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Article in *Transboundary and Emerging Diseases* · July 2019

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WILEY

Newly emerged African swine fever virus strain Belgium/Etalle/wb/2018: Complete genomic sequence and comparative analysis with reference p72 genotype II strains

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Funding information

This study is supported by a grant from the Public Service of Wallonia and a grant from the University of Liège's Research Council.

Abstract

In a new example of pathogens hopscotching the globe, African swine fever virus hit north-western Europe's wildlife in summer 2018, marking a further spread of a disease that had invaded Central and Eastern Europe recently. The complete genomic sequence of the Belgium/Etalle/wb/2018 virus is reported, with the hope it will provide a valuable tool for tracing geographical spread and biologic evolution of the virus.

KEYWORDS

African swine fever virus, Belgium, emergence, whole genome sequence, wild boar

1 | INTRODUCTION

African swine fever (ASF) is a highly contagious, fulminant, usually deadly haemorrhagic disease of pigs and wild boars. It has the potential for rapid spread, serious socio-economic consequence and is of major importance in the international trade of animals and animal products (EFSA Panel on Animal Health & Welfare, 2014). Its causative agent is African swine fever virus (ASFV; family *Asfarviridae*, genus *Asfivirus*), a large, enveloped, double-stranded DNA virus that is highly adapted for both tick-dependent sylvatic and tick-independent domestic transmission cycles (Alonso et al., 2018). By sequencing the C-terminal region of only one of its genes (*B646L*), more than 20 ASFV genotypes have been identified (Bastos et al., 2003).

After the first report of ASF in 1921 in Kenya, the disease was confined in sub-Saharan Africa. In 1957, it was introduced into Portugal and then spread to other European countries, Cuba, Brazil, Dominican Republic and Haiti (Sanchez-Vizcaino, Mur, & Martinez-Lopez, 2012). ASF has been eradicated in these countries apart

from Italy-Sardinia, where it remains endemic (Iglesias, Rodriguez, Feliziani, Rolesu, & Torre, 2017). In June 2007 however, ASF was confirmed for the first time in Georgia in the Caucasus region, then spread rapidly into vast areas of western and southern Russia, where it circulated out of control in domestic and wild pig populations. The virus then spread to Eastern and Central Europe with outbreaks reported in Ukraine (2012), Belarus (2013), Lithuania, Estonia, Latvia and Poland (2014), Romania and the Czech Republic (2017) and Hungary (2018). In August 2018, a new outbreak of ASF was reported in Liaoning province of China (Ge et al., 2018; Zhou et al., 2018).

2 | THE CONTEXT

At the beginning of September 2018, the virus was detected in a wild boar population in southern Belgium, more than 1,000 km west of the nearest foci in the Czech Republic (Linden et al., 2019). At the time of writing (on June 20, 2019), 823 wild boar carcasses had proved ASFV-positive. Although no domestic pig farms have been involved so far,

Gautier Gilliaux and Mutien Garigliany equally contributed to the study.

TABLE 1 Census of African swine fever virus complete genomic sequences publicly available

Name	GenBank no.	Origin	Year	p72 genotype	Length (bp)	Host
Kenya 1950	AY261360	Kenya	1950	XX/I	193,886	Pig
Portugal L60	KM262844	Portugal	1960	I	182,362	Pig
Malawi Tengani 62	AY261364	Malawi	1962	V/I	185,689	Pig
Portugal NHV 1968	KM262845	Portugal	1968	I	172,051	Pig
Spain/BA71	KP055815	Spain	1971	I	180,365	Pig
Spain E75	FN557520	Spain	1975	II	181,187	Pig
South Africa/Mkuzi/1979	AY261362	South Africa	1979	I/VII	192,714	Tick
Namibia:Warthog	AY261366	Namibia	1980	IV	186,528	Warthog
Malawi/Tick/Lil-20-1/1983	AY261361	Malawi	1983	VIII	187,612	Tick
South Africa/Tick:Warmbaths	AY261365	South Africa	1987	III/I	190,773	Tick
Portugal/OURT 88/3	AM712240	Portugal	1988	I	171,719	Tick
South Africa/Pretorisuskop/96/4	AY261363	South Africa	1996	XX/I	190,324	Tick
Benin 97/1	AM712239	Benin	1997	I	182,284	Pig
Ken05 Tk1	KM111294	kenya	2005	X	191,058	Tick
Ken06.Bus	KM111295	Kenya	2006	IX	184,368	Pig
Georgia 2007/1	FR682468	Georgia	2007	II	189,344	Pig
Italy/47/Ss/2008	KX354450	Italy	2008	I	184,638	Pig
Georgia 2008/1	MH910495	Georgia	2008	II	189,465	NF
Georgia 2008/2	MH910496	Georgia	2008	II	189,315	NF
Italy 26544/OG10	KM102979	Italy	2010	I	182,906	Pig
Russia/Kashino:04/13	KJ747406	Russia	2013	II	189,387	Wild boar
Estonia 2014	LS478113	Estonia	2014	II	182,446	Wild boar
Russia/Odintsovo/02/14	KP843857	Russia	2014	II	189,333	Wild boar
Uganda R35 2015	MH025920	Uganda	2015	IX	188,629	Pig
Uganda R7 2015	MH025917	Uganda	2015	IX	188,628	Pig
Uganda R25 2015	MH025918	Uganda	2015	IX	188,630	Pig
Uganda R8 2015	MH025916	Uganda	2015	IX	188,627	Pig
Uganda N10 2015	MH025919	Uganda	2015	IX	188,611	Pig
POL 2015/Podlaskie	MH681419	Poland	2015	II	189,394	Pig
Pol16 20186-07	MG939583	Poland	2016	II	189,401	Pig
Pol16 20538-09	MG939584	Poland	2016	II	189,399	Pig
Pol16 29413-023	MG939586	Poland	2016	II	189,393	Pig
Pol16 20540-010	MG939585	Poland	2016	II	189,585	Pig
Pol17 04461-C210	MG939588	Poland	2017	II	189,401	Pig
Pol17 03029-C201	MG939587	Poland	2017	II	189,405	Pig
Pol17 05838-C220	MG939589	Poland	2017	II	189,393	Pig
China/AnhuiXCGZ/2018	MH766894	China	2018	II	189,354	Pig
ASFV/Belgium/Etalle/wb/2018	NA	Belgium	2018	II	195,276	Wild boar

Abbreviations: NA, not applicable yet; NF, not found.

the costs incurred by public authorities to contain the spatial expansion of the virus and the losses of the private sector active in tourism, the timber industry and the livestock sector are already exorbitant. In this context, the search for a culprit is ongoing. In this regard, the judicial

investigations launched shortly after the identification of the index case in September 2018 have recently led to the detention of several persons allegedly responsible for the outbreak. To prevent such events from happening elsewhere and to contribute to the objective establishment

of possible liabilities, it is crucial to understand how the virus was able to cross these 1,000 km (at least). Many hypotheses flourish. Infected, still asymptomatic wild boars could have been imported and released illegally with the aim of artificially increasing game density, thus the attractiveness of the hunt. Someone may have disposed of contaminated meat products from a region known to be infected. The virus could also have reached Belgium indirectly. For example, equipments (boots, shoes, vehicles, etc.) used in a region deemed infected could have not been properly disinfected before being reused in the forest concerned. This is plausible since round trips between the infected zone in Belgium and infected regions in Eastern Europe are objectively identified, either in the context of bilateral military exercises (Ministry of Defence & Armed Forces of the Czech Republic, 2018) or because groups of Belgian hunters regularly participate to hunting parties in infected regions of Eastern Europe. Finally, the fact remains that the hypothesis of a malicious act perpetrated intentionally cannot be dismissed *ex officio*. In this context, having the complete genomic sequence of the viral strain would provide a first tool to study these questions. In addition, this resource is an essential prerequisite for providing the means to detect future potentially attenuated variants. Accordingly, the complete genomic sequence of the virus present in the spleen of the index case was reconstructed *de novo*. The ASFV double-stranded DNA genome varies in length from about 170 to 193 kbp, depending on the isolate, and contains between 150 and 190 ORFs. It has a conserved central region (CCR) of about 125 kb, while the ends are variable in size. The genome termini are covalently closed by imperfectly base-paired hairpin loops that are present in two forms that are complementary and inverted with respect to each other (Dixon, Chapman, Netherton, & Upton, 2013). The first complete genome sequence was determined in 1995 from a cell culture adapted strain (Yanez et al., 1995). A total of 151 genes were annotated. The left variable region (LVR) and the right variable region (RVR) contain different number of five multigene family (MGF) genes, MGF 100, 110, 300, 360 and 505/530, named after the average number of encoded amino acids. The CCR contains genes involving virus replication, assembly and host cell function modulation. Since then on, 37 genomic sequences from different origin and virulence have been deposited in GenBank (Table 1). In this paper, we reveal the complete genomic sequence of the most recently emerged strain, ASFV/Belgium/Etalle/wb/2018 (Linden et al., 2019).

3 | THE STUDY

On September 10–12, forest officers found 4 dead and 1 dying wild boars located close to each other in the *Bois de Buzenol*, the index location of the Belgian outbreak. On September 13th, spleen or long bone samples of these animals proved positive for the genome of the African swine fever virus by qPCR (Linden et al., 2019). A first genetic characterization was performed by using standard genotyping procedure on viral DNA directly extracted from the homogenized kidney (found-dead adult sow) or spleen (dying piglet). First, the segment of the *B646L* gene encoding the C-terminal end of the p72 protein was obtained by PCR as recommended (World Organisation for Animal Health, 2013). The DNA sequences retrieved were identical

in both animals (GenBank accession no MH998358). Alignments were performed using ClustalW implemented in Geneious v10.0.9 (Biomatters, Auckland, New Zealand), and a first phylogenetic analysis was performed (Garigliany et al., 2019). The Belgian strain of African swine fever clearly belonged to genotype II. To further define its genome, a PCR targeting a ~350-bp fragment in the variable intergenic region between the *I73R* and *I329L* genes was performed according to Gallardo et al. (Gallardo et al., 2014). Again, identical DNA sequences were retrieved from both animals (Genbank accession no. MH998359). Sequence alignments revealed that the isolate ASFV/Belgium/Etalle/wb/2018 shares a 10-nucleotide (TATATAGGAA) insertion at position 106. It is therefore a so-called intergenic region (IGR) II variant according to the nomenclature of Gallardo et al. (2014).

3.1 | Sequencing

Because unaffected by a significant post-mortem decay and because of its high concentration in viral DNA ($C_t = 23.3 \pm 1$), the piglet spleen was used as a source of viral DNA for sequencing and *de novo* reconstruction of the ASFV genome. Briefly, 500 mg of spleen tissue was homogenized and submitted to a viral enrichment step and total DNA extraction as described in Garigliany et al. (2019, 2017). The sequencing library was prepared using Illumina's Nextera XT DNA library Prep kit, and the MiSeq reagent kit v3 (ref. # MS-102-3003, read length up to 300 bp) was used for sequencing on the MiSeq instrument.

