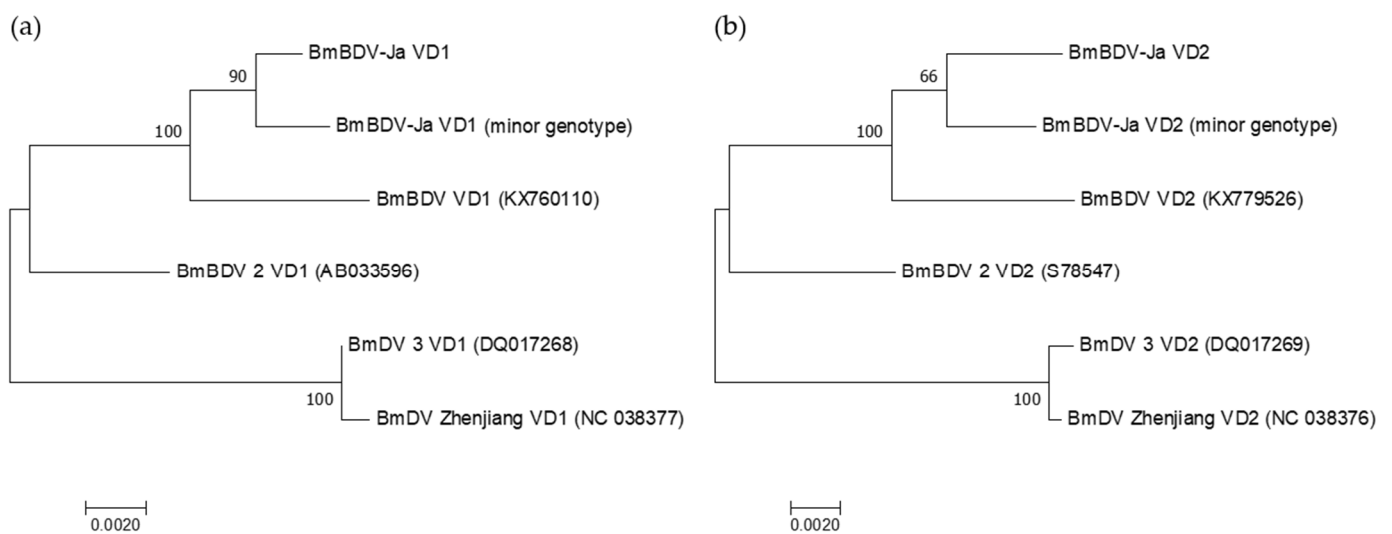


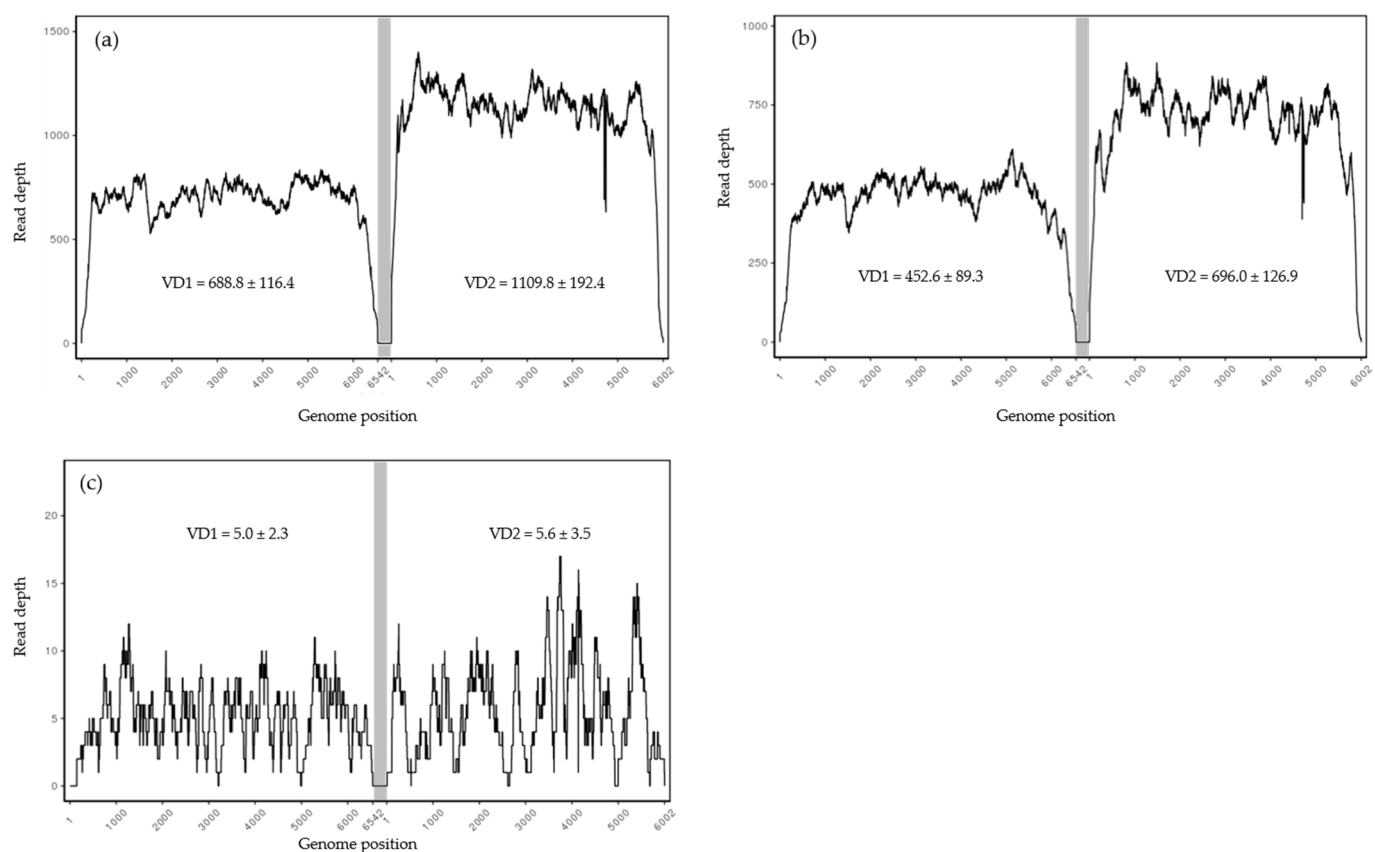
**Supplementary Material:**

1–50 nt CGATCCACGAACATCCACCTGATTACGAGTGTCTGTTAGGGGCTTATCAGC  
 51–100 nt TCCATGGGTTAATCTAGGTATAAGTCACGAAGCGACACCGAGAAGAGGCT  
 101–150 nt CAAGCCCCCAAATTCCATAAAGCTACGGAAGGGGACACCCTGGGCAGCG  
 151–200 nt ATGCGCAGGGTAGTCCGTTTTATATCATACGCGTCCGCGGTTAATATACT  
 201–250 nt ATTTGCATTTTCCACAACCTGTTGCATAGCGCGACGGCAGGCCCTTAGTA  
 251–300 nt CAGTTAGAGGAGATACAAGCCTGCACCCTGTTGCCCTACCATCTGATACG

**Figure S1.** Random 300 nt linker sequence that was used for concatenating VD1 and VD2 of BmBDV-Ja.



**Figure S2.** Maximum likelihood tree of the (a) VD1 and (b) VD2 genome molecules of BmBDV-Ja in comparison to BmBDV, BmBDV2, BmDV 3 and BmDV Zhenjiang (for details see Figure 6). The BmBDV-Ja (minor genotype) consensus sequence included all variable SNPs that were detected in the BmBDV-Ja based SNP analysis with a frequency  $f > 10\%$ .



**Figure S3.** Read depth of the BmBDV alignments created from the sequenced (a) BmNPV-My, (b) BmNPV-De and (c) BmBDV-Ja samples. Both genome molecules (VD1 and VD2) of the bipartite BmBDV-Ja genome were concatenated by a 300 nt random spacer sequence (Figure S1) marked by a vertical grey box, resulting in a single genome molecule that was used as reference sequence. From the aligned reads, the mean read depth  $\pm$  standard deviation were calculated separately for VD1 and VD2.

