COWPEA WIRUSES IN SENEGAL, WEST AFRICA: IDENTITIES, DISTRIBUTION, SEED-TRANSMISSION, AND SOURCES OF GENETIC RESISTANCE

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Contribution of the USDA Agricultural Research Service in cooperation with the Department of Botany and Plant Pathology, Agricultural Experiment Station, Oregon State University, Corvallis. Technical paper 10177, Oregon Agricultural Experiment Station.

This research was partially supported by the Bean/Cowpea Collaborative Research Support Program of the United States Agency for International Development, Grant No. DAN-131D-SS-6008-00.

ABSTRACT

Ndiaye, M., Bashir, M., Keller, K., and Hampton, R. O. 1993. Cowpea viruses in Senegal, West Africa: Identities, distribution, seed-transmission, and sources of genetic resistance.

Viral diseases of cowpea in Senegal were surveyed during the rainy seasons of 1990 and 1991. Sixty-six viral-symptomatic plant samples from five cowpea production areas were assayed for seven viruses by DAC- or DAS-ELISA. The following four recognized viruses were detected, all of which are seed-transmissible in *Vigna unquiculata*: cowpea aphid-borne mosaic potyvirus (CABMV) (34/66), cowpea mottle carmovirus (CPMoV) (2/66), cowpea severe mosaic

comovirus (CSMV)(1/66), and southern bean mosaic sobemovirus (SBMV)(1/66). In addition to these four viruses, variants of an unknown potyvirus were detected in 21 of the 66 samples by use of potyvirus-selective monoclonal antibodies (Agdia PTY and BCMV II-197). These potyvirus variants occurred principally in new improved CABMV-resistant cowpea genotypes, and their combined incidence was exceeded in plant samples only by CABMV. Isolates of the unknown potyvirus were seed-borne in Senegal cowpea lines and were efficiently transmitted non-persistently by the cowpea aphid, *Aphis craccivora*. Selected seed-borne isolates of this potyuirus were distinguishable principally by differentially resistantcowpea genotypes and by either weak (isolate Vl-1) or strong (isolate V17-14) reactions to potyvirus-selective monoclonal antibodies. Thirty-five selected cowpea genotypes were tested as possible sources of resistance to the unknown potyviruses. Of these, six (TVU-401, TW-408P2, TVU-1000, TW-1016-1, TW-1582, and White Acre-BVR) were resistant to all isolates of the potyvirus. These genotypes have been included in the existing Senegal cowpea breeding program for development of virus-resistant cultivars.

Cowpea [*Vigna unguiculata* (L.) Walp.] is second in importance only to groundnut, among Senegal legume crops. Senegal cowpeas are annually grown on some 63,000 hectares, with an annual production

of 18,000,000 kg. Doubling the cowpea yield there should be readily achievable, since the average yield of 280 kg/ha represents only 14 to 28% of the 1,000 to 2,000 kg/ha yields in experimental fields, in Senegal (19). Several factors contribute to low yields of cowpea in Senegal, and viral diseases are considered a major limitation.

Among cowpea viruses reported in West Africa (13, 15, 17, 1.9, 22), cowpea yellow mosaic comovirus (CPYMV) and cowpea aphid-borne mosaic potyvirus (CABMV) are considered economically most important. Other viruses known to occur in West Africa include cowpea mottle carmovirus (CPMoV) (1, 18) and southern bean mosaic sobemovirus (SBMV) (7, 14). Cowpea mild mottle carlavirus (CMMV), cowpea severe mosaic comovirus (CSMV), and cucumber mosaic cucumovirus (CMV) had been previously detected in seed lots from Burkina Faso, Nigeria, Senegal, and Ghana, respectively (8).

Seed-borne viruses were considered a major constraint to cowpea yield in Senegal farm fields (Gaikwad, D. G., unpublished results). Seed-borne viruses are especially destructive because emerging plants are exposed early to seed-borne inoculum that is acquired and progressively spread by insect vectors, particularly by aphid and beetle species. Two cowpea breeding lines, IS86-275N (released in 1992 as cv Mouride) and IS86-283-15N had been recently developed to increase sustainable cowpea production in Senegal.

