The first genome sequence of a metatherian herpesvirus: Macropodid herpesvirus 1

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Abstract

Background: While many placental herpesvirus genomes have been fully sequenced, the complete genome of a marsupial herpesvirus has not been described. Here we present the first genome sequence of a metatherian herpesvirus, Macropodid herpesvirus 1 (MaHV-1).

Results: The MaHV-1 viral genome was sequenced using an Illumina MiSeq sequencer, de novo assembly was performed and the genome was annotated. The MaHV-1 genome was 140 kbp in length and clustered phylogenetically with the primate simplexviruses, sharing 67 % nucleotide sequence identity with Human herpesviruses 1 and 2. The MaHV-1 genome contained 66 predicted open reading frames (ORFs) homologous to those in other herpesvirus genomes, but lacked homologues of UL3, UL4, UL56 and glycoprotein J. This is the first alphaherpesvirus genome that has been found to lack the UL3 and UL4 homologues. We identified six novel ORFs and confirmed their transcription by RT-PCR.

Conclusions: This is the first genome sequence of a herpesvirus that infects metatherians, a taxonomically unique mammalian clade. Members of the Simplexvirus genus are remarkably conserved, so the absence of ORFs otherwise retained in eutherian and avian alphaherpesviruses contributes to our understanding of the Alphaherpesvirinae. Further study of metatherian herpesvirus genetics and pathogenesis provides a unique approach to understanding herpesvirus-mammalian interactions.

Keywords: Marsupial, Herpesvirus, Genome, Wildlife, Macropod, Kangaroo, Herpes simplex

Background

Members of the Herpesviridae have a linear double-stranded DNA genome, 120–245 kbp in length, and cause significant morbidity and mortality in diverse groups of animals. Members are further classified into three subfamilies; the Alpha-, Beta- and Gammaherpesvirinae. Reports of herpesvirus infections in the Marsupialia date back to the 1970s. The first isolation of a marsupial herpesvirus was from a fatal outbreak of severe respiratory disease and systemic organ failure in a zoological collection of Parma wallabies (Macropus parma) [1]. The isolation of this alphaherpesvirus, designated Macropodid herpesvirus 1 (MaHV-1), was closely followed by the isolation of a second, related, herpesvirus (Macropodid herpesvirus 2, MaHV-2) from fatal cases of disease in several vulnerable macropod species [2]. The macropodid viruses were detected in animals displaying some clinical signs of disease similar to those caused by Human herpesviruses 1 and 2 (HHV-1 and −2) infection, such as conjunctivitis and vesicular anogenital lesions, but also included hepatic disease [1, 3]. In the following 30 years, before the identification of additional marsupial herpesviruses, evidence of herpesvirus infection in metatherians was largely observed through electron microscopy or sero-epidemiological surveys. These sero-prevalence studies measured neutralising antibodies to MaHV-1, which were detected in both wild (23–69 %) and captive (41 %) populations of...
marsupials [4, 5]. Since 2008, eleven additional marsupial herpesviruses have been identified, including a closely-related alphaherpesvirus, *Macropodid herpesvirus 4* (MaHV-4), in free-ranging eastern grey kangaroos (*Macropus giganteus*) with clinical signs of respiratory and possible neurological disease [6] and two gamma-herpesviruses from macropods [7–9]. A further eight herpesviruses have been identified in other (non-macropodid) marsupial species, though little sequence data are available for these viruses [9–13].

Despite its classification as a *Simplexvirus*, early genome hybridization studies of MaHV-1 identified a type D genome arrangement (as defined by [14]) of approximately 135 kbp in length, containing a short unique (U<sub>S</sub>) region, flanked by large inverted repeat sequences (internal repeat and terminal repeat; IR<sub>S</sub>/TR<sub>S</sub>) joined to a long unique (U<sub>L</sub>) region [15, 16]. MaHV-1 occurs as only two equimolar genomic isomers [15]. These genomic features are characteristic of *Varicelloviruses* such as varicella zoster virus (VZV) and pseudorabies virus (PRV) and contrast with those of MaHV-2. MaHV-2 has a type E genome arrangement, more typical of the *Simplexviruses*, and occurs as four equimolar genomic isomers [17]. To date MaHV-1 is the only alphaherpesvirus that encodes both ICP34.5 (RL1) and the host-derived oncogene thymidylate synthase [18]. Sequence analysis of two conserved ORFs in MaHV-1, –2 and –4, as well as analyses of their antigenic relationships, has clustered these macropodid viruses closely with the primate *Simplexviruses* [3, 6, 19]. As metatherian and eutherian mammals are believed to have diverged over 85 million years ago [20], this viral phylogenetic grouping differed from the typical virus-host co-evolutionary pattern observed within the *Herpesviridae* [3, 19, 21, 22] and was instead suggestive of a recent and complex speciation event.

