1 **Supplemental Material**

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3 **The P1N-PISPO Trans-frame Gene of Sweet Potato Feathery Mottle Potyvirus is Produced During Virus Infection and Functions**

4 **as RNA Silencing Suppressor**

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Table S1. Primers used in this study

Primer	Sequence (5'-3')	Application
FMCPFdeg	GCATCATCAAAGGGTG**Y**GAG	Detection of an SPFMV CP amplicon (389bp) with a degeneration (Y=C or T) in order to amplify most SPFMV strains/isolates.
MFRdeg	ACTGCATG**R**TCCAACAATGG	Detection of an SPFMV CP amplicon (389bp) with a degeneration (R=G or A) in order to amplify most SPFMV strains/isolates.
CSCPF	cctctaga<u>ATG</u>GCTGATAGCACTAAAG	Detection of an SPCSV CP amplicon (790bp).
PCSCR	ccctcgag<u>TCA</u>ACAGTGAAGACCTGTTC	Detection of an SPCSV CP amplicon (790bp).
FMP1seqF	GAATGCGTACCTTAGTGATG	Sequencing of the different transframed P1 versions.
FMP1F	ccac<u>ATG</u>GCAACTGTAATGGC	Directional cloning of P1wt in pENTRY-D-TOPO.
1PMFR	<u>CTA</u>ATACTGGATGATGTATGGTAG	Cloning of SPFMV P1wt in pENTRY-D-TOPO.
FMHCF	cacc<u>ATG</u>AGCTCTACTATGGAAAG	Directional cloning of SPFMV HcPro in pENTRY-D-TOPO.
CHMFR	<u>CTA</u>GCCTACTATGTAGTGTTTCAT	Cloning of SPFMV HcPro in pENTRY-D-TOPO.
FMPISPOF	cacc<u>ATG</u>GAAAAAACTGGACGAACAAT**A**G	Directional cloning of SPFMV PISPO in pENTRY-D-TOPO with stop in P1 frame.
OPSIPMFR	<u>CTA</u>CCAAGTTTCATTCGTGCG	Cloning of SPFMV PISPO in pENTRY-D-TOPO.
FMP1onF	GGAAAAAACT**T**GACGAACAATTGG	Site-directed mutagenesis of SPFMV P1 in order to stop the PISPO frame.
no1PMFR	CCAATTGTTCGTC**A**AGTTTTTTCC	Site-directed mutagenesis of SPFMV P1 in order to stop the PISPO frame.
FMP1NPISPOF	GG**(+G)**AAAAAACTGGACGAACAAT**A**G	Site-directed mutagenesis of SPFMV P1 in order to force the PISPO frame and to stop the P1 frame.
OPSIPN1PMFR	C**T**ATTGTTCGTCCAGTTTTTT**(+C)**CC	Site-directed mutagenesis of SPFMV P1 in order to force the PISPO frame and to stop the P1 frame.
FMP1ΔF	CAAT**A**GGCCACAAGGAAC	Site-directed mutagenesis of SPFMV P1 in order to generate a truncated P1.
Δ1PMFR	GTTCCTTGTGGCC**T**ATTG	Site-directed mutagenesis of SPFMV P1 in order to generate a truncated P1.
FMPISPOΔF	GGGGGTCC**TAGC**GCGAGTC	Site-directed mutagenesis of SPFMV P1 in order to generate a truncated P1N-PISPO.
ΔOPSIPMFR	GACTCGC**GCTA**GGACCCCC	Site-directed mutagenesis of SPFMV P1 in order to generate a truncated P1N-PISPO.
GFP1F	CAACTTCAAGACCCGCCACA	qRT-PCR for GFP.
1PFGR	TCTGGTAAAAGGACAGGGCCA	qRT-PCR for GFP.
UBIF	TCCAGGACAAGGAGGGTATCC	qRT-PCR for Ubiquitin.
IBUR	TAGTCAGCCAAGGTCCTTCCAT	qRT-PCR for Ubiquitin

[1]Lowercase indicates the restriction sites used for cloning or the motive required for directional cloning in pENTRY-D-TOPO (underlined). Introduction of start/stop codons are denoted with underlined capital letters. Bold letters indicate nucleotide replacement/insertions used for mutagenesis.

Table S2. Expected gene products deriving from SPFMV isolate AM-MB2[1]

