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Research paper

A comparison of virus genome sequences with their host silkworm, *Bombyx mori*

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ABSTRACT

With the recent availability of the genomes of many viruses and the silkworm, *Bombyx mori*, as well as a variety of Basic Local Alignment Search Tool (BLAST) programs, a new opportunity to gain insight into the interaction of viruses with the silkworm is possible. This study aims to determine the possible existence of sequence identities between the genomes of viruses and the silkworm and attempts to explain this phenomenon. BLAST searches of the genomes of viruses against the silkworm genome were performed using the resources of the National Center for Biotechnology Information. All studied viruses contained variable numbers of short regions with sequence identity to the genome of the silkworm. The short regions of sequence identity in the genome of the silkworm may be derived from the genomes of viruses in the long history of silkworm-virus interaction. This study is the first to compare these genomes, and may contribute to research on the interaction between viruses and the silkworm.

1. Introduction

The Silkworm, *Bombyx mori*, is not only an important economic insect for its silk production, but also a model system for study of the Lepidoptera. *B. mori* viral disease is a serious source of huge economic losses in sericulture (Bao et al., 2008; Bao et al., 2009; Zhou et al., 2013). A study on the interaction between virus and silkworm is of vital importance for prevention of viral disease. Not all exposures to viruses cause disease. In fact, most of the pathologic effects of these interactions are not caused directly by the viruses but by the effects of the immune response to the viruses. Viruses only aim to replicate themselves without killing the host. In contrast, hosts try to eradicate all disease-causing viruses (Lin & Li, 2009).

Many studies have been proposed to investigate the relationship between viruses and *B. mori*, mainly focused on the silkworm immune response to infection by viruses and the viral infection patterns (Bao et al., 2008; Bao et al., 2009; Dong et al., 2014; Singh et al., 2014). In the past decade, the *B. mori* genome sequence was published (Wang et al., 2005; Xia et al., 2004). The successful sequencing of many different silkworm viral genomes, and the recent availability of a variety of Basic Local Alignment Search Tool (BLAST) programs (Altschul et al., 1997), may provide a new opportunity to investigate the relationship between genome sequences of viruses and *B. mori*. Many studies on the relationships between humans and viruses or bacteria have been performed using BLAST programs (Lin & Li, 2009; Kerr & Boschetti, 2006), and the results indicated that there were many short regions of sequence identity between the genomes of human and bacteria or viruses; the genes contained in these sequences are involved in cell signal transduction, cell metabolism, and DNA replication, through coding of enzymes, receptors, gene regulators, and other proteins.

The aim of this study is to identify the regions of sequence identity between the genomes of *B. mori* and five viruses that infect *B. mori* using the resources of the National Center for Biotechnology Information (NCBI). The results of this study may provide new opportunities for further study of the interaction between viruses and the silkworm.

2. Methods

A BLAST search of several virus genomes against the genome of the silkworm was performed with the resources of the NCBI (http://blast.ncbi.nlm.nih.gov/Blast.cgi?PROGRAM=blastn&PAGE_TYPE=BlastSearch&LINK_LOC=blasthome). On the web search page above, type in "*Bombyx mori*" in Organism Optional and choose the program "Somewhat similar sequences (blastn)" The search parameters are shown in Table S1. Readers can perform the alignments of all the viruses of interest with the method we introduced. The virus genomes are accessible on the NCBI web site.

Abbreviations: BmNPV, *Bombyx mori* nucleopolyhedrovirus; BmCPV, *Bombyx mori* cytoplasmic polyhedrosis virus; BmDNV-1, *Bombyx mori* densonucleosis virus1; BmDNV-5, *Bombyx mori* densonucleosis virus 5; BmMLV, *Bombyx mori* macula-like virus; BmIFV, Infectious flacherie virus.

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Table 1
BLAST result of BmNPV.

Name of region of sequence identify	BmNPV sequence nt	Sequence of identity	*B. mori* genes containing sequence, n	Accession no. of *B. mori* gene	Features of *B. mori* gene	E value
NPV-Bm-1	46,442–46,474	AAAAAATGCCCCAATCCCAAGTTTTTGACACCT	1	GenBank: AK381567.1	*B. mori* mRNA, clone: fwgP03H15	9.00E-08
NPV-Bm-2	25,209–25,231	TACAATATTCAAAAGGAATCTAC	4	XM_004929624.1: XM_004929623.1 GenBank: AK386429.1 NM_001043374.1	polyubiquitin-C-like polyubiquitin-C-like *B. mori* mRNA, clone: fprW07J10 polyubiquitin (Ubi3)	0.096 0.096
NPV-Bm-3	52,295–52,317	AATGATTTAAAAACTCAAATAAT	1	XM_004928678.1	intracellular protein transport protein USO1-like	0.096
NPV-Bm-4	1780–1802	GGTGGTGGTGGTGGAGGTGGAGG	4	XM_004925015.1 XM_004925014.1 XM_004925013.1 GenBank: AK385902.1	tubulin-specific chaperone A-like tubulin-specific chaperone A-like leucine-rich repeat-containing protein AAC1-like *B. mori* mRNA, clone: fphe13C15	0.096
NPV-Bm-5	87,377–87,398	CCGTCACCGCCGCCGCCGCCAC	1	XM_004928771.1	serine/arginine repetitive matrix protein 1-like	0.038
NPV-Bm-6	9605–9626	TGTACAAATACATGTCGGTGAG	2	XM_004926236.1 GenBank: AK384743.1	acid phosphatase-like protein 2-like *B. mori* mRNA, clone: fcaL35M10	0.038
NPV-Bm-7	41,486–41,507	AAGTAGCGCTTGGAAAAATTAT	1	GenBank: AK387906.1	*B. mori* mRNA, clone: bmte22J15	0.038
NPV-Bm-8	112,845–112,866	ATAGAGAATAAATTTTTTTATT	1	GenBank: AK381987.1	*B. mori* mRNA, clone: fdpe03A22	0.038
NPV-Bm-9	66,829–66,850	ATATTTTTATTTGATAAAACCT	1	GenBank: AP009002.1	genomic DNA, chromosome 9, BAC	0.038
NPV-Bm-10	44,099–44,120	TAATAGTTTCTAATTTTTTTAT	1	NCBI Ref: XM_004925399.1	mucin-22-like	0.038
NPV-Bm-11	47,576–47,597	CATCGTCATCATCATCATCATT	1	GenBank: AK387227.1	*B. mori* mRNA, clone: bmov01O13	0.038

