

## SUPPLEMENTARY TEXT

### Core proteins special cases: *Basic protein P6.9*

Three of the baculoviral genomes deposited in GenBank, *Clanis bilineata* NPV (CBN), *Spodoptera litura* GV (SLG) and *Neodiprion abietis* NPV (NAN), lack the P6.9 protein annotation.

The CBN GenBank file does not contain small polypeptides. However, in the corresponding paper, the authors described several proteins in addition to the annotated ones. These sequences are generally small, and among them was P6.9 [S1]. Using the ORFinder tool of NCBI, the presence of P6.9 was confirmed.

Since SLG genome analysis has not been published, the P6.9 protein was not annotated. With a local implementation of NCBI Blast program, a tBlastN search was carried out over local baculovirus genome databases, using as query a file containing all the other *Betabaculovirus* P6.9 proteins. This approach facilitated the detection of a potential coding sequence for SLG P6.9 protein (nucleotides 57,132/57,315; **Suppl. Figure 1.A**). The translation product was aligned with the other *Betabaculovirus* basic proteins, showing a high degree of similarity (**Suppl. Figure 1.B**).

A tBlastN search, using the *Neodiprion lecontei* NPV (NLN) P6.9 as query against the genome of NAN, allowed the detection of a short segment with significant identity (21 amino acids, 18 identities, 21 positives) corresponding to the N-terminal region, and encoded in the frame -1 (nucleotides 30,921/30,832; **Suppl. Figure 2.A**). This finding led to a deep analysis of the surrounding nucleotide region. Surprisingly, the following 247 nucleotides constitute a highly conserved region between NAN and NLN (247 residues, 214 positives, **Suppl. Figure 2.B**). A three frame translation analysis showed that the amino acid sequence encoded in frame -2 corresponds to the rest of the NAN P6.9 protein, highly conserved with respect to the P6.9 protein of NLN (82 amino acids, 69 identities, 73 positives; **Suppl. Figure 2.C**). Taking into account the P6.9 function, the presence of this protein in every other baculoviruses and the

intriguing evolution constraints that led to a highly sequence conservation (102 amino acids, 87 identities, 94 positives), the concatenated amino acid sequence shown in **Suppl. Figure 2.C.** is proposed as NAN P6.9 protein. Frame shifting could be explained in two ways: a sequencing error, one C elimination (**Suppl. Figure 2.B.**) concatenates frames -1 and -2 in the same open reading frame; or a ribosomal slippage in the previous purine/pyrimidine stretch (**Suppl. Figure 2.B.**) that could lead to a -1 frame shift rendering a full length P6.9 protein.

#### **Core proteins special cases: *Desmoplakin***

Desmoplakin is present in every lepidopteron-specific baculoviruses, but was not reported in the Gamma and Deltabaculoviruses. However, the assigned function during virion-release from virogenic stroma to cytoplasm could be considered as a core function. A comparative analysis of the reported lepidopteron-specific baculovirus Desmoplakins shows that these are the most divergent putative core protein sequences (**Figure 5**). Divergence is not only observed in sequence, but also in length, ranging from 540 to 892 residues. Curiously, the genome of *Apocheima cinerarium* NPV (APO) deposited in GenBank reports a very short Desmoplakin containing only 260 amino acids (ORF45; nucleotides 51,915/51,133, frame -2) that aligns with the N-terminal region of other Desmoplakin sequences. Sequence analysis of the 2,000 nucleotides downstream led to the finding that the product encoded in APO ORF44 (nucleotides 50,800/49,433, frame -1) had significant BlastP matches with Desmoplakins of other Group II alphabaculoviruses (AIN, CBN, CCN, EUN, LDN, LXN, SLN and TNN) (**Suppl. Figure 3.A.** and **3.B.**). These results suggest that the final polypeptide product could derive from both frames through a ribosomal slippage mechanism such as the annotated by Zhang *et al.* [2009, unpublished] for APO ORF46 (DNA Polymerase), ORF62 (Helicase) and ORF81 (poly ADP-ribose glycohydrolase). Also, a sequencing error could not be discarded.

On the other hand, the sequence divergence in lepidopteron-specific baculovirus Desmoplakins is in the range from 9.97% (EPN/XCG) to 100% (MCN/MC4) of amino

acid identity. The extremely broad range of sequence identity and divergence in length, brings up about the problem of detecting new orthologous proteins using conventional bioinformatics tools. In view of this, the use of PSI-Blast [S2], Block Maker [S3-S6], MACAW [S7], and MetaMEME [S8] tools were explored.

Using several *Alpha* and *Betabaculovirus* Desmoplakins as query in PSI-Blast searches, three putative Desmoplakins of hymenoptera-specific NPVs were detected (encoded by NAN ORF13, NLN ORF21 and NSN ORF29). The identities were 24.10% (NAN/NSN), 26.30% (NLN/NSN), and 61.40% (NAN/NLN), falling within a range of 9.12% (NAN/OPN) to 16.33% (NSN/COG) with respect to the lepidopteron ones (**Suppl. Figure 4.A.**). The assigned identities were assessed by pairwise and multiple alignments. Similarity values obtained from pairwise alignments with the lepidopteron-specific NPV Desmoplakins were in the range of 20.75% (NAN/OPN) to 30.80% (NSN/COG) and 30.81% (NAN/CLG). These results support that NAN ORF13, NLN ORF21 and NSN ORF29 might be considered as the Desmoplakins of *Gammabaculovirus*.

The misalignments obtained with standard global alignment methods are one of the main obstacles in remote orthologous finding. In particular, this problem increases when there is a significant difference in length among the sequences compared. The number and position of gaps could significantly affect the quality of the global alignment. In this case, the local low-gapped or ungapped alignment approaches would become more reliable approaches.