Predicted Gene Product	Genome position (first)	Genome position (last)	Size (aas)	MW (Da)	pI (calc.)	Sequence
P1	118	2103	664	74107,71	9,24	MATVMASAKPAGKRKLTWKECCNKWGRAAMEQQQQQQSKKTVHLGRDHLAAYLLAFVPETEWHKYYYGSRGGPSPALLILKGAIEHGEVYKWESELTFCAECD DVLDGHNCDSCGHRHIKRDDNIADNMNAIARALGGYDAYYASNWAVYETAKYELDQVAPTAGMLYKQAKEAEKLLGKRPTRREIQEVEDLWAEYEEAAAREAVEA SEASNGHATSEVANKNAYLSDEEDDEEFPPLVVTVEKVVPTTTIIESTPEVGKTIEVQTPLEPVPEVLAATTFVEATIEGKDAPTGSIQFGTIVCALEPIKASEAGIVKEP TTGFFFGTIPAIVPLPTIPLLKLEPTIVEPIATPVVEVTSSEIVKVPIATPTEVEKASKAPLPKHLYPWTAKTQTPGEVHHKMVRKWVQKTQQAAAEKEKLVWKKLDEQL ATRNEIRKGLKVKWRWGLYRLVKKTRKDNQRQRRQRRMEKEQQLLMAMPPQVLTGISIAGGPSASLEMTPTPNGKIFCTPSMKKKKTLKSPKLTQEKIHELTQAVL KIACRKRMSIELVGKKSTKGQYRKFQGANYLFLHLKHMEGLRESVDLRIHTTTQNLVLQAAKVGAWKRPVKTTMLSKGSSGMVLNPDKLLGPRGHAPHGMLVVRG ALRGVLYDARMKLGRSVLPYIIQY
P1N-PISPO	118	2072 (+1)	654	72726,52	6,17	MATVMASAKPAGKRKLTWKECCNKWGRAAMEQQQQQQSKKTVHLGRDHLAAYLLAFVPETEWHKYYYGSRGGPSPALLILKGAIEHGEVYKWESELTFCAECD DVLDGHNCDSCGHRHIKRDDNIADNMNAIARALGGYDAYYASNWAVYETAKYELDQVAPTAGMLYKQAKEAEKLLGKRPTRREIQEVEDLWAEYEEAAAREAVEA SEASNGHATSEVANKNAYLSDEEDDEEFPPLVVTVEKVVPTTTIIESTPEVGKTIEVQTPLEPVPEVLAATTFVEATIEGKDAPTGSIQFGTIVCALEPIKASEAGIVKEP TTGFFFGTIPAIVPLPTIPLLKLEPTIVEPIATPVVEVTSSEIVKVPIATPTEVEKASKAPLPKHLYPWTAKTQTPGEVHHKMVRKWVQKTQQAAAEKEKLVWKK**TGRTI GHKERDQKRSQSKMEVGTLQTSQEDQEGQPKTAPTEAHGEGTAIIDGYATSSSDGHLHCWGSIGESGNDSNSEWEDFLHAFHEEEENFKISQINTRENSRAHA GSSENCVQEKDEHRIGGQEVHKRAVQEISRSKLFVPSFKTYGRLKRVSGFKNSHNNSKPRTSSCQGWSMEKTCKDNNVVQRFKWHGAESRQTVGPKRSCTTR NARGAWGFTRSAIRRTNETW**
HCPro	2020	3477	488	52149,48	7,86	SSTMERFLSGFDNKFKQMRQTDLNHVCESSYDAEQAGSVAAISHHMLYPMGRTTCKFCINNVEDMSRDEWCEYVRSFISRNKILCQSEYKNFVHLPQIMDFLSDSL VNTNKNLKAFNEIQNLIGDRTDAPFTSVCEVNKVLVKGGRAKSDELIKASENLLEVARYLKNRTENIKKGSLQSFRNKISQKSSVNLALMCDNQLDKNGNLIWGERGY HSKRFFANYFDVIDPSQGYEKYVIRENPNGSRKLAIGKLIVSTNFSVFREQMKGEPIQKQKLDNHCTSLRDGNFVYPCCCVTLDDGQPLESEFKL**P**TKNHLVIGNSG DPKYVDMPPEISKNMYIAKDGYCYVNIFLAMLVNVNEAEAKDFTKQVRDVLMEKLGKWPTMFDVATACAFMSVFYPETRNAELPRILVDHSTKTMHVVDSFGSLST GYHVLKANTVSQLIQFSSSSLESEMKHYIVG
P3	3484	4533	352	39639,25	8,52	GVTALPDVQERCIRTIIKGVYKPDVMYTILSEDPYALLLSVMSPRILLALLNSGSLDRSMEAWITEDQEVAVIIGTLQELAKKVSTSRVLEKQLKVIESQAHTLLFDPAFV RSRTPSFALSQKIIRGLAEGRESNRVLYEQGHSIASYAASHELMEKIWDRLLKEEYEGLPWHGKCAQIMRSSKRACGLLSIPTWPKIGALSDRATDLCTTLHTKSVTF KNTCRNGVVQRIADAHIKCVRTIMRTSLAAIKFAIPDVLKFVNMLLVINLLLQIAKVARDMSMKHRQAQIDLNAYLFDQEIDKVNVIYDAYCLKIGGEPTMDEFLGHVEYI NPTLSGTAKWLCYTADMEVKHQ
P3N-PIPO	3484	4145 (+1)	223	25461,58	9,35	GVTALPDVQERCIRTIIKGVYKPDVMYTILSEDPYALLLSVMSPRILLALLNSGSLDRSMEAWITEDQEVAVIIGTLQELAKKVSTSRVLEKQLKVIESQAHTLLFDPAFV RSRTPSFALSQKIIRGLAEGRESNRVLYEQGHSIASYAASHELMEK**NLGSSFKGGIRRTALAWKMCTNHAIIKTCMWFTKYSNMAKNRRFKRQSNRLMYYLTHEE CHIQEYL**