**Table S1.** Open reading frames (ORF), features and nucleotide (nt) and amino acid (aa) similarity in comparison to the BmNPV-India (JQ991010) isolate.

ORF	Feature	Start	End	Length (nt)	nt identity (%)	aa identity (%)
<i>bm1</i>	<i>polh</i>	1	> 738	738	100	100
<i>bm2</i>	<i>orf1629</i>	768	< 2411	1644	98.97	99.1
<i>bm3</i>	<i>pk1</i>	2410	> 3240	831	99.28	99.3
<i>bm4</i>	<i>hypothetical protein</i>	3266	< 4288	1023	99.61	100
<i>bm5</i>	<i>hypothetical protein</i>	4630	< 5625	996	99.6	99.7
<i>bm6</i>	<i>lef-1</i>	5505	< 6317	813	99.88	100
<i>bm7</i>	<i>egt</i>	6432	> 7952	1521	99.41	98.4
<i>bm8</i>	<i>odv-e26</i>	8094	> 8783	690	99.13	98.7
<i>bm9</i>	<i>hypothetical protein</i>	8752	> 9384	633	99.37	99.5
<i>bm10</i>	<i>hypothetical protein</i>	9414	< 10484	1071	99.16	98.6
<i>bm11</i>	<i>hypothetical protein</i>	10486	> 10818	333	99.4	100
<i>bm12</i>	<i>airf-1</i>	11001	< 12347	1347	99.03	98.7
<i>bm13</i>	<i>pif-2</i>	12384	> 13532	1149	99.65	99.5
<i>bm14</i>	<i>f-protein</i>	13635	> 15656	2022	99.95	99.9
<i>bm15</i>	<i>pkip</i>	15687	< 16196	510	99.22	100
<i>bm16</i>	<i>dbp</i>	16236	< 17192	957	99.58	99.7
<i>bm17</i>	<i>hypothetical protein</i>	17268	> 17657	390	100	100
<i>bm18</i>	<i>iap1</i>	17659	> 18534	876	99.2	99.3
<i>bm19</i>	<i>lef-6</i>	18539	> 19060	522	100	100
<i>bm20</i>	<i>hypothetical protein</i>	19183	< 19398	216	100	100
<i>bm21</i>	<i>hypothetical protein</i>	19454	< 20872	1419	99.72	99.6
<b>bm22</b>	<i>bro-a</i>	20907	< 21878	972	94.66	93.6
<b>bm23</b>	<i>sod</i>	22056	> 22511	456	100	100
	<i>hr1</i>	22607	23482			
<b>bm24</b>	<i>fgf</i>	23540	> 24088	549	99.64	100
	<i>hr2</i>	24148	24336			
<b>bm25</b>	<i>hypothetical protein</i>	24401	< 25048	648	100	100
<i>bm26</i>	<i>ubiquitin</i>	25069	> 25302	234	99.57	100
<i>bm27</i>	<i>39k</i>	25352	< 26188	837	100	100
<i>bm28</i>	<i>lef-11</i>	26182	< 26520	339	100	100
<i>bm29</i>	<i>bv-e31</i>	26483	< 27136	654	99.54	100
<i>bm30</i>	<i>p43</i>	27204	< 28292	1089	99.63	99.4
<i>bm31</i>	<i>p47</i>	28300	< 29499	1200	99.75	99.7
<i>bm32</i>	<i>lef-12</i>	29504	> 30037	534	99.06	97.2
<i>bm33</i>	<i>gta</i>	30112	> 31632	1521	99.34	99.2
<i>bm34</i>	<i>hypothetical protein</i>	31646	> 31882	237	100	100
<i>bm35</i>	<i>hypothetical protein</i>	31863	> 32258	396	98.74	100
<i>bm36</i>	<i>hypothetical protein</i>	32260	> 32844	585	98.97	99
<i>bm37</i>	<i>odv-e66</i>	32829	> 34955	2127	99.86	99.9