3.2 | Genome assembly

Raw read trimming was performed using Geneious v10.0.9 with a Phred quality score (Q) of 30 or higher. Retrieved library was then blasted in a hit/no_hit check against all ASFV genomes referenced in NCBI database, using an E value of $1e-10$, a scoring match–mismatch of 2–3, a K-mer of 15 and a 5–2 open extended gap cost. Finally, assembling of the complete genomic sequence of Belgium/Etalle/wb/2018 was achieved from a collection of 1,168,132 reads (9.9% of 11,818,334 total reads) using the Geneious *de novo* algorithm under the 'Highest Sensitivity/Slow' condition. The genome was sequenced to $748 \times$ average depth and 100% breadth of coverage of the reference genome, at a minimum depth of 32 reads. Search for low coverage (<75 average depth) regions highlighted two sites, from nt 14731 to nt 14781 (average depth = 73) and from nt 19074 to nt 19096 (=67). Both sites displayed a highly repeated nucleotide, a poly-C tract ($N = 20$) and a poly-G tract ($N = 13$), respectively. The complete genomic sequence is 190202 nt long and was deposited in GenBank (#MK543947).

3.3 | Open reading frame prediction and genome annotation

Open reading frames (ORFs) were first automatically detected employing the rapid annotation tool built in Geneious software. Further, protein homology searches of nucleotide sequences and manual annotation of putative translated ORF products were carried out using blastx against NCBI nonredundant protein sequence

TABLE 2 ORFs annotated in ASFV Belgium/Etalle/wb/2018 strain

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
1	MGF 360-1L	896–1.729	834	reverse	AYW33974.1; QBH90466.1; QBH90651.1	MK128995, MK333180, MK333181	unknown
2	MGF 360-2L	2.063–3.151	1.089	reverse	AXZ95934.1; AXZ95945.1; AXZ95965.1; AXZ96059.1; AXZ96217.1; AYW33954.1; AZP54003.1; CBW46644.1; QBH90467.1; QBH90652.1	FR682468, MG939583, MG939584, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene
3	KP177R; MGF 360-2L	3.292–3.825	534	forward	AXZ95770.1; AXZ95948.1; AXZ95950.1; AXZ95967.1; AXZ96062.1; AXZ96222.1; AYW33955.1; AZP54061.1; QBH90468.1; QBH90653.1	MG939583, MG939585, MG939586, MG939587, MG939588, MG939589, MH910495, MK128995, MK333180, MK333181	unknown
4	L83L	3.962–4.207	246	reverse	AXZ95771.1; AXZ95951.1; AXZ95968.1; AXZ96063.1; AYW33973.1; AZP54104.1; CBW46646.1; QBH90469.1; QBH90654.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-L83L)
5	L60L	4.308–4.466	159	reverse	AXZ95772.1; AXZ95952.1; AXZ95969.1; AXZ96064.1; AYW33975.1; AZP54119.1; CBW46647.1; QBH90470.1; QBH90655.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (Pretorisuskop-L60L)
6	MGF 360-3L	4.625–5.695	1.071	reverse	AXZ95773.1; AXZ95953.1; AXZ95970.1; AXZ96065.1; AYW33956.1; AZP54007.1; CBW46648.1; QBH90471.1; QBH90656.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene
7	MGF 110-1L	6.141–6.731	591	reverse	AXZ95774.1; AXZ95954.1; AXZ95971.1; AXZ96066.1; AYW33957.1; QBH90473.1; QBH90658.1	MG939583, MG939586, MG939587, MG939588, MK128995, MK333180, MK333181	unknown
8	ASFV G ACD 00090	6.730–6.843	114	forward	AYW33976.1; AZP54136.1; CBW46651.1; QBH90474.1; QBH90659.1	FR682468, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_Final_2-009
9	MGF 110-2L	6.911–7.225	315	reverse	AYW33958.1; AZP54096.1; CBW46652.1; QBH90475.1; QBH90660.1	FR682468, MH910495, MK128995, MK333180, MK333181	110 Multigene
10	MGF 110-3L	7.322–7.696	375	reverse	AXZ95776.1; AXZ95956.1; AXZ95973.1; AXZ96068.1; AYW33963.1; AZP54083.1; CBW46653.1; QBH90476.1; QBH90661.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	110 Multigene
11	ASFV G ACD 00120	7.807–8.031	225	forward	QBH90477.1; QBH90662.1	MK333180, MK333181	unknown
12	MGF 110-4L	8.010–8.384	375	reverse	AXZ95777.1; AXZ95957.1; AXZ95974.1; AXZ96069.1; AYW33962.1; AZP54082.1; CBW46655.1; QBH90478.1; QBH90663.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	110 Multigene
13	MGF 110-5L-6L	8.573–9.190	618	reverse	AXZ95778.1; AXZ95958.1; AXZ95975.1; AXZ96070.1; AYW33959.1; AZP54050.1; CBW46656.1; QBH90479.1; QBH90664.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	110 Multigene

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
14	MGF 110-5L-6L; MGF 110-7L	9.397–9.810	414	reverse	AYW33960.1; AZP54076.1; CBW46657.1; QBH90480.1; QBH90665.1	FR682468, MH910495, MK128995, MK333180, MK333181	110 Multigene
15	ASFV G ACD 00160	10.151–10.279	129	reverse	AYW33977.1; QBH90481.1; QBH90666.1	MK128995, MK333180, MK333181	unknown
16	MGF 110-8L	10.538–10.615	78	reverse	QBH90482.1; QBH90667.1	MK333180, MK333181	unknown
17	MGF 100-1R	11.139–11.513	375	forward	AXZ95780.1; AXZ95960.1; AXZ95977.1; AXZ96072.1; AYW33961.1; AZP54084.1; CBW46660.1; QBH90483.1; QBH90668.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	100 Multigene
18	ACD 00190; ASFV G ACD 00190	11.539–11.664	126	reverse	AXZ95781.1; AXZ95961.1; AXZ95978.1; AXZ96073.1; AZP54131.1	MG939583, MG939586, MG939587, MG939588, MH910495	unknown
19	MGF 110-9L	11.673–12.545	873	reverse	AXZ95782.1; AXZ95962.1; AXZ95979.1; AXZ96074.1; AYW33964.1; AZP54029.1; CBW46662.1; QBH90485.1; QBH90670.1	FR682468, MG939583, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	110 Multigene
20	ASFV G ACD 00210	12.544–12.735	192	forward	AYW33979.1; AZP54114.1; CBW46663.1; QBH90486.1; QBH90671.1	FR682468, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ final-021
21	MGF 110-11L	12.836–13.195	360	reverse	AXZ95784.1; AXZ95937.1; AXZ95964.1; AXZ95981.1; AXZ96076.1; AYW33965.1; AZP54089.1; CBW46664.1; QBH90487.1; QBH90672.1	FR682468, MG939583, MG939584, MG939586, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	110 Multigene
22	ACD 00240; ASFV G ACD 00240	13.653–13.763	111	forward	AXZ95786.1; AXZ95939.1; AYW33980.1; QBH90489.1; QBH90674.1	MG939583, MG939584, MK128995, MK333180, MK333181	unknown
23	MGF 110-12L	13.844–14.203	360	reverse	AYW33981.1; AZP54090.1; CBW46667.1; QBH90490.1; QBH90675.1	FR682468, MH910495, MK128995, MK333180, MK333181	110 Multigene
24	ASFV G ACD 00.270	15.142–15.255	114	reverse	AYW33982.1; AZP54137.1; CBW46669.1; QBH90492.1; QBH90677.1; SP573427.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ final-027
25	MGF 360-4L	15.298–16.461	1.164	reverse	AYW33968.1; AZP53998.1; CBW46670.1; QBH90493.1; QBH90678.1; SP573428.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	360 Multigene
26	ACD 00300; ASFV G ACD 00300	17.017–17.133	117	reverse	AXZ95789.1; AXZ95942.1; AYW33983.1; AZP54134.1; CBW46672.1; QBH90494.1; QBH90679.1; SP573429.1	FR682468, LS478113, MG939583, MG939584, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ Final_2-030
27	MGF 360-6L	17.277–18.404	1.128	reverse	AXZ95790.1; AXZ95943.1; AYW33969.1; AZP54001.1; CBW46673.1; QBH90495.1; QBH90680.1; SP573430.1	FR682468, LS478113, MG939583, MG939584, MH910495, MK128995, MK333180, MK333181	360 Multigene