6K1	4540	4689	52	6048,15	8,87	GKSRKEMQYERIIAFVSLLLMIVDSEKSDCVYKILQKLKGLMGTINNDVYHQ
CI	4696	6618	643	72047,24	6,62	SLDDITNVLEEKNLTVDFELQSGEHPTNPCTDSTFDEWWRRQIETNNTITHYRTEGVFIEFTRSNAVSVVNNIATIDAKDILIRGAVGSGKSTGLPFYLSRKGRVLLLEP TRPLAENVHRQLGGEPFMVQATLRMRGLTVFGSHPINIMTTGFAFHYYANNPEQIGEYDFIMFDECHVHDAQAMAFRCLLKEHEFKGKILKTSATPPGREVEFTTQY PVQIKVEERLSFKAFVEAQGTGSNADVVTIADNILVYVASYNEVDELSRMLVEANYKVTKVDGRTMKVGNVEIQTCGSPQKKHFIVATNIIENGVTLDIEAVVDFGTKV TAYLDVDLRALHMSKGPISYGERIQRLGRVGRNKAGVALRIGFTEKGLTEIPQTTATEAAFLCFAYGLPVMTPNVSTSLLSTCTVKQARTMLQFELTPFYMVNMVRY DGSMHPAIHSILKKYKLRDAETDLNKMAIPNRGVTGWLSVGEYAKSGKRMDIDDSVRIPFLNPSMPERLHVDIWDAITKYKHEAGFGRISCINSCKVAYTLQTDLYAIP RTIKIIDALIADEMRKKEHYKTITGRTVSSSSFTLNSIATLWRNRYAQDYTSENIAVLSSVRSQLLEFENLSVDSSFNSMGEAALRAYVRETGATSCVLHQ
6K2	6625	6777	53	5929,98	9,4	TKDSLSKHLRLKGVWNKSVITQDLFILAGVFAGGLWMIMAGLKESFDQTVLHQ
NIa	6784	8082	435	48985,93	8,29	GKEKRQMQKLKFRKARDNKLGFEVHADDGTIEHFFGSAYTKKGKQKGKVTGMGSKNRKFINMYGFDPTEYSFVRFVDPLTGAVMDDSPYTDILLVQEKIGEARLNA IKEDELSREKVAQNPGIHAYYINEITNAALKVDLTPHNPLLACERHSTIAGHPEYEGVLRQTGPPIKMTLNDVPVNPEEASLVGHESKSLFRGLRDYNPIASVICHLMN EADGRTSDCFGIGYGGLIITNRHLFKRNNGTLTIKSRHGEFVIKNTTQLGMKPCADRDILIIRMPKDIPPFPQRIKFRVPKENERICLVGSNFQDKSITSTISETSVTCHV PNSHFWKHWIDTKDGHCGLPLVSTTDGALLGVHSLSNLTNTQNFFASFPENFEVDYLKTPEAMDWIKKWSYNPDEICWGTLELKTGQPVAPFKVSKLITDLEGIQVY AQ
VPg	6784	7353	192	21543,47	7,23	GKEKRQMQKLKFRKARDNKLGFEVHADDGTIEHFFGSAYTKKGKQKGKVTGMGSKNRKFINMYGFDPTEYSFVRFVDPLTGAVMDDSPYTDILLVQEKIGEARLNA IKEDELSREKVAQNPGIHAYYINEITNAALKVDLTPHNPLLACERHSTIAGHPEYEGVLRQTGPPIKMTLNDVPVNPEEASLVGHE
NIb	8089	9645	521	59773,15	5,59	TRSDRWVQDRLYGNLKAVGQCPAQLVTKHVVKGKCMLFDLYLQQDQSEREYFKPLMGAYGKSRLNKEAYNKDLFKYATQIQAGDVQVDTFELAERSVVSMLTSK GFEKCNYITDPEEILRALNMKAAVGAMYSGKKKDYFEGMSDHDVEDHLFHSCKRLFMGHKGLWNGSLKAELRPMEKVELNKTRTFTAAPLDTLLGGKVCVDDFNN MFYNHHLKCPWTVGITKFYQGWDRLLTSLPEGWVYCDADGSQFDSSLSPYLINSVLNIRREFMEDWDVGDQMLRNLYTEIVYTPILTPDGTIVKKFKGNNSGQPST VVDNTLMVVLAVHYTLLKLGIQESEFDKCCVFFAN**G**DDLLLAMRPDTAHLLDEFGGCFSELGLNYDFSSRTNKKEDLWFMSHCGVKRDGIFIPKLEPERIVSILEWDR SHEPIHRLEAICAAMVESWGYDELLHHIRKFYAWV**L**DQAPYNELARNGKAPYIAETALKALYTGVQPNASELSAYTRVLKEMYDDSVLQENDLEVYHQ
CP	9652	10590	315	35146,61	6,66	SSESTEFK**N**AGADPPAPKPKNIPPPPTITEITDPEDPKQAALKAARAKQPAVIPESYGRDTSKERESIVGASSKGVKDKDVNVGTVGTFVVPRVKMNANKKRQPMVN GRAIINFQHLSTYEPEQFEVANTRSTQEQFQAWYEGVKGDYGVDDTGMGILLNGLMVVWCIENGTSPNINGVWTMMDGDEQVTYPIKPLLDHAVPTFRQIMTHFSD VAEEAYIEMRNRTKAYMPRYGLQRNLTDMSLARYAFDFYELHSTTPARAKEAHLQMKAAALKNARNRLFGLDGNVSTQEEDTERHTTTDVTRNIHNLLGMRGVQ