ORF	Feature	Start	End	Length (nt)	nt identity (%)	aa identity (%)
bm38	<i>ets</i>	35055	< 35324	270	99.63	98.9
bm39	<i>lef-8</i>	35574	< 38177	2604	99.77	100
bm40	<i>hypothetical protein</i>	38234	> 39193	960	99.69	100
bm41	<i>hypothetical protein</i>	39184	< 39768	585	98.97	97.9
bm42	<i>hypothetical protein</i>	39770	> 40189	420	100	100
bm43	<i>lef-10</i>	40186	> 40422	237	100	100
bm44	<i>vp1054</i>	40280	> 41377	1098	100	100
bm45	<i>hypothetical protein</i>	41459	> 41680	222	94.02	93.5
bm46	<i>hypothetical protein</i>	41682	> 41936	255	100	100
bm47	<i>hypothetical protein</i>	42190	> 42675	486	99.59	99.4
bm48	<i>hypothetical protein</i>	42690	< 43205	516	100	100
bm49	<i>ac60</i>	43217	< 43465	249	100	100
bm50	<i>fp25</i>	43611	< 44255	645	100	100
bm51	<i>lef-9</i>	44359	> 45831	1473	99.86	100
bm52	<i>hypothetical protein</i>	45892	> 46359	468	99.57	100
bm53	<i>gp37</i>	46433	< 47317	885	98.87	97.6
bm54	<i>dnapol</i>	47447	< 50413	2967	99.73	100
bm55	<i>hypothetical protein</i>	50422	> 52839	2418	99.83	99.9
bm56	<i>lef-3</i>	52842	< 53999	1158	100	100
bm57	<i>odv-nc42</i>	54018	> 54422	405	100	100
bm58	<i>hypothetical protein</i>	54400	> 55188	789	100	100
bm59	<i>iap2</i>	55355	> 56104	750	99.87	100
bm60	<i>hypothetical protein</i>	56163	> 56345	183	100	100
bm61	<i>hypothetical protein</i>	56356	< 56655	300	100	100
bm62	<i>hypothetical protein</i>	56652	< 57461	810	99.88	100
bm63	<i>hypothetical protein</i>	57479	< 57880	402	99	99.2
bm64	<i>hypothetical protein</i>	57899	< 58156	258	100	100
bm65	<i>vlf-1</i>	58172	< 59326	1155	98.1	97.9
bm66	<i>hypothetical protein</i>	59332	< 59664	333	99.7	99.1
bm67	<i>hypothetical protein</i>	59667	< 59981	315	100	100
bm68	<i>gp41</i>	59984	< 61189	1206	99.67	99.8
bm69	<i>hypothetical protein</i>	61179	< 61886	708	99.72	100
bm70	<i>hypothetical protein</i>	61729	< 62277	549	100	100
bm71	<i>p95</i>	62243	> 64756	2514	99.64	99.6
	<i>hr3</i>	64778	66264			
bm72	<i>vp15</i>	66308	> 66688	381	99.48	100
bm73	<i>cg30</i>	66693	< 67493	801	99.25	98.9
bm74	<i>vp39</i>	67496	< 68542	1047	100	100
bm75	<i>lef-4</i>	68561	> 69958	1398	99.64	100
bm76	<i>hypothetical protein</i>	69955	< 70416	462	99.78	99.3
bm77	<i>p33</i>	70452	< 71231	780	99.62	100
bm78	<i>hypothetical protein</i>	71230	> 71715	486	99.59	100

