVDRIEYRPVTANTSETS NATKTNLALMLLNLGISLASLGSF DINIPLVDSDLLPASPSLVKDVINAFDKMIQKLRWL VIGSITNVSLFT EWDALTPKLP SVSNKND AQLRATLCNRNERLEYNGPPTAPADL SCAWSKLS EIALDFNVCDNGSII LCTVLNRC SF LKTAKLSNVCSLDD GFLNDRNLCTPMLNCLHEKCHVVCVVELL KMLKKGFIKKLYLTLV ADPHDHCQKKMYNLDKIASYTG EYSEIYSNLLHIT	267 (partial)	3,E-109	ADI40483 .1	IVSPER	U19	<i>Hyposoter didymator</i>	660	174/281 (62%)
DN10347_c3_g1_i4	2,423	2,515.27	Ba_IVSP_4L-2	>Ba_IVSP4L-2_aa MTPCSMIRSKQC VSLNTVSVPCVPLKHPKMIKFSSKTYFDISFVHT GRKVYTVEEALRTVRTVSWATASIDKVKKEILKALSAWKFPTRKS RNMFDLAFRFGLOHFYRYCCICEGTKLVYDETYFDELTEYLNESG YTSQQLMWLPPPLICETLLFIKDYNESIDPQPELGNNNAGNPQSAP GSTLNVMTSYTEAKRAIVCFIKEVLSLESPVNDVLDFFSKQWLSN MYKGCYRFTSREAFCVFFNNIGAFEFSPHVMFRVPDIHEKFTERLV IPEITVKNEQIQTTSKVSNMHSMTGKTGDDKISDILGQVCGFKLIE NAPTSEINAIAMKLLKRIPSMVIRMCPNNGETMSADGGQFR TAGEI LGTLH	373 (partial?)	3,E-164	ADI40484 .1	IVSPER	IVSP4-2	<i>Hyposoter didymator</i>	431	221/398 (56%)

DN10416_c3_g2_i2	5,617	2,246.17	Ba_IVSP_Ngene-1	>Ba_IVSP_Ngene-1_aa MNTLDDDDSRGSIGSPIRDEFDGHGSISEFEVYLDEVYNDDAENSE AENDHAVSPVVESTSPEPPVAVSLKIPKRKTPAAKNFPIVKS TDDIAQAVNAGAFKKKATTVPRKRPTVEPVAKSDSDELGVETPA AKRKPVSRPKHPVEGGIHLPLIDESGKKPKTAVRRSRKLVATATN QPPVAKGRRDVTRQPDDEVSSAQAMTEVPALTPFVVEAQVHARP HVNVSQRNVTFKETPASSSSVVNSEFADNRFWMGILADDFKSLDY NALLKNSQFTEQQTYYLQQSFYQLCRKLSICTYSDRFMKTHKICIE CEFSISHQCVSINFTQYVPSSADLTGVTITTSQSTTMCICQFSFFHS HATQTRVKLVNNLSLRGSSRMLEHNRSVSVSCPRCHMNVVMKN RNHDVCCDFTNWNSLEGANRRQFYGSLENRLQTAKMSKPYLNEL YACSKQCCHLHRCVENAIANNTIPMRPQ	479	0.0	ADI40491.1	IVSPER	IVSP N-2 gene	<i>Hyposoter didymator</i>	492	314/492 (64%)
			Ba_IVSP_2L-1	>Ba_IVSP2L-1_aa_Cterm DNYTCYEITQGLSRSGHGFHFMPPMLRHGYLILKMPYIRAMVTSK STDYLFKLNKMMVVEKIEHIAPPLCFDIRSGKVVDDEAIFMSDG CSDVDWADGVENFISLPSTRDLSKLTAAASKLLAISSTSHGSPQNS DDADSKAVADVSEDDGDNITIGESLEQYKTLRAIHDFIKTIEDEQN WSPSVVDLLEFVNRFRVVMKRKKPSLLKMRSGVVIQNMMSKVPELSI AGSEDDQTSAAFEDLVKKSYNMFIHRDADEIMRSCWNEIFSSVE EAPGLSGLRALNKRTRSSTSLVSNVVKHRKIKR	308 (partial)	3,E-121	ADI40459.1	IVSPER	IVSP2-1	<i>Hyposoter didymator</i>	509	191/308 (62%)
DN10416_c3_g1_i1	1,780	1,659.95	Ba_IVSP_2L-2	>Ba_IVSP2L-2_aa_Nterm MATRANLAAYQEESAFAFEDRSVTLKSIQQLRQNVIGQLDAFNELF GLSNPLIPLSYSLHKSKEYFVDFGYKLHREHEVLIGPIDMYGLCTL TGDNRNSNGKVEADVNRNERFMMFIPNCDNMSNAPSGSLLSLIL RDMANKLELVLRNEEVVNKITSRYPKFNNGSAFAKNKESIFQKYITG KESDARGLIRLVRVDVAPTRGETYNCYEIAQGFCSRSGHGFHFMPT LRHGYLVLKIPLIRAMVTSKSTDYLFKLNKMMVVEKIEH	267 (partial)	9,E-123	ADI40459.1	IVSPER	IVSP2-1	<i>Hyposoter didymator</i>	509	175/267 (66%)
			Ba_IVSP_U5L	>Ba_U5L_aa MLLTVAATASISYAISYFISSGLTSCRKRCDELREQMRAVEVKYRRN GGNSVCILWADQQCAMWHNQKLYIYDYWNSKNEAGASTFNIANL YLRSSMVLVYDFHERKYMQKHFPNEYMLREMFEVNDFPIPEEI MMDFRTRSDDNFPMLVKRLTYTDELNIISVIYSALEEKILT	177	9,E-73	ADI40458.1	IVSPER	U5	<i>Hyposoter didymator</i>	176	111/182 (61%)
DN7233_c1_g1_i3	587	1,983.84	Ba_repeat-element-gene-1	>Ba_repeat-element-gene-1_aa_Cterm LYMSKFLDFVDYRNFIRSFPCPNYEKSDILRAKLWRLSTHEVTIPFLN GKLIQIEYNYDPSRTEEEERVLINVDMLPIFGGWVSPAMDGFRSAS KLHNFTMIHILNRCSGFYACCPCHLPNVNASSARAFERPSVTA	138 (partial)	1,E-50	BAF45626.1	Segment	f3.2	<i>Tranosema rostrale</i>	237	77/136 (57%)

