

FIG.1

PPV5A DNA Sequence

PPV5A_Reference:

gene 87..1967
 /label="Predicted replicase"
 gene 1975..2844
 /label="Predicted gene of unknown function /
 ORF3"
 gene 2845..5547
 /label="Predicted Capsid"

Sequence:

TATTTGCAGGCTTTTCCCTGATATTGGGAAGATTCCTGGGGTGA CTCTGAGCGGTATATTTAT
 GCTGTAAACGTGAGTACCCGTAATGGGCAAAAGTGGCCGAAAGTTGGGACCGAGGGGCCATTGG
 CTGCAGGTGTCTTACAGGGGGAGGCCCTTTTCCGTGAGACCCTTAAAGAGGTCCGGAAGGTGTG
 CCGGCTGCCGCAAGACCCCCCATCTTTTCTTTCAATTGGAGAAAGTTGATTCCAAAGGGGGTCT
 TCACCTTCATTTTTGTATTAGTGTGCTGCTGGCACTCCTAGAGATGTGTCTTCGATGTTTAAA
 GCCATTGAGCGTCGAGTTTCCTTTTACTACTTTGGTGTAGAGGGCTTGACTTTTTTTACTCCTC
 ATAAAAATAAGCATGGGGCTTGGAAGAGTAATGATGAGGGCTTTATTGTGAATTATCTTCTTAA
 AAAATTGCCTTTGTCTGAGTGTGTGTATGCGTGGACTAATATGGATGGGGTGATTGGCGATGCC
 TGTCTGAATGAAGATAAGCGCAGGGAATTGTTGTCTGAGCGTCAAGATCAGGGAGTCATTAAAG
 AGCTCACTGCTCCTACTTTTAAAGCTGCTACGGGTGATAAAATGTTGAGTGTGGTGGATTGGAT
 GTGTGATAATGATGTGACTACGGAGCGCCGATGGGAGGAAATATCGGCTGCGTCCCTGTACTCT
 TTCCTTGCTACCCAGCTGGCACTCATTGGCTAAACAGTGTCTTAGAGCTGCGAATCAGCGTA
 TTGTGAGCACTAAAACCTCTTG GTTGAGTCTCTGTAAATTTGCCAGTGAAAAGGAGCTTCGTGC
 TTTTCAAAATGGGGATCCTGAGTTGTCTTCAGACAACAATAGGATCTATTACTTATTTGCTATG
 AATAATTACTGCCCTGATATGGCCAGTATGATTTTCTTTTGGTGGTCTATGCGCCAAACGGGTA
 AGAGAAACAGTATTTGGCTGTTTGGACCTGCTACAACCGGTAAACCAATTTAGCAAGTGCTAT
 TGCACATACTGCTGCCAGTTATGGGTGTGTTAACTGGAATAACGCAAATTTCCCGTTTCAAGAC
 ATTGTGAATGTGCAACTGGGTTGGTGGGAGGAAGGAAAGATGACAGAGGATGTGGTTGAATGTG
 CTAAGGCATTGCTAGGGGGAAGTAATGTAAGAGTTGACCGCAAATGTATGCAATCTGCGGAAGT
 GCAATCTCCTCCTTTTATTATCACATCCAATACGGATATGTGCCTTGTTTCTCAAGGCAGTTAC
 ATCAGTTTTGAGCACCAGCAGCCTCTCCAGGATAGAATGATTAAATTTGAGTTTAAACCATGTTT
 TTCCTGGCAATTTTCGGCCTCATTCTGAAAGATGAAGTTGTGGCCTTCTTCAGAAATGGTGCTTA
 TAATGTGTTGAAGCATGCGTACATGAGAAAGGCCAGCTTTTGTCTCTCGGTCCAGCTTCCTTG
 CCATATAAGCCCCCTACGGGTGAATTAGTGTGTATAGACCAAGCTAAGTCTCCTTCTCCCTCTG
 CTTCTCGCCGCAGTGTGAGAAATTGGATGACGTGTCCCCCTGATCCTGTCCAGGACGATCCCGC
 TGA ACTGGACGAGTATTTTCTCCAGATACTCCTCCAGAGGATTGTCCTTGTCTTATTTCTCCT
 GTGAGGGAGTCTTGTCCTCGCCAGGGCCTTGCCCTACCCCTCCTCGCAAAAACAACGGAAGA
 GCAAGCATTGCTCCTTGCTGTCTCTGCGGGTAAAGTTCTGTGGTGGTTGTGGGTGATTCTGA
 CTCAGTCCCCCCCCGAAGAAAAAGAAAAAGAGGAAGTTTCCGTGGGGGAATCCCAGGATCCACAA
 CTGTACTGGGACCTAACTCTCAGTCAATCCGACGTTCTGTGCCTGAAGACGAGAGTACCCAGT
 TTCTTGACGACGCTGTGGACGCTTCTGATCTCATTGCTGAACAGTAGTTAAGGTATGAGCCGTT
 CTACTCAAAGAGATCTTTGGTCTTTGTTAAGGGAGAGACTTGAAAGGTATAAGGATCGAGTTAA
 ATATTATGGTATTTTGGTGCCAGAACGTCCTTCTACCTTAGCATCTTATTTTAGTAAAGACCCA
 CCTCCAGATCCTCCA ACTGTTAAATTTGATAAACCTATCAGGATGTAGATAGATTCTGGTTTC

