

A Novel Ambisense Densovirus, Acheta domesticus Mini Ambidensovirus, from Crickets.

Hanh T Pham, Qian Yu, Max Bergoin, Peter Tijssen

▶ **To cite this version:**

Hanh T Pham, Qian Yu, Max Bergoin, Peter Tijssen. A Novel Ambisense Densovirus, Acheta domesticus Mini Ambidensovirus, from Crickets.. Genome Announcements, 2012, 1 (6), pp.1-5. 10.1128/genomeA.00914-13 . pasteur-01132108

HAL Id: pasteur-01132108

https://riip.hal.science/pasteur-01132108

Submitted on 16 Mar 2015

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 4.0 International License

genomeA
Journals.ASM.org

A Novel Ambisense Densovirus, *Acheta domesticus* Mini Ambidensovirus, from Crickets

Hanh T. Pham, Qian Yu, Max Bergoin, Peter Tijssen

INRS-Institut Armand-Frappier, Laval, QC, Canada

The genome structure of *Acheta domesticus* mini ambidensovirus, isolated from crickets, resembled that of ambisense densoviruses from *Lepidoptera* but was 20% smaller. It had the highest (<25%) protein sequence identity with the nonstructural protein 1 (NS1) of *Iteravirus* and VP of *Densovirus* members (both with 25% coverage) and smaller (0.2- versus 0.55-kb) Y-shaped inverted terminal repeats.

Received 30 September 2013 **Accepted** 2 October 2013 **Published** 7 November 2013

Citation Pham HT, Yu Q, Bergoin M, Tijssen P. 2013. A novel ambisense densovirus, *Acheta domesticus* mini ambidensovirus, from crickets. Genome Announc. 1(6):e00914-13. doi:10.1128/genomeA.00914-13.

Copyright © 2013 Pham et al. This is an open-access article distributed under the terms of the Creative Commons Attribution 3.0 Unported license.

Address correspondence to Peter Tijssen, peter.tijssen@iaf.inrs.ca.

The cricket industry has been devastated worldwide recently by the *Acheta domesticus* densovirus (AdDNV) (1–4). We also observed several, thus far unknown, viruses such as volvoviruses, which have circular, single-stranded DNA (ssDNA) genomes (5), and a new densovirus (parvovirus).

Two genera of insect parvoviruses, named densoviruses (6), are particularly relevant for this new densovirus. The *Densovirus* genus contains ambisense densoviruses from *Lepidoptera*, with genomes of 6 kb, Y-shaped inverted terminal repeats (ITRs) of about 0.55 kb, and sequence identities of about 85% (7–11). The *Iteravirus* genus contains monosense densoviruses, also from *Lepidoptera*, with 5-kb genomes, J-shaped 0.25-kb inverted terminal repeats (ITRs), and about 75% sequence identities (12–15).

A new virus with morphology and size similar to densoviruses was detected in some cricket samples from the United States. Virus was purified and DNA extracted as described previously (5). Digestion of viral DNA with EcoRI yielded 2 bands of about 700 bp and 4,200 bp on agarose gels. DNA was blunt ended with T4 DNA polymerase and a large Klenow fragment in the presence of dNTPs at room temperature (RT), ligated into the EcoRV site of pBlueskript KS(+), and transformed into SURE cells. DNA of clones with expected sizes were subcloned. Digestion with EcoNI within the terminal hairpins yielded clear reads of ITR sequences. Several complete clones were sequenced in both directions by use of Sanger's primer-walking method as described previously (11). Contigs were assembled by use of the CAP3 program (http://pbil.univ-lyon1.fr/cap3.php/) (16).

Surprisingly, the genome structure and gene organization of this virus strongly resembled those of ambisense densoviruses from the *Densovirus* genus (7–11), but the genome sequence was only 4,945 nucleotides (nt) long, instead of about 6,035 nt, and lacked nucleotide sequence identity (best E value of 0.017, with a query coverage of 1%). Protein sequence identities were for the major nonstructural protein 1 (NS1) closest to *Iteravirus* members and, oddly, for the structural proteins (VP) closest to *Densovirus* members (both at best 25% identity for 25% coverage [or higher for shorter coverage]).

ITRs of AdMADV were smaller than those of densovirus members (199 versus about 545 nt) and Y-shaped, with a 113-nt hairpin. The 45-nt-long stem contained two side arms in the middle, nt 46 to 68, that occurred in two sequence orientations (flip/flop). It had a high GC content (63%) and contained inboard TATA boxes, at 193 to 199 for the NS cassette and at 4747 to 4753 for the VP cassette. This structure is identical to that of *Densovirus* ITRs.

The NS cassette consisted, as for *Densovirus* members, of NS3, followed by NS1 and an overlapping NS2. Splicing, as for *Densovirus*, would remove the NS3 open reading frame (ORF) and allow expression of NS1 and NS2 by leaky scanning. As for *Densovirus*, the putative splice acceptor site was located just upstream of the initiation codon of NS1 (1172-CAG/aATG$_{NS1}$..N$_{19}$..ATG$_{NS2}$) (in GmDNV, 1395-CAG/ATG$_{NS1}$..N$_4$..ATG$_{NS2}$). As for members of the *Densovirus* genus, the VP on the complementary strand also contained the phospholipase A2 motif (4,590 to 4,680 nt) (17) and the stop codons of NS1 and VP were neighbors (2661-TAG/AAT-2666), suggesting a small overlap of their transcripts, as for GmDNV.