This study aimed to sequence and analyse the full genome of the metatherian alphaherpesvirus, MaHV-1, with particular attention to novel genomic features.

**Results and discussion**

**Whole genome sequence analysis**

The genome of MaHV-1 is the first metatherian herpesvirus to be sequenced. Excluding the genomic termini, which remained unresolved, the final genome length of MaHV-1 was approximately 140.1 kbp (Fig. 1) [GenBank:KT594769], larger than previously predicted. This difference appears to be due to a larger than predicted inverted repeat region [15]. This included a 98.8 kbp U<sub>L</sub> region and a 15.3 kbp U<sub>S</sub> region flanked by 13 kbp inverted repeat sequences (IR<sub>S</sub>/TR<sub>S</sub>). The MaHV-1 genome had a G + C content of 52.9 %, but had a higher G + C content (up to 61.7 %) within the IR<sub>S</sub>/TR<sub>S</sub> regions. The final genome assembly had a mean depth of 2,168.
reads per bp (2.05 million mapped reads) and approximately 95 % of reads had a quality score of at least Phred$_{20}$. Three origins of replication were identified. The origin of lytic replication (oriLyt) was located between UL29 and UL30 in the $U_L$ region and the oriS was located within the IRs/TRs regions. Thus two copies of oriS were present, as in the genomes of HHV-1 and -2.

Conserved alphaherpesvirus ORFs

The $U_L$ region of the MaHV-1 genome encoded 54 ORFs common to other herpesviruses (Table 1). The predicted protein sequences of these ORFs shared between 41 % and 73 % aa pairwise identity (up to 86 % aa similarity) with HHV-1 and -2 homologues. In the $U_S$ region the MaHV-1 genome encoded seven ORFs common to other simplexviruses (US1 to US4 and US6 to US8), with the predicted protein sequences sharing between 32 and 59 % aa pairwise identity (up to 73 % aa similarity) with HHV-1 and -2 homologues. The IR$_S$/TR$_S$ regions encoded five ORFs, including those for thymidylate synthase, ICP0 and ICP34.5. There were no homologues of UL3, UL4, UL56 or US5 (glycoprotein J, gJ) identified in the MaHV-1 genome. Also, the US4 (glycoprotein G, gG) homologue was predicted to be non-functional, as the ORF was prematurely truncated (120 aa residues compared to 583 aa in MaHV-4). This is consistent with previous published sequence data reporting a truncation of the MaHV-1 gG ORF [6, 23]. Phylogenetic analyses using translated protein sequences of three core herpesvirus genes (UL27, UL30 and US6) are shown in Fig. 2. These analyses show that MaHV-1 clusters most closely with other macropodid herpesviruses (MaHV-2 and MaHV-4), as well as with the simplexviruses that infect primates. It also groups with the herpesvirus of an Indonesian pteropodid bat. Comparison of other viral core genes yielded similar clustering patterns. Comparison of the MaHV-1 UL27 and UL30 ORFs with those of the recently sequenced fruit bat herpesvirus 1 (FbHV-1) [GenBank:BAP00706 and GenBank:YP_009042092; UL27 and UL30, respectively] showed that these ORFs shared 71 and 67 % pairwise aa identity, respectively (83 and 78 % aa similarity). This similarity is comparable to that seen between MaHV-1 and HHV-1/HHV-2 (Table 1 and Fig. 2), which may offer some insight into their evolutionary relationship, for example, may suggest transmission of herpesviruses from primates to bats, and then to marsupials. Sequencing of herpesviruses from other metatherians, as well as other Australasian mammals, will be needed to determine the significance of this clustering.