These lines were resistant to CABMV, bacterial blight *(Xanthomonas campestris* p v *vignicola)* , storage weevil *(Callosobruchus maculatus),* striga *(Striga gesnerioides),* and drought (19). However, viral diseases in field trials of these lines in 1989-90 suggested the incidence of unrecognized indigenous viruses or perhaps undescribed pathotypes of CABMV. The present study was conducted to isolate and partially characterize these viruses and to identify resistant cowpea genotypes for use in developing virus-resistant cultivars (16).

Materials and Methods

Field survey and collection of viral isolates. During the rainy seasons of 1990 and 1991 fields were surveyed for viral diseases in the five cowpea production areas of Senegal. A total of 66 samples was collected from viral symptomatic plants in 37 farm fields and station trials. The samples were desiccated over $CaCl_2$ for serological studies and to provide sources of reference isolates. These samples and experimental seedlots from virus-inoculated plants were subsequently shipped and/or brought to the Virology Laboratory, Botany and Plant Pathology, Oregon State University, Corvallis, for investigation.

Serology. Field samples from the five areas in Senegal were tested by either double antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) (5, 6) or by direct-antigen-coating (DAC) ELISA (8) for the possible presence of seven seed-borne viruses (Table 1): blackeye cowpea mosaic (BlCMV) and cowpea aphid-borne mosaic (CABMV) potyviruses, cowpea mosaic (CPMV) and cowpea severe mosaic (CSMV) comoviruses, cowpea mottle carmovirus (CPMoV), cucumber mosaic cucumovirus (CMV), and southern bean mosaic sobemovirus (SBMV). The samples were also tested by DAC-ELISA against either potyvirus-selective monoclonal antibody (MAb) Agdia PTY (11) or anti-BCMV MAb II-197 (21).

Antisera to BlCMV and SBMV were kindly provided by Dr. Cedric Kuhn; antisera to CPMV and CSMV were kindly provided by Dr. 0. W. Barnett; and MAb II-197 was kindly provided by Dr. G. 1. Mink. The other antisera were produced by the Virology Laboratory, USDA ARS, Dept of Botany & Plant Pathology, Oregon State University.

Virus isolates derived from infected seeds of four advanced Senegal cowpea lines (Table 2, except that no seed-transmission was observed in cv. IS86-283-15) were also tested by DAS-ELISA against immunogammaglobulin G (IgG) to BlCMV, CABMV, pea seed-borne mosaic potyvirus (PSbMV) and CMV (as possible contaminant), and by DAC-ELISA against antisera of the following potyviruses: BlCMV, CABMV, clover yellow vein virus (CYW), peanut mottle virus (PeMV), peanut

stripe virus (PStV), PSbMV, white lupin mosaic virus (WLMV) and also against PTY MAbs. Isolates reactive in DAC-ELISA only to the monoclonal antibodies were tested a second time by DAC-ELISA for- possible contamination with CPMoV, CPMV, CSMV and SBMV.

In the concluding phase of this study, antisera to unknown potyvirus isolate V17-14 were produced in two young laying chickens. A series of five breast-intramuscular injections of 150 to 200 ug of purified potyvirus were made at weekly or bi-weekly intervals. Eggs were saved during a period of 10 weeks. IgG was extracted from the yolks of selected egg clutches, by the- methods of Jensenius et al (10). Four wk after the final injection, the chickens were anesthetized and exsanguinated. IgG derived from the blood was compared with yolk-derived IgG, and blood-derived IgG was chosen for comparisons of serological affinities among selected BlCMV and CABMV and isolate V17-14, by DAS-ELISA (Table 4).

Absorbance values were reco:rded by a Bioteck Mode1 EL-309 ELISA reader, typically 90 min after addition of enzyme substrate, p-nitrophenyl phosphate. Tested antigens were buffered extracts from fresh or desiccated tissues of virus-infected plants.

Electron microscopy. Potyvirus-like virions were visualized in leaf-dip extracts and partially purified virus preparations, by means of a Philips EM 12 electron microscope. For viewing, the preparations were adsorbed to carbon-coated copper grids and

negatively stained with 2% ammonium molybdate (pH 7.0). For estimations of virion sizes, the scope was calibrated using both interna1 and external magnification standards.