As a first approximation to evaluate the putative existence of a Desmoplakin encoded in the genome of CNN, a BlastP search was carried out. Using 20 selected *Alpha* and *Betabaculovirus* Desmoplakin sequences as query, a product encoded by CUNI092 ORF was identified as a good candidate to be a Desmoplakin of *Deltabaculovirus*. The most significant matches showed a degree of query coverage from 50.00% (CNN/SLG) to 72.83% (CNN/ASG), with similarities in the range of 36.00% (CNN/CDN) to 42.00% (CNN/SLG). The global similarity of CUNI092 protein

with respect to the ones of Alpha, Beta and Gammabaculoviruses is in the range of 10.26% (CNN/AOG) to 16.85% (CNN/AON). Block Maker and MACAW, both with a Gibbs sampling approach [S9], and MetaMEME, with a Hidden Markov Model approach, were used in order to detect ungapped common motifs in a complete or partial set of baculoviral Desmoplakins (MACAW program limits to a maximum of 30 sequences), including CUNI092 protein. As shown in the **Suppl. Figure 4.B.**, three common motifs were detected by Block Maker and MACAW in a partial set, which represent Alpha, Beta, Gamma and Deltabaculoviruses. Interestingly, MetaMEME has also detected two motifs that were inside the previously identified motifs 1 and 2. These results support the hypothesis that ORF CNN92 might be considered as the Desmoplakin of *Deltabaculovirus*.

#### SUPPLEMENTARY REFERENCES

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## SUPPLEMENTARY FIGURE LEGENDS

**Supplementary Figure 1. *Spodoptera litura* Granulovirus P6.9 protein. A.** Coding region and translated product. **B.** *Betabaculovirus* P6.9 protein multiple alignment. The identical residues shared by all GVs are shaded in yellow, while in pink are indicated the amino acids conserved in at least 50% of analyzed proteins.

**Supplementary Figure 2. *Neodiprion abietis* NPV P6.9 protein. A.** Result of the tBlastN search using P6.9 of NLN as query. **B.** Comparison of nucleotide sequences of NLN p6.9 ORF and NAN genomic region comprising a putative p6.9 ORF. An overall view depicts the high nucleotide identity among them. Three in-frame stop codons contained within the NAN sequence are shown in red characters. Also, two cytosine

residues are highlighted by a light blue shadow. One of them could be a sequence error or the site for a ribosomal slippage bypass (frame shift -1). Boxed characters indicate a putative slipping nucleotide sequence, a purine cluster followed by a pyrimidine cluster. **C.** Comparison between concatenated amino acid sequence of NAN P6.9 protein and the P6.9 of NLN. Amino acids derived from frame -1 are shaded in yellow; while those derived from frame -2 are in orange.

**Supplementary Figure 3. *Apocheima cinerarium* NPV Desmoplakin protein. A.**

Partial results of the BlastP searches obtained using APO annotated Desmoplakin as query (frame -2). **B.** Partial results of the BlastP searches obtained using APO amino acid sequence derived from frame -1 as query (including the amino acid sequence of ORF44). **C.** Putative amino acid sequence of APO Desmoplakin. Residues encoded by ORF45 are shaded in yellow (frame -2), the residues encoded by ORF44 in orange (frame -2), and the residues encoded in the same frame of ORF44 corresponding to the nucleotide sequence found between the mentioned ORFs in green. The polypeptide concatenation could occur by a ribosomal slippage.

**Supplementary Figure 4. Desmoplakins of *Gamma* and *Deltabaculovirus*. A.**

Partial results of the PSI-Blast searches obtained using the annotated Desmoplakin of CLG as initial query. After six iterations, three hymenoptera-specific NPV proteins were recruited: the polypeptides encoded by NAN ORF13, NLN ORF21 and NSN ORF29 (shaded in yellow). **B.** Summary of the ungapped block analyses. Grey horizontal bars represent the protein sequences, and violet rectangles indicate blocks of significant similarity. Three common motifs were found in all sequences (blocks identified with red numbers). Motifs 1 to 3 were detected by Block Maker and MACAW. Motifs 1 and 2 were also detected by MetaMEME. Sequence logos corresponding to motifs 1 and 2 are shown at the bottom. Desmoplakins from Gamma and Deltabaculoviruses are shaded in orange.

**Supplementary Table1. Homologues in Alphabaculovirus Group I**

	ACN	AGN	APN	AP2	BMN	BON	CFN	CDN	EPN	HCN	MVN	OPN	PXN	RON
<b>Core genes</b>														
lef-2	6	3	4	144	135	141	3	3	4	147	126	6	6	4
lef-1	14	19	13	136	6	6	13	17	11	139	6	13	14	12
pif-2	22	12	20	129	13	14	20	10	18	131	13	20	21	19
p47	40	44	40	109	31	32	40	40	37	110	29	45	40	37
lef-8	50	51	49	100	39	40	48	47	45	102	35	54	50	47
vp1054	54	55	53	96	43	45	52	51	49	96	40	58	55	52
lef-9	62	62	59	89	50	52	59	58	56	89	46	65	62	59
DNA pol	65	65	61	87	53	55	61	61	58	85	49	70	65	62
Desmoplakin	66	66	62	86	54	56	62	62	59	84	50	71	66	63
	68	68	64	84	56	58	64	64	61	82	52	73	68	65
vlf-1	77	76	73	76	63	66	72	72	69	74	60	80	77	74
gp41	80	79	76	73	66	69	75	75	72	71	63	83	80	77
	81	80	77	72	67	70	76	76	73	70	64	84	81	78
vp91/p95	83	82	79	70	69	72	78	78	75	68	66	86	83	80
vp39	89	86	81	67	72	76	81	82	77	65	67	90	88	86
lef-4	90	87	82	66	73	77	82	83	78	64	68	91	89	87
P33	92	89	84	64	75	79	84	85	80	62	69	93	91	89
helicase	95	92	87	61	78	82	87	88	83	59	72	96	94	92
19K	96	93	88	60	79	83	88	89	84	58	73	97	95	93
38 K	98	94	90	58	82	85	91	90	85	55	75	99	96	94
lef-5	99	95	91	57	83	86	92	91	86	54	76	100	97	95
p6.9	100	96	92	56	84	87	93	92	87	53	77	101	98	96
odv-ec43	109	107	101	47	92	95	100	103	95	46	85	109	106	104
PIF-3	115	114	107	42	95	99	106	111	102	39	89	115	111	109
pif-1	119	117	111	38	97	102	110	114	106	35	91	119	115	113
Alk-exo	133	129	124	25	110	116	126	128	118	23	102	131	129	126
p74	138	134	129	20	115	122	130	132	121	19	106	134	134	131
p49	142	138	133	16	118	125	135	135	124	15	110	139	137	134
odv-e18	143	139	134	15	119	126	136	136	125	14	111	140	138	135
odv-e27	144	140	135	14	120	127	137	137	126	13	112	141	139	136
odv-e56	148	144	139	10	124	131	141	141	130	9	116	146	143	140
<b>Alpha + Beta + Gamma</b>														
polyhedrin	8	1	1	1	1	1	1	1	1	1	1	3	8	6
dbp	25	42	38	111	16	17	38	38	35	112	16	43	24	22
p48	103	99	95	53	87	90	96	95	90	50	80	104	101	99
	145	141	136	13	121	128	138	138	127	12	113	142	140	137
pp34/PEP	131	127	122	27	108	114	124	126	116	25	100	129	127	124
odv-e25	94	91	86	62	77	81	86	87	82	60	71	95	93	91
p40	101	97	93	55	85	88	94	93	88	52	78	102	99	97
	106/107	104	99	49	90	93	98	100	93	48	83	107	104	102
<b>Alpha + Beta + Delta</b>														
F-protein	23	22	21	128	14	15	21	21	19	130	14	21	22	20
<b>Alpha + Beta</b>														
pk-1_protein kinase 1	10	151	146	4	3	3	145	148	135	3	3	1	10	8
38,7Kda	13	20	12	137	5	5	12	18	10	140	5	12	13	11
lef-6	28	39	35	114	19	20	35	35	32	115	19	40	27	25
pp31/39k	36	25	24	125	27	28	24	24	22	127	25	24	36	33
	38	23	22	127	29	30	22	22	20	129	27	22	38	35
	53	53	51	98	42	43	50	49	47	98	38	56	53	50
25K FP	61	61	58	90	49	51	58	57	55	90	45	64	61	58