Although UL3 and UL4 are conserved in all other alphaherpesviruses examined to date, gene deletion studies in the human simplexviruses have found that deletion of UL3 and UL4 does not affect viral replication or cell-to-cell spread in vitro [24]. In vivo functions of the UL3 and UL4 encoded accessory proteins are not well understood, but they colocalise and directly interact with the transcriptional repressor ICP22, encoded by US1, in small dense nuclear bodies and may also be involved in the late phase of viral replication [25–27]. The absence of gJ is also of note. This is the third Simplexivirus found to lack an ORF encoding a gJ homologue, which is otherwise conserved in the Simplexivirus genus. The other two simplexviruses lacking gJ are leopordid herpesvirus 4 and FbHV-1 [28, 29]. In other herpesviruses gJ inhibits host cell apoptosis by inducing an increase in concentrations of reactive oxygen species in the host cell [30]. It is unclear whether the absence of UL3, UL4 and gJ might be related to adaptation to a new host (marsupials) or whether it may be the result of virus passage in vitro. In respect to gJ, the former scenario could be more likely, as the absence of this ORF in other non-primate herpesviruses shows that it is not strictly conserved within the genus. Sequencing of other marsupial alphaherpesviruses, particularly field isolates, would help to resolve this finding.

Unique or hypothetical ORFs

Seven unique hypothetical ORFs were identified; one in the $U_L$ region, two located in the IR$_S$/TR$_S$ regions, and four in the $U_S$ region. Viral transcript analyses by qRT-PCR confirmed that six of the seven predicted ORFs were transcribed at both 4 and 12 h post infection (hpi) under in vitro conditions (Additional file 1: Figure S1). No transcripts for these six ORFs were detected in the uninfected cell controls at any time point. The seventh predicted ORF, which was located in the large inverted repeat region flanked by ICP0 and ICP34.5, was excluded from further analyses as qRT-PCR targeting this ORF could not confirm transcription. The six ORFs for which transcription was confirmed were annotated PW1 to PW6. PW1 was encoded in the TR$_S$/IR$_S$ repeat region (and thus two copies were present), and no significant structural or sequence domains or motifs were identified within it. Four novel ORFs, PW2 to PW5, were encoded in the $U_S$ region as a cluster downstream of US8 (Fig. 1). No putative conserved domains were detected in the polypeptides encoded by PW2 and 4, although PW3 and 5 had increased internal hydrophobicities, suggestive of transmembrane domains. Structural prediction analyses using I-TASSER suggested potential structural homologues for PW3 (C. elegans SMG5-7 complex for nonsense-mediated mRNA decay, [PDBHit:3zheB2], TM-score = 0.805, RMSDa = 2.69, 94.3 % coverage) and PW4 (Phage Phi6 capsid subunit, [PDBHit:4btgA], TM-score = 0.797, RMSDa = 2.64, 87.6 % coverage). No significant structural homologues were predicted for any of the other novel ORFs. Analysis of the predicted amino
| ORF       | Length (nt) | Length (aa) | Description (putative) | MaHV2 | MaHV4 | HHV1 | HHV2 |
|-----------|-------------|-------------|------------------------|-------|-------|------|------|
| US1       | 1392        | 463         | Infected cell protein 22; ICP22 | 29    | 35    |
| US2       | 867         | 288         | Tegument protein        | 49    | 49    |
| US3       | 1449        | 482         | Protein kinase          | 56    | 59    |
| US4       | 360         | 119         | Glycoprotein G; predicted non-functional | 59    | 63    | 32   | 35   |
| US6       | 1188        | 395         | Glycoprotein D          | 74    | 56    | 57   |
| US7       | 1392        | 463         | Glycoprotein I          | 58    | 38    | 39   |
| US8       | 1599        | 532         | Glycoprotein E          | 63    | 34    | 32   |
| PW2       | 342         | 113         | Unique hypothetical     |       |       |      |      |
| PW3       | 582         | 193         | Unique hypothetical     |       |       |      |      |
| PW4       | 1023        | 340         | Unique hypothetical     |       |       |      |      |
| PW5       | 1233        | 410         | Unique hypothetical     |       |       |      |      |
| ICP4      | 3708        | 1235        | Infected cell protein 4; ICP4 | 51    | 50    |
| TS        | 951         | 316         | Thymidylate synthase; host-derived |       |       |      |      |
| ICP34.5   | 900         | 299         | Infected cell protein 34.5; ICP34.5 | 62    | 56    |
| ICP0      | 1629        | 542         | Infected cell protein 0; ICP0 | 50    | 51    |
| UL1       | 579         | 192         | Glycoprotein L          | 41    | 47    |
| UL2       | 906         | 301         | Uracil-DNA glycosylase   | 59    | 60    |
| UL5       | 2601        | 866         | Helicase-primase helicase subunit | 73    | 73    |
| UL6       | 2007        | 668         | Capsid portal protein   | 62    | 63    |
| UL7       | 888         | 295         | Tegument protein        | 51    | 49    |
| UL8       | 2253        | 750         | Helicase-primase subunit | 38    | 39    |
| UL9       | 2616        | 871         | DNA replication origin-binding helicase | 70    | 70    |
| UL10      | 1347        | 448         | Glycoprotein M          | 51    | 48    |
| UL11      | 246         | 81          | Myristoylated tegument protein | 45    | 59    |
| UL12      | 1749        | 582         | Alkaline exonuclease; deoxyribonuclease | 56    | 56    |
| UL13      | 1845        | 614         | Tegument serine/threonine protein kinase | 48    | 47    |
| UL14      | 645         | 214         | Tegument protein        | 60    | 63    |
| UL15      | 2100        | 699         | DNA packaging terminase subunit 1 | 70    | 71    |
| UL16      | 1098        | 365         | Tegument protein        | 51    | 54    |
| UL17      | 2184        | 727         | DNA packaging tegument protein | 51    | 50    |
| UL18      | 951         | 316         | Capsid triplex subunit 2 | 68    | 68    |
| UL19      | 4131        | 1376        | Major capsid protein    | 69    | 70    |
| UL20      | 648         | 215         | Envelope protein        | 45    | 43    |
| UL21      | 1596        | 531         | Tegument protein        | 43    | 43    |
| UL22      | 2631        | 876         | Glycoprotein H          | 45    | 45    |
| UL23      | 1062        | 353         | Thymidine kinase        | 76    | 42    | 44   |
| UL24      | 702         | 233         | Nuclear protein         | 52    | 53    |
The MaHV-1 genome lacked an identifiable UL56 homologue. Studies in HHV-2 have shown that UL56 encodes a tegument protein involved in relocalising ubiquitin ligase Nedd4 in HHV-2 infected cells, and has a role in intracellular virion transport and/or virion release from the cell surface [31, 32]. UL56 polypeptide interacts and complexes with UL11 polypeptide as they co-localise in the Golgi apparatus and in aggresome-like structures [33]. In HHV-2, UL56 is dispensable for virus growth in vitro, but deletion of it results in reduced production of cell-free infectious virus [31]. In vivo, the presence of UL56 is important for pathogenicity of HHV-1, with deletion mutants having reduced neuroinvasiveness [34]. The hydrophobic C-terminal region of UL56 is particularly important for pathogenicity [35].