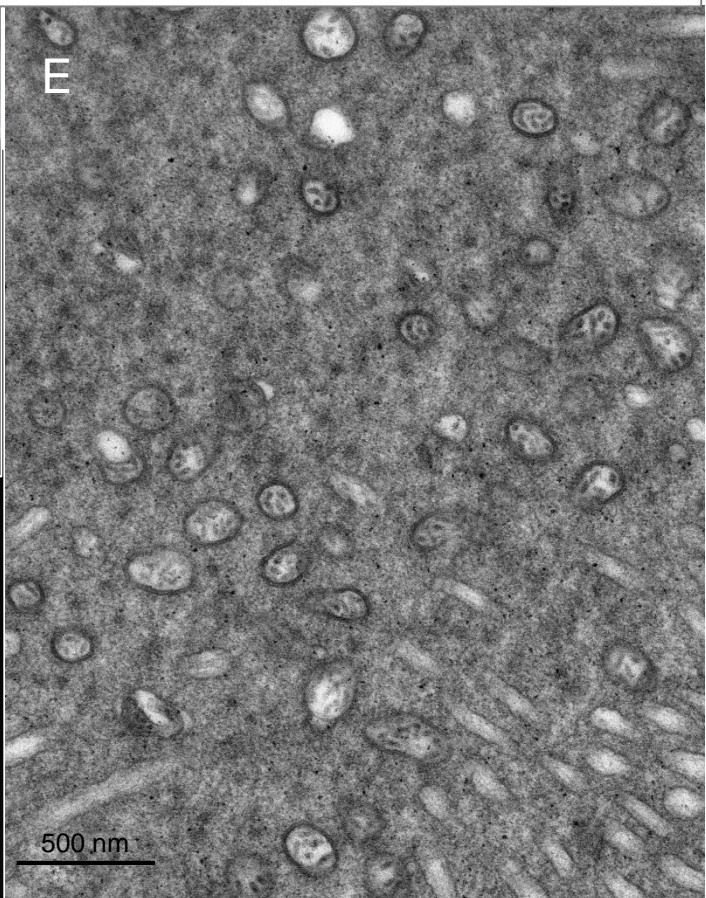
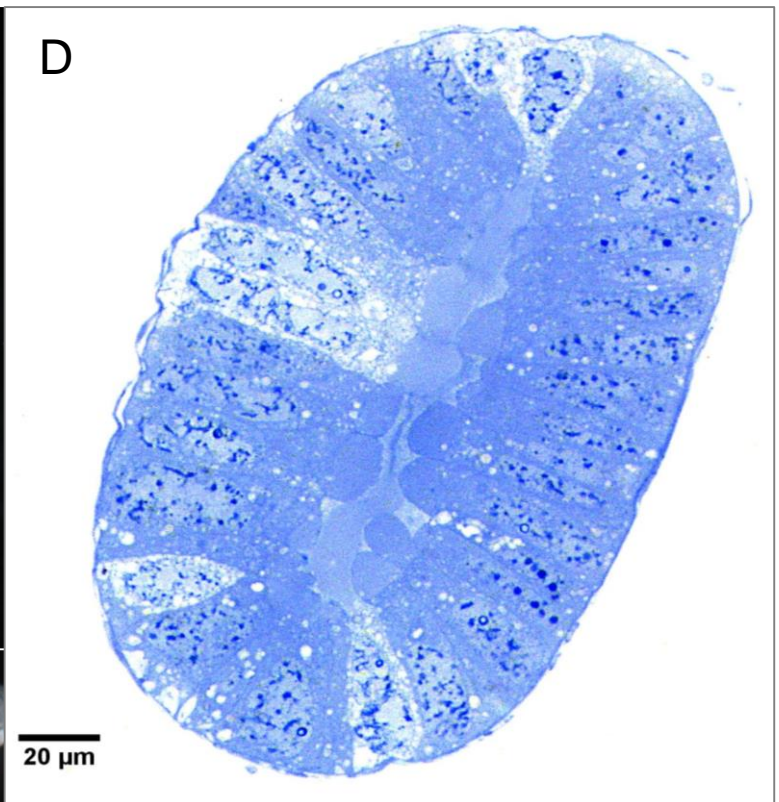
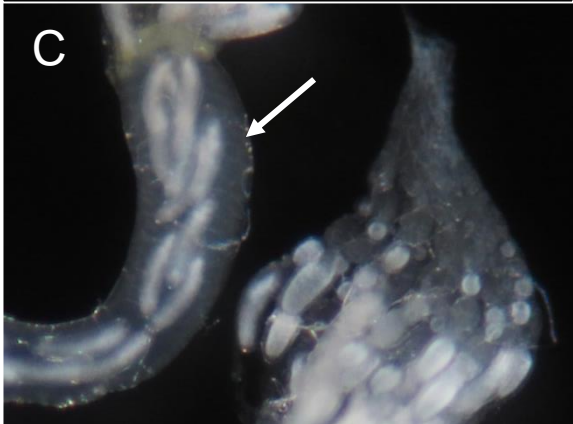
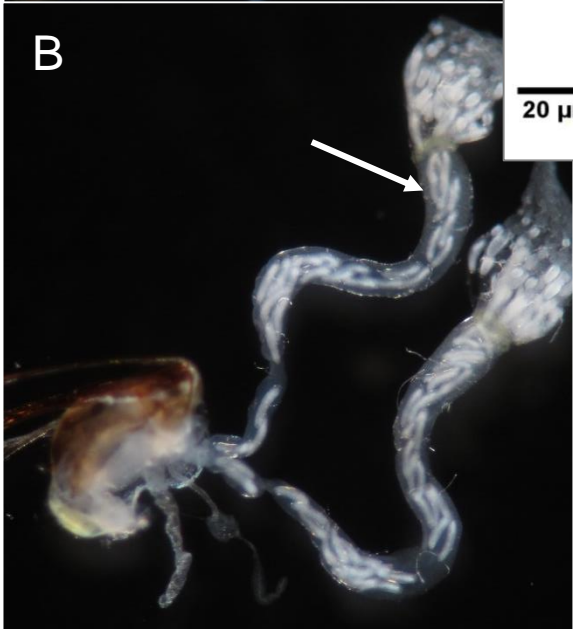
DN10385_c0_g1_j2	5,252	1,342.13	>Ba_IVSP3L_aa MSLLRKILGSWVYTYISNRLDDDDVIEQYRVDLAVPGPDEMYRF YTFLLKTEIIMRDEVHGGRFQWLKEGLHFKIPTTEFGKPIWKYK CLCRLHHSFNTLKNDEKFSVLKHHVSDVVRNLDLTKTEPVYASLL FALQLNGNLRNRTVSFNSLDELHRRLLATDDPLVNGLFKLTGKQS YVYVNSVLDLALILFEPILQYLPADENKSLTIINLVSERLPEPLLOQT LWKNLATSPNEVGSSDVRVRSSKQEQGSLCWEFITGLTSQEY YDDVLTDKIFEKVDFERLRSPVKATLAHDDGNEHDHANTVDKQQV FKLSMYSMSTLLLLSSKTMVHCHCASKTIQFISLIFSTCDEMKLRAQ SLPNSKVLVFAAHELAKFPMVRPSEFRHFRNIFITYRQADIFERPTG TIFQHKYLNELNFVRIETSGLEPTHTLLHLLMLKNDSSVLPDF LHSQLVRAIEQSFGLGRITSDFNNEVIEMRYRTMSEKNLLRLHGT GVYDAINIFCLSYYHKMAYFAQGVVINATHLIPLHLIDLNTRNKEYP ITWAMLQMYIRQMPGRHINAVDLTSPSVDNQQVETRTMFKYLSLV VNVMIQEQTKEGYTMVDLIEHAGGITLY	629	0.0	ADI40465 .1	IVSPER	IVSP3-1	<i>Hyposoter didymator</i>	630	405/626 (65%)
			>Ba_IVSP1L_aa MHDNTATNSKPIEVVSAVVLSDDDIPQNKLAYFTKDRNRRSRLSD ALNTIHKIATEPQVLAWVAAILFFAGSVSDLFLDFTYITNHSLLVAGS IFWMFHALAKKEYPMFLQHVVMSISVYVFTKQLNVGKFPYLTAAL LCTSCAVYRHENVMSTDLGPCPNATNANLNDTPMPWSPRPPIC ELETINIALDEKVNVRKLEILVDIKGNRGEDGPLDNSEYHHVYIAA RAQMNDILHSLETKLAQC	249	7,E-71	ADI40464 .1	IVSPER	IVSP1-2	<i>Hyposoter didymator</i>	196	104/194 (54%)
DN9406_c3_g1_j3	1,849	1,102.93	>Ba_U7L_aa MPHTSSKQSINDILGERVLLNTSGTLENQQLSHSNHNDNLRPP TTAEQFFQPAQNISGSVQHIDQPVIKFEQYKVCNSVEKMFSCNGN SANLVNTTDSLRRKHTRTLWSYDNLFKILMLLLFAIYVEVRKSDGS MVDGQSFDSFNNSFITSAVGYSDDTMEKIADACTYGRQTYDTMY QNAKLIYHRIKKALSLSAS	201	8,E-70	ADI40463 .1	IVSPER	U7	<i>Hyposoter didymator</i>	212	129/203 (64%)
			>Ba_repeat-element-gene-2_aa MSQSPSTSQLPTSEPIVLPFDIIRYMSKFLDFVDYRNFILSFCPNYE KNVDLRKEVWRMSTHRVTVPFINGKIDMEYNDPSRTEEDRVLI NVDSCLAIFGGWISPAMDKFTTSLKLRHYIKKYVHLNICSGLQYAC CPCHFNVDDPSVQAFERPSVTTCYGHYHYCWRHVVAWIVQV HFFVEELENKPLAEEYARLDIRVLDKAVFFPGK	216	4,E-61	BAF4562 6.1	Segment	f3.2	<i>Tranosema rostrale</i>	237	92/181 (51%)
DN9191_c0_g3_i1	478	1,026.46	>Ba_repeat-element-gene-3_aa_Nterm MSQAPSTLPLPTSEPIVLPDIILYMSKFLSFVDYRNFISICPNYDE SDIFRPTLWRLSTHKITTKFLNGELMQIEYNYDPSREDRVLINLDSL LPVFGGFVLPAMDKFTSPSKLRNFIAMHVHLNMCSDRRYACCP HLPNVDDHSAIAFERP	155 (partial)	4,E-65	BAF4561 0.1	Segment	d5.1	<i>Tranosema rostrale</i>	229	105/156 (67%)
DN10332_c3_g1_j2	2,637	768.56	>Ba_U22L_aa MNKKYVVKLVTKKLMVRVATGLESKAAKKIFSRVLSVALKKAARIAV KAAAKFAVRYAAAAILACTGPVGLAIDVIFVILDVISFISDLIDVNNYA LAYTRETVMQNSLEDEWKKETLEKLGSGIMDPEYPVEVNYLGV SSTQEWITDDEVTAKSLSYSNTLLNLNVNSLGEVIDLKALGDSG ADTDDRLLLTHPPSWNECVQSQSIVKSNERAMIQHHELDGCECKQI NALASISWITFLTVGCTIALTALKRRTFFTRHATNPKP	270	1,E-54	ADI40487 .1	IVSPER	U22	<i>Hyposoter didymator</i>	257	94/251 (37%)