LEF-3	67	67	63	85	55	57	63	63	60	83	51	72	67	64
	75	74	70	78	61	64	70	70	67	76	58	78	75	72
	76	75	72	77	61	65	71	71	68	75	59	79	76	73
tlp20	82	81	78	71	68	71	77	77	74	69	65	85	82	79
p18	93	90	85	63	76	80	85	86	81	61	70	94	92	90
P12	102	98	94	54	86	89	95	94	89	51	79	103	100	98
	108	106	100	48	91	94	99	102	94	47	84	108	105	103
p24	129	125	120	29	106	112	122	124	114	27	98	127	125	122
me53	139	136	131	18	116	123	132	133	122	17	107	137	135	132
	146	142	137	12	122	129	139	139	128	11	114	144	141	138
ie-1	147	143	138	11	123	130	140	140	129	10	115	145	142	139
<b>Alpha</b>														
orf1629 capsid	9	152	147	3	2	2	146	149	136	2	2	2	9	7
	19	14	18	131	11	12	18	12	16	133	11	18	19	17
pkip-1	24	43	39	110	15	16	39	39	36	111	15	44	23	21
	34	27	26	123	25	26	26	26	24	125	23	26	34	31
	51	52	50	99	40	41	49	48	46	101	36	55	51	48
iap-2	58/59	59	56	92	47	49	56	55	53	92	43	62	59	56
	104	100	96	52	88	91	97	96	91	49	81	105	102	100
p87/vp80	141	137	132	17	117	124	134	134	123	16	109	138	136	133
ie-0	71	70	66	82	58, 60	61	66	66	63	80	54	74	71	68
<b>Alpha, Group I</b>														
ptp-1/bvp	1	9	9	140	130	137	9	8	7	142	123	10	1	1
	5	4	5	143a	134	140	4	4	5	146	125	7	5	3
odv-e26	16	17	15	134	8	9	15	15	13	137	8	15	16	14
iap-1	27	40	36	113	18	19	36	36	33	114	18	41	26	24
	30	37	33	116	21	22	33	33	30	117	21	38	29	27
	72	71	67	81	58a	61	67	67	64	79	55	75	72	69
	73	72	68	80	59	62	68	68	65	78	56	76	73	70
	114	114	106	43	94	98	105	109	100	40	88	114	110	108
	124	121	114	35	101	107	113	118	108	32	93	122	120	117
gp64	128	124	119	30	105	111	119	123	112	28	97	126	124	121
p25	132	128	123	26	109	115	125	127	117	24	101	130	128	125
ie-2	151	145	141	8	127	134	142	143	131	6	119	151	146	143

AP2 ORF143a, 124901-125122 (tBlastN finding, shaded in yellow)



Supplementary Table 2. Homologues in Alphabaculovirus Group II (part 1)