Table 1 Predicted open reading frames (ORFs) identified in different structural regions of the Macropodid herpesvirus 1 genome and percentage pairwise amino acid identity to ORFs in related alphaherpesviruses (Continued)

| ORF | Sequence Length | Percentage ID | Human herpesvirus 1 | Human herpesvirus 2 |
|-----|----------------|---------------|---------------------|---------------------|
| UL25 | 1740           | 579           | DNA packaging tegument protein | 61 61 |
| UL26 | 1761           | 586           | Capsid maturation protease | 53 52 |
| UL27 | 2664           | 887           | Glycoprotein B | 83 82 72 70 |
| UL28 | 2325           | 774           | DNA packaging terminase subunit 2 | 64 63 |
| UL29 | 3579           | 1192          | ICP8; single stranded binding protein | 70 69 |
| UL30 | 3675           | 1224          | DNA polymerase | 66 66 |
| UL31 | 921            | 306           | Nuclear egress lamina protein | 73 72 |
| UL32 | 1731           | 576           | DNA packaging protein | 62 61 |
| UL33 | 390            | 129           | DNA packaging protein | 61 60 |
| UL34 | 837            | 278           | Nuclear egress membrane protein | 44 43 |
| UL35 | 408            | 135           | Small capsid protein | 53 50 |
| UL36 | 8535           | 2844          | Large tegument protein | 48 48 |
| UL37 | 3150           | 1049          | Tegument protein | 46 45 |
| UL38 | 1359           | 452           | VP19C; capsid triplex subunit 1 | 56 56 |
| UL39 | 2916           | 971           | Ribonucleotide reductase subunit 1 | 65 66 |
| UL40 | 990            | 329           | Ribonucleotide reductase subunit 2 | 65 65 |
| UL41 | 1566           | 521           | Tegument host shutoff protein | 60 61 |
| UL42 | 1422           | 473           | DNA polymerase processivity subunit | 44 44 |
| UL43 | 1296           | 431           | Glycoprotein C | 36 34 |
| UL44 | 516            | 171           | Membrane protein | 42 40 |
| UL45 | 2343           | 780           | VP11/12; tegument protein | 49 49 |
| UL46 | 2133           | 710           | VP13/14; tegument protein | 43 42 |
| UL47 | 1497           | 498           | VP16; transactivating tegument protein | 47 47 |
| UL48 | 777            | 258           | VP22; tegument protein | 67 67 |
| UL49A| 324            | 107           | Glycoprotein N | 39 35 |
| UL50 | 1035           | 344           | Deoxyuridine triphosphatase | 39 35 |
| UL51 | 741            | 246           | Tegument protein | 67 66 |
| UL52 | 3102           | 1033          | Helicase primase subunit | 59 58 |
| UL53 | 1023           | 340           | Glycoprotein K | 46 47 |
| UL54 | 1524           | 507           | ICP27; multifunctional expression regulator | 52 52 |
| UL55 | 540            | 179           | Nuclear protein | 40 36 |
| PW6  | 630            | 209           | Unique hypothetical | 6 |