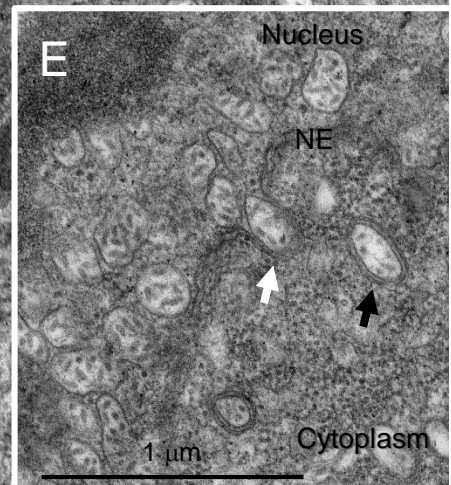
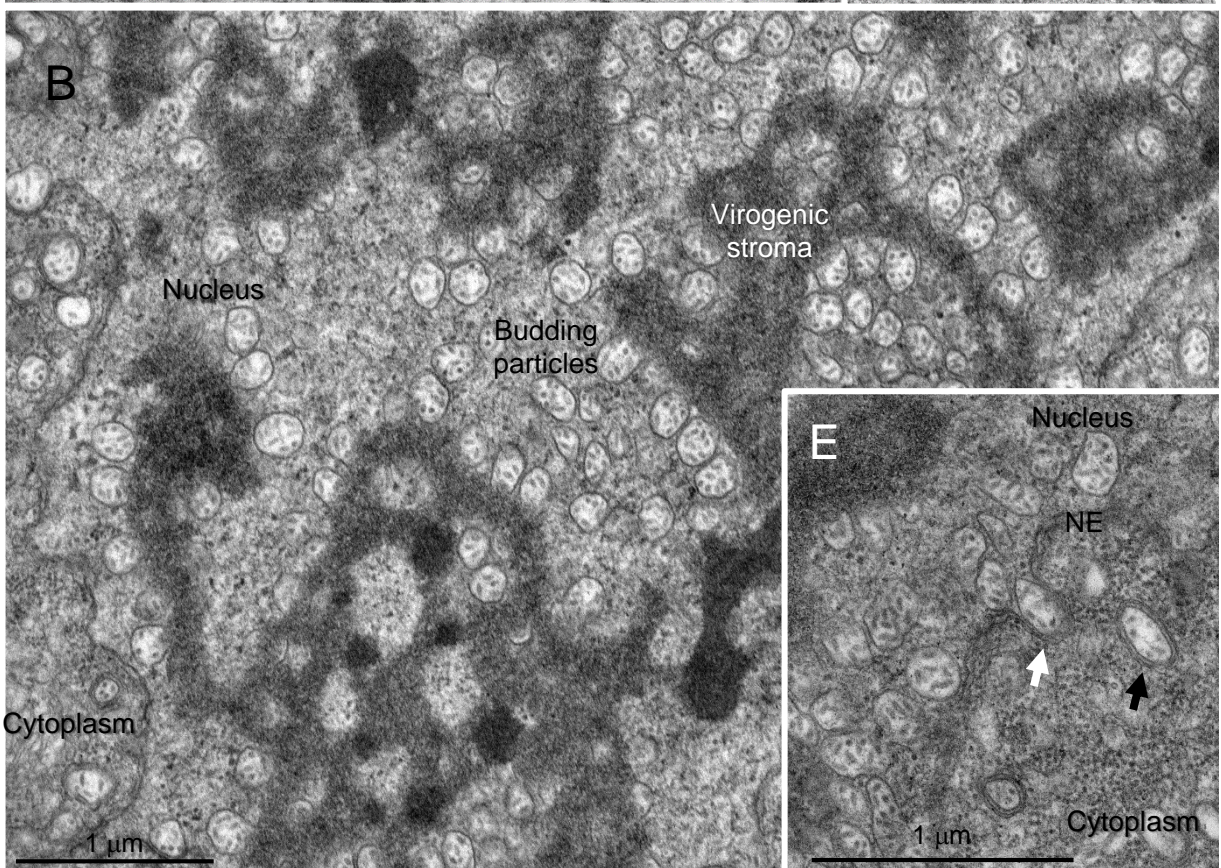
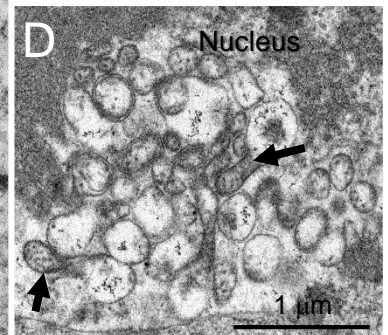
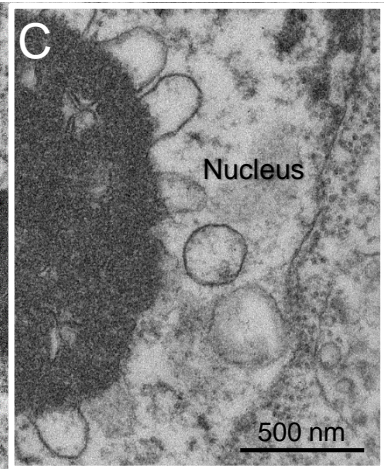
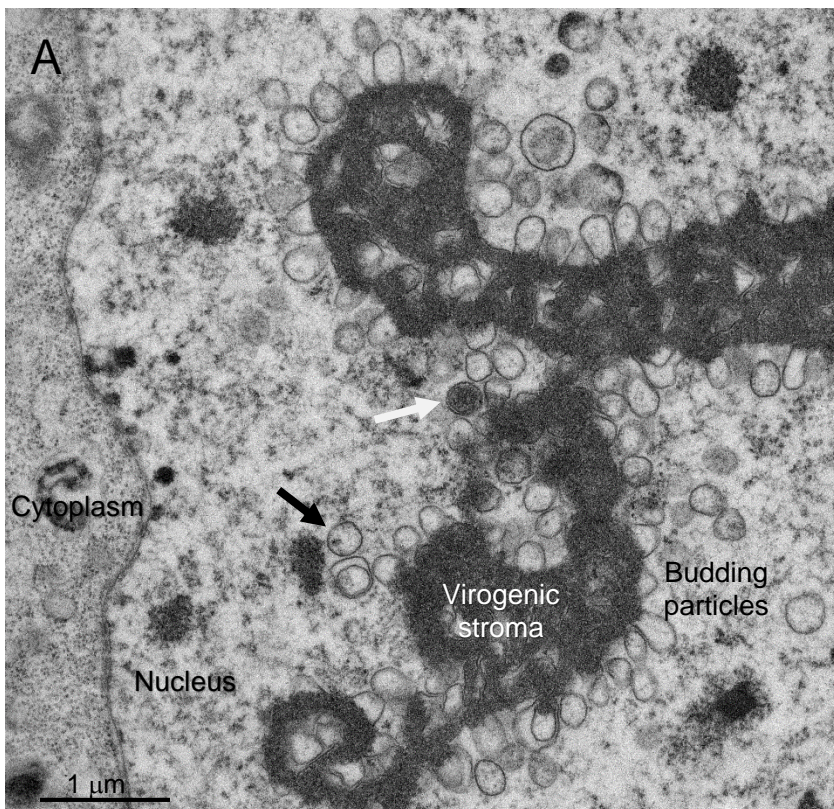
DN10351_c0_g1_i3	4,957	755.81	Ba_IVSP2L-3	>Ba_IVSP2L-3_aa_Cterm TLRHGYLVKLIPLIRAMVTSKSTDYLFKLNAMIMVEKIENTAPPYC FNIRTGKIVDDTDTFMLDECSDDDCADNVESVITIPSTRELSKLT ATSEPPSILPASHGPLQDFNDDSKSGPDAFEDDDADITTDVSVD RYKTLRSRTINDFIKSIQNEGNWSPSIDNLIIEFVNRFRALKRQKASLL GTNSGTIVVNVKIVHELVSAGGEGNQTLASVEDLVVQSYEKFRLL CDADEIMRLCWNETLSHIERTLELTKVQTVNKRKRSSTPTINNATK TRKIKH	284 (partial)	1,E-114	ADI40459 .1	IVSPER	IVSP2-1	<i>Hyposoter didymator</i>	509	180/282 (64%)
			Ba_IVSP_Ngene-2	>Ba_IVSP_Ngene-2_aa_Nterm MHAHDDDDSRGSGVGSPTQGQFVRGVSPECEDDSEEEYNDDAGN SGVEIDHAVSSDDEFDSTVVIQPLPVVESISPELPTVPSLKKITKR KTAATAAKNAPLAKTRKSDNNAQAANAGGSEKKAIIIVPKNRSIVEPV AKFDSVEFAKRSPATKKKPVSKAKDPEEERSHMLPIDETRNPVKV VVKKSKLVATATDEPPVKKGRDFKHQPEDVSSPQVTNEVLSTS FSVVEAVHASPQANVVRKHKTSKTSKAKNFVSLNSESADRRFFWM ETLAGDFKSSGYNALLKNSQFTEQQTNVLQHSFYQLYR	308 (partial)	9,E-116	ADI40491 .1	IVSPER	IVSP N- 2 gene	<i>Hyposoter didymator</i>	492	193/309 (62%)
DN10165_c1_g1_i1	1,941	497.28	Ba_IVSP_U15L	>Ba_U15L_aa MESFIFMASGTLAMTKIIQKCLDVSTAGTAASLTREPPILSNDSE RHFQTRTYFNIDKTHYPPVIDVHELQATASCNNTDECTVRFQDGF SCILIRPVQLTITIDGVDKIVYDADINSNVASSNQSLDCKRCVLTG