	ACN	AHN	AON	AIN	APO	ASN	CCN	CBN <sup>1</sup>	EON	EUN	HAN	HA1	HA4	HAS
<b>Core genes</b>														
lef-2	6	100	95	17	87	13	136	109, 119	103	118	13	117	117	123
lef-1	14	124	120	22	3	17	138	123, 133	124	128	29	124	124	131
pif-2	22	95	90	42	84	36	148	107, 117	106	121	42	132	133	140
p47	40	10	10	134	92	126	33	36, 41	29	25	137	35	35	35
lef-8	50	49	46	130	20	121	37	32, 37	32	21	133	38	38	38
vp1054	54	42	39	122	27	113	45	39, 46	39	36	125	44	47	47
lef-9	62	35	33	113	34	105	52	47, 54	46	29	116	52	55	55
DNA pol	65	58	55	106	46	100	58	77	58	66	107	67	67	69
Desmoplakin	66	57	54	105	45	99	59	76	57	65	106	66	66	68
	68	55	52	103	42	97	61	73	55	63	104	64	64	66
vlf-1	77	61	58	99	49	93	76	71, 80	61	69	98	71	71	73
gp41	80	63	60	97	51	91	78	73, 82	63	71	96	73	73	75
	81	64	61	96	52	90	79	74, 83	64	72	95	74	74	76
vp91/p95	83	66	63	94	54	88	81	76, 85	66	74	93	76	76	78
vp39	89	67	64	92	56	86	82	78, 87	68	76	91	78	78	80
lef-4	90	68	65	91	57	85	83	79, 88	69	77	90	79	79	81
P33	92	69	66	89	59	83	84	80, 89	71	79	88	80	80	82
helicase	95	72	69	86	62	80	87	83, 92	74	82	85	84	84	86
19K	96	73	70	85	63	79	88	84, 93	75	83	84	85	85	87
38 K	98	74	71	81	64	74	91	85, 94	77	85	80	86	86	88
lef-5	99	75	72	80	65	73	92	86, 95	78	86	79	87	87	89
p6.9	100	76	73	79	66	72	93	96	79	87	78	88	88	90
odv-ec43	109	82	79	73	72	66	99	92, 102	85	93	72	94	94	96
PIF-3	115	108	103	59	79	56	110	100, 110	111	102	59	98	98	101
pif-1	119	117	113	43	19	37	131	120, 130	98	115	43	111	111	114
Alk-exo	133	2	2	47	15	41	127	117, 127	93	111	47	114	114	117
p74	138	27	26	151	106	144	17	14, 17	14	17	153	20	20	19
p49	142	24	23	160	109	151	11	10, 13	11	13	160	9	9	9
odv-e18	143	23	22	158	110	150	12	12	10	12	159	10	10	10
odv-e27	144	22	21	156	111	149	13	9, 11	9	11	158	11	11	11
odv-e56	148	8	8	9	115	6	7	6, 7	5	7	6	15	15	15
<b>Alpha + Beta + Gamma</b>														
polyhedrin	8	1	1	1	1	1	1	1	1	1	1	1	1	1
dbp	25	28	27	146	105	139	22	27, 32	27	44	148	25	25	24
p48	103	79	76	76	69	69	96	89, 99	82	90	75	91	91	93
	145	21	20	155	112	148	14	10	8	10	157	12	12	12
pp34/PEP	131	104	99	54	76	49	121	114, 124	108	106	53	120	120	127
odv-e25	94	71	68	87	61	81	86	82, 91	73	81	86	82	82	84
p40	101	77	74	78	67	71	94	87, 97	80	88	77	89	89	91
	106/107	110	105	62	82	59	107	97	116	100	62	101	101	104
<b>Alpha + Beta + Delta</b>														
F-protein	23	118	114	12	9	8	150	129, 139	118	134	8	133	133	141
<b>Alpha + Beta</b>														
pk-1_protein kinase 1	10	5	5	3	117	3	3	3	3	3	3	3	3	3
38,7Kda	13	125	121	21	2	16	137	122, 132	125	127	30	123	123	130
lef-6	28	29	28	147	104	140	21	17, 21	16	53	149	24	24	23
pp31/39k	36	13	13	139	96	132	28	24, 28	24	47	143	31	31	31
	38	11	11	137	94	130	30	25, 30	26	45	141	33	33	33
	53	47	44	126	23	117	41	28, 33	35	40	129	43	43	43
25K FP	61	36	34	114	33	106	51	46, 53	45	30	117	50	53	53

LEF-3	67	56	53	104	43	98	60	74	56	64	105	65	65	67
	75	59	56	107	47	101	57	68, 78	59	67	108	69	69	71
	76	60	57	108	48	102	56	69, 79	60	68	109	70	70	72
tlp20	82	65	62	95	53	89	80	75, 84	65	73	94	75	75	77
p18	93	70	67	88	60	82	85	81, 90	72	80	87	81	81	83
P12	102	78	75	77	68	70	95	98	81	89	76	90	90	92
	108	83	80	72	73	65	100	93, 103	86	94	71	95	95	97
p24	129	102	97	15	89	11	134	111, 121	101	125	11	118	118	125
me53	139	26	25	10	107	7	8	12, 15	13	15	7	16	16	16
	146	20	19	154	113	147	15	8, 9	7	9	156	13	13	13
ie-1	147	19	18	153	114	146	16	7, 8	6	8	155	14	14	14
<b>Alpha</b>														
orf1629 capsid	9	4	4	2	118	2	2	2	2	2	2	2	2	2
	19	91	87	49	13	44	126	115, 125	91	109	48	115	115	118
pkip-1	24	98	93	38	86	33	146	108, 118	104	119	39	130	131	138
	34	18	17	143	100	136	25	21, 25	20	49	146	27	27	27
	51	48	45	129	21	120	38	31, 36	33	43	132	39	39	39
iap-2	58/59	39	36	118	31	109	49	44, 51	43	32	121	48	51	51
	104	80	77	75	70	68	97	90, 100	83	91	74	92	92	94
p87/vp80	141	25	24	161	108	152	10	11, 14	12	14	161	8	8	8
ie-0	71	53	50	101	41	95	62	63, 71	54	62	102	62	62	64

<sup>1</sup> Grey numbers correspond to the original GenBank ORF numbering (lacking small ORFs). Black numbers correspond to the published list of ORFs (including small ORFs)

**Supplementary Table 2. Homologues in Alphabaculovirus Group II (part 2)**

	ACN	HZN	LSN	LDN	LXN	MCN	MCB	MC4	OLN	SEN	SF9	SF2	SL2	SLN	TNN
<b>Core genes</b>															
lef-2	6	121	137	137	118	14	13	14	114	12	15	16	114	14	128
lef-1	14	128	150	123	134	35	30	35	132	14	17	18	129	16	130
pif-2	22	136	163	119	138	48	43	48	112	35	33	34	135	36	141
p47	40	35	41	48	44	145	144	145	52	115	115	116	36	121	31
lef-8	50	38	43	51	48	141	140	141	45	112	112	113	38	118	33
vp1054	54	48	64	57	55	133	132	133	38	105	104	105	49	110	42
lef-9	62	56	78	64	61	124	123	124	31	97	96	97	59	101	49
DNA pol	65	69	84	83	79	115	114	115	67	93	91	92	69	97	54
Desmoplakin	66	68	83	82	78	114	113	114	66	92	90	91	68	96	55
	68	66	81	80	76	112	111	112	64	90	88	89	66	94	57
vlf-1	77	73	89	86	82	106	105	106	70	82	83	84	74	88	70
gp41	80	75	91	88	84	104	103	104	72	80	81	82	76	86	72
	81	76	92	89	85	103	102	103	73	79	80	81	77	85	74
vp91/p95	83	78	94	91	87	101	100	101	75	77	78	79	79	83	76
vp39	89	81	96	92	88	99	98	99	77	75	76	77	81	81	77
lef-4	90	82	97	93	89	98	97	98	78	74	75	76	82	80	78
p33	92	83	98	94	90	96	95	96	80	73	74	75	83	79	79
helicase	95	87	101	97	93	93	92	93	83	70	71	72	86	76	82
19K	96	88	102	98	94	92	91	92	84	69	70	71	87	75	83
38 K	98	89	103	99	95	88	87	88	85	67	66	67	88	71	86
lef-5	99	90	104	100	96	87	86	87	86	66	65	66	89	70	87
p6.9	100	91	105	101	97	86	85	86	87	65	64	65	90	69	88
odv-ec43	109	97	111	107	103	80	79	80	93	59	58	59	96	63	94
PIF-3	115	101	131	143	112	68	67	68	102	50	48	49	107	53	105
pif-1	119	114	148	155	148	49	44	49	126	36	34	35	124	37	123
Alk-exo	133	117	134	157	150	54	48	54	124	41	38	39	109	42	119
p74	138	19	24	27	24	160	159	160	15	131	132	134	21	137	17