1 Putative function of encoded polypeptides in MaHV-1
2 Amino acid identities with homologues in Human herpesvirus 1 and 2 (HHV1 and HHV2) and Macropodid herpesviruses 2 and 4 (MaHV2 and MaHV4)
terminus of PW6, which was encoded directly downstream of UL55. This may indicate that PW6 is a distant UL56 homologue, although it only shared 17 % aa pairwise identity (27 % aa similarity) with HHV-1 UL56. However, at this stage any structural or functional similarities between PW6 and UL56 remain unclear, particularly as preliminary analyses of predicted tertiary structures did not identify significant structural similarities.

In the absence of conserved motifs or domains, the sequences of PW1 to PW4 provide no indication of the potential functions of these novel polypeptides. The identification of a rhoptery antigen domain in PW5 may suggest an association with organelles, but little else can be inferred. High relative levels of transcript of PW2 to PW5 at 4 hpi may indicate that they are transcribed at an early stage of the replication cycle, but further studies are necessary to better differentiate the kinetics of expression of these ORFs. It is not clear whether these genes are important for in vitro replication or in vivo pathogenicity. Gene deletion studies or functional studies of the products of these ORFs would be necessary to elucidate their function. The clustering of novel ORFs identified in the US/IR region, PW1 to PW5, suggest that they may have been acquired in a single event, possibly from an unknown host or another virus during virus speciation. Sequence comparisons with other marsupial herpesviruses would help determine whether the novel ORFs are unique to MaHV-1, or are instead ORFs common to herpesviruses infecting metatherians.

Conclusions
This is the first genome sequence of a herpesvirus that infects metatherians, a taxonomically unique mammalian clade. Members of the Simplexvirus genus are remarkably conserved, so the absence of ORFs otherwise conserved in eutherian and avian alphaherpesviruses contributes to our understanding of the Alphaherpesvirinae more generally. Together with the sequence similarities observed to the human herpesviruses, these conclusions indicate that further study of metatherian herpesvirus genetics and pathogenesis will provide a unique approach to understanding herpesvirus-mammalian interactions.
Methods
Viral genome sequencing and analysis
The MaHV-1 isolate selected for sequencing (MaHV1.3076/08) was originally isolated from a Parma wallaby with clinical signs of disease [1]. The viral nucleocapsid genomic DNA was purified and sequenced as previously described [6, 36]. Briefly, 50 ng of viral genomic DNA was used to prepare libraries using the Illumina Nextera DNA library preparation kits according to the manufacturer’s instructions. The libraries were pooled in equimolar concentrations and loaded onto an Illumina MiSeq. Sequencing was carried out using a 300 cycle V2 SBS kit (Illumina, Inc.) in paired-end 150 bp format. Over 350 Mbp of sequence data were obtained from 2.69 million paired reads with a mean length of 137 bp (standard deviation of 26.3) and were submitted to the Short Read Archive [SRA:SRP067309]. Reads were trimmed to an error probability limit of 0.5 % and de novo assembly was performed using medium-low default sensitivity settings on the bioinformatics package Geneious version 6.1.7 [37] (Biomatters Ltd). This yielded four large contigs (52.6 kbp, 37.3 kbp, 14.9 kbp and 17 kbp) with consensus sequences that corresponded to herpesvirus sequence, according to Blastx and Blastn searches of GenBank databases [38, 39]. These consensus sequences were used as references in further assemblies, where reads were reiteratively mapped until there was no further contig extension. Previously published MaHV-1 genome sequence data [GenBank:AY048539, GenBank:AF188480] was used to aid scaffold construction. Medium and high sensitivity default settings with a minimum of 90–95 % overlap identity in Geneious version 6.1.7 were used in these assemblies.