QSRRLKCNALTSVAVGSAVYSPQTRGFNAHWVGESLYPDMFSK DSESGDITISHACGAAENRQGLVHEETGLSWDEHYKRYGRYDPA DSLVCCECYPPFKPEDVPANRSLYSDNIIIVLPSTSTCRRSTCAPGR PHLSEPESECEPRGYVSCPVIGLNTNEQFHRRLCWGSYVRNHEG HPMPTCVRDPCLPRGTLTASSGMCVSNKYEEVKAFNEIHVLPKVT WSIL	367	1,E-142	ADI40477 .1	IVSPER	U15	<i>Hyposoter didymator</i>	410	198/384 (52%)
DN8699_c0_g2_i1	483	418.96	Ba_IVd7.3L	>Ba_IVd7.3L_aa FFFYYSFFPPVLR LAPITGSARVSSRPPGCLVRISNETPMPRHPT SPSVAHLPWHSIPWARGNCGKPELPVPGFASRSRSYVTSC	88 (partial)	6,E-13	BAF4561 8.1	Segment	d7.3	<i>Tranosema rostrale</i>	117	32/43 (74%)
DN10436_c0_g1_i1	3,628	345.61	Ba_IVSP_U4L	>Ba_IVSP_U4L_aa MVRNPPKRRRRHNESNRRETPTTVLFLKFLSTTCSTMLAFVIGRQ FWHTRPKWMEHDAALLRYRKRTRLVKFCGFGFGQREKYLLRL LESSVTNNDETSLIMHILFPYLSITEEFAPSDNALGN	126	2,E-34	ADI40456 .1	IVSPER	U4	<i>Hyposoter didymator</i>	131	58/115 (50%)
DN10332_c6_g1_i2	5,354	318.96	Ba_IVSP_U23L	>Ba_IVSP_U23L MVDYKQTSWCANTTIQKNPVLSDAYLIKIIRTFEELDDLTISCNDM LTKILSMFRNAIARGGLQRILDGFMLFLCGKKENSHSHIPRIVTYWD LKILIAGLIRRFNSDKTLKDVLELDNGNGTTDIYSLRLNGNMLSTMA TEAHAGISLLPPRKIIIVLDPKQAAVLVFLFQAYSNNSVIDDSSVHN FMRELERIDENIHGSIVVKESELRAVKSCSTRESLLKTYCGTSLVVQ RYIMGQYSYIFSMLECFRDFLNTDRLPETDPRRQAKSLMLNLYL TVFIGWNTSPPEWSVWSKNINEVGMNTLYDMLNSGAINDFLSY VLLKSLLFTEPGDGEQASYGDQFSANQREVDSLQKQYKNINP YIEGVTRKDPGLINKEKLVKIKISEALLRLRGTTTSE	409	2,E-155	ADI40488 .1	IVSPER	U23	<i>Hyposoter didymator</i>	415	229/406 (56%)