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
28	ASFV G ACD 00320	18.632–18.757	126	forward	AYW33984.1; AZP54132.1; CBW46674.1; QBH90496.1; QBH90681.1; SPS73431.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ final-031
29	ASFV G ACD 00330	18.944–19.057	114	forward	AYW33985.1; AZP54138.1; CBW46675.1; QBH90497.1; QBH90682.1; SPS73432.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ final-032
30	ASFV G ACD 00360	19.253–19.369	117	reverse	AYW33986.1; AZP54135.1; CBW46677.1; QBH90499.1; QBH90684.1; SPS73433.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ Final_2-035
31	X69R	19.281–19.490	210	forward	AYW33987.1; CBW46678.1; QBH90500.1; QBH90685.1; SPS73434.1	FR682468, LS478113, MK128995, MK333180, MK333181	unknown (BA71V-X69R)
32	MGF 300-1L	19.788–20.594	807	reverse	AXZ95792.1; AXZ96218.1; AYW33970.1; AZP54034.1; CBW46679.1; QBH90501.1; QBH90686.1; SPS73435.1	FR682468, LS478113, MG939583, MG939589, MH910495, MK128995, MK333180, MK333181	300 Multigene
33	MGF 300-2R	21.422–21.904	483	forward	SPS73436.1	LS478113	unknown
34	MGF 300-4L	21.994–22.986	993	reverse	AXZ95793.1; AXZ96219.1; AYW33971.1; AZP54019.1; CBW46680.1; QBH90502.1; QBH90687.1; SPS73437.1	FR682468, LS478113, MG939583, MG939589, MH910495, MK128995, MK333180, MK333181	300 Multigene
35	MGF 360-8L	23.100–24.059	960	reverse	AXZ95794.1; AXZ95982.1; AXZ96077.1; AYW33972.1; CBW46681.1; QBH90503.1; QBH90688.1; SPS73438.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	360 Multigene
36	MGF 360-9L	24.221–25.273	1.053	reverse	AYW33988.1; AZP54012.1; CBW46682.1; QBH90504.1; QBH90689.1	FR682468, MH910495, MK128995, MK333180, MK333181	360 Multigene
37	MGF 360-10L	25.459–26.496	1.038	reverse	AZP54014.1; CBW46683.1; SPS73440.1	FR682468, LS478113, MH910495	360 Multigene
38	MGF 360-11L	26.523–27.584	1.062	reverse	AXZ95797.1; AXZ95985.1; AXZ96080.1; AYW33990.1; CBW46684.1; QBH90506.1; QBH90691.1; SPS73441.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	360 Multigene
39	MGF 505-1R	27.792–29.387	1.596	forward	AXZ95798.1; AXZ95986.1; AXZ96081.1; AYW33991.1; AZP53979.1; CBW46685.1; QBH90507.1; QBH90692.1; SPS73442.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	505 Multigene
40	MGF 360-12L	29.440–30.492	1.053	reverse	AXZ95799.1; AXZ95987.1; AXZ96082.1; AYW33992.1; AZP54013.1; CBW46686.1; QBH90508.1; QBH90693.1; SPS73443.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene
41	MGF 360-13L	30.653–31.714	1.062	reverse	AXZ95800.1; AXZ95988.1; AXZ96083.1; AYW33993.1; AZP54011.1; CBW46687.1; QBH90509.1; QBH90694.1; SPS73444.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene
42	MGF 360-14L	31.899–32.972	1.074	reverse	AXZ95801.1; AXZ95989.1; AXZ96084.1; AYW33994.1; AZP54006.1; CBW46688.1; QBH90510.1; QBH90695.1; SPS73445.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database that are 100% identical to that encoded by said ORF	Function
43	MGF 505-2R	33.178–34.758	1.581	forward	AXZ95802.1; AXZ95990.1; AXZ96085.1; AYW33995.1; AZP53983.1; CBW46689.1; QBH90511.1; QBH90696.1; SPS73446.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	505 Multigene
44	MGF 505-3R	34.845–35.687	843	forward	AXZ95803.1; AXZ95991.1; AXZ96086.1; AYW33996.1; AZP54031.1; CBW46690.1; QBH90512.1; QBH90697.1; SPS73447.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	505 Multigene
45	ASFV G ACD 00520	35.765–35.887	123	reverse	AYW33997.1; AZP54133.1; CBW46691.1; QBH90513.1; QBH90698.1; SPS73448.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_Final_2-049
46	MGF 505-4R	35.855–37.375	1.521	forward	AXZ95993.1; AXZ96088.1; AYW33998.1; AZP53986.1; CBW46692.1; QBH90514.1; QBH90699.1; SPS73449.1	FR682468, LS478113, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	505 Multigene
47	MGF 505-5R	37.404–38.900	1.497	forward	AYW33999.1; AZP53988.1; CBW46693.1; QBH90515.1; QBH90700.1; SPS73450.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	505 Multigene
48	MGF 505-6R	39.101–40.678	1.578	forward	AXZ95807.1; AXZ95995.1; AXZ96090.1; AYW34000.1; AZP53984.1; CBW46694.1; QBH90516.1; QBH90701.1; SPS73451.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	505 Multigene
49	MGF 505-7R	40.808–42.391	1.584	forward	AYW34001.1; AZP53982.1; CBW46695.1; QBH90517.1; QBH90702.1; SPS73452.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	505 Multigene
50	MGF 505-9R	42.695–44.215	1.521	forward	AXZ95808.1; AXZ95996.1; AXZ96091.1; AYW34002.1; QBH90518.1; QBH90703.1; SPS73453.1	LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown
51	MGF 505-10R	44.627–46.255	1.629	forward	AXZ95809.1; AXZ95997.1; AXZ96092.1; AYW34003.1; AZP53977.1; CBW46697.1; QBH90519.1; QBH90704.1; SPS73454.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	505 Multigene
52	A224L	46.372–47.046	675	reverse	AXZ95810.1; AXZ95998.1; AXZ96093.1; AYW34004.1; CBW46698.1; QBH90520.1; QBH90705.1; SPS73455.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	IAP homolog
53	ASFV G ACD 00600	47.085–47.237	153	reverse	AYW34005.1; AZP54121.1; CBW46699.1; QBH90521.1; QBH90706.1; SPS73456.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_final-055
54	A104R	47.407–47.721	315	forward	AXZ95811.1; AXZ95999.1; AXZ96094.1; AYW34006.1; AZP54097.1; CBW46700.1; QBH90522.1; QBH90707.1; SPS73457.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Histone like structural protein
55	A240L	47.718–48.428	711	reverse	AXZ95812.1; AXZ96000.1; AXZ96095.1; AYW34007.1; AZP54044.1; CBW46701.1; QBH90523.1; QBH90708.1; SPS73458.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Thymidylate kinase
56	A118R	48.34–48.522	183	forward	AYW34008.1; AZP54117.1; CBW46702.1; QBH90524.1; QBH90709.1; SPS73459.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-A118R)

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TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
57	A151R	48.737–49.192	456	forward	AXZ95813.1; AXZ96001.1; AXZ96096.1; AYW34009.1; AZP54071.1; QBH90525.1; QBH90710.1; SPS73460.1	LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown
58	MGF 360-15R	49.431–50.300	870	forward	AXZ95814.1; AXZ96002.1; AXZ96097.1; AZP54030.1; CBW46704.1; SPS73461.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495	360 Multigene
59	A238L	50.536–51.216	681	reverse	AYW34011.1; AZP54046.1; CBW46705.1; QBH90527.1; QBH90712.1; SPS73462.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	IkB-like protein
60	A859L	51.266–53.842	2.577	reverse	AXZ95816.1; AXZ96004.1; AXZ96099.1; AYW34012.1; AZP53972.1; CBW46706.1; QBH90528.1; QBH90713.1	FR682468, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Helicase (BA71V-A859L)
61	A179L	53.844–54.383	540	reverse	AXZ95817.1; AXZ96005.1; AXZ96100.1; AYW34013.1; AZP54060.1; CBW46707.1; QBH90529.1; QBH90714.1; SPS73464.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	bcl-2-bax homolog
62	A137R	54.616–55.029	414	forward	AXZ95818.1; AXZ96006.1; AXZ96101.1; AYW34014.1; AZP54077.1; CBW46708.1; QBH90530.1; QBH90715.1; SPS73465.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-A137R)
63	F317L	55.062–56.015	954	reverse	AYW34015.1; AZP54023.1; CBW46709.1; QBH90531.1; QBH90716.1; SPS73466.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-F317L)
64	F334L	56.041–57.045	1.005	reverse	AXZ95820.1; AXZ96008.1; AXZ96103.1; AYW34016.1; AZP54018.1; CBW46710.1; QBH90532.1; QBH90717.1; SPS73467.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Ribonucleotide reductase small subunit
65	F778R	57.066–59.402	2.337	forward	AXZ95821.1; AXZ96009.1; AXZ96104.1; AYW34017.1; CBW46711.1; QBH90533.1; QBH90718.1; SPS73468.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	Ribonucleotide reductase large subunit
66	F165R	59.435–59.932	498	forward	AXZ95822.1; AXZ96010.1; AXZ96105.1; AYW34018.1; CBW46712.1; QBH90534.1; QBH90719.1; SPS73469.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-F165R)
67	F1055L	59.919–63.065	3.147	reverse	AXZ95823.1; AXZ96011.1; AXZ96106.1; AYW34019.1; AZP53968.1; CBW46713.1; QBH90535.1; QBH90720.1; SPS73470.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Helicase/Probable origin binding protein (BA71V-F1055L)
68	K205R	63.259–63.876	618	forward	AXZ95824.1; AXZ96012.1; AXZ96107.1; AYW34020.1; AZP54051.1; CBW46714.1; QBH90536.1; QBH90721.1; SPS73471.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-K205R)
69	K78R	63.965–64.201	237	forward	AYW34021.1; AZP54107.1; CBW46715.1; QBH90537.1; QBH90722.1; SPS73472.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	DNA binding p10

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database that are 100% identical to that encoded by said ORF	Function
70	K196R	64.198–64.788	591	forward	AXZ95826.1; AXZ96014.1; AXZ96109.1; AYW34022.1; AZP54055.1; CBW46716.1; QBH90538.1; QBH90723.1; SPS73473.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Thymidine kinase
71	K145R	64.804–65.241	438	forward	AYW34023.1; CBW46717.1; QBH90539.1; QBH90724.1; SPS73474.1	FR682468, LS478113, MK128995, MK333180, MK333181	unknown (BA71V-K145R)
72	K421R	65.275–66.543	1.269	forward	AXZ95828.1; AXZ96016.1; AXZ96111.1; AYW34024.1; AZP53994.1; CBW46718.1; QBH90540.1; QBH90725.1; SPS73475.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-K421R)
73	EP1242L	66.584–70.312	3.729	reverse	AXZ95829.1; AXZ96017.1; AXZ96112.1; AYW34025.1; AZP53964.1; CBW46719.1; QBH90541.1; QBH90726.1; SPS73476.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	RNApol2
74	EP84R	70.391–70.645	255	forward	AYW34026.1; CBW46720.1; QBH90542.1; QBH90727.1; SPS73477.1	FR682468, LS478113, MK128995, MK333180, MK333181	unknown (BA71V-EP84R)
75	EP424R	70.681–71.937	1.257	forward	AXZ95830.1; AXZ96018.1; AXZ96113.1; AYW34027.1; AZP53996.1; CBW46721.1; QBH90543.1; QBH90728.1; SPS73478.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-EP424R)
76	EP152R	72.431–72.889	459	forward	AXZ95831.1; AXZ96019.1; AXZ96114.1; AYW34028.1; AZP54070.1; CBW46722.1; QBH90544.1; QBH90729.1; SPS73479.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-EP152R)
77	EP153R	72.892–73.368	477	forward	AXZ95832.1; AXZ96020.1; AXZ96115.1; AYW34029.1; AZP54069.1; CBW46723.1; QBH90545.1; QBH90730.1; SPS73480.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Lectin like protein
78	EP402R	73.438–74.520	1.083	forward	AXZ95833.1; AXZ96021.1; AXZ96116.1; AYW34030.1; AZP54004.1; CBW46724.1; QBH90546.1; QBH90731.1; SPS73481.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	CD2v like protein (EP402R)
79	EP364R	74.590–75.699	1.11	forward	AXZ95834.1; AXZ96022.1; AXZ96117.1; AYW34031.1; CBW46725.1; QBH90547.1; QBH90732.1; SPS73482.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-EP364R)
80	M1249L	75.763–79.512	3.75	reverse	AXZ95835.1; AXZ96023.1; AXZ96118.1; AYW34032.1; AZP53963.1; CBW46726.1; QBH90548.1; QBH90733.1; SPS73483.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-M1249L)
81	M448R	79.552–80.898	1.347	forward	AXZ95836.1; AXZ96024.1; AXZ96119.1; AYW34033.1; AZP53991.1; CBW46727.1; QBH90549.1; QBH90734.1; SPS73484.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-M448R)
82	C129R	80.985–81.374	390	forward	AXZ95837.1; AXZ96025.1; AXZ96120.1; AYW34034.1; AZP54078.1; CBW46728.1; QBH90550.1; QBH90735.1; SPS73485.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-C129R)