FIG.1 (Cont.)

PPV5A DNA Sequence

CAACAGACGATTATACTGACTGGTATGTCTGGCATGGAGAGGACAGACCTCCTAGATTTACCGA
GCATTCCGGTGTTTCAGGGTTTTAAACTAGGTGTGAGGGGGGGCTTCCTTTAATGCCCAGTGAT
CCCAAATTTTGCCCCATACAAAATTTTGGGATCAGTTCGCTAATTTTGATGAGGGGTCTCCGT
CCACCCAGATCGGTGAGAGTGTTTCATGGAGTGATCATTTTGGAAGTCCCGATCCCTCTCATCA
TCAGGAGGTGAGGGATGCTGATGAAGTTACTTCCGAGCGGCAGCAATATAAAAATAGGATTGTC
ACCTTACTAAGAAAAGTTTATTGGGCTAAGCAGTGGTCTGGGAAATTACAAATTAATGTTTCCTT
CCCTCGAAAGCCTTTATGAGCAGATCCCCTATATGCTAGCCTATATGGACGCCGATAATTGGCG
TCAGAATTTGTTAGCTGCTAAACTCTGCGAACCCTTTGGAAGCATTTTCCTGTGTTCCAGAT
CCTTCCACGTGCGATGTCACAATCTCCACACCCCTATCTGGTGAAACGGATCCCGCCTCTTTTG
CAAAATACTTATGTTCCCTTGTATGCAACAGGTCTCAAGAAAAAGAACAGGCGCAGACGCCTTC
TTTGTCTCCATCTAAGCAAAAAGGGCAGATGTCAAGTCTGATTCTGCATCGATCTCCCAACCT
CCCCCTGAAAGTCACAAGGATAGACTGCTTCCTAAACTGATCCCCTTCAGGAAGCAGGGCCCC
TTCCCGCTCCCCCTACAGCTCAGAAGCCTATTATCTCTAAGGGTGCAGGCGGTGGAGGGTTCGTC
TGGCTTCATAATCCCTCCAAAACCTCCTAGCCCCGATCATACTAAAGATCCCCCCCCCTCCTCCT
CCTCCCTCTCCAATTCCTCCTCCTACATCTGCGCCTGACGCAGAGGAGCACGAGCTAGAGCGTG
CTAAGCAGGAGAAACAAGAGGAAGATGAGCTCATTGAAAGAATCAAATCAGGAGAAGGAGAAGG
AGAACGAGGAGGCTTCGTCTTGCCTTCTCACCCTACACTGGTCTAGAAATCCTGTCCCAGCT
GGCAAGCCTGCTGACCCCGTTGATGAATCTTCTGCGAGACATGACATCAGGTATGGGCAACGTC
TTAAACATGGAGACTGGCCATACCTGTGGGGGAAGGACTTGGATAATGCTCAGCGAGATGAGAT
TATCAAAGCTCTTCATAGTCATGTCAAAGTGGGAACCCAATTGGCAGGGAATATAGTGAGGAGT
ATCTGGAAGGCTAAGGAGCTCTTAACAGAACCTGTGTATGAGCTGTTAAAGTCTATTCTCCCTC
CTTCAGATTTATCTAAAGTTCCTCTTCCTCATTCCCAACAGACAGACAGAACAGAAGATCCAGA
AACTCCAGGGGAGACTAGAGGAACTGGATCAGACAGTCTCGATCTCCTCGGCCTTCTGGATCA
ACTGAAGACGGGGGAGGTCCTTCTTCCGAGTCCAGATTACCTGGGAGTAAAGTTCCAGTAGACC
CATCTGCCACCACGTCTGAAGCAAAGAGGCAGAGGACTGAGGAGGGGATGGACATATCTTCATG
CGGTCCAGGGGGGATTTCTGCTTCTGGGGCTGCTTCAAATAACTCTGGTCTTGTGTTGGGGGT
GGGGGGGGTACTAATTTAGGGACAGAATCTCTTGTATCCGGCTGTCAGTTTGGTAAAACTCTG
TGATCACTTCATCTTTTAGACGATGTCTTATTTACCCCTGGCCTGATAAATACTGTTGTTCTTC
TGCTCACGATCTTATTCCCGGAGTGGTCTACGAGACCCCTTGGTGCTATTATGATCTGAACGTC
ATCTCAAGCTACATTTTTTCTCCTTCTGCTTGGCAGAGGCTTTTGGAGGATTATGATGCCTTTC
GACCTAAATCCCTTAAAGTTACCATCCAGTCTTTAGTTTTAAAGATGTCTGTCAAGGTGCAGAA
AAAACAAACTACAGTTCAGGATTCCCAGTCAGCCACTATTGCTATCTTTGAGGATAAAGACTAT
GACTACCCCTATGTGATGGGAGGGGGTCAAAAACAGTTCGGGGTCACTTGCCCGGTCAACCTT
ATAATCTTCCCAAGTATTCTTACAGAACCTTGGTTTCAAGTCAAAGAAAGTAATAGGGCCAGTAT
GGGCGGTTCAGGGTACACTTTCAAATCCAATCAAGATACGGAATTGTTTCCTGCTTGAAACACAT
GATGCCACTCTTATTTCGAGGCGGGGGTACTTTTGAGCAGTACTATGAATTTCCAAACGATCTTC
CTTTCGAAAATTTGACTCAGTATCCTTGGGATATCCGCCGTCAGGATAACCCCTCTATCAGCA
GAGGATCACTGTCATGTCAGGTTCTGACAGAGATACGGTAGGCATTCTAGATGGAGATTTTTAC
TCTCCTTTTCGGTTCAAAGGACATGATAGACCCGCCATGTGGCTGCCAGGACAGAGGTTGATTC
AGGGCAAATTCATAGATACGCACCCAATACCCAATACAGGGAGGAGTGGGGTTCATCCTAATGA
TTTTACACAAGGGGCGATGGTCATGGTGACCCCATAGAACACATGAAGAGAGGATCTACAGT
CTAGATACAGGTCTTGCTGCTATGCCACGTGCCGCTCATAGACCCACCCTTCAGCCCGGACCTA