Disease reactions, seed transmission, and host range tests. Seedling plants of five advanced cowpea lines/cultivars (Table 2) were dusted with silicon carbide powder and mechanically inoculated with four Senegal viral field isolates, for tria1 reproduction of the previously observed disease symptoms. Viral isolates V-l a:nd V-2 were collected from naturally infected cowpea plants in Kolda, and isolates V-17 and V-54 were taken from comparable plants in Diourbel. Inoculated plants were maintained under both field and screenhouse conditions near Bambey, and were inoculated a second time to increase the potential for virus transmission. Insecticide was applied as needed to control potential insect vectors. Disease incidence in plots (% symptomatic: plants) was recorded biweekly from 7 to 45 days after inoculation.

Seeds were harvested from plants in these Isolate x Genotype treatments and tested for seed-borne virus by growing out seedlings in insect-free glasshouses, at Oregon State University. Seedling infection was examined first by visual inspection and then by ELISA. Two-wk-old symptomatic and selected viral-symptomatic seedlings were assayed for seed-borne potyviruses by DAC-ELISA with potyvirus-selective monoclonal antibodies Agdia PTY and 11-197.

Potyviral isolates derived from individual infected seedlings of cv 58-57 or Mougne (i.e., screenhouse-grown, inoculated mother plants) *were* assigned distinct sub-numbers (Tables 3, 5, 6) and thereafter referred to as PTY+ (i.e., detectable by monoclonal antibody PTY). Stock cultures of such isolates were preserved in desiccated infected tissues at - 30 C and maintained in infected seeds of: selected cowpea cultivars. A small set of selected plant species/genotypes (Table 5) and a strategic set of cowpea genotypes (3, 4)(Table 6) were tested for susceptibility to five selected seed-borne PTY+ potyviral isolates. Eight to ten plants of each species/genotype were inoculated under glasshouse Conditio:ns (temperature, 28-30 C; 14 hr photoperiod; and solar irradiant equivalence of 87 to 121 kJm^{-2} day^{-1}. Symptomless inoculated plants were assayed for asymptomatic infection, using Agdia PTY MAb 'by DAC-ELISA, 5 wk after inoculation.

Aphid transmission. Aphid-transmissibility of seed-borne PTY+ isolates V1-1 and V17-14 was tested using an *Aphis craccivora* colony reared on healthy cowpea plants (Table 7). Plant to plant transmission was carried out as follows: after a 2-hr fasting period, groups of 4th or 5th instar apterae were deposited on detached virus-infected cowpea leaves for 3 to 4 min acquisition periods. Apterae found in feeding position were then carefully transferred with a fine camel-hair brush to healthy plants of

Senegal cowpea cv 58-57. For each virus isolate, 26 to 35 test plants were inoculated using three aphids per test plant. The aphids were allowed to feed overnight on test plants before removal by insecticide. Inoculated plants were observed for symptom developiment for 4 wk after aphid inoculations. Symptomless plants were assayed by DAC-ELISA using PTY MAb. Each transmission test was repeated.

RESULTS

Field survey and virus detection. Of 66 samples collected from five cowpea growing areas of Senegal, 36 reacted positively with one or more of the seven test antisera or with MAb (Table 1). Neither BlCMV, CMV, nor CPMV was detected among the Senegal test samples. Thirty-four of 66 (52%) samples contained CABMV. One sample from Diourbel contained both CSMV and CPMoV. SBMV was detected in only one sample from Louga in mixture with CPMoV. Twenty-one samples (32%) reacted with potyvirus MAb 11-197, but reacted with none of the seven polyclonal antibodies. Based on these unique reactions and supplementary serology, isolates V1-1 and V17-14 were concluded to be an unknown potyviruses (i.e., designated PTY+). This unknown potyvirus and CABMV were the predominant cowpea viruses at all locations surveyed in Senegal.

Inoculations and seed transmission. The disease incidence in mechanically virus-inoculated plants (screenhouse and field) of five Senegal cowpea genotypes ranged from 8% to 100% (Table 2). Cowpea line 1886-283-15 was partially resistant or tolerant to two of four viral field isolates, V1 and V2. Results from screenhouse and field inoculations were essentially the same.