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
83	C84L	81.422–81.676	255	reverse	AYW34035.1; QBH90551.1; QBH90736.1; SPS73486.1	LS478113, MK128995, MK333180, MK333181	unknown
84	C717R	82.156–84.309	2.154	forward	AXZ95839.1; AXZ96027.1; AXZ96122.1; AZP53974.1; CBW46730.1; QBH90552.1; QBH90737.1; SPS73487.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK333180, MK333181	unknown (BA71V-C717R)
85	C122R	84.296–84.613	318	forward	AXZ95840.1; AXZ96028.1; AXZ96123.1; AYW34036.1; CBW46731.1; QBH90553.1; QBH90738.1; SPS73488.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-C122R)
86	C257L	85.026–85.799	774	reverse	AXZ95841.1; AXZ96029.1; AXZ96124.1; AYW34037.1; AZP54037.1; CBW46732.1; QBH90554.1; QBH90739.1; SPS73489.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-C257L)
87	C475L	85.778–87.205	1.428	reverse	AXZ95842.1; AXZ96030.1; AXZ96125.1; AYW34038.1; AZP53989.1; CBW46733.1; QBH90555.1; QBH90740.1; SPS73490.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-C475L)
88	C315R	87.258–88.205	948	forward	AXZ95843.1; AXZ96031.1; AXZ96126.1; AYW34039.1; CBW46734.1; QBH90556.1; QBH90741.1; SPS73491.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-C315R)
89	C147L	88.273–88.716	444	reverse	AXZ95844.1; AXZ96032.1; AXZ96127.1; AYW34040.1; AZP54072.1; CBW46735.1; QBH90557.1; QBH90742.1; SPS73492.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	RNApol subunit6
90	BA71V-C62L; C62L	88.876–89.064	189	reverse	AYZ2262.1; AJZ77191.1; AOO54406.1; AYW34041.1; AZP54115.1; CAN10170.1; CBH29171.1; CBW46736.1; QBH90558.1; QBH90743.1; SPS73493.1	AM712239, FN557520, FR682468, KM102979, KM262844, KX354450, LS478113, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-C62L)
91	C962R	89.146–92.034	2.889	forward	AXZ95845.1; AXZ96033.1; AXZ96128.1; AYW34042.1; AZP53969.1; CBW46737.1; QBH90559.1; QBH90744.1; SPS73494.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Putative DNA primase
92	ACD 01020; ASFV G ACD 01020	91.985–92.143	159	reverse	AXZ95846.1; AXZ96034.1; AXZ96129.1; AYW34043.1; AZP54120.1; CBW46738.1; QBH90560.1; QBH90745.1; SPS73495.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia, final-099
93	B962L	92.172–95.060	2.889	reverse	AXZ95847.1; AXZ96035.1; AXZ96130.1; AYW34044.1; AZP53970.1; CBW46739.1; QBH90561.1; QBH90746.1; SPS73496.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	RNA helicase (BA71V-B962L)
94	B119L	95.020–95.379	360	reverse	AXZ95848.1; AXZ96036.1; AXZ96131.1; AYW34045.1; AZP54091.1; CBW46740.1; QBH90562.1; QBH90747.1; SPS73497.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B119L)

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database that are 100% identical to that encoded by said ORF	Function
95	B318L	95.360–96.316	957	reverse	AYW34046.1; AZP54022.1; CBW46741.1; QBH90563.1; QBH90748.1; SPS73498.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	Prenyltransferase
96	B438L	96.283–97.599	1.317	reverse	AXZ95850.1; AXZ96038.1; AXZ96133.1; AYW34047.1; AZP53992.1; CBW46742.1; QBH90564.1; QBH90749.1; SPS73499.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B438L)
97	B169L	97.612–98.106	495	reverse	AXZ95851.1; AXZ96039.1; AXZ96134.1; AYW34048.1; AZP54068.1; CBW46743.1; QBH90565.1; QBH90750.1; SPS73500.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B169L)
98	B475L	98.123–99.550	1.428	reverse	AXZ95852.1; AXZ96040.1; AXZ96135.1; AYW34049.1; AZP53990.1; CBW46744.1; QBH90566.1; QBH90751.1; SPS73501.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B475L)
99	B354L	99.685–100.749	1.065	reverse	AXZ95853.1; AXZ96041.1; AXZ96136.1; AYW34050.1; AZP54009.1; CBW46745.1; QBH90567.1; QBH90752.1; SPS73502.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B354L)
100	B602L	100.76–102.352	1.593	reverse	AXZ95854.1; AXZ96042.1; AXZ96137.1; AYW34051.1; AZP53980.1; CBW46746.1; QBH90568.1; QBH90753.1; SPS73503.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B602L)
101	B385R	102.407–103.564	1.158	forward	AXZ95855.1; AXZ96043.1; AXZ96138.1; AYW34052.1; CBW46747.1; QBH90569.1; QBH90754.1; SPS73504.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-B385R)
102	B646L	103.661–105.601	1.941	reverse	AXZ95856.1; AXZ96044.1; AXZ96139.1; AYW34053.1; AZP53976.1; CBW46748.1; QBH90570.1; QBH90755.1; SPS73505.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	Structural protein p72
103	B125R	105.641–106.018	378	forward	AXZ95857.1; AXZ96045.1; AXZ96140.1; AYW34054.1; AZP54081.1; CBW46749.1; QBH90571.1; QBH90756.1; SPS73506.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B125R)
104	B117L	105.991–106.338	348	reverse	AXZ95858.1; AXZ96046.1; AXZ96141.1; AYW34055.1; AZP54093.1; CBW46750.1; QBH90572.1; QBH90757.1; SPS73507.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B117L)
105	B407L	106.345–107.583	1.239	reverse	AXZ95859.1; AXZ96047.1; AXZ96142.1; AYW34056.1; AZP53997.1; CBW46751.1; QBH90573.1; QBH90758.1; SPS73508.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B407L)
106	B175L	107.611–108.138	528	reverse	AXZ95860.1; AXZ96048.1; AXZ96143.1; AYW34057.1; AZP54062.1; CBW46752.1; QBH90574.1; QBH90759.1; SPS73509.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B175L)

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
107	B263R	108.185–108.976	792	forward	AXZ95861.1; AXZ96049.1; AXZ96144.1; AYW34058.1; AZP54036.1; CBW46753.1; QBH90575.1; QBH90760.1; SPS73510.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B263R)
108	B66L	108.973–109.173	201	reverse	AXZ95862.1; AXZ96050.1; AXZ96145.1; AYW34059.1; AZP54111.1; CBW46754.1; QBH90576.1; QBH90761.1; SPS73511.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-B66L)
109	G1340L	109.179–113.201	4.023	reverse	AXZ95863.1; AXZ96051.1; AXZ96146.1; AYW34060.1; CBW46755.1; QBH90577.1; QBH90762.1; SPS73512.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-G1340L)
110	G1211R	113.242–116.862	3.621	forward	AXZ95864.1; AXZ96052.1; AXZ96147.1; AYW34061.1; AZP53965.1; CBW46756.1; QBH90578.1; QBH90763.1; SPS73513.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	DNApol
111	CP123L	116.859–117.227	369	reverse	AXZ95865.1; AXZ96053.1; AXZ96148.1; AYW34062.1; AZP54086.1; CBW46757.1; QBH90579.1; QBH90764.1; SPS73514.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-CP123L)
112	CP2475L	117.333–124.763	7.431	reverse	AXZ95866.1; AXZ96054.1; AXZ96149.1; AYW34063.1; CBW46758.1; QBH90580.1; QBH90765.1; SPS73515.1	FR682468, LS478113, MG939583, MG939587, MG939588, MK128995, MK333180, MK333181	220kDa Polyprotein
113	CP204L	124.867–125.451	585	reverse	AXZ95867.1; AXZ96055.1; AXZ96150.1; AYW34064.1; AZP54056.1; QBH90581.1; QBH90766.1; SPS73516.1	LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	unknown
114	CP530R	125.482–127.074	1.593	forward	AXZ95868.1; AXZ96056.1; AXZ96151.1; AYW34065.1; AZP53981.1; CBW46760.1; QBH90582.1; QBH90767.1; SPS73517.1	FR682468, LS478113, MG939583, MG939587, MG939588, MH910495, MK128995, MK333180, MK333181	60kDa Polyprotein
115	CP80R	127.077–127.319	243	forward	AYW34066.1; AZP54105.1; CBW46761.1; QBH90583.1; QBH90768.1; SPS73518.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	RNApol subunit10
116	CP312R	127.361–128.284	924	forward	AYW34067.1; AZP54025.1; CBW46762.1; QBH90584.1; QBH90769.1; SPS73519.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-CP312R)
117	O174L	128.305–128.829	525	reverse	AXZ95871.1; AXZ96154.1; AZP54063.1; CBW46763.1; QBH90585.1; QBH90770.1; SPS73520.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK333180, MK333181	DNApol beta like protein
118	O61R	128.879–129.064	186	forward	AXZ95872.1; AXZ96155.1; AYW34069.1; AZP54116.1; CBW46764.1; QBH90586.1; QBH90771.1; SPS73521.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Attachment protein p12
119	NP1450L	129.144–133.526	4.383	reverse	AXZ95873.1; AXZ96156.1; AZP53961.1; CBW46765.1; SPS73522.1	FR682468, LS478113, MG939583, MG939588, MH910495	RNApol1