Nucleotide sequence accession number. The GenBank accession number of AdMADV is KF275669.

ACKNOWLEDGMENTS

This work was supported by the Natural Sciences and Engineering Research Council of Canada to P.T.; H.T.P. and Q.Y. acknowledge tuition fee waivers at INRS and scholarships from INRS and the People's Republic of China.

REFERENCES

1. **Liu K, Li Y, Jousset FX, Zadori Z, Szelei J, Yu Q, Pham HT, Lépine F, Bergoin M, Tijssen P.** 2011. The *Acheta domesticus densovirus*, isolated from the European house cricket, has evolved an expression strategy unique among parvoviruses. J. Virol. **85:**10069–10078.
2. **Szelei J, Woodring J, Goettel MS, Duke G, Jousset FX, Liu KY, Zadori Z, Li Y, Styer E, Boucias DG, Kleespies RG, Bergoin M, Tijssen P.** 2011. Susceptibility of North-American and European crickets to *Acheta domesticus densovirus* (AdDNV) and associated epizootics. J. Invertebr. Pathol. **106:**394–399.
3. **Weissman DB, Gray DA, Pham HT, Tijssen P.** 2012. Billions and billions

Downloaded from http://genomea.asm.org/ on May 7, 2015 by INSTITUT PASTEUR Bibliothèque

sold: pet-feeder crickets (*Orthoptera*: *Gryllidae*), commercial cricket farms, an epizootic densovirus, and government regulations make a potential disaster. Zootaxa **3504:**67–88.
4. **Pham HT, Iwao H, Szelei J, Li Y, Liu K, Bergoin M, Tijssen P.** 2013. Comparative genomic analysis of *Acheta domesticus* densoviruses from different outbreaks in Europe, North America, and Japan. Genome Announc. **1**(4)**:**e00629-13. doi:10.1128/genomeA.00629-13.
5. **Pham HT, Bergoin M, Tijssen P.** 2013. *Acheta domesticus Volvovirus*, a novel single-stranded circular DNA virus of the house cricket. Genome Announc. **1**(2)**:**e00079-13. doi:10.1128/genomeA.00079-13.
6. **Tijssen P, Agbandje-McKenna M, Almendral JM, Bergoin M, Flegel TW, Hedman K, Kleinschmidt JA, Li Y, Pintel DJ, Tattersall P.** 2011. Parvoviridae, p 375–395. *In* King AMQ, Adams MJ, Carstens E, Lefkowitz EJ (ed), Virus taxonomy: classification and nomenclature of viruses: ninth report of the International Committee on Taxonomy of Viruses. Elsevier, San Diego, CA.
7. **Pham HT, Nguyen OT, Jousset FX, Bergoin M, Tijssen P.** 2013. *Junonia coenia* densovirus (JcDNV) genome structure. Genome Announc. **1**(4)**:** e00591-13. doi:10.1128/genomeA.00591-13.
8. **El-Far M, Szelei J, Yu Q, Fediere G, Bergoin M, Tijssen P.** 2012. Organization of the ambisense genome of the *Helicoverpa armigera* densovirus. J. Virol. **86:**7024. doi:10.1128/JVI.00865-12.
9. **Huynh OT, Pham HT, Yu Q, Tijssen P.** 2012. *Pseudoplusia includens* densovirus genome organization and expression strategy. J. Virol. **86:** 13127–13128.
10. **Fédière G, El-Far M, Li Y, Bergoin M, Tijssen P.** 2004. Expression strategy of densonucleosis virus from *Mythimna loreyi*. Virology **320:** 181–189.
11. **Tijssen P, Li Y, El-Far M, Szelei J, Letarte M, Zádori Z.** 2003. Organization and expression strategy of the ambisense genome of densonucleosis virus of *Galleria mellonella*. J. Virol. **77:**10357–10365.
12. **Yu Q, Hajek AE, Bergoin M, Tijssen P.** 2012. *Papilio polyxenes* densovirus has an iteravirus-like genome organization. J. Virol. **86:**9534–9535.
13. **Yu Q, Fédière G, Abd-Alla A, Bergoin M, Tijssen P.** 2012. Iteravirus-like genome organization of a densovirus from *Sibine fusca* Stoll. J. Virol. **86:** 8897–8898.
14. **Fédière G, Li Y, Zádori Z, Szelei J, Tijssen P.** 2002. Genome organization of *Casphalia extranea* densovirus, a new iteravirus. Virology **292:**299–308.
15. **Li Y, Zádori Z, Bando H, Dubuc R, Fédière G, Szelei J, Tijssen P.** 2001. Genome organization of the densovirus from *Bombyx mori* (BmDNV-1) and enzyme activity of its capsid. J. Gen. Virol. **82:**2821–2825.
16. **Huang X, Madan A.** 1999. CAP3: A DNA sequence assembly program. Genome Res. **9:**868–877.
17. **Zádori Z, Szelei J, Lacoste MC, Li Y, Gariépy S, Raymond P, Allaire M, Nabi IR, Tijssen P.** 2001. A viral phospholipase A2 is required for parvovirus infectivity. Dev. Cell **1:**291–302.

Downloaded from http://genomea.asm.org/ on May 7, 2015 by INSTITUT PASTEUR Bibliothèque