Seed transmission rates of the four potyvirus isolates in five Senegal cowpea genotypes varied from 0 to 30 % (Table 2). Isolate V17 was seed-transmitted in cv 58-57 at a rate of 30%; however, larger :numbers of seeds are required to assess real differences in seed-transmission rates among field isolates. Senegalcv 58-57 was most seed-transmission prone, whereas no seed transmission of PTY+ occurred in line IS86-283-15 N.

Serological relationships. Seed-borne isolates of potyvirus PTY+ were tested by DAS-ELISA and found to be serologically unrelated to potyviruses BlCMV, CABMV or PSbMV, and also to be free of ELISA detectable CMV (Table 3). The same isolates reacted to var-ying degrees in DAC-ELISA with antisera to five selected potyviruses (BlCMV, CABMV, PeMV, PMV, PSbMV and PStV), but not with antisera to CYVV, or WLMV, as would be expected of this less discriminating version of ELISA. The PTY+ isolates were verified to be free of ELISA-detectable CPMoV, CSMV, PStV, or SBMV. All PTY+ isolates reacted with both MAbs Agdia PTY and 11-197; however,

the reactions of isolate Vl-1 were consistently weaker with either MAb.

IgG to PTY+ isolate V17-14 reacted indistinguishably to all sister isolates of PTY+. However, this IgG reacted neither to 10 selected BlCMV isolates nor to 9 of 11 selected CABMV isolates (Table 4). Reactions by CABMV isolates RN-27C and RN-28C were unexpected, since they were previously considered typical, pure CABMV isolates. We did not determine whether the results indicated the sha:ring of coat protein epitope(s) between RN isolates and PTY+ V17-14 or contamination of RN isolates with PTY+. Both RN isolates had originated in cowpea seeds obtained from Botswana (3, 4).

Electron microscopy. Plants infected with PTY+ isolates contained flexuous rod-shaped particles, visualized by electron microscopy in leaf dip or partially purified preparations. The modal length of >100 particles was approximately 725 nm, thus fitting within the recognized 710 to 900 nm size range of potyvirus particles,

Preliminary host-range tests. Few differences were found in the host range/reactions of five seed-borne potyvirus isolates (Table 5), including minor variations in symptoms induced in Senegal cowpea genotypes and *Chenopodium amaranticolor* Coste & Reyn. and susceptibility to asymptomatic infection in *Phaseodus vulgaris* L. (bean cv Topcrop). Generally, the host ranges for

these isolates were more narrow than those for typical isolates of CABMV (3, 4).

Screening of cowpea cultivars for resistance. The reactions of cowpea lines/cultivars to mechanical inoculation with five seed-borne PTY+ isolates were determined (Table 6). Five International Institute of Tropical Agriculture (IITA) TW lines, TW-401, TVU-408P2, TW-1000, TW-1016-1, and TW-1582 and one U.S.A. cv White Acre-BVR were immune to all isolates (i.e., asymptomatic and free of ELISA MAb-detectable virus. Some genotypes were susceptible to all PTY+ isolates. Other genotypes were susceptible to specific isolates, e.g., cv Serido was susceptible only to PTY+ V17-14; cv TVU-410 was susceptible only to PTY+ V54-23, whereas TW 984 was resistant only to this isolate. No attempt was made to classify PTY+ pathotypes using these cowpea genotypes; however, the genotypes provided evidence that the isolates were pathogenically diverse.

Aphid transmission. Seed-borne PTY+ isolates V1-1 and V17-14 were both efficiently transmitted nonpersistently by *Aphis craccivura.* In replicated trials, isolate V1-1 was transmitted to >60% (42 of 61) of the plants inoculated by 3 apterae/plant and, in parallel tests, isolate V17-14 was transmitted to 59 of 59 plants inoculated. We believe that *A. craccivora* is a probable vector of all seed-borne potyviruses in Senegal and that indigenous biotypes

can transmit isolates of potyvirus PTY+ at rates comparable to these experimental results.

DISCUSSION

Cowpea viruses are increasingly important in all cowpea growing areas of Senegal. The survey reported herein was prompted because new pathogen/pest-resistant breeding lines had been damaged by viral diseases. Moreover, seed-borne viruses were designated priority pathogens in these studies, since they have historically inflicted heavy losses through unknowing establishment of seed-borne field inoculum, followed by secondary spread by insect-vector species (8).