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TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database that are 100% identical to that encoded by said ORF	Function
120	NP419L	133.579–134.838	1.26	reverse	AXZ95874.1; AXZ96157.1; AYW34071.1; QBH90588.1; QBH90773.1; SPS73523.1	LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	unknown
121	NP868R	134.903–137.509	2.607	forward	AXZ95875.1; AXZ96158.1; AYW34072.1; AZP53971.1; CBW46767.1; QBH90589.1; QBH90774.1; SPS73524.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Guanylyltransferase
122	D205R; D250R	137.566–138.318	753	forward	AXZ95876.1; AXZ96159.1; AYW34073.1; AZP54038.1; CBW46768.1; QBH90590.1; QBH90775.1; SPS73525.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	8-Hydroxy-dGTPase
123	D129L	138.498–138.887	390	reverse	AXZ95877.1; AXZ96160.1; AYW34074.1; AZP54079.1; CBW46769.1; QBH90591.1; QBH90776.1; SPS73526.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-D129L)
124	BA71V-D79L (g7L); D79L; DP79L	138.960–139.199	240	reverse	AYZ2295.1; AJZ77183.1; AOO54461.1; AXZ95878.1; AXZ96161.1; AYW34075.1; AZP54106.1; CAN10203.1; CBH29204.1; CBW46770.1; QBH90592.1; QBH90777.1; SPS73527.1	AM712239, FN557520, FR682468, KM102979, KM262844, KX354450, LS478113, MG939583, MG939588, MH910495, MK128995, MK333181	unknown (BA71V-D79L)
125	D339L	139.268–140.287	1.02	reverse	AXZ95879.1; AXZ96162.1; AYW34076.1; AZP54016.1; CBW46771.1; QBH90593.1; QBH90778.1; SPS73528.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-D339L)
126	D1133L	140.419–143.820	3.402	reverse	AXZ95880.1; AXZ96163.1; AYW34077.1; CBW46772.1; SPS73529.1	FR682468, LS478113, MG939583, MG939588, MK128995	Helicase (BA71V-D1133L)
127	D117L	144.051–144.404	354	reverse	AXZ95881.1; AXZ96164.1; AYW34078.1; AZP54092.1; CBW46773.1; QBH90595.1; QBH90780.1; SPS73530.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Structural protein p17
128	D205R 1; D205R	144.461–145.078	618	forward	AXZ95882.1; AXZ96165.1; AYW34079.1; AZP54052.1; CBW46774.1; QBH90596.1; QBH90781.1; SPS73531.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	RNApol subunit5
129	D205R; D345L	145.105–146.142	1.038	reverse	AXZ95883.1; AXZ96166.1; AYW34080.1; AZP54015.1; CBW46775.1; QBH90597.1; QBH90782.1; SPS73532.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-D345L)
130	S183L	146.142–146.693	552	reverse	AYW34081.1; AZP54059.1; CBW46776.1; QBH90598.1; QBH90783.1; SPS73533.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-S183L)
131	S273R	146.754–147.575	822	forward	AXZ95884.1; AXZ96167.1; AYW34082.1; AZP54033.1; CBW46777.1; QBH90599.1; QBH90784.1; SPS73534.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-S273R)
132	P1192R	147.610–151.188	3.579	forward	AXZ95885.1; AXZ96168.1; AYW34083.1; AZP53966.1; CBW46778.1; QBH90600.1; QBH90785.1; SPS73535.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Topoisomerase II

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
133	H359L	151.220–152.299	1.08	reverse	AXZ95886.1; AXZ96169.1; AYW34084.1; AZP54005.1; CBW46779.1; QBH90601.1; QBH90786.1; SPS73536.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	RNA pol subunit 3
134	H171R	152.334–152.849	516	forward	AXZ95887.1; AXZ96170.1; AYW34085.1; AZP54064.1; CBW46780.1; QBH90602.1; QBH90787.1; SPS73537.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-H171R)
135	BA71V-H124R; H124R	152.889–153.263	375	forward	AIY22306.1; AJZ77164.1; AOO54481.1; AXZ95888.1; AXZ96171.1; AYW34086.1; AZP54085.1; CAN10215.1; CBH29215.1; CBW46781.1; QBH90603.1; QBH90788.1; SPS73538.1	AM712239, FN557520, FR682468, KM102979, KM262844, KX354450, LS478113, MG939583, MG939588, MH910495, MK128995, MK333181	unknown (BA71V-H124R)
136	H339R	153.286–154.305	1.02	forward	AXZ95889.1; AXZ96172.1; AYW34087.1; AZP54017.1; CBW46782.1; QBH90604.1; QBH90789.1; SPS73539.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-H339R)
137	H108R	154.317–154.643	327	forward	AXZ95890.1; AXZ96173.1; AYW34088.1; AZP54095.1; CBW46783.1; QBH90605.1; QBH90790.1; SPS73540.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-H108R)
138	H233R	154.603–155.304	702	forward	AXZ95891.1; AXZ96174.1; AYW34089.1; CBW46784.1; QBH90606.1; QBH90791.1; SPS73541.1	FR682468, LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-H233R)
139	H240R	155.419–156.144	726	forward	AXZ95892.1; AXZ96175.1; AYW34090.1; CBW46785.1; QBH90607.1; QBH90792.1; SPS73542.1	FR682468, LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-H240R)
140	R298L	156.137–157.033	897	reverse	AXZ95893.1; AXZ96176.1; AYW34091.1; AZP54027.1; CBW46786.1; QBH90608.1; QBH90793.1; SPS73543.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Serine protein kinase
141	Q706L	157.008–159.128	2.121	reverse	AXZ95894.1; AXZ96177.1; AYW34092.1; AZP53975.1; CBW46787.1; QBH90609.1; QBH90794.1; SPS73544.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Helicase (BA71V-Q706L)
142	QP509L	159.086–160.615	1.530	reverse	AXZ95895.1; AXZ96178.1; AYW34093.1; AZP53985.1; CBW46788.1; QBH90610.1; QBH90795.1; SPS73545.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Helicase (BA71V-QP509L)
143	QP383R	160.605–161.756	1.152	forward	AXZ95896.1; AXZ96179.1; AYW34094.1; AZP54000.1; QBH90611.1; QBH90796.1; SPS73546.1	LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database that are 100% identical to that encoded by said ORF	Function
144	E184L	161.704–162.258	555	reverse	AYW34095.1; AZP54057.1; CBW46790.1; QBH90612.1; QBH90797.1; SPS73547.1	FR682468, LS478113, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-E184L)
145	E183L	162.302–162.856	555	reverse	AXZ95897.1; AXZ96180.1; AYW34096.1; CBW46791.1; QBH90613.1; QBH90798.1; SPS73548.1	FR682468, LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-E183L)
146	E423R	162.887–164.158	1.272	forward	AXZ95898.1; AXZ96181.1; AYW34097.1; CBW46792.1; QBH90614.1; QBH90799.1; SPS73549.1	FR682468, LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-E423R)
147	E301R	164.309–165.214	906	forward	AXZ95899.1; AXZ96182.1; AYW34098.1; AZP54026.1; CBW46793.1; QBH90615.1; QBH90800.1; SPS73550.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Proliferating cell nuclear antigen
148	E146L	165.248–165.688	441	reverse	AXZ95900.1; AXZ96183.1; AYW34099.1; AZP54073.1; CBW46794.1; QBH90616.1; QBH90801.1; SPS73551.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-E146L)
149	E199L	165.925–166.524	600	reverse	AXZ96184.1; AYW34100.1; CBW46795.1; QBH90617.1; QBH90802.1; SPS73552.1	FR682468, LS478113, MG939588, MK128995, MK333180, MK333181	unknown (BA71V-E199L)
150	E165R	166.552–167.049	498	forward	AXZ95902.1; AXZ96185.1; AYW34101.1; AZP54067.1; CBW46796.1; QBH90618.1; QBH90803.1; SPS73553.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	dUTPase
151	E248R	167.072–167.818	747	forward	AXZ95903.1; AXZ96186.1; AYW34102.1; AZP54039.1; CBW46797.1; QBH90619.1; QBH90804.1; SPS73554.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-E248R)
152	E120R	167.860–168.228	369	forward	AXZ95904.1; AXZ96187.1; AYW34103.1; AZP54087.1; CBW46798.1; QBH90620.1; QBH90805.1; SPS73555.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	DNA-binding structural protein p14.5
153	EP296R	168.258–169.148	891	forward	AXZ95905.1; AXZ96188.1; AYW34104.1; AZP54028.1; CBW46799.1; QBH90621.1; QBH90806.1; SPS73556.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	AP endonuclease class II
154	E111R	169.151–169.486	336	forward	AXZ95906.1; AXZ96189.1; AYW34105.1; AZP54094.1; CBW46800.1; QBH90622.1; QBH90807.1; SPS73557.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-E111R)
155	E66L	169.569–169.721	153	reverse	AXZ95907.1; AXZ96190.1; AYW34106.1; AZP54122.1; CBW46801.1; QBH90623.1; QBH90808.1; SPS73558.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-E66L)
156	I267L	169.725–170.528	804	reverse	AXZ95908.1; AXZ96191.1; AYW34107.1; QBH90624.1; QBH90809.1; SPS73559.1	LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	unknown

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database that are 100% identical to that encoded by said ORF	Function
157	I226R	170.680–171.360	681	forward	AXZ95909.1; AXZ96192.1; AYW34108.1; AZP54047.1; CBW46803.1; QBH90625.1; QBH90810.1; SPS73560.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-I226)
158	I243L	171.357–172.088	732	reverse	AXZ95910.1; AXZ96193.1; AYW34109.1; AZP54040.1; CBW46804.1; QBH90626.1; QBH90811.1; SPS73561.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Transcription factor SII homolog
159	I73R	172.172–172.390	219	forward	AXZ95911.1; AXZ96194.1; AYW34110.1; AZP54108.1; CBW46805.1; QBH90627.1; QBH90812.1; SPS73562.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-I73R)
160	I329L	172.610–173.599	990	reverse	AXZ95768.1; AXZ96060.1; AYW34111.1; AZP54020.1; CBW46806.1; QBH90628.1; QBH90813.1; SPS73563.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-I329L)
161	I215L	173.888–174.526	639	reverse	AXZ95912.1; AXZ96195.1; AYW34112.1; AZP54049.1; CBW46807.1; QBH90629.1; QBH90814.1; SPS73564.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Ubiquitin-conjugation enzyme
162	I177L	174.567–174.767	201	reverse	AXZ95913.1; AXZ96196.1; AYW34113.1; AZP54112.1; CBW46808.1; QBH90630.1; QBH90815.1	FR682468, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-I177L)
163	I196L	175.093–175.701	609	reverse	AXZ95914.1; AXZ96197.1; AYW34114.1; AZP54053.1; CBW46810.1; QBH90632.1; QBH90817.1; SPS73566.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-I196L)
164	DP238L	175.795–176.511	717	reverse	AXZ95915.1; AXZ96198.1; AYW34115.1; AZP54042.1; CBW46811.1; QBH90633.1; QBH90818.1; SPS73567.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-DP238L)
165	DP63R; MGF 360-16R	176.688–177.746	1.059	forward	AXZ96199.1; AYW34116.1; QBH90634.1; QBH90819.1; SPS73568.1	LS478113, MG939588, MK128995, MK333180, MK333181	unknown
166	MGF 505-11L	177.826–179.454	1.629	reverse	AXZ95917.1; AXZ96200.1; AYW34117.1; CBW46814.1; QBH90635.1; QBH90820.1; SPS73569.1	FR682468, LS478113, MG939583, MG939588, MK128995, MK333180, MK333181	505 Multigene
167	MGF 100-1L	179.573–179.998	426	reverse	AXZ95918.1; AXZ96201.1; AYW34118.1; AZP54075.1; CBW46815.1; QBH90636.1; QBH90821.1; SPS73570.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	100 Multigene
168	MGF 100-3L	180.363–180.671	309	reverse	SPS73571.1	LS478113	unknown

