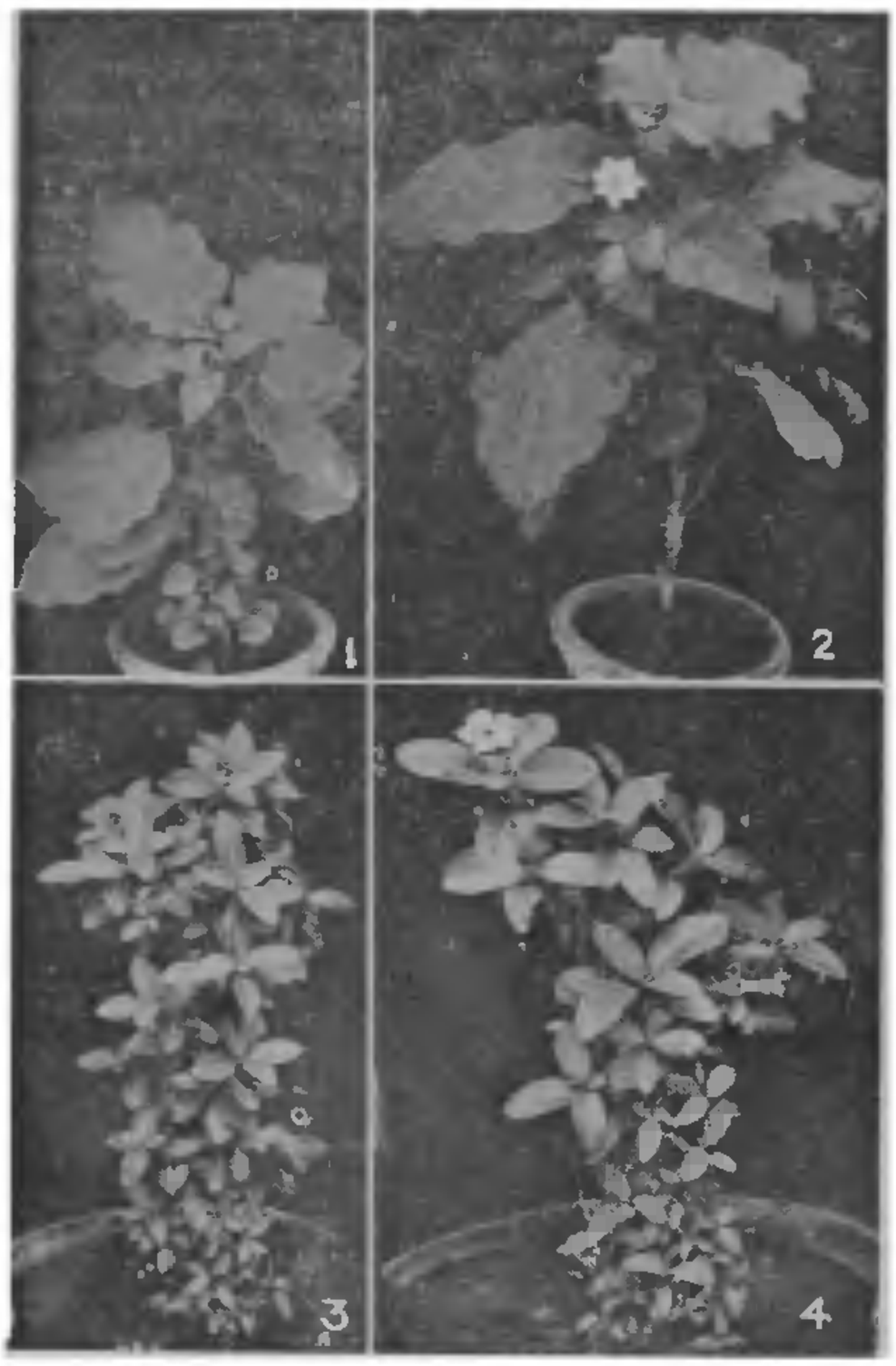
healthy and bore normal-sized leaves and also healthy flowers (Figs. 3 and 4). Axillary buds in these shoots were dormant.



FIGS. 1–4. **Fig. 1.** Eggplant untreated control—45 days after graft-inoculation. **Fig. 2.** Eggplant treated with 500 ppm chlortetracycline—45 days after graft-inoculation. **Fig. 3.** *Vinca rosea* untreated control—90 days after inoculation. **Fig. 4.** *Vinca rosea* treated with 500 ppm chlortetracycline—90 days after inoculation and 40 days after commencement of treatment. Spraying with antibiotic was done at three-day intervals.

Maramorosch *et al.*[6] have suggested that amenability to cure by comparatively low temperatures may be another characteristic of plants infected by mycoplasma-like agents. This is illustrated by the fact that aster yellows disease is inactivated by exposures to temperatures of 38°–42° C.[5] We have observed that when fully little leaf diseased *Vinca rosea* plants were exposed to 40° C. for 15 days or 44° C. for 8 days, the disease symptoms were completely reversed.