The present study of 66 strategic cowpea samples with virus-like symptoms indicated the presence in Senegal of four recognized seed-borne viruses, CABMV, CSMV, CPMoV, and SBMV, and an apparently new potyvirus herein designated PTY+. SBMV had already been reported from the Casamance region of Senegal (7). Hampton et al (8), had detected CSMV in cowpea germplasm accessions from Senegal. CPMoV was previously reported only from Nigeria (1, 18), until recently when it was reported in Pakistan-grown cowpeas (2). CPMoV was also detected in cowpea samples collected from screening

nurseries in Riverside, California, U.S.A (M. Bashir, unpublished results). The seed-borne nature of CPMoV (1, 18) and these recent detections suggest that the virus is now spreading through seeds to other parts of the world. However, CABMV and potyvirus PTY+ were the prevalent viruses, occurring in 83% of the 66 samples and accounting for 55 of the 57 samples in which viruses were ELISA-detected. Based on prior investigations (8, and unpublished results), CMV and CPMV were expected to occur in Senegal-grown cowpeas, but neither was detected.

Multiple-virus infections tendto be common among samples from field-grown cowpeas, world-wide. Such mixed infections are known to modify and complicate symptoms, essentially precluding field diagnosis (9, 12). In these studies, however, mixtures of seed-borne viruses were found in only two of the 66 cowpea tissue samples, CSMV + CPMoV and SBMV + CPMoV.

The five seed-borne PTY+ potyvirus isolates examined by DAS-ELISA did not react with IgGs to CABMV and BlCMV (Table 3), a:nd most CABMV and BlCMV isolates were non-reactive to IgG to PTY+ isolate V17-14 (Table 4). Despite clear serological distinctions among these three viruses, the interactions of PTY+ isolates with cowpea genotypes resembled CABMV, lacking the ability to infect IITA accessions TVU-401 and TVU-1582, previously proven resistant to all tested CABMV isolates (3, 4). It is therefore conceivable

that PTY+ is a distinct serotype and pathotype of CABMV and that TVU-401 and TVU-1582 contain multiple genes/alleles against all tested CABMV variants.

While various controlmeasures may impede cowpea viraldisease development, including control of insect vectors, removing diseased plants from seed fields, and production of virus-free seed, we believe the development of resistant cultivars is the most practical and economical control measure for such diseases. In this study, we identified six cowpea genotypes as sources of resistance to all isolates of PTY+. These genotypes have now been incorporated in the extant Senegal cowpea breeding program for development of improved disease/pest-resistant cultivars for Senegal cowpea production areas.

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Table 1. Viruses detected by DAC-ELISA in field samples of cowpea collected in five districts of Senegal (West Africa)

District surveyed/ sampled	No. samples collected	No. of samples reacting positively with antiviral antisera/potyvirus MAb.							
		BlCMV	CABMV	CMV	CPMoV	CPMV	CSMV	SBMV	MAB II-197
Diourbel	28	- [1]	10	-	1		1		11 [2]
Kolda	4		1	-					2
Louga	20		10	-	1	-		1	7
Tambacounda	10		9	-					1
Thies	4		4	-					
Total	66		34	-	2		1	1	21

[1] - , indicates virus not detected by ELISA.

[2] Samples reacting to monoclonal antibody II-197 (21) contained no virus detectable by other anti-viral polyclonal antisera.

Table 2. Disease incidence[1] and seed transmission[2] associated with Senegal potyvirus PTY+ field isolates

Virus isolate	Cultivars/ lines	Disease incidence (%)	No. of seeds germinated/ planted	Seed transmission Incidence	%
v 1	Baye Ngagne	100	37/50	1/37	3
	IS86-275N	61	41/50	0/41	0
	IS86-283-15	8	29/50	0/29	0
	Mougne	97	46/50	2/46	4
	58-57	100	46/50	6/46	13
v 2	Baye Ngagne	100	46/100	0/46	0
	IS86-275N	47	37/100	0/37	0
	1686-283-15	18	44/100	0/44	0
	Mougne	100	92/100	1/92	1
	58-57	55	83/100	7/83	8
v 17	Baye Ngagne	81	35/50	0/35	0
	IS86-275N	50	40/50	2/40	5
	1886-283-15	52	23/50	0/23	0
	Mougne	97	47/50	0/47	0
	58-57	93	43/50	13/43	30
v 54	Baye Ngagne	86	27/50	0/27	0
	IS86-275N	88	40/50	2/40	5
	1586-283-15	82	28/50	0/28	0
	Mougne	97	49/50	0/49	0
	58-57	89	44/50	1/44	2

[1] Experiments conducted in field and screenhouse plots, Bambey, Senegal.