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI data-base encoding proteins 100% identical to that encoded by said ORF	Function
169	I7L	180.770–181.078	309	reverse	AXZ95919.1; AXZ96202.1; AYW34119.1; AZP54099.1; CBW46816.1; QBH90637.1; QBH90822.1; SPS73572.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (Malawi-I8L)
170	I8L	181.292–181.603	312	reverse	AIY22341.1; AJZ777175.1; AOO54525.1; AXZ95920.1; AXZ96203.1; AYW34120.1; AZP54098.1; CAN10249.1; CBH29251.1; CBW46817.1; QBH90638.1; QBH90823.1; SPS73573.1	AM712239, FN557520, FR682468, KM102979, KM262844, KX354450, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (Malawi-I8L)
171	ACD 01870; ASFV G ACD 01870	181.698–181.835	138	forward	AXZ95921.1; AXZ96204.1; AYW34121.1; AZP54126.1; CBW46818.1; QBH90639.1; QBH90824.1; SPS73574.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_ final-182
172	I9R	181.798–182.088	291	forward	AXZ95922.1; AXZ96205.1; AYW34122.1; AZP54100.1; CBW46819.1; QBH90640.1; QBH90825.1; SPS73575.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (Malawi-19R)
173	I10L	182.164–182.676	513	reverse	AXZ95923.1; AXZ96206.1; AYW34123.1; AZP54065.1; CBW46820.1; QBH90641.1; QBH90826.1; SPS73576.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	Structural protein p22
174	L11L; L11L EST-A; L11L EST-B	182.915–183.196	282	reverse	AXZ95924.1; AXZ96207.1; AYW34124.1; AZP54102.1; CBW46821.1; QBH90642.1; QBH90827.1; SPS73425.1; SPS73577.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (Warthog-111L)
175	MGF 360-18R; MGF 360-18R EST-A; MGF 360-18R EST-B	183.426–184.139	714	forward	AXZ95925.1; AXZ96208.1; AYW34125.1; AZP54043.1; CBW46822.1; QBH90643.1; QBH90828.1; SPS73424.1; SPS73578.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene
176	DP71L; DP71L EST-A; DP71L EST-B	184.122–184.334	213	reverse	AXZ95926.1; AXZ96209.1; AYW34126.1; AZP54109.1; CBW46823.1; QBH90644.1; QBH90829.1; SPS73423.1; SPS73579.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-I14L)
177	DP71L	184.408–184.434	27	reverse	AOO54533.1	KX354450	unknown
178	DP96R; DP96R EST-A; DP96R EST-B	184.433–184.723	291	forward	AXZ95927.1; AXZ96210.1; AYW34127.1; AZP54101.1; CBW46824.1; QBH90645.1; QBH90830.1; SPS73422.1; SPS73580.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	unknown (BA71V-DP96R)
179	ASFV G ACD 01940; ASFV G ACD 01940 EST-A; ASFV G ACD 01940 EST-B	185.023–185.181	159	reverse	AYW34128.1; QBH90646.1; QBH90831.1; SPS73421.1; SPS73581.1	LS478113, MK128995, MK333180, MK333181	unknown

(Continues)

TABLE 2 (Continued)

#	ORF name	ORF position in genome (nt)	ORF length (bp)	ORF direction	Proteins found in NCBI database that are 100% identical to that putatively encoded by said ORF	DNA sequences found in NCBI database encoding proteins 100% identical to that encoded by said ORF	Function
180	ACD 01940	185.153–185.260	108	forward	AXZ95928.1; AXZ96211.1	MG939583, MG939588	unknown
181	MGF 360-19R EST-A; MGF 360-19R EST-B	185.334–186.143	810	forward	SPS73420.1; SPS73582.1	LS478113	unknown
182	ACD 01960; ASFV G ACD 01960; ASFV G ACD 01960 EST-A; ASFV G ACD 01960 EST-B	186.495–186.626	132	reverse	AXZ95929.1; AXZ96212.1; AYW34129.1; AZP54128.1; CBW46826.1; QBH90647.1; QBH90832.1; SPS73419.1; SPS73583.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_Final_2-187
183	MGF 360-21R; MGF 360-21R EST-A; MGF 360-21R EST-B	187.072–188.142	1,071	forward	AXZ95930.1; AXZ96213.1; AYW34130.1; AZP54008.1; CBW46827.1; QBH90648.1; QBH90833.1; SPS73418.1; SPS73584.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	360 Multigene
184	ACD 01980; ASFV G ACD 01980; ASFV G ACD 01980 EST-A; ASFV G ACD 01980 EST-B	188.131–188.325	195	reverse	AXZ95931.1; AXZ96214.1; AZP54113.1; CBW46828.1; SPS73417.1; SPS73585.1	FR682468, LS478113, MG939583, MG939588, MH910495	ASFV-Georgia_Final_2-189
185	ACD 01990; ASFV G ACD 01990; ASFV G ACD 01990 EST-A; ASFV G ACD 01990 EST-B	188.832–188.978	147	reverse	AXZ95932.1; AXZ96215.1; AYW34131.1; AZP54124.1; CBW46829.1; QBH90649.1; QBH90834.1; SPS73416.1; SPS73586.1	FR682468, LS478113, MG939583, MG939588, MH910495, MK128995, MK333180, MK333181	ASFV-Georgia_final-194
186	DP60R; DP60R EST-A; DP60R EST-B	189.099–189.278	180	forward	AXZ95933.1; AXZ96216.1; QBH90650.1; QBH90835.1; SPS73415.1; SPS73587.1	LS478113, MG939583, MG939588, MK333180, MK333181	unknown

Abbreviations: ORF, open reading frame.

TABLE 3 Variations detected between ASFV Belgium/Etalle/wb/2018 and other genotype II virulent strains

Belgium/Etalle/wb/2018	Georgia/2007/1	Russia/Odintsovo/02/14	Poland/2015/Podlaskie	China/2018/AnhuiXCGQ
Annotation (ORF position)	Genome position ^{a,b} and type of modification			
N.C.G.R.	0 ins TTGTAACAACATTTTTTTT CGATCGGCAATAGATAAGTA	0 ins TTGTAACAACATTTTTTTT CGATCGGCAATAGATAAGTAG	0 ins TTGTAACAACATTTTTTTT CGATCGGCAATAGATAAGTA	0 ins TTGTAACAACATTTTTTTT CGATCGGCAATAGATAAGTAGA
N.C.G.R.	98_99 ins A	97_98 ins A	98_99 ins A	97_98 ins A
N.C.G.R.	405_406 ins A	404_405 ins A	N.A.	N.A.
N.C.G.R.	423_424 ins C	N.A.	424_425 del C	422_423 ins CC
N.C.G.R.	433_434 ins T	N.A.	N.A.	N.A.
N.C.G.R.	440_441 ins A	N.A.	N.A.	N.A.
N.C.G.R.	N.A.	791_792 ins A	N.A.	N.A.
MGF_360-1L (896 ← 1729)	1601_1604 del TT	N.A.	N.A.	N.A.
MGF_360-1L (896 ← 1729)	1620_1621 ins T	N.A.	N.A.	N.A.
N.C.G.R.	N.A.	1994_1995 ins TT	N.A.	1994_1995 ins T
MGF_360-2L (2063 ← 3184)	N.A.	2114_2115 ins T	N.A.	N.A.
N.C.G.R.	3238_3239 ins A	3235_3236 ins A	N.A.	N.A.
N.C.G.R.	3854_3855 ins A	3851_3852 ins A	N.A.	N.A.
L83L (3962 ← 4207)	N.A.	4106_4108 del T	N.A.	N.A.
N.C.G.R.	5662_5663 ins A	N.A.	N.A.	N.A.
N.C.G.R.	N.A.	N.A.	5819_5821 del T	N.A.
N.C.G.R.	5863_5865 ins A	N.A.	N.A.	N.A.
MGF_110-1L (6141 ← 6731)	C6095T	N.A.	C6104T	N.A.
ACD_00120 (7807 → 8031)	7815_7816 ins T	7815_7816 ins T	N.A.	N.A.
ACD_00120 (7807 → 8031)	7934_7935 ins A	N.A.	N.A.	N.A.
N.C.G.R.	8501_8502 ins A	N.A.	N.A.	N.A.
N.C.G.R.	10459_10460 ins A	10461_10462 ins A	N.A.	N.A.
ACD_00190 (11539 ← 11664)	11601_11602 ins A	11603_11604 ins A	11614_11615 ins A	11607_11608 ins A
MGF_110-14L (12836 ← 13654)	13257_13259 del C	13257_13258 ins CC	13268_13269 ins CC	13261_13262 ins CC
ACD_00240 (13653 → 13763)	13657_13658 ins A	13656_13657 ins A	N.A.	N.A.
MGF_110-13L (14289 ← 14858); MGF 110-14L (14746 ← 15117)	14697_14698 ins CCCC	14695_14696 ins CCCCCCCCCC	14707_14708 ins CCCC	14700_14701 ins CCCC
ACD 00270 (15142 ← 15255)	N.A.	15085_15086 ins A	N.A.	N.A.
N.C.G.R.	16653_16655 del G	16645_16646 ins G	16664_16665 del G	16656_16657 ins GG
N.C.G.R.	N.A.	16657_16659 del G	N.A.	N.A.
N.C.G.R.	N.A.	16796_16798 del A	N.A.	N.A.

(Continues)

TABLE 3 (Continued)

Belgium/Etalle/wb/2018	Georgia/2007/1	Russia/Odintsovo/02/14	Poland/2015/Podlaskie	China/2018/AnhuiXCGQ
ACD-00350 (16896 → 17027)	N.A.	16861_16868 del CGGGGG	16880_16883 del GG	16869_16870 ins G
ACD-00350 (16896 → 17027)	N.A.	16880_16882 del C	N.A.	N.A.
N.C.G.R.	18728_18729 ins T	18727_18728 ins T	N.A.	N.A.
N.C.G.R.	N.A.	N.A.	18837_18840 del GG	N.A.
N.C.G.R.	19030_19033 del GG	19029_19032 del GG	19042_19043 ins GGGG	N.A.
N.C.G.R.	19453_19454 ins T	19452_19453 ins T	N.A.	N.A.
N.C.G.R.	20662_20663 ins A	N.A.	N.A.	N.A.
N.C.G.R.	N.A.	20824_20826 del G	20836_20837 ins G	20824_20825 ins G
BA71-J154R; MGF 300-2R; 300-2R (21422 → 21904)	21580_21581 ins A	21581_21582 ins A	N.A.	N.A.
N.C.G.R.	N.A.	21923_21924 ins T	N.A.	N.A.
N.C.G.R.	23019_23020 ins A	23019_23020 ins A	N.A.	N.A.
MGF 360-10L; MGF 360-11L (25459 ← 26496)	N.A.	N.A.	N.A.	C25454T
MGF 360-10L; MGF 360-11L (25459 ← 26496)	N.A.	N.A.	G26050A	N.A.
N.C.G.R.	N.A.	N.A.	26459_26461 del T	26447_26449 del T
N.C.G.R.	31671_31672 ins A	31671_31672 ins A	N.A.	N.A.
MGF 505-2R; BA71-A489R (33178 → 34758)	N.A.	34105_34106 ins A	N.A.	N.A.
ACD 00520 (35765 ← 35887)	N.A.	35777_35778 ins T	N.A.	N.A.
MGF 505-4R; A505R (35855 → 37375)	N.A.	37261_37262 ins A	N.A.	N.A.
N.C.G.R.	39016_39017 ins T	39013_39014 ins T	39031_39033 del T	N.A.
N.C.G.R.	40722_40723 ins T	40719_40720 ins T	N.A.	N.A.
N.C.G.R.	42608_42609 ins T	42605_42606 ins T	N.A.	N.A.
MGF 505-9R; BA71-A506R (42,695 → 44,215)	A43599G	N.A.	A43618G	N.A.
N.C.G.R.	44542_44543 ins T	44539_44540 ins T	N.A.	N.A.
N.C.G.R.	N.A.	46258_46259 ins A	N.A.	N.A.
N.C.G.R.	47319_47320 ins A	N.A.	N.A.	N.A.
N.C.G.R.	48657_48658 ins A	48654_48655 ins A	N.A.	N.A.
A179L; 5-HL; BA71V-A179L (53844 ← 54383)	N.A.	54192_54193 ins T	N.A.	N.A.

