

Short report

Open Access

Bioinformatic analysis suggests that the Cypovirus I major core protein cistron harbours an overlapping gene

Andrew E Firth* and John F Atkins

Address: BioSciences Institute, University College Cork, Cork, Ireland

Email: Andrew E Firth* - A.Firth@ucc.ie; John F Atkins - j.atkins@ucc.ie

* Corresponding author

Published: 20 May 2008

Received: 16 April 2008

Virology Journal 2008, 5:62 doi:10.1186/1743-422X-5-62

Accepted: 20 May 2008

This article is available from: <http://www.virologyj.com/content/5/1/62>

© 2008 Firth and Atkins; licensee BioMed Central Ltd.

This is an Open Access article distributed under the terms of the Creative Commons Attribution License (<http://creativecommons.org/licenses/by/2.0>), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Abstract

Members of the genus *Cypovirus* (family *Reoviridae*) are common pathogens of insects. These viruses have linear dsRNA genomes divided into 10–11 segments, which have generally been assumed to be monocistronic. Here, bioinformatic evidence is presented for a short overlapping coding sequence (CDS) in the cypovirus genome segment encoding the major core capsid protein VPI, overlapping the 5'-terminal region of the VPI ORF in the +1 reading frame. In Cypovirus type I (CPV-1), a 62-codon AUG-initiated open reading frame (hereafter ORFX) is present in all four available segment I sequences. The pattern of base variations across the sequence alignment indicates that ORFX is subject to functional constraints at the amino acid level (even when the constraints due to coding in the overlapping VPI reading frame are taken into account; MLOGD software). In fact the translated ORFX shows greater amino acid conservation than the overlapping region of VPI. The genomic location of ORFX is consistent with translation via leaky scanning. A 62–64 codon AUG-initiated ORF is present in a corresponding location and reading frame in other available cypovirus sequences (2 CPV-14, 1 CPV-15) and an 87-codon ORFX homologue may also be present in *Aedes pseudoscutellaris reovirus*. The ORFX amino acid sequences are hydrophilic and basic, with between 12 and 16 Arg/Lys residues in each though, at 7.5–10.2 kDa, the putative ORFX product is too small to appear on typical published protein gels.

Findings

The genus *Cypovirus* (cytoplasmic polyhedrosis viruses; CPVs) is one of ≥ 12 genera within the *Reoviridae*, a family of segmented dsRNA viruses. While other members of the family infect mammals (e.g. *Bluetongue virus*), including humans (e.g. rotaviruses, coltivirus, mammalian orthoreoviruses and seadornaviruses), CPVs infect insects. CPV species have been divided into 16 or more types (CPV-1, CPV-2, etc) based on electrophoretic migration of the genome segments [1]. Of the 352 *Reoviridae* RefSeqs in GenBank (10 Apr 2008; 33 species \times 9–12 segments per species), only $\sim 5\%$ are multicistronic. Among these are a

few examples of fully overlapping genes apparently translated via leaky scanning, for example in mammalian *Orthoreovirus* segment S1 [2], *Phytoreovirus* segment S12 or S9 [3], and (currently not experimentally verified) *Orbivirus* segment 9 [4]. Such overlapping CDSs can be difficult to detect using conventional gene-finding software [5], especially when short. The software package MLOGD, however, was designed specifically for identifying such CDSs, and includes explicit models for sequence evolution in double-coding regions as well as models for single-coding and non-coding regions [5,6]. Using MLOGD, we recently identified – and subsequently experimentally ver-

ified – a new short CDS in the *Potyviridae* family that overlaps the P3 cistron but is translated in the +2 reading frame [7]. When we applied MLOGD to the cypoviruses we also found evidence for a short overlapping CDS. Here we describe the bioinformatic analysis.