The present results indicate that the eggplant little leaf disease is probably caused by mycoplasma or psittacosis-lymphogranuloma-trachoma-like agents. Electron micrographic studies to confirm the above results are in progress.

Dept. of Plant Pathology,
Agricultural College and
Research Institute,
Coimbatore-3, *April* 18, 1969.

A. ANJANEYULU.
K. RAMAKRISHNAN.

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SOME STUDIES ON *GOSSYPIUM* SPECIES AND THEIR F_1 HYBRIDS

1. Alcohol Leaf Extract Coloration

IN certain *Gossypium* species and species hybrids, five main stem leaves were fixed in absolute alcohol for 24 hours for subsequent observations on leaf stomata. An incidental observation reported here is the coloration of the alcohol fixative drawing the pigments from the leaves of the various species and hybrids subsequent to fixation.

G. herbaceum (A_1), *G. arboreum* (A_2), *G. anomalum* (B_1), *G. sturtianum* (C_1), *G. thurberi* (D_1), *G. armourianum* (D_2), *G. klotszchianum* (D_3-1), *G. aridum* (D_4), *G. raimondii* (D_5), *G. gossypioides* (D_6) and *G. stocksii* (E_1) F_1 (*G. arboreum* × *G. raimondii*), F_1 (*G. arboreum* × *G. armourianum*), F_1 (*G. arboreum* × *G. stocksii*) at the diploid level, F_1 (*G. hirsutum* × *G. raimondii*), F_1 (*G. hirsutum* × *G. armourianum*) at the triploid level and *G. hirsutum* race *mariegalante* and *G. barbadense* at the tetraploid [2 (AD)] level were taken for study in the present instance. (Symbols in parenthesis denote the genomes.)

An interesting feature noted was that the leaves of *G. raimondii* gave a very dark brownish-green colour, entirely different from any other species. The same colour was observed in the two hybrids involving this wild species as one of the parents and also in the two tetraploids [2 (AD)]. In no other species or hybrid combination was this characteristic colour evident. *G. anomalum* gave a pale orange coloration while the other species (excepting *raimondii*) were observed to have a pale olive green alcohol coloration.

If the *raimondii* pigment could be observed in the synthesised hybrids having this species as one of the parents at the diploid and triploid level, it is presumed that by the same token of hybridization, the *raimondii* coloration has been imparted to the tetraploids also. The tetraploid cottons (AD genome) are believed to have arisen due to natural hybridisation between the A and D genomes at the diploid level and subsequent spontaneous doubling to form amphidiploids. Of the several D genome species, *G. raimondii* has been suggested as the most likely species to have hybridized with A genome based on morphological, cytological and genetic tests.[1-3]

The observations in the present study also tend to confirm the postulate of the previous investigators that *G. raimondii* is the most likely species to have contributed its genome to the tetraploid cottons.

a similar pigmentation on the anther cases of this species. In the F_1 hybrids mentioned above, the petal spot and the filament pigmentations are expressed very markedly while there is an incomplete expressivity for the androecium base colour. The red anther case colour is not observed in such F_1s.

In *G. armourianum*, the R_1^{ARM} gene controls the petal spot.[5] Again, there is no information available if this gene is responsible for the orange-red androecium base colour and organge-yellow anther case colour in this species. In F_1 hybrids, between this species as the male parent and the cultigens mentioned above, the petal spot and androecium base pigmentations are dominant in hybrids with *G. hirsutum*, while the anther case colour is recessive and with *G. arboreum*, all the three characters are expressed fully.

The data are as in Table I.

TABLE I

Sl. No.	Species and crosses	Anther case		Pollen colour	Filaments	Androecium base
		Shape	Colour			
1	*G. arboreum* race *indicum*	Reniform	Yellow	Yellow	Pale yellow	Pale yellow
2	*G. arboreum* race *soudanense*	,,	,,	,,	Red for basal filaments and pale yellow for top filaments	,,
3	*G. hirsutum*	,,	Pale yellow	,,	Pale yellow	,,
4	*G. raimondii*	Horseshoe	Red	Cream	Red	Red
5	*G. armourianum*	Reniform	Orange-yellow	Yellow	Pinkish-white	Orange red
	F_1 (1×4)	Horseshoe	Yellow	,,	Red	Red spots on pale yellow background
	F_1 (3×4)	,,	Pale yellow	,,	,,	Pale yellow
	F_1 (2×5)	Reniform	Orange-yellow	,,	Pinkish-red	Red
	F_1 (3×5)	,,	Pale yellow	,,	Pinkish-white	Orange-red

2. Anther Cases and Colour

In the species of *Gossypium*, the anther cases are generally reniform in shape. Exception to this generality is seen in the wild American diploid species *G. raimondii* Ulb., in which the anther cases are usually the shape of a horseshoe. In hybrids between the wild species as the pollen parent and the cultivated *G. arboreum* (diploid) and *G. hirsutum* (tetraploid), which possess reniform anthers, it has been observed that in the F_1s, the horseshoe shape is dominant over the reniform shape. As the F_1s are sterile, it has not been possible to follow the inheritance further.