[2] Seeds taken from potyvirus inoculated plants, Bambey screenhouse plots. Experiments conducted in greenhouses, Corvallis, OR, U.S.A.

Table 3. Comparisons of eight recognized potyviruses with five seed-borne Senegal cowpea potyvirus isolates, by DAS- and DAC-ELISA. The Senegal isolates were also tested for the possible presence of four seed-borne non-potyviruses

	A_{405} values [1]						
	Seed-borne isolates of Senegal potyvirus, PTY+					Homologous virus [2]	Healty-plant extract
Antiserum	V1-1	V17-2	V17-14	V54-3	V54-23		
DAS-ELISA							
BlCMV [3]	0.00	0.01	0.01	0.00	0.01	0.95	0.01
CABMV	0.01	0.01	0.01	0.01	0.03	1.15	0.01
PSbMV	0.00	0.00	0.00	0.00	0.00	1.87	0.00
CM-V	0.01	0.00	0.01	0.00	0.00	1.27	0.02
DAC-ELISA							
BlCMV	0.26	1.20	0.36	0.37	0.21	2.81	0.02
CABMV	1.68	1.65	1.51	1.30	1.41	2.48	0.02
CYVV	0.11	0.10	0.08	0.05	0.08	>3.00	0.01
PeMoV	1.63	1.38	2.03	1.27	1.58	>3.00	0.03
PStV	1.90	1.50	1.75	1.10	1.92	>3.00	0.02
PMV	1.86	0.54	0.23	0.78	0.51	>3.00	0.02
PSbMV	1.65	1.58	1.51	1.86	2.11	>3.00	0.01
WLMV	0.01	0.02	0.01	0.02	0.04	>3.00	0.01
CPMoV	0.03	0.02	0.02	0.02	0.00	>3.00	0.03
CSMV	0.16	0.10	0.11	0.15	0.13	>3.00	0.12
SBMV	0.00	0.00	0.00	0.00	0.02	>3.00	0.01
II-197 (BCMV MAb)	0.31	0.77	1.40	0.57	0.70	0.58 [4]	0.00
Agdia (PTY MAb)	0.22	NT [5]	0.70	0.78	0.86	0.77 [6]	0.00

Table 3, cont.

[1] A_{405} values recorded after 90 min incubation with substrate, p-nitrophenyl phosphate.

[2] Virus homologous to each antiserum, e.g., the viral homologue of BlCMV antiserum is blackeye cowpea mosaic potyvirus.

[3] Antisera to potyviruses are: BlCMV, blackeye cowpea mosaic virus; CABMV, cowpea aphid-borne mosaic virus; CYW, clover yellow vein virus; PMV, pea mosaic virus, PeMoV, peanut mottle virus; PSbMV, pea seedborne mosaic virus; PStV, peanut stripe virus; and WLMV, white lupin mosaic virus. Antisera to other viruses seed-borne in cowpea are: CMV, cucumber mosaic virus; CSMV, cowpea severe mosaic virus; SBMV, southern bean mosaic virus; and CPMoV, cowpea mottle virus. The Agdia monoclonal antibody (11) reacts to >90% of all tested potyviruses; monoclonal antibody II-197 (21), produced against bean common mosaic virus, reacts to its homologue and several other potyviruses.

[4] BlCMV isolate RF-26B was selected as a positive control for MAb II-197.

[5] NT = Not tested.

[6] CABMV isolate 9-7C was selected as a positive control for the Agdia PTY MAb.