[1] Prediction of the SPFMV protein products based on the preliminary nucleotide annotated sequence deposited in GeneBank (Accession Number KU511268).

Table S3. Expected gene products deriving from SPV2 isolate AM-MB2[1]

Predicted Gene Product	Genome position (first)	Genome position (last)	Size (aas)	MW (Da)	pI (calc.)	Sequence
P1	118	1971	618	70385,46	9,33	MACVTNGTAFARKKKMTWKECCNKWGRAAMEQQQGKGSAYTTEVSRDQLAANIFAFIPTTEWHSYYVARVGLSANALKLKYAISFGEKYEHGANFNRCPECDCAI DEHYCDECEIRFKKADDNIIKNMNGTAKALGGWDNYYAATWKQFEAAKYDMEQIAPTAGMLERRAKEAEKLLGKKAKKHEIAEVQQLWEEFEAAKELEAEEETFFE HEASLSSIPEPTTYEEAFPQLKVTSDVSTNTSQASGVVEDNLGFFFGEIPAKIALPTIPILEILPAAPILNLNGELNDITEVKQPEVIDEVCVTTQPKETDIIQSGLKKYELV NGKFQKVKKLPKTLYPWGDRKTTPGKTQHAMVTKWVRKKMSEEADKEEKIWSAWEHTKKQQLEKRLDLKVKWRYGMFRLAKKTRKDNQRQRLKQRAMLEQKKL EMMPQQIVSTISIGGGLAPSHMEEATQKSGMIFCTPSMKKRKLFKPLVISNGNLDNLTQAVLKIACKKEMNVEFIGKRVIKGDYTRKENVRHLRLQLKHMKGLRHSID LRIPSDLQALIVKAAHVAAWKKIYNTQNVVKGMSGFVLNPQRLQGKTGHAPQGIFVVRGAFKGVLYDARMKIGRSILPYMEQF
P1N-PISPO	118	1919 (+1)	601	68297,56	6,61	MACVTNGTAFARKKKMTWKECCNKWGRAAMEQQQGKGSAYTTEVSRDQLAANIFAFIPTTEWHSYYVARVGLSANALKLKYAISFGEKYEHGANFNRCPECDCAI DEHYCDECEIRFKKADDNIIKNMNGTAKALGGWDNYYAATWKQFEAAKYDMEQIAPTAGMLERRAKEAEKLLGKKAKKHEIAEVQQLWEEFEAAKELEAEEETFFE HEASLSSIPEPTTYEEAFPQLKVTSDVSTNTSQASGVVEDNLGFFFGEIPAKIALPTIPILEILPAAPILNLNGELNDITEVKQPEVIDEVCVTTQPKETDIIQSGLKKYELV NGKFQKVKKLPKTLYPWGDRKTTPGKTQHAMVTKWVRKKMSEEADKEEK**NLECVGTHKETATREAIGPESEMALWDVSPRQKDTKGQPKTTSETACNARAEET RNDAPTDSLNNINWGWSSTESYGGSHSEEWDDFLHAFYEEEEAFQTTSNFEWELRQSHTSSSKDRLQERNERGVHWKTCDKRRLHAQGKCKASSPSVEAYE RLAPLHRSKNPFRPTSSHCKGSTRGSVEKDLQHAKCCKRNERVCLKPSATARENRTRTTRNFRGTWSFQRRPV**
HCPro	1972	3375	458	52595,4	7,9	SQTGDRFWNGYDQMYRDLRGNEQDHICKSDLDVSEAGKLAAVMQHLCLPMNRITCLTCANKILEMSSSEWVEHIRMFVNSKLEFIRKECPNYKHVHWMIETMTKN LVHENKNLKAFNEIQQLIGDRTDAPFSTVNEINKILVGSGSAPISIMTSGFAFNYYAHNPDQLREYEFVIFDECHVNDAHAMAFRCLLHEHAFNGKVLKVSATPPGREVEFST QYPVKIKTEERLSFQAFVDAQGTGSNSDVISSADNILVYVASYNEVDELSKMLIDRGHKVTKVDGRTMKVGNVEIITSGTSNKKHFIVATNIIENGVTLDIEAVVDFGTK VTVYLDVDSRMIRPCKGPITYGERIQRLGRVGRNKAGIALRIGFTERGLCEIPQTVATEAAFLSFAYGLPVMTNNVSTSLLSTCTVRQARTVLQFELTPFYTVNLVRYD GSMHQAIHNLLKKYKLRDSEIVLNKLAIPNRGITGWLSCCDYIRIGQRMDLDDSIRIPFLNNAMPVRLHQEIWDVIQKYKHEAGFGRLSCISACKIAFTLQTDMYAIPRTI KILDALIESEMRKKEHFKTVTGRTTSSHHFTLNSIATMWRARYAQDYTSENIAILTAAKSQLLEFANLSTDVSFNEMSESMLSSYIRDSGAVSCVQHQ
P3	3346	4401	352	40115,96	8,42	GIVGVSKDEERCLRSIIKSVFKPELMHQILEEDPYVLLLSILSPRVLLALFNSGSLDRSLEKWLTKDQEVSTILGILIELSRKVTVARTLDEQLNVIEGHASYLIDNLWIEG RKTVAHALSYKIARGLSEKREANKVLYEQGHRITAFISSSHEMMEKIWDQLLLEAWNELSWQEKCCSMMRSLKYAKPLQGGFPQVNIGGLKDKVGESLTTLHTKSAVI GKECKKSVIDNVASLYKSMIRNTINVTLSTVRLLMPDILKFVNILLVINLLLQIAKTAKSMNQKTKQMKIDLGEFMLDQEIDKINVIYNSMCSKEGKLPTKEEFLEKVEYLN PQLLGTAKWLVYAYDSDVFHQ