(Continues)

TABLE 3 (Continued)

Belgium/Etalle/wb/2018	Georgia/2007/1	Russia/Odintsovo/02/14	Poland/2015/Podlaskie	China/2018/AnhuiXCGQ
F317L; BA71V-F317L (55062 ← 56015)	N.A.	55758_55759 ins T	N.A.	N.A.
N.C.G.R.	55966_55967 ins A	55961_55962 ins A	N.A.	N.A.
F165R; BA71V-F165R (59435 → 59932)	N.A.	59431_59432 ins T	N.A.	N.A.
F1055L (59919 ← 63065)	N.A.	N.A.	A62220T	N.A.
N.C.G.R.	63839_63840 ins T	N.A.	N.A.	N.A.
N.C.G.R.	63855_63856 ins A	N.A.	N.A.	N.A.
N.C.G.R.	63865_63866 ins T	63861_63862 ins T	N.A.	N.A.
N.C.G.R.	63869_63870 ins T	63865_63866 ins T	N.A.	N.A.
K421R; BA71V-K421R (65275 → 66543)	N.A.	66265_66266 ins A	N.A.	N.A.
EP1242L; BA71V-EP1242L (66584 ← 70312)	N.A.	N.A.	A68551G	N.A.
EP424R (70681 → 71937)	N.A.	70833_70834 ins A	N.A.	N.A.
N.C.G.R.	72279_72281 del T	72273_72275 del T	72306_72308 del T	72293_72295 del T
CD2v; EP402R (73438 → 74520)	N.A.	73752_73753 ins A	N.A.	N.A.
EP364R (74590 → 75699)	N.A.	74831_74832 ins A	N.A.	N.A.
M1249L; BA71V-M1249L (75763 ← 79512)	N.A.	79149_79150 ins T	N.A.	N.A.
M448R; BA71V-M448R (79552 → 80898)	N.A.	79635_79636 ins G	N.A.	N.A.
C84L (81422 ← 81676)	81518_81519 ins T	81508_81509 ins T	N.A.	N.A.
N.C.G.R.	81611_81612 ins A	81601_81602 ins A	N.A.	N.A.
B438L; BA71V-B438L (p49) (96283 ← 97599)	N.A.	97124_97125 ins T	N.A.	N.A.
B354L; BA71V-B354L; L09PL (99685 ← 100749)	N.A.	N.A.	A99664G	N.A.
B354L; BA71V-B354L; L09PL (99685 ← 100749)	N.A.	100402_100403 ins T	N.A.	N.A.
B602L; B602L protein (100760 ← 102352)	N.A.	100796_100797 ins T	N.A.	N.A.
N.C.G.R.	N.A.	N.A.	N.A.	102338_102340 del G
N.C.G.R.	N.A.	103570_103571 ins T	N.A.	N.A.

(Continues)

TABLE 3 (Continued)

Belgium/Etalle/wb/2018	Georgia/2007/1	Russia/Odintsovo/02/14	Poland/2015/Podlaskie	China/2018/AnhuiXCGQ
B125R; I09YR; BA71V-B125R (105641 → 106018)	N.A.	105652_105653 ins A	N.A.	N.A.
N.C.G.R.	113162_113163 ins A	N.A.	N.A.	N.A.
G1211R; BA71-G1211R (113242 → 116862)	N.A.	116204_116205 ins A	N.A.	N.A.
G1211R; BA71-G1211R (113242 → 116862)	N.A.	116453_116454 ins A	N.A.	N.A.
N.C.G.R.	117173_117174 ins T	117157_117158 ins T	N.A.	N.A.
N.C.G.R.	124699_124700 ins A	124683_124684 ins A	N.A.	N.A.
CP204L; phosphoprotein p30; BA71-CP204L; C'204L (124867 ← 125451)	124796_124797 ins TT	124780_124781 ins T	N.A.	N.A.
O174L; BA71V-O174L (128305 ← 128829)	N.A.	N.A.	N.A.	A128448G
O174L; BA71V-O174L (128305 ← 128,829)	N.A.	N.A.	N.A.	A128552G
O174L; BA71V-O174L (128305 ← 128829)	N.A.	N.A.	N.A.	A128577G
N.C.G.R.	133458_133459 ins A	133443_133444 ins A	N.A.	N.A.
N.C.G.R.	N.A.	133496_133470 ins T	N.A.	N.A.
NP419L; BA71V-NP419L (g3L) (133579 ← 134838)	T133521C	N.A.	T133556C	N.A.
NP868R; BA71-NP868R; BA71V-NP868R (g4R) (134903 → 137509)	N.A.	135790_135791 ins A	N.A.	N.A.
N.C.G.R.	N.A.	G137442A	N.A.	N.A.
N.C.G.R.	138414_138415 ins T	138397_138398 ins T	N.A.	N.A.
D79L; DP79L; BA71V-D79L (g7L) (138960 ← 139199)	N.A.	139027_139028 ins T	N.A.	N.A.
N.C.G.R.	143750_143751 ins A	143732_143733 ins A	N.A.	N.A.
N.C.G.R.	152788_152789 ins A	152770_152771 ins A	N.A.	N.A.
N.C.G.R.	N.A.	N.A.	T155265C	N.A.
H240R; BA71V-H240R (j7R) (155419 → 156144)	N.A.	N.A.	A155933G	N.A.
QP383R; BA71V-QP383R (j11R) (160605 → 161756)	161244_161246 del A	N.A.	N.A.	N.A.
QP383R; BA71V-QP383R (j11R) (160605 → 161756)	161290_161291 ins A	N.A.	N.A.	N.A.

(Continues)

TABLE 3 (Continued)

Belgium/Etalle/wb/2018	Georgia/2007/1	Russia/Odintsovo/02/14	Poland/2015/Podlaskie	China/2018/AnhuiXCGQ
N.C.G.R.	N.A.	N.A.	T165756C	N.A.
N.C.G.R.	N.A.	N.A.	T165800C	N.A.
N.C.G.R.	N.A.	N.A.	T165818C	N.A.
N.C.G.R.	N.A.	N.A.	T165820C	N.A.
E199L; BA71V-E199L (j18L) (165925 ← 166524)	N.A.	N.A.	T166104C	N.A.
N.C.G.R.	N.A.	166957_166958 ins T	N.A.	N.A.
N.C.G.R.	167754_167755 ins A	167735_167736 ins A	N.A.	N.A.
EP296R; E296R; BA71V-E296R (k4R) (168258 → 169148)	N.A.	168540_168541 ins A	N.A.	N.A.
N.C.G.R.	169454_169455 ins T	169434_169435 ins T	N.A.	N.A.
N.C.G.R.	169455_169456 ins A	T169436A	N.A.	N.A.
I267L; BA71V-I267L (k7L) (169725 ← 170528)	169733_169734 ins T	169714_169715 ins T	N.A.	N.A.
I267L; BA71V-I267L (k7L) (169725 ← 170528)	T169862A	T169843A	T169904A	N.A.
I226R; BA71V-I226R (k8R) (170680 → 171360)	N.A.	171096_171097 ins A	N.A.	N.A.
N.C.G.R.	172008_172009 ins T	171988_171989 ins T	N.A.	N.A.
N.C.G.R.	172380_172381 ins TATATAGGAA	N.A.	172423_172424 ins TATATAGGAA	N.A.
N.C.G.R.	173559_173560 ins A	N.A.	N.A.	N.A.
I177L (174567 ← 175100)	174950_174951 ins A	174941_174942 ins A	N.A.	N.A.
I196L (175093 ← 175701)	N.A.	C175367T	N.A.	N.A.
N.C.G.R.	175623_175624 ins A	175614_175615 ins A	N.A.	N.A.
DP63R; MGF 360-16R; BA71-DP311R (176688 → 177746)	177486_177487 ins A	177477_177478 ins A	N.A.	N.A.
N.C.G.R.	179371_179372 ins A	179362_179363 ins A	N.A.	N.A.
I7L; BA71-M102L (180770 ← 181078)	N.A.	180907_180908 ins T	N.A.	N.A.
I9R; BA71-M98R (181798 → 182088)	N.A.	N.A.	G182013A	N.A.
N.C.G.R.	183302_183303 ins T	N.A.	N.A.	N.A.
N.C.G.R.	183306_183307 ins T	183297_183298 ins T	N.A.	N.A.
DP96R (184433 → 184723)	N.A.	184610_184611 ins A	N.A.	N.A.
ACD 01940 (185023 ← 185181)	184960_184962 del T	N.A.	N.A.	N.A.

(Continues)

TABLE 3 (Continued)

Belgium/Etalle/wb/2018	Georgia/2007/1	Russia/Odintsovo/02/14	Poland/2015/Podlaskie	China/2018/AnhuiXCGQ
N.C.G.R.	186345_186346 ins T	186334_186335 ins T	N.A.	N.A.
DP60R (189099 → 189278)	N.A.	N.A.	189066_189067 ins A	N.A.
DP60R (189099 → 189278)	189100_189101 ins A	189089_189090 ins A	189149_189150 ins A	189148_189149 ins A
DP60R (189099 → 189278)	N.A.	189114_189115 ins A	N.A.	N.A.
N.C.G.R.	N.A.	N.A.	A189272G	N.A.
N.C.G.R.	N.A.	N.A.	G189275A	N.A.
N.C.G.R.	N.A.	N.A.	G189302A	N.A.
N.C.G.R.	189278_189279 ins T	N.A.	N.A.	N.A.
N.C.G.R.	189344 ins AATTTAATCTTTGACGCC.... TAAATTTGACCTGCTTT (754 nt)	189,333 ins AATTTAATCTTTGACGCC.... TAAATTTGACCTGCTTT (754 nt)	189,394 ins AATTTAATCTTTGACGCC.... TAAATTTGACCTGCTTT (754 nt)	189,393 ins AATTTAATCTTTGACGCC.... TAAATTTGACCTGCTTT (754 nt)
% identity	99.945	99.937	99.963	99.975

Abbreviations: N.A. Non applicable; N.C.G.R. Non-coding genomic regions; ORF, open reading frame.