The following viruses were compared: *B. mori* nucleopolyhedrovirus (BmNPV), *B. mori* cytoplasmic polyhedrosis virus (BmCPV), *B. mori* densonucleosis virus1 (BmDNV-1), *B. mori* densonucleosis virus 5 (BmDNV-5), *B. mori* macula-like virus (BmMLV), and *B. mori* infectious flacherie virus strain ZheJiang01/CHN (BmIFV).

3. Results

We compared five virus genomes with the *B. mori* genome database using a BLAST program. These viruses included a dsDNA virus (BmNPV), an ssDNA virus (BmDNV), a dsRNA virus (BmCPV), and ssRNA viruses (BmMLV and BmIFV). The largest virus is BmNPV, with a genome size of 24,758 base pairs (bp); the genome size of BmDNV5 is only 5078 nucleotides (nt). Unexpectedly, we found that all the viruses except BmIFV that were compared to *B. mori* contained a different number of short regions identical to the human genome (100% identity). The BLAST results are shown in Tables 1–5. According to the BLAST results, we found that a DNA virus or a virus with a larger genome often has more identical regions than an RNA virus or a smaller virus. For a specific virus, different subtypes contained different numbers of identical regions, but some of the identical regions were identical. The BLAST results for the genome of BmIFV against the genome of *B. mori* are shown in Table 6. There was a 171 nt similar sequence identity of 94% between the genome of BmIFV and the genome of *B. mori*. It was noted that all the similar sequences between the genome of BmIFV and the genome of *B. mori* are located on the same gene (GenBank accession No: AK377204.1). In addition, more than two regions containing similar sequences against the same sequence were identified on the gene.

Most of the identical regions had 20–30 nt and some were found at multiple sites within the *B. mori* genome. In addition, some were located on different genes encoding the same protein; for example, three of the four genes contained the sequence NPV-Bm-2 and encode polyubiquitin-like protein, and two of the four genes contained the sequence NPV-Bm-4 and encode tubulin-specific chaperone A-like protein. The identical regions were found in either the plus or minus orientation in the *B. mori* genome. The 171 nt similar sequence in the BLAST result of the genome of BmIFV against the genome of *B. mori* might be related to miRNA sequences, but needs further study for verification. The lengths of these identical regions never exceeded 33 nt, and they were widespread on the *B. mori* chromosomes. These short identical sequences were unrelated to miRNA sequences.

According to the Gene Ontology (GO) database (Ashburner & Lewis, 2002; Blake & Harris, 2002), most of the *B. mori* genes that contain identical sequences have functions that can be generally termed metabolism. They encode many kind of enzymes, binding proteins, and transporters involved in the transcriptional complex, protein-binding, post-transcriptional modification of proteins (polyubiquitin, phosphorylation), substance transportation, and cell apoptosis.

4. Discussion

The publication of the *B. mori* genome sequence has provided the opportunity to analyze host-virus interactions in a new way. Kerr et al. (Kerr & Boschetti, 2006) compared the genomes of parvoviruses and their respective hosts and found several short identical sequences; the ontology of host genes with identical regions highlighted several

Table 2
BLAST result of densovirus5.

Name of region of sequence identify	BmDNV5 sequence nt	Sequence of identity	*B. mori* genes containing sequence, n	Accession no. of *B. mori* gene	Features of *B. mori gene*	E value
DNV-5-Bm-1	976–996	CTTTTGAGAATAATACAGTTA	2	XM_004927825.1 GenBank: AK386673.1 GenBank: AK377684.1	CCR4-NOT transcription complex subunit 7-like *B. mori* mRNA, clone: fprW21M16_K01639 *B. mori* mRNA, clone: fe8d16F24_K01171	0.06
DNV-5-Bm-2	3478–3497	CCTGAATTTCGACATTTAGC	3	GenBank: AK383657.1 NM_001046804.1	*B. mori* mRNA, clone: MFB-15P14 phosphoserine aminotransferase (Psat1)	0.24