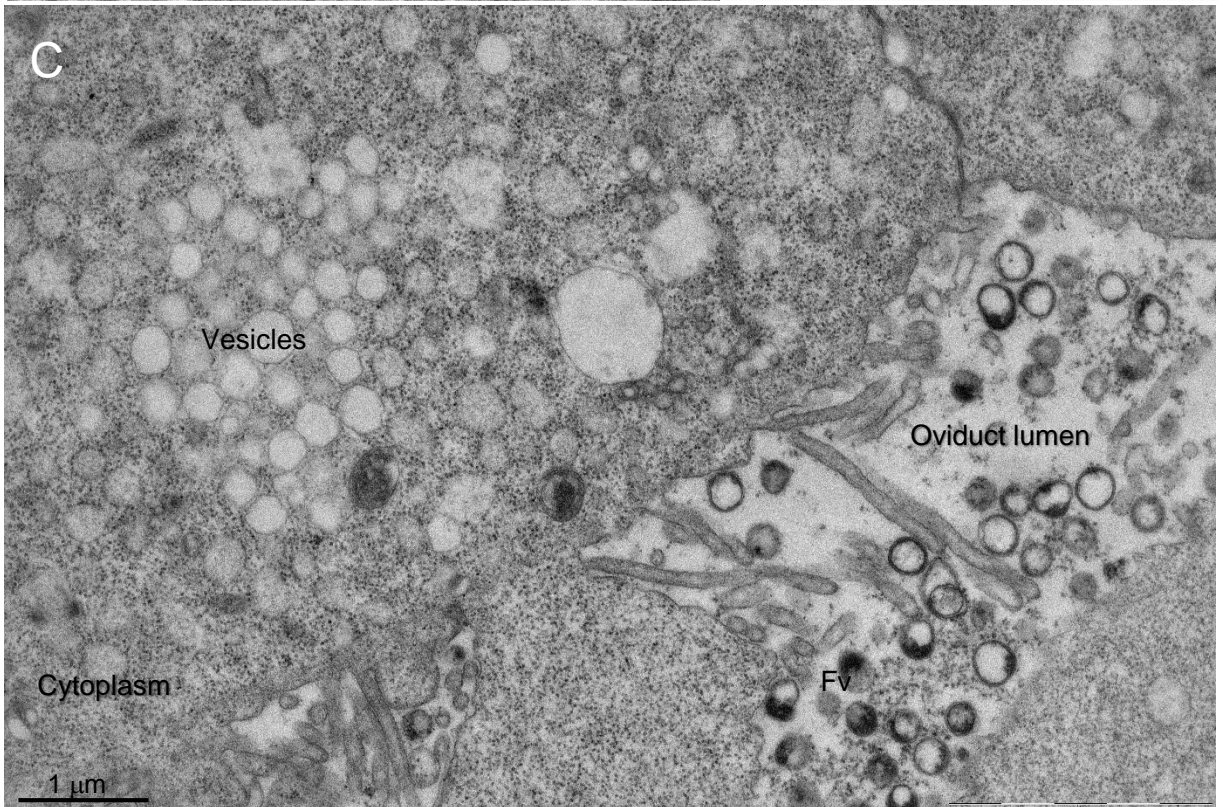
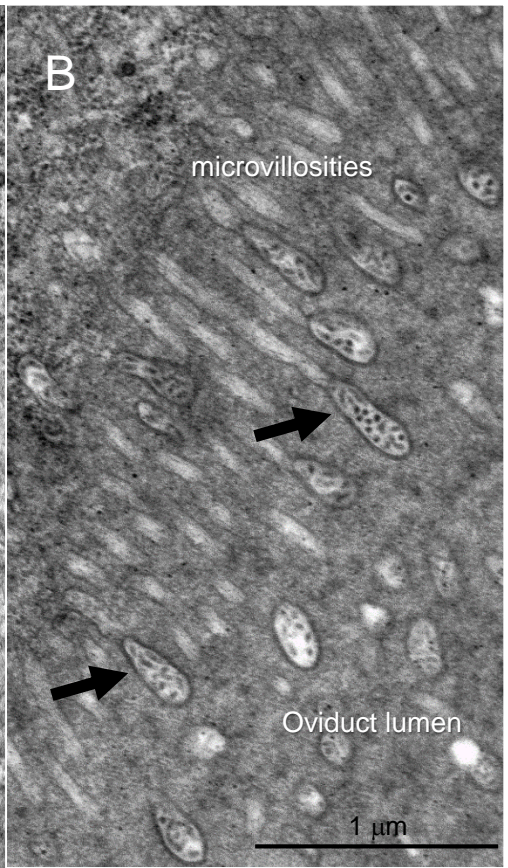
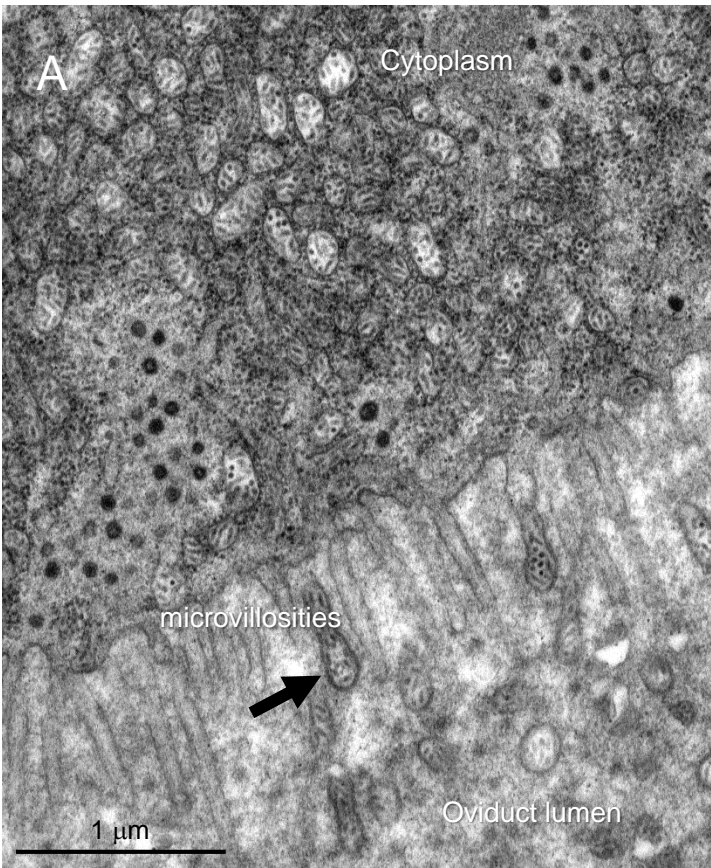
DN6598_c0_g1_i2	3,083	288.46	Ba_IVSP_U24L	<p>>Ba_IVSP_U24L_aa MKYFAKMDIAPYHLQVERVFSRLADLVLNWEDDEPGDSDGPEPMV FYLFMIENRNQRKNLAVESFCDVGMNQISSIEKDSAETHALIEHNHGK HTDSTSCAIGFCQSQSNFVPMEAHESCNHGKADAGMVSNRGIFR SVNQNEVEVVLTAHYYPWLLGDIGSVFATLPDWWQLRVEILFILG ELMFGYLSKVESFLNVNTRSASLQHDKQSCNDAQAQARMYFQLL DAVCARASKGKKCIADLIKQSLASHGHQSVKLILKSKIMHSYLKNR MNCPPVRDKKFNQPFPSRLTNVFPDCLLALIFSNVHTWRSFVGF QKMYDLNVELFAAYTMCPDQNDLLIVLFDINTAQQSAANRFGST PWNCNYGYLDEPLLQRALRKTHTITQSYMYGFLHDISKDVCTARL FRNLTTINGNMETIVKDLCGTVRSTMLQGMNDLLLALHITRLAE NFGIASSCGFMEYMLRNEVSKMSFRNVVDTFLNSIRKNAKHAIIIE YVFLHRMCHVRSALCEFNVFANVIVSQTLPKE</p>	529	0.0	ADI40490.1	IVSPER	U24	<i>Hyposoter didymator</i>	563	372/564 (66%)
DN10406_c0_g3_i3	9,174	235.02	Ba_IVSP_U10L	<p>>Ba_IVSP_U10L_aa MEPTAIKKCFSSIEIQPLASGFEELSDNGRVVKKRRHKVTTGVNLKYY EFILTLEKICSNIASVPEPAYSSVIGELFRTLANYRVLICDPMANMLV DALQRLSELNIIYVLKQTELIVMNILLPETVKDSDAIHMFTISLRLLVL NMFVCGLARRDHNAISFSTRERSTLDYELDVQCAAMHTQSNHC CLCIAENYPKRIDERGAIDLDDVRKEFVNYSRITTCCKCIANSNLC DQCLCSLRESLYLTYIFYKFEDEKKSMSMRDKNAELRIFKAKSLAK REARLRATTEKIKLQAAGTNTPPVLNKRVRNLTKELETPVNTDI DHQKSQKIVYEDSDLQLRVRKSGAIGFKRKSANGYDEIVILSERKD PPKTAHKLMSMGLPSGKFRFRGRLPERSNTVSRTFINKLINDLNPQ TRKRSEEIPRAQSSILCAKPKGLAQRVVKVISTALLNNERLLTESVIA ELCKVVLKLRGVSLEMTRCNCEECKNTVSDALSTEDMRPIIALFL HNEILNSNFLMDICNDKMFMSLQMPRRSAKMYFNIVDNRSKITKD KLAEARTRIHNTSSFMLYDVSKGVAKPISLCFAIRKYGTQLHDMYR LDLNAGLRNPNENLVWLKNCNTKNDAAFLYKSEQESSLIGQATLH YNTAYHTYHASKPEDNKTFSSEMFPWSSAAGTSILRQGPVATSR TLNRYNKMNRNPKYAAISGVAVKSVKRDFFRVNGDGINRKRSDV HRGKEAILCCQANESELEATILQMFDSMLLGHLLRVYCNILSNQIEC HDTDYRGFYDQFHLYLNRTTRSTERYESDIFVLIADRTFKATEKVMIE GNVLLRNKGPLSMKNIPRIVKYARSTLDAFTKFEFNGTLIVLFRPT GNNYFVIQFENDRSIIHQHAKCILVELVSKDPLDADAPLTSTERYFE NVDNALFSRNEVVAIQNFLNTDNMLPKADSSYSTLMFLVGGNHND ESWDEAIHDCERIAEVMKVKTVAIQDRCASIVFNKLEAAWNLQP VSYTRQIDERTLACIPAYDADEICTWTREEHITLCTAAKYAVVAVGQ LLVMSDYNVLDMLLDCFRRRISVLKCSSRAGVVIPLNRIPNCEKE VALFLKNGINHIENYRCIHENIPRHMLVHDPFAVMTATTTALHLSL DSMRAIRRNKLNMGFMHGRHSNTGFLTTSANRLLLAIAATVLIANT YHREYFTLKSSLLLLSEHGLNEVNFARLRYIVQKIVLADGYIVSKES QSYDYKKLISLLLVEQAALLMHQIPLNNDRLVKSVMGHYHRLHLV YVYRKLIDYFTSQYSDMPMECDPTVFMNLIVSNAKKFILHFEKRTVI RVPLRYK</p>	1350	0.0	ADI40468.1	IVSPER	U10	<i>Hyposoter didymator</i>	1355	1120/1355 (83%)
			Ba_IVSP_U11L	<p>>Ba_IVSP_U11L_aa MEYKNSSMEFSETLLDVLNFDIGYDLSTMDVINGHSPIDNLAMLI DEDSHEEKLHHMYSNQNMFKRPNIIYGEDEVSVQKDDVYQSTK GVLVLQAEAVKSWSGLIESDLYKRHCDDLHIEEVSVAVTLDYTAMI PINTFIDTVLIEEVTTKSQAFLLKFFVLPVKELVHLHRCNLKLNHPFM SSIVYCKKCGFIATDIQHTNFRMMRELKKSQENVRMMINAVLVDV FTYPAILPWGIRENRSTVQSAVLGKISSAYRSLIRDRSFMDFL EVFVEYYRAIALQYRGNISTAYYELQNLFSFGT</p>	313	0.0	ADI40469.1	IVSPER	U11	<i>Hyposoter didymator</i>	316	245/316 (78%)