p49	142	9	11	20	17	167	166	167	12	137	139	141	11	146	11
odv-e18	143	10	12	19	16	166	165	166	11	136	138	140	12	145	12
odv-e27	144	11	13	18	15	165	164	165	10	135	137	139	13	144	13
odv-e56	148	15	17	14	10	6	6	6	6	6	8	9	17	7	8
<b>Alpha + Beta + Gamma</b>															
polh	8	1	1	1	1	1	1	1	1	1	1	1	1	1	1
dbp	25	24	31	47	43	155	154	155	53	126	126	127	30	132	22
p48	103	94	108	104	40	83	82	83	90	62	61	62	93	66	91
	145	12	14	17	14	164	163	164	9	134	136	138	14	143	14
pp34/PEP	131	124	158	136	120	60	61	60	109	46	44	45	132	47	113
odv-e25	94	85	100	96	92	94	93	94	82	71	72	73	85	77	81
p40	101	92	106	102	98	85	84	85	88	64	63	64	91	68	89
	106/107	104	123	140	115	71	70	71	99	53	51	52	101	56	102
<b>Alpha + Beta + Delta</b>															
F-protein	23	137	166	130	126	9	8	9	127	8	11	12	136	10	143
<b>Alpha + Beta</b>															
pk-1	10	3	3	3	3	3	3	3	3	3	3	3	3	3	3
38,7Kda	13	127	149	122	135	36	31	36	133	13	16	17	128	15	129
lef-6	28	23	30	38	34	156	155	156	18	127	127	128	29	133	21
pp31/39k	36	31	36	44	40	150	149	150	56	120	120	121	33	126	26
	38	33	38	46	42	148	147	148	54	118	118	119	35	124	28
	53	44	60	54	52	137	136	137	41	108	108	109	45	114	38
25K FP	61	54	76	63a	60	125	124	125	32	98	97	98	57	102	48
LEF-3	67	67	82	81	77	113	112	113	65	91	89	90	67	95	56
	75	71	87	84	80	116	115	116	68	94	92	93	72	98	53
	76	72	88	85	81	117	116	117	69	95	93	94	73	99	52
tlp20	82	77	93	90	86	102	101	102	74	78	79	80	78	84	75
p18	93	84	99	95	91	95	94	95	81	72	73	74	84	78	80
P12	102	93	107b	103	99	84	83	84	89	63	62	63	92	67	90
	108	98	112	108	104	79	78	79	94	58	57	58	97	62	95
p24	129	122	139	133b	24	12	11	12	116	10	13	14	116	12	126
me53	139	16	27	23	21	7	7	7	14	7	9	10	27	8	9
	146	13	15	16	13	163	162	163	8	133	135	137	15	142	15
ie-1	147	14	16	15	12	162	161	162	7	132	134	136	16	141	16
<b>Alpha</b>															
orf1629 capsid	9	2	2	2	2	2	2	2	2	2	2	2	2	2	2
	19	118	135	159	152	55	49	55	122	42	39	40	112	43	118
pkip-1	24	134	159	110	106	45	40	45	113	32	30	31	133	32	139
	34	27	18	42	38	153	152	153	60	124	124	125	18	128b	24
	51	39	44	51b	49	140	139	140	44	111	111	112	39	117	34
iap-2	58/59	52	71	61	58	129	128	129	34	101	100	101	52	105	46
	104	95	109	105	41	82	81	82	91	61	60	61	94	65	92a
p87/vp80	141	8	8	21	18	168	167	168	13	138	140	142	8	147	10
ie-0	71	64	80	79	75	110	109	110	63	88	86	87	91	91	58

LDN ORF51b, 51312-52307; LDN ORF133b, 130920-131216; LSN ORF107b, 107429-107812; SLN ORF128b, 127186-127776 (tBlastN finding, shaded in yellow)