FIG.1 (Cont.)

GGACTCTGTCTCATGCCGTACGCAGACCCGATGGTTCCACCGTGGTCACGGCTAATGCGTGTGC
TTACGCTTACACCCAGGAGAATCCTCATCAGGAACCCTGGAGTGATCTCAATGTCAGACATACC
ATGTATAGGTTAGCCTATCAACGTCAAAAAGGTTTTTCAGCAACCCGGGGACCCTCTTCATATTC

GAACCCATGCTTGTTATGGGGACGGGGATGTTACCATTCCTTATGGCCTAC
TGTTCTGGGTAGTTGCACAGAAAAGTCCCCTGCCTGTTTAGAGTCCCAGATTTGGTGTAACA
CCAAATGTGGACATGGTCTATGGAGAACACACACCCCCCTCTTGCTTTATGGGGTATGCATGCTC
CCCCACCCCATGTATTTCTCAGGATGCTTGCTCAAGAGGGTCCTCCTAATGTCAGTACTTGCAG
ACCGGCTCAATCTGGTCAGACCTTCATCAATCAATATGGTCAGTTTCTCCTCTGTTTTACCATG
GTATGGGAAGTTAAGCCTAGACCCAAGTCCATCAAGCAGTGGAATCCACGTCCGCCCATCAGCA
TTCCTGTTGGTCAGTCTGGTCCTGCTTTCATTCTCGATCAAGATGGCTACTACCGTCTCCCAGA
ACATGTCTGGTCTGCCAGGGAACGTATCCGCAGCAAACGCTAGTGCCCCCAGCAATACACTTAC
TACAGTATTGATGTGTCAGGCATTCTGGTTGATTGTTTTATTTTGGCTCCGCCTACTGTATGGC
CCATGTAAACGCATCTATTATGAAAATAAAATACGTCAATTGCTGATGTAATTCGTGTTGTAAT
TCTTGTTTTGAAAAGCGCATATTTTCTTGCCGGTCTGAGTAACACCACCTATGACATCATATAA
ATTTGATTACGTAACCTTCCTCTTTTTTACTTCCGTCTTTTTTTGATTACGCAATATACACAATTC
TAGCAGTTAACTATTACACAATATCACAC