The characteristic red pigmentation in the petal spot, filaments and base of androecium is controlled by the R^{RAI} gene in *G. raimondii*.[4] It is not known if this gene is responsible for

From the observations, it would appear that the horseshoe shape of the anther cases in *raimondii* may be under the influence of a gene (or genes) as this shape is markedly dominant over reniform shape in F_1s with the cultigens.

The 'R' locus-controlling pigmentation on the anther cases in the wild species would seem to be incapable of expressing the colour, when transferred to the cultigen background except in the case of *arboreum-armourianum* hybrid. The varied aspect, in the expression of anther case colour alone, is suggestive of an independent gene control for this character.

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Agricultural College and Research Institute, Coimbatore-3, *January* 28, 1969

MANOHAR BAHAVANDOSS

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A NEW BACTERIAL DISEASE OF *BIOPHYTUM SENSITIVUM*

Biophytum sensitivum (L) D.C., a member of the Geraniaceæ, is found commonly growing in fields during rainy season. In September-October 1967, a leaf spot disease was noticed on this plant at Machhad near Navsari, Gujarat State. The morphological, cultural and physiological characteristics of the pathogen showed it to belong to the genus *Xanthomonas*. Similar disease on two other members of Geraniaceæ, *viz.*, on *Pelargonium* sp. by *X. pelargonii* (Brown) Starr and Burkh. and on *Geranium* sp. by *X. geranii* (Burkh.) Dowson has been reported.[1,2] *B. sensitivum* appears to be the third member of this family to show an infection by *Xanthomonas*.

The disease at first appears as minute water-soaked spots, round to irregular, measuring 1 to 3 mm. in diameter. They are mostly hypophyllous but are also found at the leaf margin which in severe cases cause blighting of the leaf. The pathogen seems to enter through stomata and hydathodes.

The causal organism was isolated on PDA and M_2 media. On inoculation of the young and mature plants of *B. sensitivum* the typical symptoms developed in about 15 days. The pathogen reisolated was identical with the original.

By artificial inoculation, the pathogen could not infect *Tamarindus indica* L., *Lawsonia alba* L., *Triticum vulgare* H., *Sorghum vulgare* P., *Capsicum annuum* L., *Vigna catjang* W., *Cajanus cajan* M., *Ricinus communis* L., *Vernonia cinerea* L., *Carissa carandus* L., *Bauhinia racemosa* L., *Clerodendron phlomides* L., *Phaseolus* sp., *Gossypium* sp., which are found in the vicinity and from which *Xanthomonas* disease was reported. *Averrhoa carambola* L., *Oxalis corniculata* L., and *Impatiens blasamina* H., which belong to Geraniaceæ, could not be infected by the pathogen under study.

Since no bacterial disease is reported from the host *B. sensitivum*, and the pathogen isolated differs from *X. pelargonii* and *X. geranii* in some of the characteristics and its host range, it is, therefore, proposed to assign a new name *Xanthomonas biophytii* nov. sp. to this pathogen. The technical description of the pathogen is as follows:

Xanthomonas biophytii Nov. Sp.

Short rods with rounded ends, usually single, rarely in pair, measuring 1–1·7 × 0·5–0·7 microns, gram-negative, motile with polar flagellum, capsulated, no endospore, non-acid-fast, colonies on PDA plate—big circular, smooth surface and entire margin, butyrous and glistening yellow. Growth on PDA slant is abundant, filiform, convex, smooth, opaque, butyrous and glistening yellow, medium remains unchanged. On nutrient agar growth is moderate, filiform, flat, smooth, opaque and glistening yellow.

Starch hydrolysed, casein digested, tributyrin hydrolysed, gelatin liquefied and hydrolysed, milk peptonised and litmus reduced, nitrates not reduced to nitrites, ammonia and hydrogen sulphide produced, indol not produced, V.P. and M.R. tests negative, uric acid utilised but not citrate, tolerates 3% sodium chloride but not 5%, acid without gas from maltose, glucose, lactose, sucrose, arobinose, fructose, mannose, inuline, cellobiose, galactose, but no acid and no gas from mannitol, xylose, raffinose, rhamnose, sorbitol, inocitol, dulcitol, glycogen, glycerol and salicin. Catalase positive, aerobic, optimum temperature 27°–31° C., thermal death point 53° C.

Pathogenic only to *B. sensitivum* producing spots as well as blighting symptoms on leaves.

Thanks are due to Rev. Fr. H. Santapau, Director, Botanical Survey of India, for suggesting the Latin name for the pathogen and to Principal P. B. Menon, Baria Science Institute, Navsari, for his interest in the present work.