**Supplementary Table 3. Homologues in Betabaculovirus**

	ACN	AOG	ASG	COG	CLG	CPG	HAG	POG	PUG	PRG	PXG	SLG	XCG
<b>Core genes</b>													
lef-2	6	32	35	29	38	41	33	37	33	33	32	32	35
lef-1	14	62	64	55	66	74	80	66	85	60	55	62	82
pif-2	22	39	43	35	45	48	42	44	43	40	37	39	45
p47	40	58	60	50	61	68	74	61	79	56	51	58	78
lef-8	50	110	118	107	119	131	149	121	155	110	109	121	148
vp1054	54	115	127	113	125	138	173	126	177	116	115	130	175
lef-9	62	100	107	96	107	117	140	109	145	99	99	107	139
DNA pol	65	94	101	90	101	111	134	103	138	93	93	101	132
Desmoplakin	66	95	102	91	102	112	135	104	139	84	94	102	133
	68	97	104	93	104	114	137	106	141	96	96	104	135
vlf-1	77	91	97	86	97	106	126	99	127	90	89	97	123
gp41	80	88	95	83	95	104	124	97	125	88	87	95	121
	81	87	94	82	94	103	123	96	124	87	86	94	120
vp91/p95	83	85	91	80	92	101	121	94	122	85	84	92	118
vp39	89	81	86	76	87	96	113	88	115	81	79	87	111
lef-4	90	80	85	75	86	95	112	87	114	80	78	86	110
P33	92	79	83	74	84	93	100	85	105	78	76	83	101
helicase	95	76	79	71	81	90	97	82	102	75	72	80	98
19K	96	75	78	70	80	89	96	81	101	74	71	79	97
38 K	98	74	77	69	79	88	95	80	100	73	70	77	96
lef-5	99	73	76	68	78	87	94	79	99	72	69	76	95
p6.9	100	72	75	67	77	86	93	78	98	71	67	75b	94
odv-ec43	109	46	48	40	53	55	48	50	51	46	43	46	53
PIF-3	115	26	29	26	34	35	30	31	30	30	29	27	32
pif-1	119	63	65	56	67	75	82	67	87	61	7	64	84
Alk-exo	133	107	115	104	115	125	146	114	152	107	106	117	145
p74	138	53	56	46	58	60	72	55	77	51	49	56	77
p49	142	11	12	13	14	15	12	13	12	15	14	11	13
odv-e18	143	10	11	12	13	14	11	12	11	14	13	10	12
odv-e27	144	82	87	77	88	97	114	89	116	82	80	88	112
odv-e56	148	12	15	14	17	18	14	16	14	16	16	13	15
<b>Alpha + Beta + Gamma</b>													
Gran.	8	1	1	1	1	1	1	1	1	1	4	1	1
dbp	25	68	69	61	72	81	87	73	92	66	61	70	89
p48	103	69	72	64	74	83	90	75	95	68	63	73	91
	145	8	10	9	8	9	10	8	10	8	12	9	11
pp34/PEP	131	17	19	18	23	22	18	20	18	21	21	19	19
odv-e25	94	77	81	72	82	91	98	83	103	76	74	81	99
p40	101	71	74	66	76	85	92	77	97	70	66	75	93
	106/107	43	46	37	50	52	45	47	47	43	42	42	50
<b>Alpha + Beta + Delta</b>													
F-protein	23	23	25	23	30	31	26	27	26	26	26	24	27
<b>Alpha + Beta</b>													
pk-1	10	3	3	3	3	3	3	3	3	3	6	3	3
38,7Kda	13	61	63	54	65	73	79	65	84	59	54	61	81
lef-6	28	67	68	60	71	80	86	72	91	65	60	69	88
pp31/39k	36	49	51	42	55	57	50	52	53	48	45	48	55
	38	59	61	51	62	69	77	62	82	57	52	59	79
	53	111	122	109	121	134	169	122	173	113	112	127	171
25K FP	61	101	108	97	108	118	141	110	146	100	100	109	140

LEF-3	67	96	103	92	103	113	136	105	140	95	95	103	134
	75	93	100	89	99	108	129	101	130	92	92	100	126
	76	92	99	88	98	107	128	100	129	91	91	99	125
tlp20	82	86	93	81	93	102	122	95	123	86	85	93	119
p18	93	78	82	73	83	92	99	84	104	77	75	82	100
P12	102	70	73	65	75	84	91	76	96	69	64	74	92
	108	47	49	41	54	56	49	51	52	47	43b	47	54
p24	129	60	62	52	63	71	78	63	83	58	53	60	80
me53	139	119	131	116	129	143	178	130	182	120	120	134	180
	146	7	9	8	7	8	9	7	9	9	11	8	10
ie-1	147	6	8	7	6	7	8	6	8	6	10	7	9
<b>Beta</b>													
	CPG4	4	6	5	4	4	6	4	6	4	8	5	7
	CPG5	5	7	6	5	5	7	5	7	5	9	6	9
	CPG20	16	18	17	20	20	16	19	16	20	20	15	17
	CPG23	18	20	19	24	23	17	21	17	22	23	18	18
	CPG29	21	23	22	28	29	24	46	24	24	25	22	25
	CPG33	25	27	24	32	33	28	29	28	28	28	26	29
	CPG39	29	34	28	36	39	32	34	32	31	31	31	34
	CPG45	36	40	32	42	45	37	40	37	36	34	36	39
Metalloproteinase	CPG46	37	41	33	43	46	38	41	38	37	35	37	40
	CPG62	19	59	49	60	62	73	60	78	55	50	57	77b
FGF-1	CPG76	64	66	57	68	76	83	69	88	62	56	66	85
	CPG79	66	67	59	70	79	85	71	90	64	59	68	87
	CPG99	83	88	78	90	99	116	92	117	83	82	89	113
	CPG100	84	90	79	91	100	119	93	120	84	83	90	116
	CPG115	98	105	94	105	115	138	107	142	97	97	105	136
IAP-5	CPG116	99	106	95	106	116	139	108	143	98	98	106	137
FGF	CPG123	105	113	102	113	123	145	116	151	105	104	116	144
	CPG135	113	124	110	122	135	170	123	174	114	113	128	172
FGF-3	CPG140	117	128	114	127	140	176	128	180	118	117	133	178

PXG ORF43b, 35622-35756; SLG ORF 75b, 57132-57315; XCG ORF77b, 74368-74059 (tBlastN finding, shaded in yellow)

**Supplementary Table 4. Homologues in Gamma and Deltabaculovirus**

	ACN	NAN	NLN	NSN	CNN
<b>Core genes</b>					
polh	8	1	1	1	
lef-2	6	57	57	57	25
lef-1	14	68	65	68	45
pif-2	22	55	52	55	38
p47	40	49	46	49	73
lef-8	50	83	78	81	26
vp1054	54	88	83	85	8
lef-9	62	39	37	40	59
DNA pol	65	12	20	28	91
Desmop.	66	13	21	29	92
	68	40	38	41	58
vlf-1	77	45	42	45	18
gp41	80	47	44	47	33
	81	48	45	48	106
vp91/p95	83	87	82	84	35
vp39	89	92	88	89	24
lef-4	90	62	59	62	96
p33	92	8	16	24	14
helicase	95	61	58	61	89
19K	96	60	57	60	90
38 K	98	59	56	59	87
lef-5	99	58	55	58	88
p6.9	100	31b	28	36	23
odv-ec43	109	71	67	70	69
PIF-3	115	69	66	69	46
pif-1	119	79	76	79	29
alk-exo	133	36	33	31	54
p74	138	50	47	50	74
p49	142	63	60	63	30
odv-e18	143	65	62	65	31
odv-e27	144	66	63	66	32
odv-e56	148	16	23	38	102
<b>Alpha + Beta + Gamma</b>					
polh	8	1	1	1	
dbp	25	6	14	22	
p48	103	34	31	33	
	145	67	64	67	
pp34/PEP	131	53	50	53	
odv-e25	94	10	18	26	
p40	101	32	29	35	
	106/107	35	32	32	
<b>Alpha + Beta + Delta</b>					
F-protein	23				104