Table 4. DAS-ELISA tests of selected BlCMV and CABMV isolates against chicken anti-V17-14 immunogammaglobulin G

Virus isolate	A_{405} values
BlCMV	
BlCMV-Ga [1]	0.003
PI-3B	0.005
RF-4B	0.012
PU-7B	0.004
PU-8B	0.003
PI-22B	0.007
PIC-23B	0.002
PI-25B	0.003
RF-26B	0.002
RF-27B	0.007
CABMV	
RN-7c [1]	
RN-10C	
RN-27C [2]	
RN-28C [2]	
RN-34c	
RN-35c	
RN-36C	
RN-37c	
PI-39c	
PI-4oc	
PI-44C6	
V17-14 (Homologue)	
Healthy-plant extract	

[1] Isolates BlCMV-Ga (Georgia) and RN-7C (Botswana) were included as type isolates of BlCMV and CABMV, respectively.

[2] Isolates RN-27C and RN--28C previously had reacted in DAS-ELISA only to CABMV antiserum produced against CABMV isolate RN-7C.

Table 5. Reactions by selected plant species to inoculations with five seed-borne isolates of Senegal potyvirus PTY+

Host species	Disease reactions to PTY+ isolates				
	V1-1	V17-2	V17-14	V54-3	V54-23
Leguminous hosts:					
Lupinus albus cv Astra	- [1]		-	-	-
Medicago sativa cv DuPuits			-	-	-
Trifolium pratense cv Kenland					-
Phaseolus vulgaris cv Monroe			-	-	-
Phaseolus vulgaris cv Top Crop			LI	-	-
Vicia faba cv Hertz Freya	VN	VN	VN	VN	VN
Non-leguminous hosts:					
Chenopodium amaranticolor, Corvallis strain	LLn	LLn	LLn.VN	LLn	LLn,VN
Nicotiana benthamiana, ATCC	SM	SM	SM	SM	SM
Gomphrena globosa, A.F. Ross Strain	-	-	-	-	-
Phlox drumondii cv Tall Mixed Color	-	-			-
Lycopersicon esculentum cv Marglobe	-	-	-	-	-
Petunia hybrida cv King Henry	-	-	-	-	-
Antirrhinum majus cv Mixed Colors	-	-			-

[1] Symbols are: - , no symptoms and no ELISA-detectable virus; LI, latent (asymptomatic), ELISA-detected infection; LLn, necrotic locallesions; VN, vein necrosis; SM, systemic mosaic.

Table 6. Responses of selected cowpea genotypes to greenhouse mechanical inoculations with five seed-borne isolates of Senegal potyvirus PTY+

Cowpea genotypes	Potyvirus isolates				
	V1-1	V17-2	V17-14	V54-3	V54-23
TVU 109P2 [1]	- [2]	+ +	++		++
TVU 196	++		++	++	++
Tvu 347	-	+ +	-	++	-
Tvu 354	++	+ +	++	++	++
Tvu 401	-		-		-
TVU 408P2	-		-		-
Tw 410	-		-		+
TVU 984	++	+ +	++	++	-
TV-U 1000	-		-		-
TVU 1016-L	-		-		-
TVU 1582	-		-		-
TVU 2657	++	+ +	++	++	++
Tvu 3433	++	+ +	++	++	++
IT 81D 1137	-	+ +	++	++	++
IT 86 27N	++	+ +	++	++	++
P:I 25122	++	+ +	++	++	++
Bambey 21	LI		-	++	++
Serido	-		++		-
Wh Acre BVR	-		-		-
Cal Bl # 5	0	0	+	++	0
Snapper	0	0	+	++	0
Blue Goose	0	0	-		0
Corona	0	0	-	-	0
Mopod	0	0	-	-	0
Tex Cr # 8	0	0	++	++	0
Tex Cr # 40	0	0	-	++	0
UCR 524B	0	0	-	-	0
Mis Purple	0	0	++	++	0
Mis Silver	0	0	++	++	0
Magnolia	0	0	++	-	0
Kn Pur Hull	0	0	-	-	0
Worthmore	0	0	++	++	0
Bettergreen	0	0	++	++	0
UCR 7964	0	0	++	++	0

[1] TW genotypes kindly provided by I.I.T.A., Ibadan, Nigeria.

[2] Symbols are: - , no symptoms and no virus detectable by ELISA, i.e., immune; + , mild systemic symptoms; ++, moderate systemic symptoms; LI, latent (asymptomatic), ELISA-detected infection; i.e., tolerant to infection; 0, not tested.