^aPositions of variations detected and ORF positions are based on the reference genome of Georgia 2007/1 (FR682468), Russia/Odintsovo_02/14/Boar (KP843857), POL/2015/Podlaskie (MH681419), and China/2018/AnhuiXCGQ (MK128995).

^bPositions of the indels refer to the position of the last nucleotide within each homopolymer region. Genome positions for indels are given by the flanking nucleotide positions.

database (E value cut-off $<10^{-4}$) to compare the homologies with known protein sequences. By doing so, 186 ORFs showing 100% identity with proteins encoded by other ASFV genomes among those publicly available were predicted and annotated on ASFV Belgium/Etalle/wb/2018 genome (Table 2). In the left (5') variable region, 13 members of *MGF_360* were identified. *MGF_110* (10 members), *MGF_505* (9 members), *MGF_300* (3 members) and *MGF_100* (1 member) were also observed. In the right (3') variable region, *MGF_360* (4 members), *MGF_100* (2 members) and *MGF_505* (1 member) were found. Besides, four additional ORFs were 95.0%–99.9% identical, *MGF_110-4L*, *MGF_110-13L*, *ASFV_G_ACD_00290* and *ASFV_G_ACD_00350*.

To further control our annotations and determine whether other ORFs may be present, a second ORF search was carried out using Glimmer software, again followed by a systematic manual comparison against duly annotated ASFV genomes and a blastx against NCBI nonredundant protein sequence database (E value cut-off $<10^{-4}$). This latter analysis confirmed the 186 aforescribed ORFs and revealed 11 new candidate ORFs. Among the latter, one encodes a pKP93L-like protein (90.5% similarity), a second encodes a pA118R-like protein (87.9%), three are referred to as hypothetical proteins and 6 are not referenced at all (no significant similarity found). These additional ORFs thus encode 35 to 124 amino acids long proteins lacking convincing similarity ($<91\%$) and were therefore not considered for the ORF annotation presented in Table 2.

3.4 | Genome comparison

Comparison with the ASFV Georgia 2007/1 (FR682468), ASFV Russia/Odintsovo/02/14 (FR682468), ASFV Poland/2015/Podlaskie (FR682468) and ASFV China/2018/AnhuiXCGQ (FR682468) nucleotide sequences revealed 73, 92, 38 and 19 differences, respectively (Table 3). Some (11) of the indels detected in ASFV Belgium/Etalle/wb/2018 were confirmed by sequencing of PCR products to rule out artefacts. Further, the said indels were also observed in DNA extracted from the spleen material collected from two ASFV-positive wild boars retrieved weeks after the two index cases. Of note, compared with ASFV Georgia/2007/1 genome, a SNP leads to a premature stop codon in the ORF *MGF_110-1L*, and insertion of a stretch of 4Cs within the ORF *MGF_110-13L* results in the gain of a glycine codon and a frameshift. Furthermore, three non-synonymous mutations were observed at nt 43599 in the gene *MGF_505_9R* (Lys to Glu), at nt 133521 in the gene *NP419L* (Asn to Ser) and at nt 169862 in the gene *I267L* (Ile to Phe). Twenty-one other indels were situated in coding regions where a frameshift is expected (Table 3). The effect on protein functions resulting from all these changes is unknown. The remaining differences were 1-nt indels within intergenic regions. Finally, the gene *EP402R*, coding the CD2-like protein is identical to that in ASFV Georgia/2007/1, thus suggesting that a functional CD2-like protein is duly present on the surface of Belgium/Etalle/wb/2018 extracellular virions where it is expected to mediate haemadsorption to infected cells (Borca et al., 1994; Rodríguez, Yáñez, Almazán, Viñuela, & Rodríguez, 1993).

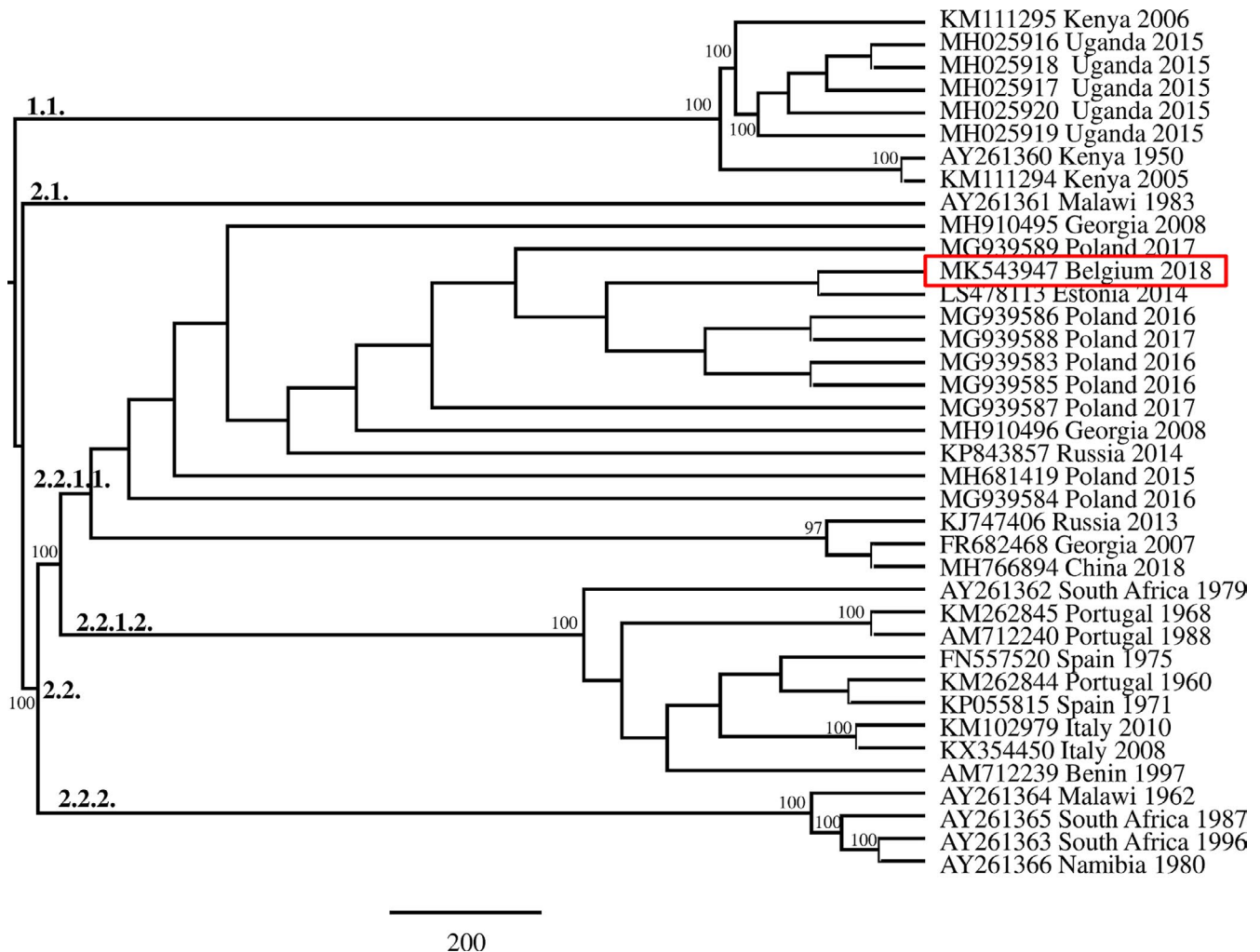


FIGURE 1 Evolutionary relationships of all currently available strains of African swine fever virus based on the phylogeny of the central conserved region of the genome. The phylogenetic analysis was performed using MEGA7 (<http://www.megasoftware.net>) and the GTR + G substitution model, as determined by a model selection analysis. Bootstrap values (>70%, based on 500 replicates) for each node are given. GenBank accession numbers, country and year of collection are indicated for each strain. Scale bar indicates nucleotide substitutions per site

3.5 | Phylogenetic analysis

We then performed a nucleotide alignment of the central conserved region (from the start of ORF A224L to the end of ORF I196L) of Belgium/Etalle/wb/2018 genome to the 37 ASFV genomes currently available in Genbank, using Clustal Omega 1.2.1 (Sievers et al., 2011). A phylogenetic analysis was subsequently performed using the maximum likelihood inference method implemented in MEGA7 (<http://www.megasoftware.net>). The tree was reconstructed using the GTR + G substitution model, as determined by a model prediction analysis in MEGA7. The phylogenetic analysis revealed that all the 38 ASFV were grouped in two clades (Figure 1). Clade 1 includes 8 East African strains, with a subclade of 6 strains belonging to genotype IX and a second subclade of 2 belonging to genotype X. Clade 2 comprises a singleton (Malawi 1983) and a subclade 2.2 containing the other 29 strains. The latter is divided into 3 clusters with unanimous

bootstrap support, with clade 2.2.1.1. gathering all 16 genotype II post-2007 euroasiatic strains, clade 2.2.1.2. grouping African and South European strains and clade 2.2.2. comprising southern African strains. Of note, within clade 2.2.1.1., the phylogenetic tree proposing a lineage by descent of the 16 post-2007 Euro-Asian strains displays knots the reliability of which remains low (bootstrap value less than 0.7), probably because the central genomic region considered has had little diversification since Georgia/2007. The phylogenetic analysis observed using the Bayesian MCMC sampling method was consistent with that inferred using the maximum likelihood method (data not shown).

In a new example of pathogens hopscothching the globe, African swine fever virus hit north-western Europe's wildlife in summer 2018, marking a further spread of a disease that had invaded Central and Eastern Europe recently. The complete genomic sequence of ASFV Belgium/Etalle/wb/2018 is reported, with the hope it provides

a valuable tool for tracing geographical spread and biologic evolution of the virus.

ACKNOWLEDGMENTS

The authors thank Laetitia Delaval and Mathieu Franssen for technical assistance.

ETHICAL APPROVAL

This study was not conducted using living animals. Therefore, the study had not to be submitted to an Ethical Committee. Instead, the authors used organ samples taken from the bodies of dead wild boars referred for autopsy by the public authorities. One of the animals had been euthanized by these same public authorities in accordance with the legislation that organizes and supervises the shooting, for humane and/or sanitary reasons, of wild animals found sick. The said legal text is the following: *Arrêté du Gouvernement wallon déterminant les personnes habilitées à détruire et à transporter des animaux de la catégorie grand gibier pour des raisons sanitaires ainsi que les conditions que celles-ci doivent remplir*. Moniteur belge, 2006, 261:41438–41439.

CONFLICT OF INTEREST

The authors declare that they are not in a position of conflict of interest with any aspect of the work presented.

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How to cite this article: Gilliaux G, Garigliany M, Licoppe A, et al. Newly emerged African swine fever virus strain Belgium/Etalle/wb/2018: Complete genomic sequence and comparative analysis with reference p72 genotype II strains. *Transbound Emerg Dis*. 2019;00:1–26. <https://doi.org/10.1111/tbed.13302>