				>Ba_IVSP_U12L_aa MTSFNLSNDMLVKRKKVTSWIIIVMDNDFDRKHLKHATCATLRLFD VVTNEVPTDLLQSVAVGVMIACKATNIDVDIDTLLYYSGGGCSIDS LLDVAPLMKVLHEEDLRVELLPYYITDLMQLTRLQGGPQPVRWII HLMNSNRYLSVETTPRMTAAIALLAYNKYLSRSSKLLAPVLLRDF SLVIKTRRYKRLERRAQ	203	2,E-132	ADI40470 .1	IVSPER	U12	<i>Hyposoter didymator</i>	203	184/203 (91%)
DN10047_c0_g 1_i1	5,425	257.48	Ba_IVSP _GfU28L	>Ba_IVSP_GfU28L_aa MYDFSHLISNNYFRSDDNGDVFIYLDLILESKQCCKSLAKLYPKVS QRFIDHDVVKVLRYSYQDNYFYRVIGHHFFNRIRSYCYMIRGVTDK RKTIQKISRDPGRGGVNILTKFELYAENRPDLNDSTLSILNYPPDR LRSVMNLWNTPRHECGFSTLFDQNTHKNILWCRIEQNHTSLVMN RQNVPRHALTSDLRRTLITDKFLAMTSKDRYATSTSDPGWLVDKQ KLRTYITAESSFGRSSYNNNAKHAVFDVDDVEMFSDMSTATTA DARLIHRECPYMTMPHSLYNTLQSRKDASYHVHNPQMKFSFDVRS LVETTTLCRALSVFQDRFSGTRIMDNGDIVAFAYDPETNDFAVEFV NGKIYFTRMNYDDNARCGSVIRPVIKTYPLPTADEINGARLKQAFS QQLKNCISIRYCVRVSSRSISVILGNRSKFIIAARDRLFVVEIDME DQDASYLRESLVKAHEISSKVVETAKNMAEKKGRRQRSTRNIKDR DIKVTLYAMIHGIHDTNLLNLARHAYIPTMLCDRDPVFFALHKS NMKEFQRRIRLEYKAVCAYSTQPCLVSDVTRGRKILSCAATTKLQD VEPPTALNSKTDNRSHSAADVHAKYKFTKSLHKKRTTYSLGEQAE SIKRYLNMGNRLVYKLSGTVEEFIDYDLTRLLYTRDRVAVFVIR WDSESTQYDIVSSGRLNPIWNRNFSINMMREKQLINACDDGTAD RCIAKHPELEHYDRDTGRSERVRFLESEKISFPMNAEVAKLLSIAN NRVNEFQVVLRQPRTKFRKSSFLRRYGIASCQAIDICERIDSNT GIYTLYYYVCSLNSRFWGLGLLFYETGHLNSNIPEVDFNVCETPYTIV IRGSVACNGSSKSFTYVYTCNLDMWVDMVQLDRNCFALYNDN PIIINVAKYCTSIARLFNDPRTPFYNLATLFADFYMDQCFSSQSEEC KTLVHWATISRSLCLDMHTEYEFDIDCWTAARKIRCSNLTVLLTVR FLLVHCSRKVKCKRKYSEESNIYARRAMFSLTTRYLDAAMKYNIYK ELEWHLNEEGMLDSLKSVFNADFSEHVYRYIFNGTETCLRSK LRKIEEFDHIFKMLMLKRAMSEVFVELAAARTYSTFVEWFKRGVCS TPTTCVNNRPVVGWYQTLNIMRYVERIIPHYSCTEVVIKRSCE TMELPLVIERQENVDKIYRNGFAWAYERETRKNKIPNKTAVRSRRF PNIMMNEHA	1247	0.0	AKD2806 0.1	IVSPER	GfU28	<i>Glypta fumiferanae</i>	1322	598/132 9 (45%)
DN9620_c0_g1 _i3	2,489	243.73	Ba_IVSP _U9L	>Ba_IVSP_U9L_aa MDIPSTVRLGKLNVSIAIKTASIANLNDANVFTRQLKNISGASTSLT EYIPFLCNVQVTDLCVVDGSGIRKTVYSLHNNTDDERDYSALVVEN IILWVCSRKSDRIRNFFSMFFTTSTNKDVCNDLDFLEHVVEDFCP DMKILTESKYCSEATVCLLDVGDGKSIDLRDWRSTMIRVMEHWKTMF KLNVRDVTTKDSKINLLYDDGSKKSTLPDISQLDNECIRDIELAFS YITPVSAPLENDGASSTLCKRRASDDVSNIDCKKAN	269	1,E-114	ADI40467 .1	IVSPER	U9	<i>Hyposoter didymator</i>	274	169/268 (63%)
DN9251_c0_g1 _i1	4,092	203.54	Ba_IVSP _U6L	>Ba_IVSP_U6L_aa MDSCHIVTLTINIQDNFVNWAPIFESVFHAAKSYEYCLANFNSQQ PAYQVLCIIIKTMTSTYDFTILDSEVNKKMVIAGKIYGYSKFAIFHL AHTIDDPLNLSVHEICGSSGFQSVMMYVKKLSVSASMDYFST AATSTFSLKQANVTIHNFAFCCEENNIACHRSVREVAGVRLIFNG RRAQFLNKLRSLLPREYITALANSASNVQFFLNVSQALIDRINSECR AFVNNHKICRELVFYCLCCMTSHLQITSGEIDEVDDSEPCQKPRI QGNPVFPQCQLPIELPHNIFAHEISSPPFLSLLHFDIHNCFYEHEV ENIENIRSNLLVKTHSLNTMYNT	349	0.0	ADI40462 .1	IVSPER	U6	<i>Hyposoter didymator</i>	349	310/349 (89%)