P3N-PIPO	3346	4004(+1)	220	25320,43	9,43	GIVGVSKDEERCLRSIIKSVFKPELMHQILEEDPYVLLLSILSPRVLLALFNSGSLDRSLEKWLTKDQEVSTILGILIELSRKVTVARTLDEQLNVIEGHASYLIDNLWIEG RKTVAHALSYKIARGLSEKREANKVLYEQGHRITAFISSSHEMMEK**NLGSTFAGSMERVKLAGKVLFNDALVKVCKTFTRRFSPSKYRRFERQSRRITYYITHKECC DR**
6K1	4402	4557	52	5733,7	8,14	AKSAKESSYERIIAFIALVLMVIDAERSDCVYKSLNKLKGLMGTIGDGVYHQ
CI	4558	6486	643	72285,5	7,04	SLDDISNEFEEKKLTIDFELQSDESHINSESDSTFGDWWKKQLETNNVIPHYRTEGHFMEFTRANAVSVANTIAMSPHKDLLIRGAVGSGKSTGLPFYLSRKGRVLLV EPTRPLAENVHRQLAGEPFMIQSTLRMRGLSVFCGSAPISIMTSGFAFNYYAHNPDQLREYEFVIFDECHVNDAHAMAFRCLLHEHAFNGKVLKVSATPPGREVEFST QYPVKIKTEERLSFQAFVDAQGTGSNSDVISSADNILVYVASYNEVDELSKMLIDRGHKVTKVDGRTMKVGNVEIITSGTSNKKHFIVATNIIENGVTLDIEAVVDFGTK VTVYLDVDSRMIRPCKGPITYGERIQRLGRVGRNKAGIALRIGFTERGLCEIPQTVATEAAFLSFAYGLPVMTNNVSTSLLSTCTVRQARTVLQFELTPFYTVNLVRYD GSMHQAIHNLLKKYKLRDSEIVLNKLAIPNRGITGWLSCCDYIRIGQRMDLDDSIRIPFLNNAMPVRLHQEIWDVIQKYKHEAGFGRLSCISACKIAFTLQTDMYAIPRTI KILDALIESEMRKKEHFKTVTGRTTSSHHFTLNSIATMWRARYAQDYTSENIAILTAAKSQLLEFANLSTDVSFNEMSESMLSSYIRDSGAVSCVQHQ
6K2	6487	6645	53	5889,02	7,92	SAEAMAKHLKLKGIWCKSLMTQDLLVLAGVFIGGIWMIMQGAKDAFDETVRHQ
NIa	6646	7956	437	49625,31	8,52	GKDKRQRQKLKFREARDKKMGFEVTADDGTIEHFFGEAYTKKGKQKGKTTGMGSKNRRFINMYGFDPTEYSLVRYVDPLTGKIIDDSIYTDVLLVQEQFTKARREAI NDDLLSNEKVAQNPGIVAYFIKEGANAALKVDLTPHNPLKACDRINTIAGFPERESELRQTGQPIQISKNQVPHNPETSDSSVVTHESKSLFRGLRDYNPIASVICHLV NTSDGRTTDVFGLGFGGLIITNRHLFKRNNGELLIKSRHGEFTIKNTTQLHMMPCSERDILVIKMPKDIPPFPQKLRFRVPKENERICLVGSNFQEKSITSTVSETSVTC RVDRSHFWKHWVDTKDGHCGLPIVSTTDGAILGLHSLSTMTNSQNFFAAFPESFEEDYLRSPESLEWVRKWSYNPDEVCWGSLELQWSQPGEPFKPTKLMSDLN AIPVYAQ
VPg	6646	7227	194	21935,72	8,84	GKDKRQRQKLKFREARDKKMGFEVTADDGTIEHFFGEAYTKKGKQKGKTTGMGSKNRRFINMYGFDPTEYSLVRYVDPLTGKIIDDSIYTDVLLVQEQFTKARREAI NDDLLSNEKVAQNPGIVAYFIKEGANAALKVDLTPHNPLKACDRINTIAGFPERESELRQTGQPIQISKNQVPHNPETSDSSVVTHE
NIb	7957	9519	521	59520,24	5,24	AKHDTWVRDRLNGNLKAVGVCPSQLVTKHVVKGKCMLFELFLQTFPDEKSFFKPLMGAYGKSKLNKEAYTKDLFKYATPISAGEVDTEVFEQAETLVIEMLREKGF TECNYVTDTDEIIEALNMKAAVGALYSGKKKEYFQDLNADDRDDLLFHSCKRLYMGRKGLWNGSLKAELRPMEKINANKTRTFTAAPLDTLLGGKVCVDDFNNMFY NHHLKCPWTVGITKFYKGWDTLLNKLPEGWLYCDADGSQFDSSLSPYLINAVLNIRLAFMEDWEIGAQMLKNLYTEIVYTPILTPDGTIVKKVKGNNSGQPSTVVDNT LMVVLAMTYSLCKLNIKPENHDQVCIYFAN**GDDLLL**AIDPTYEWILDSLGKLFRELGLNYDFSSRTNDKEELWFMSHRGMKRDGIYIPKLEPERIVSILEWDRASEPVH RLEAICAAMVEAWGYDDLLQHIRKFYAWILD**QAP**YSELARVGKAPYIAETALKALYTCVEPSAEDLSEYVRVLNLMYDDAVESNDCEPVYHQ
CP	9520	10515	332	37117,62	6,2	SGTEEIK**DAG**TPTPAKSVKTRTGQTQPLKAPEGSTNPTDPPPPTVEEIIEEETPAQKALREARGKQPATQPSYTYGRDTGPRSPRQVTTTSRVRDRDVNAGTVGTFI VPRLQITSSKKRLPIVDGRPVINLDHLA?YDPEQTNLANTRSTQEQFKAWYEGVNGDYGVSDDEMSILLNGLMVWCIENGTSPNINGMWVMMDGEEQVTYPIKPLL DHAVPTFRQIMTHFSDIAEAYIEKRNRIKAYMPRYGLQRNLTDMSLARYAFDFYELHSNTPVRAREAHMQMKAAALKNAQNRLFGLDGNVSTQEEDTERHTTTDVT RNIHNLLGMRGVQ