The putative new CDS (hereafter ORFX) was first identified in an alignment of the RefSeq [GenBank: [NC_003016](#)] with its CPV-1 genome neighbours. Subsequently, all homologous CPV sequences in GenBank were located by applying tblastn [8] to the [NC_003016](#) VP1 amino acid sequence, resulting in the sequences [GenBank: [AF389462](#)] – *Lymantria dispar cypovirus 1* segment 1 (CPV-1), [GenBank: [AF323781](#)] – *Bombyx mori cypovirus 1* segment 1 (CPV-1), [GenBank: [AY163247](#)] – *Dendrolimus punctatus cypovirus 1* segment 1 (CPV-1), [GenBank: [AY388398](#)] – *Bombyx mori cypovirus 1* segment 1 (CPV-1), [GenBank: [AF389453](#)] – *Lymantria dispar cypovirus 14* segment 2 (CPV-14), [GenBank: [DQ388474](#)] – *Heliothis armigera cypovirus 14* segment 2 (CPV-14), [GenBank: [AF291684](#)] – *Trichoplusia ni cypovirus 15* segment 2 (CPV-15), and [GenBank: [DQ087278](#)] – *Aedes pseudoscutellaris reovirus* segment 3 (APRV). APRV has only 9 segments and is not classified as a cypovirus [9], but was nonetheless included in the analysis. Note that the GenBank RefSeqs [NC_003016](#), [NC_003007](#) and [NC_002558](#) were derived, respectively, from [AF389462](#), [AF389453](#) and [AF291684](#).

In the four CPV-1 sequences, ORFX has 62 codons (nt coords [AF389462:77..262](#); 7.5 kDa) and overlaps the 5'-terminal region of the VP1 ORF (nt coords [AF389462:40..4038](#)) in the +1 reading frame (Figure 1). Here the VP1 ORF starts at AUG2 (context [acgAUGc](#)) while ORFX starts at AUG3 (context [aauAUGa](#)).

Interestingly, AUG1 (context [\[g/u\]guAUGu](#); nt coords [AF389462:11..13](#)) is also in the ORFX frame and, in [AY163247](#) and [AF323781](#), could allow a 22-aa N-terminal extension of ORFX; however, in [AF389462](#), there is an in-frame termination codon four codons 3' of AUG1 and, furthermore, the MLOGD results (Figure 1; see below) do not support the N-terminal extension.

In order to measure the coding potential of ORFX in CPV-1, we used MLOGD [5]. Applied to an alignment of the four CPV-1 sequences, MLOGD detected a strong coding signature for ORFX, with three non-overlapping – and hence completely independent – positively scoring windows in the ORFX region (Figure 1). The number of independent base variations across the alignment within the ORFX region is $N_{\text{var}} \sim 33$, and the total MLOGD score is $\log(\text{LR}) \sim 23.4$ (see [6] for details). Extensive tests with known single-coding and double-coding virus sequence

alignments indicate that ' $N_{\text{var}} \geq 20$ ' and ' $\log(\text{LR}) \geq \frac{1}{6} \times N_{\text{var}}$ ' signals robust detection (<1% false positive rate) of an overlapping same-strand CDS [6] (and unpublished data). Moreover, the MLOGD results showed that the ORFX amino acid sequence is considerably more conserved at the amino acid level than the overlapping region of VP1 (Figure 1). Indeed, in pairwise comparisons between [AF389462](#) and each of the other three CPV-1 sequences, there was 92–100% amino acid identity in ORFX, but only 74–77% amino acid identity in the overlapping region of VP1.

In the two CPV-14 sequences, ORFX has 64 codons (nt coords [DQ388474:70..261](#); 7.7 kDa) and overlaps the 5'-terminal region of the VP1 ORF (nt coords [DQ388474:39..3947](#)) in the +1 reading frame. In [DQ388474](#), the VP1 ORF starts at AUG2 (context [gauAUGu](#)) while ORFX starts at adjacent AUG [34] (contexts [aagAUGaUGa](#)). AUG1 (context [uagAUGa](#)) at nt coords [DQ388474:20..22](#) is in the -1 frame relative to the VP1 ORF and heads a 15-codon ORF terminating at a UAA codon which is separated from the ORFX AUG codon by a 2-nt spacer. In [AF389453](#), the annotated VP1 ORF starts at nt 261 (the first VP1-frame AUG codon), however, by homology with [DQ388474](#), VP1 initiation likely (also) occurs at a GUG (context [gauGUGu](#)) codon aligning with the VP1 AUG codon in [DQ388474](#). AUG2 itself overlaps the GUG codon in the +1 frame relative to the VP1 ORF and heads a 6-codon ORF terminating at a UAA codon which is separated from the ORFX AUG codons (adjacent AUG [34]) by a 12-nt spacer. As in [DQ388474](#), AUG1 heads a 15-codon ORF that overlaps the VP1 ORF GUG codon and terminates just 5' of AUG3.