FIG. 2

PPV5A REPLICASE PROTEIN SEQUENCE

MGKSGRKLGPGRHWLQVSYRGRPF SVRPLKRSGRCAGCRKTPHLFFQLEKVDSKGGHLHLHFCIS
 VAAGTPRDVSSMFKAIERRVSFYFYGVEGLTFFTTPHKNKHGAWKSNDEGFIVNYLLKKLPLSEC
 VYAWTNMDGVIGDACLNEDKRRELLSERQDQGVIKELTAPT FKAATGDKMLSVDWMCDNDVTT
 ERRWEEISAASLYSFLATPAGTHLAKQCLRAANQRIVSTKTSWLSLCKFASEKELRAFQNGDPE
 LSSDNNRIYYLFAMNNYCPDMASMIFFWWSMRQTGKRNSIWLFGPATTGKTNLASAIHTAASY
 GCVNWNANANFPFQDIVNVQLGWWEKGKMTEDVVECAKALLGGSNVRVDRKCMQSAEVQSPFFII
 TSNTDMCLVSQGSYISFEHQQLQDRMIKFEFNHVLPGNFGLISEDEVVAFFRNGAYNVLKHAY
 MRKAQLFALGPASLPYKPPTGELVCIDQAKSPSPSASRRSVRNWMTCPDPVQDDPAELDEYFP
 PDTPPEDCPCPI SPVRESCPSGPCPTPPRKKQRKSKHCSLSVSAGKVPVVVVGSDSDSVPPEEK
 EKEEVSVGESQDPQLYWDLTLSQSDVPVPEDESTQFPDDAVDASDLIAEQ

FIG.3

PPV5A ORF3

MSRSTQRDLWSLLRERLERYKDRVKYYGILVPERPSTLASYFSKDPPDPPTVKFDKPYQDVDR
 FWFPTDDYTDWYVWHGEDRPPRFTEHSGVQGFKTRCEGGLPLMPSPDKFCPIQNFWDQFANFDE
 GSPSTQIGESVSWSDHFGSPDP SHHQEVRDADEVTSERQQYKNRIVTLLRKVYWAKQWSGKLQI
 NVPSLESLEYEQIPYMLAYMDADNWRQNLLAAKTLRTTLEAFSCVPDPSTCDVTISTPLSGETDP
 ASFAKYLCSLVCNRSQEKEQAQTPSLSPSKQKGQ

Fig. 4:

PPV5A CAPSID PROTEIN SEQUENCE

MQRINSGEGERGERGGFVLPSHHYTGPRNPVPAGKPADPVDESSARHDIRYGQRLKHGDWPYLVG
 KDLDNAQRDEIIKALHSHVKVGTQLAGNIVRSIWKAKELLTEPVYELLKSILPPSDL SKVPLPH
 SQQTDRTEDPETPGETRGTGSDSPRSPRPSGSTEDGGGPSSESRLPGSKVPVDPSATTSEAKRQ
 RTEEGMDISSCGPGGISASGAASNNSGLACGGGGGTNLGTESLVSGCQFGKNSVITSSFRRLCI
 SPWPKDYCCSSAHDLPVGVYETPWCYIDLNVISSYIFSPSAWQRLLEDYDAFRPKSLKVTIQS
 LVLKMSVKVQKKQTTVQDSQSATIAIFEDKDYDYPYVMGGGQKTVPGHLPGQPYNLPKYSYRTL
 GSVKESNRASMGSGYTFSNQDTELFLETHDATLIRGGGTFEQYYEFPNDLPFENLTQYPWD
 IRRQDNPLYQQRITVMSGSDRDTVGILDGDFYSPFRFKGHDRPAMWLPGQRLIQGKFIDTHPIP
 NTGRSGVHPNDFHTRGDGHGDTHRTHEERIYSLDTGLAAMPRAAHRPTLQPGPRTL SHAVRRPD
 GSTVVTANACAYAYTQENPHQEPWSDLNVRHTMYRLAYQRQKGFQQPGDPLHIRTHACYGDGDV
 TIPKEESLWPTVLGSCTEKSPACLESQIWCKTPNVDMVYGEHTPPLALWGMHAPPPHVFLRMLA
 QEGPPNVSTCRPAQSGQTFINQYGQFLLCFTMVWEVKPRPKSIKQWNPRPPISIPVGQSGPAFI
 LDQDGYRYRLPEHVWSARERIRSKR