Table S4. Expected gene products deriving from SPVC isolate AM-MB2[1]

Predicted Gene Product	Genome position (first)	Genome position (last)	Size (aas)	MW (Da)	pI (calc.)	Sequence
P1	157	2118	654	73232,81	8,95	MASATVSVKPAGKRKLTWKECCNKWGRAAMEQQQAAHSRRRVELSRNQLAANIFAFVPETEWHKYYFGNRGGPSPQLEVLSNAIQYGEAFKYKFDFTFCPDCDEFLEGHKCEECGTTFRKTDDNLADNMNVVARELGGYDAYYASTWSEFEQAKLELEEVAPTAGQLRKQAQAAEKLLDKRSTRKEKEYVNSLWEAVEEAEATETGEASDASEKAAELSGIPSSATAGEMFPPLVGHKNTEVITATSDVVVSECSNIQFGQITEFMPEENKDEKVVESLIEEVENATASAVMPIETGFFFGTIPAIIPLPVVVPQQGSMGVLQPAFMQVGTMPVNGIALADTHLETKETAVKEIEPAKEDIDVGAQKSTSLPAHLYPWAPRSKNSGATHHQMVRKWVKKTQEAEEMKQRAVWKKLDEQLAARNEARKDLKVKWRWGLYRLVKKTRKDNQRQRQKKRMEKEQQLLAMPPQILTGISIAGGPVASLQETPTVNGKISSTPSMKRKRILKSPTLSSDKIQELIKATLKIACKQGLQVEIINKKTVKGVYRRHGGTNHLFLHLKHMEGWRKPVDLHIHQEDIELVTMAARVGAWNKRFRTSQLCKGTSGLVLNPDKLTGPRGHAPKGLFVVRGALAEVVYDARMRLGRSTLPYIEQF
P1N-PISPO	157	2087(+1)	644	71988,27	5,98	MASATVSVKPAGKRKLTWKECCNKWGRAAMEQQQAAHSRRRVELSRNQLAANIFAFVPETEWHKYYFGNRGGPSPQLEVLSNAIQYGEAFKYKFDFTFCPDCDEFLEGHKCEECGTTFRKTDDNLADNMNVVARELGGYDAYYASTWSEFEQAKLELEEVAPTAGQLRKQAQAAEKLLDKRSTRKEKEYVNSLWEAVEEAEATETGEASDASEKAAELSGIPSSATAGEMFPPLVGHKNTEVITATSDVVVSECSNIQFGQITEFMPEENKDEKVVESLIEEVENATASAVMPIETGFFFGTIPAIIPLPVVVPQQGSMGVLQPAFMQVGTMPVNGIALADTHLETKETAVKEIEPAKEDIDVGAQKSTSLPAHLYPWAPRSKNSGATHHQMVRKWVKKT**GRTIGSSERSKERPQSEMEVGPLQAGQKDQKGQPKAAAEETNGKGATTAPCNATSDFNGHFNSWWPSSESAGDSYSEWKDFIDAFYEAEKDFKISNPIIRQDTRVDKSNFKDCLQTRTSSGDYQQENRERSLQTTRRNKPFVPSFKTHGRMEEACGSAYPPRRYRACNNGSSRRCMEQEIPYKPTMQRYQWVSSQSGQIDRSARSRAQGALRGSWGFSRSSIRRADAAW**
HCPro	2119	3492	458	52382,02	8,11	SSTMERFLRGFDEKFKQLRQVDSDHVCESTYDAEQAGAVAAILHHMVCPMNRTTCKHCSNKIEDLSKDEWCDYVRDFTNKNRLPLQLEFKDFKHLPLIMDFIAESLVQTNKDVRAFNEIQTLIGNRIDAPFTTVCEVNKVLVKGGRAKGTEFTKASEALLELARYLKNRTENIKKGSLQSFRNKISQKAAMNLALMCDNQLDKNGNLIWGERGYHSKRFFSNYFDEINPEEGYSRYIVRNNPNGTRKLAIGKLIVSTNFSVFREQMKGEPIHKQKLDNHCTSTLDGNFIYPCCCVTYDDGQPMESEFKLPTKNHLVIGNSGDPKYVDMPPEISKKMYIAKEGYCYINIFLAMLVNVNEAEAKDFTKQVRDVLMEKLGKWPTMFDVATACAFMSVFYPETRNAELPRILIDHTTKTMHVIDSFGSLSTGYHILKANTVSQLIKFANSSLDSEMKHYLVG
P3	3493	4548	352	39955,17	7,25	GLTALPANEERCVRTVIKGVYRPKILYEILSEDPYMLMLSVISPCIILALFNSGSLDRAMDTWITKDQEVAVIIGTLSELARKVSTSRVLEQQLQIIESQSHTLLFDDSTARRRTPSFALSQRVIRSLSERRETNRVLHEQGHTVSAYATSHELMEKIWDTLLLKQEYAELALLEKCSLIMRSSRYMRCIQGTYLRQSIDDFKGRVDASYTALHTKSVALSNTCKEGFVSRVAGAHARCVRTIVQTSLSAIRFAVPDILKFVNLLLVVNLILQIAHVARNMVQKHQQAQIDLNAYLFDQEIDKINVIYDSFCKKIGGEPTMDEFLAHIEYINPTLLGTAKWLCYTADVEVEHQ
P3N-PIPO	3478	4145(+1)	223	25598,61	9,58	GLTALPANEERCVRTVIKGVYRPKILYEILSEDPYMLMLSVISPCIILALFNSGSLDRAMDTWITKDQEVAVIIGTLSELARKVSTSRVLEQQLQIIESQSHTLLFDDSTARRRTPSFALSQRVIRSLSERRETNRVLHEQGHTVSAYATSHELMEK**NLGHSFKAGVRRTCLVGKMLTNHAIIQVYALYTRYVSATKYRRFQRQSRRILYCITHKECSIEQHL**
6K1	4549	4704	52	5933,02	8,73	GKSRKEVQYERIIAFISLLLMVIDSERSDCVYKILSKLRGLMGCIDGGVYHQ
CI	4705	6633	643	72287,37	6,8	SLDDITNILEEKNLTVDFELQGDEQLSNAMTDATFDEWWRKQLETNRTITHYRTEGTFIEFTRSNAVSVANNIATLPANDILVRGAVGSGKSTGLPFYLSRKGRVLLLEPTRPLAENVHRQLGGDPFMVQTTLRMRGLTVFGSHPINIMTTGFAFHYYANNPEQLREYEFIIFDECHVNDAQAMAFRCLLKEHEFSGKIIKASATPPGREVEFTTQHPVQIKVEESLSFKAFVEAQGTGSNADVVAVADNILVYVASYNEVDELSRLLVEANHKVTKVDGRTMKVGNVEIKTTGTSNKKHFIVATNIIENGVTLDIEAVVDFGTKVTAYLDVDLRMIRTSKGPISYGERIQRLGRVGRNKAGTALRIGYTEKGLVDIPQTVATEAAFLCFAYGLPVMTPNVSTSLLGSCTVRQARTMLQFELTPFYMVNMVRFDGSMHHAIHQLLKRYKLRDAETTLNKLAIPNRGITGWMSAADYRKVGQRLDIEDQIRIPFYHQSMPEKLHSDIWEAIQRYKHEAGFGRVSCINSCKIAYTLQTDVYAIPRTIKILDALIADEMRKKEHYKTITGRTVSSSSFTLNSIATLWRNRYAQDYTSENIAVLSSARAQLLEFENLSMDASYNEMSKGILETYVRESGATTCVLHQ
6K2	6634	6792	53	5843,78	8,11	TKSDLAKHLQLKGIWNKSVITQDLLVLAGVFVGGVWMVFSGAKESFEQTVTHQ
NIa	6793	8097	435	48917,56	8,5	GKEKRQRQKLKFRQARDRKLGFEVHADDGTIEHYFGSAYTAKGKQKGKVTGMGVKNRKFINMYGFDPTEYSFVRFVDPLTGLVFDDSPYTDIQLVQEKIGDARHKAILEDKLSRERVSYNPGVSAYYINEITNAALKVDLTPHNPLLACERHSTIAGHPDHEGELRQTGAAVKVDIKDVPENPEEASLVGHESKSLFRGLRDYNPIASVICHLVNEADGRTSDSYGIGYGGLIITNRHLFKRNNGTLTIRSRHGEFVIKNTTQLGMKPCADRDILIIKMPKDIPPFPQRLQFRIPKENERICLVGSNFQDKSITSTVSETSVTCHVPNSHFWKHWIDTKDGHCGLPLVSTVDGAILGVHSLSNLTNTQNFFAAVPANFEVDYLKTPEATEWIKKWSYNPSEICWGTLELKTGQPVAPFKVTKLITDLDSMQVYAQ
VPg	6793	7368	192	21627,34	7,26	GKEKRQRQKLKFRQARDRKLGFEVHADDGTIEHYFGSAYTAKGKQKGKVTGMGVKNRKFINMYGFDPTEYSFVRFVDPLTGLVFDDSPYTDIQLVQEKIGDARHKAILEDKLSRERVSYNPGVSAYYINEITNAALKVDLTPHNPLLACERHSTIAGHPDHEGELRQTGAAVKVDIKDVPENPEEASLVGHE
NIb	8098	9660	521	59582,23	5,52	ARSDRWVLDRLYGNLKAVGQCPAQLVTKHVVKGKCMLFDLYLQQDCDVRSFFKPLMGAYGKSRLNKEAYNKDLFKYATPINAGDVCHKTFEQAELAVVDMLKANGFHKCNYITDPEEIVKALNMKAAVGAMYSGKKKDYFDGMDDKDIENLLFHSCKRLYMGQKGLWNGSLKAELRPMAKVELNKTRTFTAAPLDTLLGGKTCVDDFNNMFYNNHLKCPWTVGITKFYQGWDRLLTSLPEDWIYCDADGSQFDSSLSPYLINAVLNIRREFMEEWDIGDQMLRNLYTEIVYTPILTPDGTIVKKFKGNNSGQPSTVVDNTLMVVLAVFYTLLKLGVSEFEISERCVFFANGDDLLIAMRPDTAHLLDNFSECFAELGLNYDFSSRTTKKEELWFMSHCGIKRDGIYIPKLEPERIVSILEWDRSHEPIHRLEAICAAMVEAWGYDELLHQIRKFYAWVLGQAPYSELARTGKAPYIAETALKSLYTGVQPSADDLSEYTRVLNEMYDDSLLQDNELSVYHQ
CP	9661	10599	313	34986,39	6,83	SGNPPEFK<u>DA</u>GANPPAPKPKGPFAAPEITEVTEPEDPKQAALREARQKQPAVTPESYGRDTGEKSMRSVSPQRVKDKDVNVGTTGTFVVPRVKLHTGKMRQPRVNGISVVNLQHL<u>AT</u>YEPEQHNIGNTRSTQEQFRAWYEGVKGDYGVDDAGMAILLNGLMVWCIENGTSPNINGVWTMMDGDEQVTYPIKPLLDHAVPTFRQIMTHFSDVAEAYIEMRNRTKAYMPRYGLQRNLTDMSLARYAFDFYELHSTTPARAKEAHMQMKAAALKNAHNRLFGLDGNVSTQEEDTERHTATDVTRNIHNLLGMRGVH