DN9992_c1_g1_i4	2,435	94.7	Ba_IVSP_U16L	<p>>Ba_IVSP_U16L_aa MIKSIIGGFTFQGCNEKQDPSSHLFPRKCMVCTPNASGYNALDLFA ASYKPKQIGKLCFQEKNGCAPERGYPIRVVDLSDNENLLESLLC EIRKLLRELLPQAEASDFKLIICILRKKQTGRFHIHLLNVVSNDLITYK NFLMVLHEKIKAVDRGAGVNYFMVFGAIKAYKQKVDPTTPVADQC YLPWKMCSAKINEIKLNNFIDLPPFTGGSSDEYCNDIQNYFNKYFQ RSSCGTLFHLLSLHRRYNPDFDVVPLPCQESIVRSSRKRTSDDSD SEGKKKIRTAKSDPINRAKESFFENVLFKLPKNYYEYDSWIGIGKII AFVKQTDGLNLFHFKFSSQSRDKYDAERVATTYEGLLEAMKVNQS DKAAKPVIHMTSALRALLLGSNSIIDQIERKMFYKWKGDTHAIVGAV TCCIQQMSPMLTFPHPLNANYLFAIEFSRVDGAYRISHDFTIQSFG GQRATIDAGVERHEHEHYERILECFIYLAIKYFNDNHRFRWRMYSAHSI LDSTPFKQHLHAKNNVEDMRSSQHSFYRRAVVQKLNKLNKLRW LLAQSNGATISSKKKNKRLWSKLYTQYEFQRALDSARKCGRYPQS VFDKAVPRSDASSCSR</p>	612	0.0	ADI40479.1	IVSPER	U16	<i>Hyposoter didymator</i>	612	487/605 (80%)
DN2005_c0_g1_i1	3,05	79.4	Ba_IVSP_p53L	<p>>Ba_IVSP_p53L_aa MPTSTIHGGGSAPTQEAAARQPPGTAQGVKPPFPVQNEQSEDSNRN TKTSILEETDNPKTETQIRVNTETDIIGDNEADAGMLEATIDEELVA EFKVNENEGMRLLKILKYPSTARHDEQSSILSHVLVKERDSKRIRV GAIVVNDAAVKGGKIKTRWDVLDKCPYKRALLSALENSSPNSVH AFHATLRYPNDFVLAVVASPNDDRIPDGAHVDPKTDENLLKYNIVV RRIKHHQTGSAPSKKNLFSRWFKRSNSKSISEGRSQTSSEPVSHR IEIKKSEIRPPSNGNKKPTPNEYVPLGGIDDSQRPIQTSAQHTKDV GLDSEKRVHFDQDQSSAFNEAQPTHRRRKRALTECQIIAPNS TNFALKAVLQIGSICGLSVGITYLLVKKSKLA</p>	397	3.E-90	CAR31590.1	IVSPER	p53-1	<i>Hyposoter didymator</i>	395	180/407 (44%)
DN10161_c0_g2_j8	1,803	71.18	Ba_VankyrinL	<p>>Ba_VankyrinL_aa MSLRNLLSERGTSGGTVFHDMVELGLVGLLKRIQAAIGKSHTDILQ MTDDHGDYAIHLAAKRHRGHKAMELIEVLVGMGADINAADKRYGL TVLHCAVEMGDSTLVELLCCQPRINLDARIGVEQTPYQKTRKDRN KKNILERNGADNQELEWSD</p>	156	1.E-27	AFH35119.1	Segment	vankyrin5	<i>Hyposoter didymator</i>	168	62/150 (41%)