Pair-wise amino acid Identity comparisons

	[1]	[2]	[3]	[4]	[5]	[6]	[7]	[8]	[9]	[10]	[11]	[12]	[13]	[14]	[15]	[16]
[1] Bovine		47.2%	52.3%	50.3%	50.5%	52.8%	52.8%	52.8%	52.6%	6.6%	22.7%	22.5%	20.7%	20.7%	21.4%	18.4%
[2] CanineMinute	43.3%		51.0%	60.2%	61.0%	50.5%	51.3%	50.5%	51.8%	7.4%	25.0%	24.7%	21.7%	21.7%	20.9%	18.1%
[3] GboV	43.7%	49.8%		50.0%	50.3%	91.3%	83.7%	83.7%	84.2%	6.6%	23.7%	23.7%	21.7%	21.7%	23.0%	17.6%
[4] PBov1a	42.8%	53.5%	49.1%		93.9%	51.8%	50.5%	49.7%	51.5%	7.1%	24.0%	24.0%	20.9%	20.9%	23.2%	19.9%
[5] PBov1b	43.3%	53.7%	49.5%	94.7%		51.8%	51.3%	49.7%	51.8%	7.9%	24.5%	24.5%	20.4%	20.4%	23.0%	20.2%
[6] HuBoca	44.2%	50.9%	93.3%	50.0%	50.7%		82.7%	82.7%	83.2%	6.9%	24.2%	24.2%	21.2%	21.2%	22.5%	17.9%
[7] HuBoca2	47.0%	50.5%	78.4%	50.0%	50.2%	80.5%		91.8%	91.1%	7.9%	23.5%	23.2%	20.9%	20.9%	22.5%	18.4%
[8] HuBoca3	44.7%	51.2%	92.6%	50.2%	50.5%	93.3%	80.0%		92.1%	8.7%	24.0%	23.7%	21.7%	21.7%	23.2%	18.6%
[9] HuBoca4	46.5%	50.2%	77.7%	50.0%	50.5%	80.2%	96.5%	79.3%		8.2%	23.5%	23.7%	21.4%	21.4%	23.2%	19.1%
[10] Dengovirus	7.9%	7.0%	6.5%	7.7%	8.1%	6.5%	6.1%	6.7%	5.8%		7.7%	7.4%	8.4%	8.2%	6.9%	6.6%
[11] Hokovirus_a	20.5%	20.7%	20.5%	22.6%	22.3%	20.9%	20.2%	20.7%	20.5%	7.9%		99.5%	33.9%	34.2%	33.4%	17.6%
[12] Hokovirus_b	20.0%	20.9%	20.5%	22.6%	22.3%	20.9%	20.2%	20.7%	20.5%	8.1%	98.6%		33.9%	34.2%	33.4%	17.9%
[13] PPV4a	21.4%	21.2%	22.1%	22.1%	21.6%	22.8%	21.2%	22.8%	21.4%	6.3%	29.1%	29.1%		99.5%	51.3%	17.1%
[14] PPV4b	21.4%	21.2%	22.1%	22.1%	21.6%	22.8%	21.4%	22.8%	21.6%	6.3%	29.3%	29.3%	99.3%		51.3%	17.1%
[15] BIVI_PPV5A	22.1%	22.3%	23.3%	23.3%	23.0%	22.8%	23.0%	22.3%	23.3%	5.1%	32.6%	32.3%	60.5%	60.2%		15.8%
[16] PPV1	18.6%	25.4%	23.3%	20.5%	21.2%	22.8%	26.1%	23.5%	25.1%	5.8%	16.5%	16.5%	18.4%	18.4%	19.3%	
Top = VP1/CAP amino acid identity																
Bottom = REP amino acid identity																