Prediction of open reading frames (ORFs) using Glimmer3 was restricted to those larger than 240 bp, and ORF annotations were determined by Blastx and Blastn searching against the NCBI non-redundant protein and nucleotide databases, respectively [38, 39]. ORF annotations followed those of HHV-1 and –2, whilst the novel ORFs were prefixed with PW (Parma wallaby). The unique MaHV-1 ORF sequences were translated to hypothetical polypeptides and compared to sequence motifs in the Pfam database to determine their putative functions. Further structural prediction analyses were performed using I-TASSER [40]. Threshold cut-off values of >1 for the normalised Z-score, < 3.0 for the RMSD and >0.7 for the TM-score were considered significant and used to identify structural homologues.

Phylogenetic analyses of the translated protein sequences of the core herpesvirus genes UL27, UL30 and US6 were performed using the neighbour - joining method in Geneious version 6.1.7 with the Jukes Cantor model of amino acid substitution [41]. Ten thousand bootstrap replicates were used to assess the significance of the phylogenetic tree topology.

Confirmation of transcription of novel ORFs
To determine if the novel ORFs were transcribed in vitro, RNA from infected cells was interrogated using quantitative reverse transcription PCR (qRT-PCR). One-step growth analyses using wallaby fibroblast JU56 cells [42] in 6-well trays was performed as previously described [6] with modifications. Briefly, JU56 cells were infected with virus at a multiplicity of infection of 3 (3 median tissue culture infective dose (TCID50) per cell). The contents of wells collected at 4 and 12 hpi. RNA was extracted using the RNeasy RNA Extraction kit (Qiagen) and 2 μg of purified nucleic acid was treated with DNase using the TurboDNase kit (Life Technologies). Complementary DNA was prepared using Superscript III reverse transcriptase (Life Technologies). Transcription was detected by qPCRs containing 500 nM of each primer (Additional file 2: Table S1), 50 μM dNTPs, 2 μM MgCl2, 8 μM Syto9 green fluorescent stain (Life Technologies) and GoTaq DNA polymerase (Promega). Reactions were incubated through 40 cycles of 95 °C for 30 s, 60 °C for 30 s and 72 °C for 60 s. Relative levels of transcription of each ORF were calculated by comparing cycle threshold (CT) values for each ORF to that of the host housekeeping gene GAPDH and to those obtained for uninfected cell controls, determining the normalised expression value as previously described [43, 44]. Further amino acid sequence analyses, as described above, were continued only on the polypeptides encoded by ORFs confirmed to be transcribed in vitro.

Availability of supporting data
The MaHV-1 genome sequence data has been submitted to GenBank and the accession number is KT594769. The Illumina read data have been submitted to the Short Reads Archive database and has the ID number SRA:SRP067309.

Additional files

Additional file 1: Figure S1. Relative transcript levels for the unique hypothetical MaHV-1 ORFs PW1 to PW6 at 4 h (grey bars) and 12 h (black bars) post infection (hpi) in wallaby fibroblast cells. Expression was normalised to the host housekeeping gene, GAPDH, and analysed by calculating mean normalised expression values. No viral transcripts were detected in uninfected cells. Error bars indicate standard deviation of three biological replicates. (TIF 8005 kb)

Additional file 2: Table S1. Oligonucleotides used for ORF transcription studies of the unique hypothetical MaHV-1 ORFs (PW1 to PW6) and the host housekeeping gene GAPDH. (DOC 37 kb)

Abbreviations
Ct: cycle threshold; DPOL: DNA polymerase; FbHV: fruit bat herpesvirus; GAPDH: Glyceraldehyde 3-phosphate dehydrogenase; gB: glycoprotein B; gD: glycoprotein D; gG: glycoprotein G; gJ: glycoprotein J; HHV: human herpesvirus; hpi: hours post infection; ICP: infected cell protein; IR/TR internal
Contributions – 

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