[1] Prediction of the SPVC protein products based on the preliminary nucleotide annotated sequence deposited in GeneBank (Accession Number KU511270).

28 **Table S5. Expected gene products deriving from unknown Sweet potato begomovirus isolate AM-MB2[1]**

Predicted Gene Product	Genome position (first)	Genome position (last)	Size (aas)	MW (Da)	pI (calc.)	Sequence
V2/MP	43	441	132	15454,85	8,11	MMTLLYKDQSGCRAWRPSMAEMWDPLQNPLPDTLYGFRCMLSVKYLQGILKKYEPGTLGFELCSELIRIFRVRQYDRANSRFAEISSLWGETGKTEAELRDSYRAL HWECCPNCCPKLCPGFKRRPDEEKEG*
V1/CP	266	1030	254	29476,86	10,04	MTGRIRVSPRFHPYGGRQVRRRLNFETAIVPYTGNAVPIAARSYVPVSRGVRMKRRRGDRIPKGCVGPCKIQDYEFKMDVPHTGTFVCVSDFTRGTGLTHRLGKR VCIKSMGIDGKVWMDDNVAKRDHTNIITYWLIRDRRPNKDPLNFGQIFTMYDNEPTTAKIRMDLRDRMQVLKKFSVTVSGGPYSHKEQALIRKFFKGLYNHVTYNHK EEAKYENQLENALMLYSASSHASNPVYQTLRCRAYFYDSHNN*
C3/REn	1480	1049	144	16864,56	9,5	MDSRTGESLSHAQTTRAVEFNTNPISVGRTAPFHLRIMYVHESTQGRTILKFQLRVNHRERRQLGFHKIFLQFRILTTRLTGAIHSWTGILERLKWHICNELANLGLFS LINLVFVIRYLPRVCSWIDEIDTIDCNDDVKVLLY*
C2/TrAp	1643	1200	148	16560,58	8,08	MSNPLSGYKRKCPIQEPLHTEAKKAKRKVPEQRTRIVWK?CGCSAFITTNCKYQHGFTHRGITKSCSDYESSRIQHQPHLCGSDCTIPS?NHVCPREHTGENHPQIP TESQPQGKEAAGIPQDLPPIQDLDDPSNWCYSQLDWYFGTP*
C1/Rep	2646	1555	364	40830,69	6,32	MPRAGRFNIKAKNYFLTYPQCSLTKEEALDQLLHLNTPTNKKFIKICRELHENGEPHLHVLLQFEGNYQCTNQRFFDLVSPSRSSHFHPNIQRAKSSSDVKSYVDKD GDTIEWGEFQVDGRSARGGQQTANDAAAEALNSGSKEAALQIIREKLPEKFIFQYHNLCGNLDRIFSPPPSVYSSPFSSSSFNAVPDIISDWAAENVMDSAARPDRP ISIVIEGPSRIGKTVWARSLGPHNYLCGHLDLSPKVYSNSAWYNVIDDVNPQYLKHFKEFMGAQKDWQSNCKYGKPVQIKGGIPTIFLCNPGEGSSFKLWLDKPEQG ALKNWATANAIFCDVQSPFWVQEEVSHSGATAHRGEEGQEESS*
C4	2495	2235	87	9533,85	9,6	MKMGNLISTCCCSSKGTTNARIRDSSTLFPHQGHHTFTLISRELNPAPMSSPTSIRTVTQLNGVSSRSTADLLEEASRLLMTQQQRP*

29 [1] Prediction of the Sweet potato begomovirus protein products based on the preliminary nucleotide annotated sequence deposited in GeneBank (Accession Number KU511271).

30 **Table S6. Expected gene products deriving from unknown Sweet potato badnavirus isolate AM-MB2[1]**