FIG. 6

Phylogenetic analysis of VP1/CAP region of PPV5A

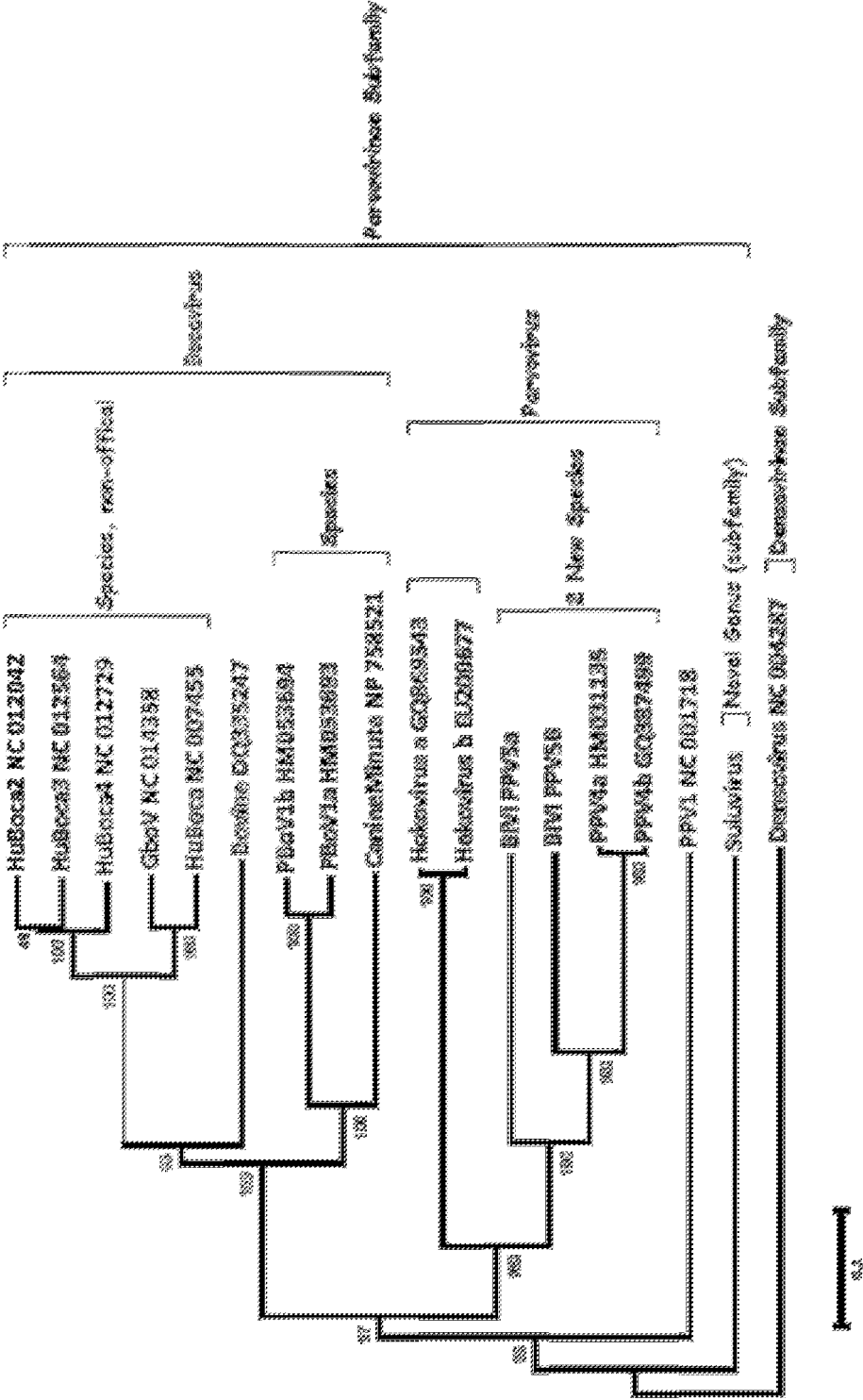


FIG. 7

BLASTp results of PPV5A_Capsid vs. Total GenBank sequences.

Closest Match: Porcine Parvovirus 4 PPV4 -- GenBank Accession ID: AFM73871
 Sequence Identities: 40% (310/774)
 Sequence Homologies: 52% (403/774)