# A

57132 ATGGTGCGCAGACGTTCCAGATCACGTTACCGTACAGGCGTCGTTCCCGAGCACGTCGT  
M V R R R S R S R S P Y R R R S R A R R  
57192 CGTTCACATCGCGCATCCGAACACATGCCGGCGAGGCGTCGATCCCGCTCTCGATCCAGG  
R S H R A S E H M P A R R R S R S R S R  
57252 TCGCCCTACAGGAGACGTTTCGCGTAGCGGTGGCCGACGTCATCACATCAACCAATATGTT  
S P Y R R R S R S G G R R H H I N Q Y V  
57312 TAA 57315  
\*

# B

ORF72_AOG	MVY--RRRPGRPRSRSRSRSR--RSRSRSY--SRQ-QTHARRRSRSRSPRRR-SR-----HINQYV--
ORF67_COG	MVY--RRRPGRPRSRSRSRSR--YSRTAAR--ARS-RSRSRSRSRSRSPRRR-SHQ-Y---HVNQYV--
ORF77_CLG	MVR--RRR-SRSPYRRRSRSRSRSGSDRSR--SRY-RSRSRSRSRSRSRSR--SPYHH---HINQYI--
ORF67_PXG	MVR--RRR-SRSPMRRRRRSRSYSPPRRSR--STA-STRRRSRSRSRSPRRR-S--NY---HINQYI--
ORF86_CPG	MVR--RRR-SRSPNRRR-----SYRSRSR--SRS-RSRSRSRSRSRSPYRS-H---Y---HINQYI--
ORF78_POG	MVR--RRR-SRSRSRSP-YGRS---RSRSR--SMGGRRRSRSRSRSPYRR-SRSS-SS-----YLYE
ORF75_ASG	MYR--RRR-SRSPGRRRSQRRR-SNSGGEY--ASSGRRRSRSRSRSGRRR-SRSRYGSHHVNQYV--
ORF93_HAG	MERTGRRR-SRSRSRSPQRRRS--YRRRSR--STSTGARRRSRS----GYRR-SRSGQRRNHVNQYV--
ORF94_XCG	MERTGRRR-SRSRSRSPQRRRS--YRRRSR--STSTGARRRSRSRS--GYRR-SRSGQRRNHVNQYV--
ORF98_PUG	MERTGRRR-SRSRSRSPQRRRS--YRRRSR--SPATGGRRRSRSRS--GYRR-SRSGQRRHHVNQYV--
ORF71_PRG	MVY--RRRPGRPRSRSRSRSR--RSPSYR-RTRT--RSRSRSRSRSRSPRR-RSRI-QHHINQYV--
SLG	MVR--RR----SRSRSPYRRRSR-ARRRSHRASEHMPARRRSRSRSPYRRRSRSGRRHHINQYV--

# A

Neodiprion abietis nucleopolyhedrovirus, complete genome  
Length=84264

Score = 42.4 bits (98), Expect = 1e-05, Method: Compositional matrix adjust.  
Identities = 20/26 (76%), Positives = 23/26 (88%), Gaps = 0/26 (0%)  
Frame = -1

Query 1 MVSESSDSKKELKPIEIMAYN 23  
MV+ESSDSKKELKP+EIMAY+  
Sbjct 30921 MVNESSDSKKELKPLEIMAYH 30832

# B

ORF28\_NLN ATGGTAAGCGAATCGTCGGATTCTAAAAAAGAATTAAAACCCATCGAAATTATGGCMTAT  
NAN ATGGTAAACGAATCTTCGGATTCCAAAAAAGAATTAAAACCTCTCGAAATTATGGCGTAT  
\*\*\*\*\*  
ORF28\_NLN AATAGAAGACCCGGTCGTC-CGCGCAAACGGCGTTCTTATGGAAACAATTCTACAAATAG  
NAN CACTAGTGAATTGGGTCGTCTCACGTAAACGACGTTCTTACGGAAACAGTTCTACAAATAG  
\* \*\* \*\*\*\*\* \* \*\* \*\*\*\*\*  
ORF28\_NLN GACAAGATCAAGATCACGATCAAGATCCCGTTCTCGTTCAAGATCTCGTTCAAGAACCGG  
NAN GACAAGATCAAGATCAAGATCACGATCACGTTCTCGTTCAAGATCTCGTTCAAGAGCCGG  
\*\*\*\*\*  
ORF28\_NLN TGGTCGACGCAGGTCGCGTTCATCATCATCGTATAACAGAAATTATCGGTCCTCGAACAG  
NAN TGGCCGACGGAGGTCGCGTTCGTATCATCATCGTATAACAGAAATTATCGGTCGTCAAACAG  
\*\*\* \*\*\*\*\*  
ORF28\_NLN CCCGTCTTCCAACAGGCAATATGGCCGAGCCGAAGTCGAAGTCGTTATCACAACG  
NAN CCCGTCTTACAACAGGCAATATGGCCGAGCCGAAGTCGAAGTCGTTATCATCGTCACGTGT  
\*\*\*\*\*  
ORF28\_NLN RAGGTATTAA  
NAN GAGATATTAA  
\*\* \*\*\*\*\*

# C

NAN MVNESSDSKKELKPLEIMAYTSDWVVSRRKRRSYGNSSTNRTRSRSRSRSRSRSRSRSRAG  
ORF28\_NLN MVSESSDSKKELKPIEIMAYNRRPGRPRKRRSYGNNSTNRTRSRSRSRSRSRSRSRRTG  
\*\* .\*\*\*\*\*:\*\*\*\*\*: .\*\*\*\*\*.\*\*\*\*\*: \*  
NAN GRRRSRSSSSYNRNYRSSNSPSYNRQYGRSRSRSRSSSRVRY  
ORF28\_NLN GRRRSRSSSSYNRNYRSSNSPSSNRQYGRSRSRSRSLSQRRY  
\*\*\*\*\* \*: \*\*



