BRILL
WAGENINGEN
ACADEMIC

JOURNAL OF INSECTS AS FOOD AND FEED 12 (2026) 1475–1476

Journal of Insects as Food and Feed
brill.com/jiff

CORRIGENDUM

Corrigendum to: A new volvovirus isolate from the Korean two-spotted cricket (*Gryllus bimaculatus*) and the analysis of its genome (*Journal of Insects as Food and Feed* 12 (2026): 939-948)

*Hyun-Soo Kim and June-Sun Yoon**

Department of Agricultural Convergence Technology, Jeonbuk National University, Jeonju 54596, South Korea; *jsyoon@jbnu.ac.kr

Received 13 December 2024 | Accepted 1 October 2025 | Published online 20 October 2025 | Published in issue 1 April 2026

In the above-mentioned article Tables 1–3 were omitted.
Please find the tables below.

TABLE 1 List of primers for sequence analysis of *Gryllus bimaculatus* volvovirus (GbVVV)

Set	Oligo name	Sequence (5’→3’)	Size (bp)	Region (nt)	Reference
	AdVVV F	TGGCTGCTTCTCGTTTGG	431	853–1283	de Miranda *et al.* (2021)
	AdVVV R	CTTTATCTCAACAGCATCGGG			
1	GbVVV_1 F	GTCGTGGGTTTGCGATTAGA	1004	496–1499	This study
	GbVVV_1 R	AACAGAAGCAGGACCAATATCC			
2	GbVVV_2 F	CGGTTGAGATGCCGGATATT	1001	1469–2469	This study
	GbVVV_2 R	CAGAGACGGCACACATACAA			
3	GbVVV_3 F	GTCCATAGTTCTTGGGTTAG	863	2282–629	This study
	GbVVV_3 R	CCAACTAAACTCTCTGGC			
4	AdVVV F	TGGCTGCTTCTCGTTTGG	792	853–1644	This study
	GbVVV_4 R	ATTTGCACGAATAACACG			
5	GbVVV_2 F	CGGTTGAGATGCCGGATATT	176	1469–1644	This study
	GbVVV_4 R	ATTTGCACGAATAACACG			

Oligonucleotide primer names, sequences of the primers for amplifying the genome regions, the size of the expected PCR product, and the genomic region where the primers bind.

DOI: 10.1163/23524588-20260005
ISSN: 2352-4588 (online)

TABLE 2 Complete genome sequences of all available volvovirus genomes from the NCBI database

Name	Host species	Isolate	GenBank ID	Size (bp)	Reference
AdVVV-IAF	*Acheta domesticus*	AdVVV-IAF	KC543331.1	2517	Pham *et al.* (2013)
AdVVV-JP	*Acheta domesticus*	AdVVV-Japan	KC794540.1	2517	Pham *et al.* (2013)
GaVVV-US	*Gryllus assimilis*	AdVVV-GA	KC794539.1	2516	Pham *et al.* (2013)
GaVVV-CACV1	*Gryllus assimilis*	Cricket-associated circular virus 1-I0180-G7-G12	MH545526.1	2516	Rosario *et al.* (2018)
AdVVV-TH	*Acheta domesticus*	AdVVV-Thailand	MW288623.1	2516	Homchan and Gupta (2024)
GbVVV-KR	*Gryllus bimaculatus*	GbVVV-South Korea	PP275066.1	2515	This study

Genome information including the host species, isolate, GenBank ID, and the size of the genome. Volvoviruses were named using basic guidelines: the species abbreviation is listed in front of VVV (volvovirus) and, in most cases, national origin follows after VVV. Therefore, the sequence isolated from *G. bimaculatus* in South Korea was designated GbVVV-KR.

TABLE 3 Results of SNP analysis and coding sequence (CDS) information for potential ORFs in volvoviruses

ORFs	Annotation	Name	Amino acid	Mutation	Synonymous	Non-synonymous
ORF1	Hypothetical protein/capsid protein-like protein	AdVVV-IAF	361	–	–	–
		AdVVV-JP	361	18	4	14
		GaVVV-US	361	5	0	5
		GaVVV-CACV1	361	6	1	5
		AdVVV-TH	361	38	4	34
		GbVVV-KR	361	31	3	28
ORF2	Hypothetical protein/ replication-associated protein	AdVVV-IAF	270	–	–	–
		AdVVV-JP	270	3	3	0
		GaVVV-US	270	0	0	0
		GaVVV-CACV1	270	0	0	0
		AdVVV-TH	270	0	0	0
		GbVVV-KR	270	5	4	1
ORF3	Hypothetical protein	AdVVV-IAF	207	–	–	–
		AdVVV-JP	207	0	0	0
		GaVVV-US	207	0	0	0
		GaVVV-CACV1	207	0	0	0
		AdVVV-TH	207	3	0	3
		GbVVV-KR	111*	5	0	5
ORF4	Hypothetical protein	AdVVV-IAF	130	–	–	–
		AdVVV-JP	130	3	0	3
		GaVVV-US	130	0	0	0
		GaVVV-CACV1	130	0	0	0
		AdVVV-TH	130	2	0	2
		GbVVV-KR	130	2	0	2

ORF3 of the reference sequences is 207 aa, reduced to 111 aa by the stop codon.