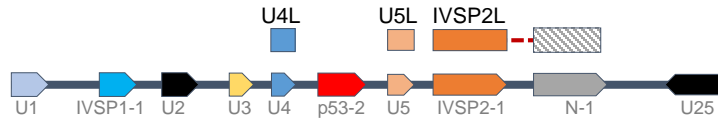






B. anurus genes

Hd_IVSPER-1
(14,020 nt)



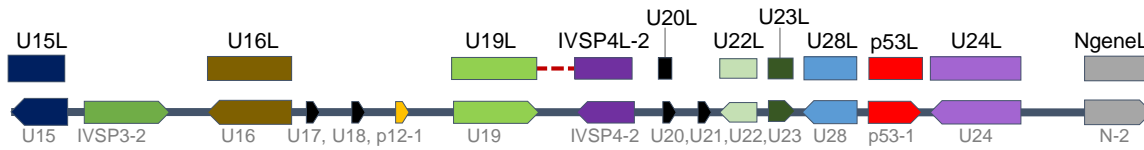
B. anurus genes

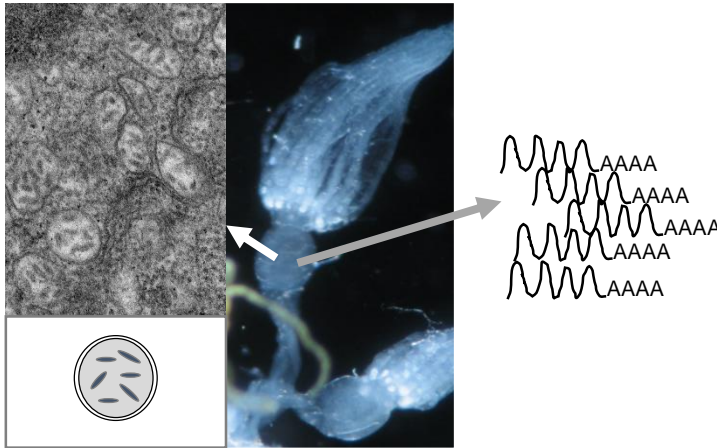
Hd_IVSPER-2
(26,611 nt)



B. anurus genes

Hd_IVSPER-3
(25,432 nt)





BlastX search results : similarities with ichnovirus (IV) genes

Blast e-value	name of the IV gene	Wasp species carrying the IV	Type of IV sequence
5E-153	IVSP4-2	<i>Hyposoter didymator</i>	IVSPER
0.0	IVSP N-2 gene	<i>Hyposoter didymator</i>	IVSPER
8E-118	IVSP2-1	<i>Hyposoter didymator</i>	IVSPER
2E-58	U5	<i>Hyposoter didymator</i>	IVSPER
1E-49	f3.2	<i>Tranosema rostrale</i>	Segment
2E-54	f3.2	<i>Tranosema rostrale</i>	Segment