PPV5A	163	KHGDWPYLWGKDLDNAQRDEIIKALHSHVKVGTQLAGNIVRSIWKAKELLTEPVYELLKS	222
		KHG WP+LW +D EI + L K+ +L N + ++W+AKE + P+YE++K	
PPV4_	3	KHGHWPPLWAPFVDRQMSQEIQQVLKGSTKLSQKLLANFIIALWRAKEKIGAPIYEIVKG	62
PPV5A	223	ILPPSDLKSVPLPHSQQTDRTEDPETPGETRGTGSDSPRSPRPSGSTEDGGGPSSSRPLP	282
		+ P D V P +P RG+ SP P+ ED	
PPV4_	63	VFPSVDKKTVESLLPHPDPIAPPSSP--QRGSKRASPPQ--SPNAHDED-----	108
PPV5A	283	GSKVPVDPSATTSEAKRQRTEEGMDISSCGPGGISASGAASNNSGLACGGGGGTNLGTES	342
		T S KRQ+T E S C + + A + L CG GGG +	
PPV4_	109	-----TMSGHKRQKTMEVE--SECDKSLLCPTQNAGADFEL--CGTGGGATNEKGT	155
PPV5A	343	LVSGCQFGKNSVITSSFRRLCLISPWDKYCCSSAHDLPGVVYETPWCYYDLNVISSYIF	402
		V G QF S+ T RRC++S +PD YC + D IP +++ TPW YYDLN++S + F	
PPV4_	156	WVGGTQFTDTSIRTFGTTRRCVLSAFPDTYCSMMSGDAIPSIIFNTPWYYYDLNIMSCH-F	214
PPV5A	403	SPSAWQRLLEDYDAFRPKSLKVTIQSLVLKMSVKVQKKQT-TVQDSQSATIAIFEDKDYD	461
		SPSA+Q L+EDYDAFRP+SL V ++ LV+K + Q Q V D+ SAT+ FED +Y+	
PPV4_	215	SPSAFQTLIEDYDAFRPRSLTVHLKELVIKDVCQQQLQAEQVSDNNSATLLAFEDVNYE	274
PPV5A	462	YPYVMGGGQKTVPGHLPQGQPYNLPKYSYRTLGS-----VKESNRASMGGSGY-----	508
		PYV+GGGQ +VPGHLPQGQPY LPKYSYRT+G V N G G+	
PPV4_	275	LPYVLGGGQVSVPGHLPQGQPYQLPKYSYRTVGKPDPNSGFVPGRNTHPDQGP GHPKASKT	334
PPV5A	509	----TFKSNQDTELFLETHDATLIRGGGTFEQYYEFPNDLPFENLTQYPWDIRRDNDNPL	564
		+ QDTE ++LE H AT++ G TF Q+Y FP DLPFE LTQY WD RRQDNPL	
PPV4_	335	IWYSQYLETQDTEFYILENHKATILHSGNTFSQHYNFP-DLPFEQLTQYMW DARRQDNPL	393
PPV5A	565	YQQRITVMSGSDRD----TVGILDGDFYSPFRFKGHRPAMWLPQRLIQGKFIDTHPIP	620
		QRI VMS D T I + PF K RPAM+L G R G + T P	
PPV4_	394	IDQRIQVMSRMYDDGPQKTFAIKVNPYIVPFTVKSTSRPAMFLAGGRFKDGDYSITGPGD	453
PPV5A	621	NTGRSGVHPND---FHTRGDGHGDTHTHEERIYSLDTGLAAMPRAAHRPTLQPGPRTLS	677
		S + ND TR DT Y + LA R QPGPR	
PPV4_	454	RDKTSFKYYNDPPWIITR-----DT-----YLFSSDLAKTERE-----QPGPRQGD	494
PPV5A	678	HAVRRPDGSTVVTANACAYAYTQENPHQEPWSDLNVRHT-MYRLAYQRQKGFQQPGDPLH	736
		VR PDG+ +VT NA AY YT E P +RLA + ++G+ PG P H	
PPV4_	495	TVVRTPDGTLIVTTNALAYGYTTEYLKNIPLLSKYHGVENFRLAVENERGYSM PGHP SH	554
PPV5A	737	IRTHACYGD-----GDVTIPKE----ESLWPTVLGSCTEKSPACLESQIWCKTPNVDMVY	787
		IR G + TI E E +P +GS EK+ A LESQIW + PN D+	
PPV4_	555	IRETLFRGKLPSEIRESTIKSEDQRKEITFPDYMGSVNEKTTANLESQIWSQIPNTDITE	614
PPV5A	788	GEHTPPLALWGMHAPPHVFLRMLAQEGPPNVSTCRPAQSGQTFINQYGQFLLCFTMVWE	847

FIG. 7 (Cont.)

		TPPL++WGM	PPP	VFLR+LAQ	GPP	S C +	T++NQY	QFLL + M W+	
PPV4_	615	KCTTPPLSIWG	MKNPPPM	VFLRLLAQM	GPPRRSACS	SGSIPSNTYL	NQYCQFLL	TYEMEWD	674
PPV5A	848	VKPRPKSIKQ	WNRPPI	SIPVG-QSG	PAFILDQD	GYRLPEHV	WSARERIR	SKR	900
		V R +	+WNP PP	IP+G + P	+IL+++G	YR+P VW+A++	R R +R		
PPV4_	675	VIKRTRKTV	RWNPIPPP	QIPMGPN	NLPVYILN	KEGQYRMPT	EVTAKQR	PRHRR	728

FIG. 8

BLASTp results of PPV5A_REP gene vs. Total GenBank sequences.