ORF	Feature	Start	End	Length (nt)	nt identity (%)	aa identity (%)
bm79	odv-e25	71724	> 72410	687	100	100
bm80	dna helicase	72449	< 76117	3669	99.78	100
bm81	odv-e28	76104	> 76625	522	98.28	97.7
bm82	bro-b	76740	> 77465	726	n.a.	n.a.
bm83	bro-c	77524	< 78522	999	93.29	92.5
bm84	38k	78665	< 79627	963	99.58	99.4
bm85	lef-5	79562	< 80359	798	99.62	99.6
bm86	p6.9	80356	< 80553	198	100	100
bm87	p40	80595	< 81686	1092	99.91	100
bm88	p12	81706	< 82083	378	100	100
bm89	p45	82064	< 83227	1164	99.48	99.7
bm90	vp80	83253	< 85337	2085	99.62	99
bm91	he65	85360	< 86229	870	99.43	99.3
	hr4L	86250	86846			
bm92	hypothetical protein	86863	< 87609	747	99.33	98.8
bm93	hypothetical protein	87610	< 87927	318	100	100
bm94	hypothetical protein	87942	< 89117	1176	99.4	99.5
bm95	hypothetical protein	89141	< 89320	180	100	100
bm96	hypothetical protein	89369	< 89572	204	100	100
	hr4R	89715	90241			
bm97	hypothetical protein	90246	< 91520	1275	99.76	99.7
bm98	pif-3	92155	< 91535	614	99.84	99.5
bm99	hypothetical protein	92333	< 92163	185	94.05	89.5
bm100	hypothetical protein	92269	< 92556	288	99.65	100
bm101	pif-1	92688	< 94271	1584	99.62	99.4
bm102	hypothetical protein	94279	< 94527	249	100	100
bm103	hypothetical protein	94630	< 94803	174	100	100
bm104	hypothetical protein	94696	< 94881	186	100	100
bm105	gcn2	94915	< 95592	678	99.56	99.1
bm106	hypothetical protein	95776	< 96510	735	99.05	98.8
bm107	lef-7	96529	< 97212	684	98.68	97.8
bm108	chitinase	97202	< 98857	1656	99.64	99.6
bm109	v-cath	98904	< 99875	972	99.9	100
bm110	gp64	99993	< 101585	1593	100	100
bm111	p24	101713	< 102300	588	99.83	100
bm112	gp16	102331	< 102651	321	100	100
bm113	pp34	102713	< 103660	948	99.79	99.7
bm114	hypothetical protein	103663	< 104325	663	99.55	99.5
bm115	alkexo	104353	< 105615	1263	99.52	99.5
bm116	p35	106082	< 106981	900	100	100
	hr5	107030	107914			
bm117	p26	107971	< 108693	723	100	100

ORF	Feature	Start	End	Length (nt)	nt identity (%)	aa identity (%)
<i>bm118</i>	<i>p10</i>	108766	< 108978	213	99.53	100
<i>bm119</i>	<i>p74</i>	109053	< 110990	1938	99.79	99.5
<i>bm120</i>	<i>me53</i>	111187	< 112542	1356	99.48	99.1
<i>bm121</i>	<i>hypothetical protein</i>	112688	< 112891	204	100	100
<i>bm122</i>	<i>ie-0</i>	112819	< 113604	786	99.62	100
<i>bm123</i>	<i>odv-nc50</i>	113619	< 115049	1431	99.86	99.8
<i>bm124</i>	<i>odv-e18</i>	115060	< 115368	309	100	100
<i>bm125</i>	<i>odv-ec27</i>	115383	< 116255	873	99.89	100
<i>bm126</i>	<i>hypothetical protein</i>	116270	< 116557	288	100	100
<i>bm127</i>	<i>hypothetical protein</i>	116552	< 117157	606	99.67	100
<i>bm128</i>	<i>ie-1</i>	117223	< 118977	1755	99.83	100
<i>bm129</i>	<i>odv-e56</i>	119093	< 120223	1131	99.29	98.7
<i>bm130</i>	<i>hypothetical protein</i>	120252	< 120572	321	100	100
<i>bm131</i>	<i>hypothetical protein</i>	120541	< 120858	318	100	100
<i>bm132</i>	<i>ie-2</i>	120891	< 122168	1278	98.51	98.4
<i>bm133</i>	<i>pe38</i>	122654	< 123583	930	100	100
<i>bm134</i>	<i>hypothetical protein</i>	123688	< 123924	237	99.58	100
	<i>hr6</i>	123929	124392			
<i>bm135</i>	<i>ptp</i>	124403	< 124909	507	99.21	98.8
<i>bm136</i>	<i>bro-d</i>	124906	< 125952	1047	94.57	92.6
<i>bm137</i>	<i>hypothetical protein</i>	126026	< 126481	456	99.12	99.3
<i>bm138</i>	<i>hypothetical protein</i>	126510	< 126839	330	99.39	99.1
<i>bm139</i>	<i>lef-2</i>	126820	< 127452	633	99.53	99.5