**A**

Accession	Description	Max score	Total score	Query coverage	E value
ADB84406.1	desmoplakin [ <i>Apocheima cinerarium</i> NPV]	508	508	100%	2e-142
YP_001650976.1	desmoplakin [ <i>Orgyia leucostigma</i> NPV]	170	170	58%	1e-40
YP_002854675.1	desmoplakin [ <i>Euproctis pseudoconspersa</i> NPV]	158	158	70%	5e-37
YP_002268135.1	agip105 [ <i>Agrotis ipsilon</i> MNPV]	143	143	60%	2e-32
YP_529769.1	ORF-99 [ <i>Agrotis segetum</i> NPV]	138	138	59%	5e-31

**B**

Accession	Description	Max score	Total score	Query coverage	E value
ADB84405.1	AciNPV44 [ <i>Apocheima cinerarium</i> NPV]	890	890	79%	0.0
YP_308945.1	orf55 [ <i>Trichoplusia ni</i> SNPV]	75.1	75.1	22%	2e-11
YP_249663.1	desmoplakin [ <i>Chrysodeixis chalcites</i> NPV]	70.9	70.9	22%	5e-10
YP_003517818.1	desmoplakin-like prot. [ <i>Lymantria xylina</i> MNPV]	61.6	61.6	18%	3e-07
YP_002854675.1	desmoplakin [ <i>Euproctis pseudoconspersa</i> NPV]	60.5	60.5	90%	7e-07
YP_002268135.1	agip105 [ <i>Agrotis ipsilon</i> MNPV]	54.7	54.7	17%	3e-05
YP_717604.1	desmoplakin [ <i>Clanis bilineata</i> NPV]	52.8	52.8	14%	1e-04
YP_002332793.1	SlnV2_gp095 [ <i>Spodoptera litura</i> NPV II]	51.2	51.2	22%	5e-04
NP_047719.1	LdOrf-82 peptide [ <i>Lymantria dispar</i> MNPV]	50.8	50.8	69%	6e-04

## C

MDFKVSHFIRFIFAVTLDDVVIMSRYNLQPKYLNTD VNASTVKHLLQTVNSISKQCKVQ	60
YANEDDLERVRSIIYLHRPHLRFRYDLHVP ELMALPNSTVSNNI PNQITHNFNYKYD	120
YNTNYPVPTIVPAPVTNVDPFGMPVVS P SPQQPQ NATGSTAVPVQNYIINTAPNNGGNVP	180
LQNNNNNNNTDLQQAPPQLYAQQQQQQQQHSLRNYKFLSNNN SNIQRF SYLNTRRPPSP	240
PPAASAAVQLIGFNQDDVAAIENQYRITS DVPSTESYHALINVLF SVSKKYIRTQVFIES	300
LTLINSFDQLENDLKAVVDAINRRTFLK LNYSSPYVANAITVVIQQYVRIVDTVFNNTFN	360
YAQLQIEQQYVEMTTQIINI IKNNTD L TDC KRSYASLET KYNENNER SERQIAEYRKEI	420
NDAGERLTQLNAIFVYLYSKSNYFGNNI IDYIKDLESTIDKLKIQIPLVRMETDFTDNLEK	480
QNKELTSSLKTLQESNNFYSS E INRIKNILSQNNINTDNPISTLISEYNTLKENLKHVPN	540
VEKMKSQFEYEVEQNAKAIENLQFQSE QKYNQLQSVVETLQRETSISNQKIIDLNNETSR	600
LRNTVVELTDRNQTLSSQNQTLSSQNQ TLSSQNQTLSSQNQTLSSQIENLHSEISIEKTR	660
QRTAYVSPTQSQESATTELDERTQQ INDRVNDLQNR LNERDKTIEQLKLLQEDKQQKLK	720
SSRSRKSAIYNKPSSTLTDDKNEIIVYSKNMVSGQEERYIEEINRLKSLLSNQTS SYELM	780
QSDIQNIKNSLETAINTSAIGPDFVALNKNIDEQTEPYAELEQKYYY	827

# A

Accession	Description	Max score	Total score	Query coverage	E value
NP_148896.1	ORF112 DESMOPLAKIN [ <i>Cydia pomonella</i> GV]	330	330	99%	3e-89
NP_891949.1	desmoplakin [ <i>Cryptophlebia leucotreta</i> GV]	309	309	100%	6e-83
YP_002268135.1	agip105 [ <i>Agrotis ipsilon</i> MNPV]	228	228	94%	2e-58
NP_037852.1	ORF92 [ <i>Spodoptera exigua</i> MNPV]	228	228	94%	2e-58
YP_529769.1	ORF-99 [ <i>Agrotis segetum</i> NPV]	224	224	95%	3e-57
ABC67293.1	desmoplakin [ <i>Pieris rapae</i> GV]	215	215	99%	1e-54
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YP_950780.1	desmoplakin-like protein [ <i>Maruca vitrata</i> MNPV]	187	187	94%	2e-46
YP_025220.1	hypothetical protein [ <i>Neodiprion lecontei</i> NPV]	184	184	97%	2e-45
YP_758380.1	ORF83 [ <i>Leucania separata</i> NPV]	182	182	94%	8e-45
YP_001650976.1	desmoplakin [ <i>Orgyia leucostigma</i> NPV]	180	180	95%	3e-44
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NP_613197.1	McnAVgp114 [ <i>Mamestra configurata</i> NPV-A]	174	174	94%	3e-42
YP_667861.1	hypothetical protein [ <i>Neodiprion abietis</i> NPV]	174	174	89%	3e-42
YP_003422478.1	desmoplakin [ <i>Pseudaletia unipuncta</i> GV]	171	171	93%	2e-41
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NP_818704.1	AhnVgp057 [ <i>Adoxophyes honmai</i> NPV]	156	156	90%	7e-37
YP_025136.1	NeseNPV_gp29 [ <i>Neodiprion sertifer</i> NPV]	155	155	91%	2e-36
YP_803460.1	AGNV_gp066 [ <i>Anticarsia gemmatilis</i> NPV]	154	154	95%	2e-36
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**B**