Closest Match: Porcine Parvovirus 4 PPV4 -- GenBank Accession ID: ADB20210
 Sequence Identities: 58% (292/504)
 Sequence Homologies: 73% (369/504)

PPV5A	15	LQVSYRGRPF SVRPLKRSGR CAGCR--KTPHLFFQLEKVDSKGGLHLHFCISVAAGTPRD	72
		L ++ R R L++ R CR P +F QLE+VDSKGGLHLH+C+SV+AGTPRD	
PPV4_	33	LVI AVRQAEALFRELQKELR-KSCRLGVDPGIFMQLEEVD SKGGLHLHWCVSVSAGTPRD	91
PPV5A	73	VSSMFKA IERRVSFY YFGVEGLTFFTPHK NKHGAWKSNDEGFIVNYLLKKLPLSEC VYAW	132
		V ++FK E++VS YYFGVEGL+FF PHKNKHGAWKS DEGF I NYLLKKLPL EC+YAW	
PPV4_	92	VTIFKNTEKKVSQYYFGVEGLSFFVPHKNKHGAWKSTDEGFIYNYLLKKLPLKECLYAW	151
PPV5A	133	TNMDGVIGDA CLNEDKRRELLSERQDQGVIKELTAPT FKAATGDKMLS VVDWMCDNDVTT	192
		T + G IGDACL N DKR+ELL RQD VI+EL+AP +K ATG+KML +V W+ DN++ +	
PPV4_	152	TTIGGAIGDA CLNTDKRKELLDNRQDPAVIEELSAPMYKCATGEKMLDIVQWLVDNNICS	211
PPV5A	193	ERRWEEISAASLYSFLATPAGTHLAKQCLRAANQRIVSTKTSWLSLCKFASEKELRAFQN	252
		E RWE +A SLYSFLAT AG ++AKQCLR A Q+++ K L+L F LR FQ	
PPV4_	212	ESRWENKNALSLYSFLATQAGGYMAKQCLRIAQQKLLKEKPLGLTLMDFKGMNALRRFQQ	271
PPV5A	253	GDPELSSDNNRIYYLFAMNNYCPDMASMIFFWWSMRQTGKRNSIWLFGPATTGKTNLASA	312
		+ E++ DNNR++Y+FA+NNY P +AS+I ++WSM+QTGKR N +W +GPATTGKTN+A A	
PPV4_	272	DEGEMTFDNNRMHYIFA INNYDPKIASVIMYFWSMKQTGKRNCVWFYGPATTGKTNMAQA	331
PPV5A	313	IAHTAASYGCVNWNANF PFQDIVNVQLGWWE EGKMTEDVVECAKALLGGSNVRVDRKCM	372
		I H++A+YG VNWNANF PFQDIV Q+GWWE EGKMT D+VE AKALLGG+ +R+DRKCM	
PPV4_	332	ICHSSANYGNVNWNANF PFQDIVGAQVGWWE EGKMTGDMVEAAKALLGGTALRIDRKCM	391
PPV5A	373	QSAEVQSPPFIITSNTDMCLVSQGSYISFEHQQPLQDRMIKFEFNHVLPGNFGLISEDEV	432
		QS EV SPPF+ITSN DM +V +GS++SFEHQQPL+DRMIKF FN LPGNFGLI+ +EV	
PPV4_	392	QSIEVNSPPFLITSNVDMTIVQEGSFVSFEHQQPLEDRMIKFSFNMTLPGNFGLITSEEV	451
PPV5A	433	VAFFRNGAYNV LKHAYMRKAQLFALGPASLPYKPPTGELVCIDQAKSPSPSASRRSVRNW	492
		+FFR GA + +F GPAS+ + P GE+ P + +	
PPV4_	452	KSFFRMGA-KLAAQPDIMNCPIFKKGPASIRHLVPVGEI-----PPPKEMKHKRQPLY	503
PPV5A	493	MTCPPDPVQDDPAELDEYFPDTP	516
		M PD +QD+P ELD +F + P	
PPV4_	504	MRAEPDEIQDNPEELDHWFE EEAP	527