Predicted Gene Product	Genome position (first)	Genome position (last)	Size (aas)	MW (Da)	pI (calc.)	Sequence
ORF1	(703)	(1131)	ND	ND	ND	MSERWEKSLQNWYDSRRSHLEYLDLETVSKPSLSQLAHNLSIV[...]YVLEEKLEEQSLLIKRLEKGLEALTEEFLSSRPLTA[...]
ORF2	ND	ND	ND	ND	ND	[...]
ORF3a	(1486)	(4999)	ND	ND	ND	[...]QGANLLITRGMVGRLSNTPNVGFNYNISAVTDYLASRGVRTLPGRRYSTADLQGLRWNIRRPREVIPRHPTEMISRNLLGGGFSLSFREYQPITTEQRRAAQHPEEDSLEEEVLGVLNVEVLDWDGLDFPEPDPTLVNFEIPEPEPQQQHPEQVVEPVSDEILEFRREYSSIWDYGSEEEALLEFVYYSTTPDDSNYWSYSNAYRELAAALEGNVSPNDVEGLEEVEGGTSTHFSGGGEVVPPSEPNCCIMCNKRGIPEDKILCQNCMDITDDSDDEREVERQERKRMQKQKEKRVTPSTSKQTSQEEIIGAIEGDPWEEFEEMVERLHAQVTQQQPNPPADPQASNTRGQSAQSPYRPPEDTTMGQPSYAPARPTVETVSGPPSFRTDSRFLKRGTNNENWSLPPAQQQGGVLLTLPEQMGLLNDVFMRWETTTLNHMSLMNIQDTQEKVDYMENLLGETAKLAWIQWRTVYEDEYKAIVAQAEGRMGTQNVISQVRRILTLSDPVQGSTAIQDQAYRDLERLQCHDVKDMVKFLNDYMRLATKTGRLYIGRELSDKLWIKMPGDLGTKIKEEFDKKHPGAEIAVIPRIFFAHKYLEDRCKEAAFTRSLKSVSFCKDIPIQGYYGSDKPKYTPRKAKTYKGKPHETHVRIDRRKNLDRNSHCKCFICEEPGHYARDCPNQKRNIKRVMMFNQVNIPDNYDIVSVQENEEDSDAIYSLTEGEEGDEIAFGIVQESVHMISHQVIGSWRAHIDMSEVQKVCRHQWQDHQEIEAPGEDTCLWCKHHINIRTRSHCPACLLTTCNICSLRYLGREVPPKAQERPLPFPDQTALIQQQQLYMNWADQDRARLKQEVEDEKRRGQLLFEAERRRTERLGEEIAQQKLRIESMEEEQKLKNDLHAHTERDLQKKIKELKRLLREEKIKRRSLRNGKDVRTGSSEDDASSEEASGSEN*
ORF3b	(5166)	(7481)	771	85643,35	9,45	MRVSIRIRGCPEFNVNAILDTGATVCCIEEERVPKEGLEESRMTAQFTGLNSTQQTRKKLKEGYMIIADHTFPLPFVYALNPMRIGRGIQFIIGCNFIRRMKGGLRIEGPTVTFYRNVSTIETQEKSTVAAAIGNINEERTMVFPRFRKEVARLIQEGYIGENPLRHWSKNKVECTLRIKNPDLVIQDPPLKHVTPAAREFFQNQVSSLIKAQLIRPSRSRHRTTAFMVESGTSVDPKTGKEVRGKQRMVLNYKRLNDNTEKDQYSLPGINTIISRVAGKKVFSKFDLKSGFHQIRMSKESIPWTAFWTPDGLYEFLVMPFGLVNAPADFQRKMDNAFRGTEAFIAVYIDDILIFSETEEDHEQHLLKFAQIVEKNGLILSPTKMKIGVKSVDFLGVKIHQNKVQLQEHILKKIGDFREEDLLTKKGLRSWLGILNYARQHIPNLGKMLGPLYGKTSPTGEIRFNAQDWKLVREIKRKIQQLPPLEIPPKDCCIVLEADGCMDGWGAICKWKQFAYDPRSKERITAYASGKFQPIKSTIDAEIFAIMNAMEAFKIYYLDKKEMVIRTDCQAIVSFFNKSASNKPSRARWISFTDYITGTGIKIRIEHIDGKDNTLADYLSRLVFSLIIAEWKTQGRRSTAHHQAQSMAQTIGSCSKQQEPLLLREPPLKQEQEGTGEGPWGIEQLTLPLERLLKGLKTGPYKNKLIIGTGLMNSLKIALRILDLSPEVIISTYKLKEGYSEMGSQEMSVHNL*LIDSPYCMKRPRRPGEAS*
ORF4	(7055)	(7636)	193	22065,72	6,99	MENARQEINSPPSSPVNGPNHRVMQQAARAFALERATVEAGARRNRGRPMGHRAVNPATRTPAQRFEDWSLQEQTYHRDWINEQFEDSLANLGPLARGYNFNIQIERRLFRDGLSGDVGTQLVANRLSLLHEAAQEARRSVMTLQRMIRDRAEHNERFVTRDNAYMDLRQPYAEAQAQIEAAAIILMACIEDL*

31 [1] Prediction of the Sweet potato badnavirus protein products based on the preliminary nucleotide annotated sequence deposited in GeneBank (Accession Number KU511272). ND, not determined.

32 [...] indicates gaps in the sequencing of the isolate AM-MB2. Provisional numbers (in brackets) are given to estimate positions, using the sequence of a Badnavirus B isolate (FJ560944.1) for the

33 alignment

34 **Table S7. Detailed indel data of the sequence of Sweet potato potyviruses found in the AM-MB2 sample**

Virus	Sample[1]	Acc. #	Position	Indel	Length to stop codon/product	%	Coverage
SPFMV	AM-MB2 (sample 1)	KU511268	1377	A insertion	231 aas/PISPO	13,21%	2172
			3943	A insertion	66aas/PIPO	1,02%	1541
			3943	A deletion	6aas/?	0,65%	3944
	AM-MB2 (sample 2)	KU511268	1377	A insertion	231 aas/PISPO	10,47%	1175
			3943	A insertion	66aas/PIPO	1,38%	799
			3943	A deletion	6aas/?	0,50%	799
	AM-MB2 + SPCSV (sample 1)	KU511268	1377	A insertion	231 aas/PISPO	6,82%	13444
			3943	A insertion	66aas/PIPO	1,02%	9837
			3943	A deletion	6aas/?	0,53%	9837
	AM-MB2 + SPCSV (sample 2)	KU511268	1377	A insertion	231 aas/PISPO	6,48%	12564
			3943	A insertion	66 aas/PIPO	0,88%	11415
			3943	A deletion	6 aas/?	0,68%	11415
SPV2	AM-MB2 + SPCSV (sample 1)	KU511269	1231	A insertion	229 aas/PISPO	3,61%	7754
			3811	A insertion	64 aas/PIPO	2,61%	3406
			3811	A deletion	14 aas/?	1,05%	3406
			5212	T deletion	25 aas /?	0,40%	1492
	AM-MB2 + SPCSV (sample 2)	KU511269	1231	A insertion	229 aas/PISPO	2,72%	8497
			3811	A insertion	64 aas/PIPO	2,57%	3153
			3811	A deletion	14 aas/?	2,57%	3153
			5212	T deletion	25 aas /?	0,37%	930
SPVC	AM-MB2 + SPCSV (sample 1)	KU511270	3953	A insertion	67 aas/ PIPO	2,58%	10183
	AM-MB2 + SPCSV (sample 2)	KU511270	3953	A insertion	67 aas/ PIPO	2,38%	5751

35 [1] Two samples of the same plant material were processed in parallel as independent libraries, and the data was analysed separately.