In [AF291684](#) (CPV-15), ORFX has 62 codons ([221..406](#); 7.8 kDa), and overlaps the VP1 ORF ([34..4119](#)) in the +1 reading frame. The VP1 ORF starts at AUG1 (context [aguAUGu](#)) but ORFX starts at AUG5 (context [aauAUGc](#)), with AUG [234] in the ORFX frame but heading two short ORFs: [AUGaacUGAucaAUGaaaAUGaguuaCUAG](#) (nt coords [83..112](#)).

In [DQ087278](#) (APRV), ORFX has 87 codons ([113..373](#); 10.2 kDa), and overlaps the VP1 ORF ([34..3639](#)) in the +1 reading frame. The VP1 ORF starts at AUG1 (context [uuuAUGa](#)) and ORFX starts at AUG3 (context [aaaAUGa](#)), with AUG2 (context [agaAUGu](#)) being in the VP1 frame, five codons 3' of AUG1.

MLOGD can not be used effectively on an alignment of all eight sequences because the pairwise divergences are too great, so we can not robustly assess the coding potential of ORFX outside of CPV-1 with the currently available

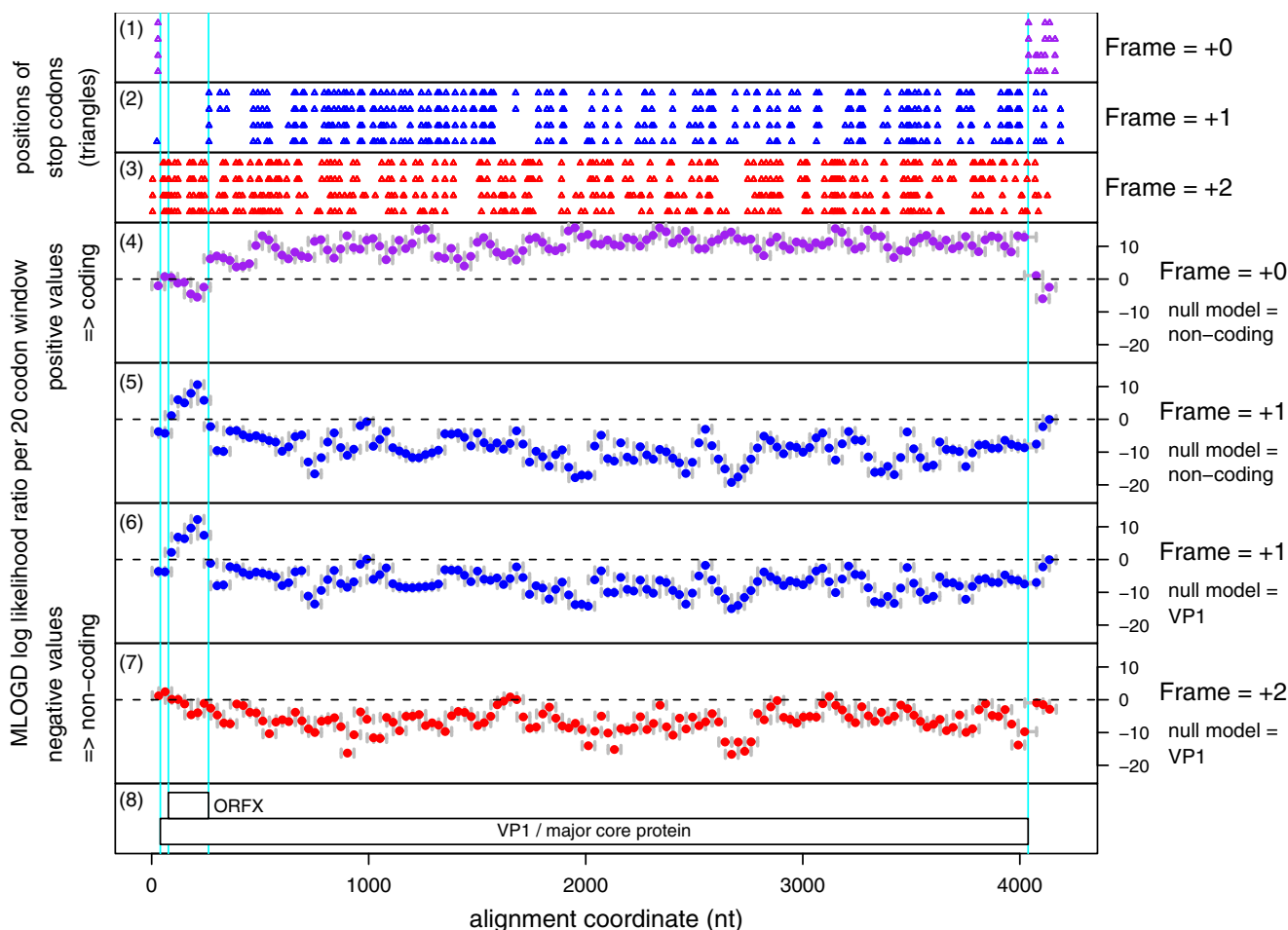


Figure 1
MLOGD statistics for the alignment of four CPV-1 segment I sequences. The four sequences were aligned with code2aln [15]; the alignment is gapless within the VP1 ORF. **(1)–(3)** The positions of stop codons in each of the four sequences in each of the three forward reading frames (frame defined by alignment to the reference sequence [GenBank: AF389462]). Note the conserved absence of stop codons in the +0 frame within the VP1 ORF and in the +1 frame in the ORFX region. **(4)–(7)** MLOGD sliding-window plots. Window size = 20 codons. Step size = 10 codons. Each window is represented by a small circle (showing the likelihood ratio score for that window), and grey bars showing the width (ends) of the window. See [6] for further details of the MLOGD software. In **(4)–(5)** the null model, in each window, is that the sequence is non-coding, while the alternative model is that the sequence is coding in the window frame. Positive scores favour the alternative model. There is a strong coding signature in the +0 frame (4) throughout the VP1 ORF, except where it overlaps ORFX. In this region there is a strong coding signature in the +1 frame (5) indicating that ORFX is subject to stronger functional constraints than the overlapping section of VP1. In **(6)–(7)** the null model, in each window, is that only the VP1 frame is coding, while the alternative model is that both the VP1 frame and the window frame are coding. Only the +1 (6) and +2 (7) frames are shown because the +0 frame is the VP1 frame which is included in the null model. Scores are generally negative with occasional random scatter into low positive scores, except for the ORFX region which has consecutive high-positively scoring windows (6). **(8)** Map of the reference sequence [GenBank: AF389462].

sequence data. However, the fact that the +1 frame ORF is present at the same alignment location in all eight sequences, even though the mean divergence of the 8-sequence alignment within the ORFX region is ~ 1.5 independent base variations per alignment nucleotide column, suggests that it is functionally important.

The genomic location of ORFX is more-or-less consistent with a leaky scanning model for ORFX translation, albeit perhaps at relatively low efficiency since the contexts of the VP1 initiation codons are not particularly weak. The frequent presence of an additional AUG codon, preceding both the ORFX and VP1 AUG codons, is a little confusing both for VP1 and ORFX translation though, in some cases,

this AUG codon may play a role in moving some ribosomes past the VP1 initiation codon, allowing them to reinitiate at the ORFX AUG codon. There may also be other *cis*-elements that promote ORFX translation (although we were unable to locate candidate RNA secondary structures for this purpose). The presence of two short intervening ORFs argues against simple leaky scanning in CPV-15. It is interesting, and possibly relevant, that in another *Reoviridae* species – *Avian reovirus* – a novel, as yet not fully understood, scanning-independent ribosome migration mechanism is used to bypass two upstream CDSs in order to translate the 3'-proximal CDS on the tricistronic S1 mRNA [10].

In AF389462 (CPV-1), the ORFX peptide sequence is MKRNINNQKLTAVQIMEKERQEHAIKQLEILRLKRELEMKRKQVQALEDRLMARAVVEQMOK. With the exception of APRV, the 62–64-aa ORFX peptide sequence is very hydrophilic ($\geq 60\%$ of residues are polar) and basic (22–27% of residues are basic) with 13–16 Arg/Lys residues. The APRV ORFX peptide sequence is longer (87 aa) but has a similar hydrophobicity profile, is also basic, and contains 12 Arg/Lys residues. One potential function for ORFX product may be suppression of silencing via dsRNA binding (cf. [11]). Alternatively, the Arg/Lys residues may mediate nuclear localization. Application of blastp [8] to the eight ORFX peptide sequences revealed no similar amino acid sequences in GenBank (10 Apr 2008). Similarly, application of InterProScan [12] returned no hits (protein motifs, domains etc).

The VP1 protein itself (~150 kDa) has been identified as the major capsid protein [13,14]. It shares some homology with the *Oryzavirus* major capsid protein P3 [13] and, expressed independently, assembles into single-shelled virus-like particles [14]. Our analysis indicates that the 5'-terminal region of the VP1 ORF encodes, in the +1 reading-frame, an additional 7.5–7.8 kDa protein. Cypoviruses have potential uses in insect pest control and are also important pathogens of commercially important insects such as silkworms. Although much remains to be discovered about even the ten known cypovirus proteins, it is important to know of any additional proteins as early as possible. In particular, if an overlapping gene remains undetected, then its functions may be wrongly attributed to the gene that it overlaps, leading to persistent and wasteful confusion. We hope that presentation of this bioinformatic analysis will stimulate an attempt to experimentally verify the expression and functional role of ORFX product. Initial verification could be by means of immunoblotting with ORFX-specific antibodies, bearing in mind, however, that it may be expressed at relatively low levels.

Competing interests

The authors declare that they have no competing interests.

Authors' contributions

AEF carried out the bioinformatic analysis and wrote the manuscript. Both authors edited and approved the final manuscript.

Acknowledgements

This work was supported by an award from Science Foundation Ireland to John F Atkins.

References

- Mertens PPC, Rao S, Zhou H: **Cypovirus, Reoviridae**. In *Virus Taxonomy, VIIIth Report of the ICTV* Edited by: Fauquet CM, Mayo MA, Maniloff J, Desselberger U, Ball LA. London: Elsevier/Academic Press; 2004:522-533.
- Ernst H, Shatkin AJ: **Reovirus hemagglutinin mRNA codes for two polypeptides in overlapping reading frames**. *Proc Natl Acad Sci USA* 1985, **82**:48-52.
- Suzuki N, Sugawara M, Nuss DL, Matsuura Y: **Polycistronic (tri- or bicistronic) phytoreoviral segments translatable in both plant and insect cells**. *J Virol* 1996, **70**:8155-8159.
- Firth AE: **Bioinformatic analysis suggests that the Orbivirus VP6 cistron encodes an overlapping gene**. *Virology* 2008, **5**:48.
- Firth AE, Brown CM: **Detecting overlapping coding sequences with pairwise alignments**. *Bioinformatics* 2005, **21**:282-292.
- Firth AE, Brown CM: **Detecting overlapping coding sequences in virus genomes**. *BMC Bioinformatics* 2006, **7**:75.
- Chung BYW, Miller WA, Atkins JF, Firth AE: **An overlapping essential gene in the Potyviridae**. *Proc Natl Acad Sci USA* 2008, **105**:5897-5902.
- Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ: **Basic local alignment search tool**. *J Mol Biol* 1990, **215**:403-410.
- Attoui H, Mohd Jaafar F, Belhouchet M, Biagini P, Cantaloube JF, de Micco P, de Lamballerie X: **Expansion of family Reoviridae to include nine-segmented dsRNA viruses: isolation and characterization of a new virus designated *Aedes pseudoscutellaris reovirus* assigned to a proposed genus (*Dinovernavirus*)**. *Virology* 2005, **343**:212-223.
- Racine T, Barry C, Roy K, Dawe SJ, Shmulevitz M, Duncan R: **Leaky scanning and scanning-independent ribosome migration on the tricistronic S1 mRNA of avian reovirus**. *J Biol Chem* 2007, **282**:25613-25622.
- González-López C, Martínez-Costas J, Esteban M, Benavente J: **Evidence that avian reovirus σ A protein is an inhibitor of the double-stranded RNA-dependent protein kinase**. *J Gen Virol* 2003, **84**:1629-1639.
- Zdobnov EM, Apweiler R: **InterProScan – an integration platform for the signature-recognition methods in InterPro**. *Bioinformatics* 2001, **17**:847-848.
- Hagiwara K, Rao S, Scott SW, Carner GR: **Nucleotide sequences of segments 1, 3 and 4 of the genome of *Bombyx mori* cypovirus 1 encoding putative capsid proteins VP1, VP3 and VP4, respectively**. *J Gen Virol* 2002, **83**:1477-1482.
- Hagiwara K, Naitow H: **Assembly into single-shelled virus-like particles by major capsid protein VP1 encoded by genome segment S1 of *Bombyx mori* cypovirus 1**. *J Gen Virol* 2003, **84**:2439-2441.
- Stocsits RR: **Nucleic Acid Sequence Alignments of Partly Coding Regions**. In *PhD thesis* University of Vienna; 2003.