Table 1 *Binding of some cell wall degrading enzymes of Fusarium oxysporum f.sp. udum by isolated host- and non-host cell walls*

Enzyme	(Control cell walls) Enzyme activity*	Cell walls	In presence of cell walls: Enzyme activity	% activity*	% inhibition	After desorption with 0.2 M NaCl: Enzyme activity	% activity of the original	% activity recovered
Exo-PL	27.7	Host	12.3	44.5	(55.5)	11.3	40.8	85.3
		Non-host	13.6	49.1	(50.9)	10.7	38.3	87.4
Exo-PAL	12.6	Host	7.3	58 0	(42.0)	3.2	25.4	83.4
		Non-host	8.4	66.7	(33.3)	2.7	21.5	88.2
Endo-xylanase	78.1	Host	54.6	70.0	(30.0)	19.3	24.8	94.8
		Non-host	53.7	68.8	(31.2)	17.3	22.2	91.0

*Enzyme activities are expressed in $IU \times 10^2$ ml^{-1}.

amount of enzyme desorbed from cell walls by adding 0.2 M NaCl, gave the per cent recovery of the enzyme.

The results (table 1) indicate that all the test enzymes were bound by host-, as well as non-host cell walls to some extent. The binding of enzymes ranged from 30 to 55.5%. Exo-PL was bound maximally by both host and non-host cell walls (by over 50%). Exo-PAL was inactivated by 42% and 33% by host and non-host cell walls respectively. Endo-xylanase was inactivated by about 30% and 31.2% by both types of cell walls.

The enzyme activity lost due to binding after incubation with cell walls and the activity of enzymes desorbed from cell walls by 0.2 M NaCl (table 1) indicate that enzymes adsorbed by cell walls were not completely recovered. In the case of pectic enzymes the recovery varied from 85.3% to 88.2%; the maximum activity was recovered for endo-xylanase (90%).

The present results suggest that enzyme binding by cell walls is not limited to endo-PG only. The exo-pectic enzymes and endo-xylanase were equally amenable to binding by cell walls. No consistent difference was noted in binding of any enzymes on incubation with host-, or non-host cell walls. The release of bound enzymes by desorption with NaCl was not total (i.e. not 100%), which could be due to the irrevocable immobilization of enzymes by cell walls, or the high binding affinity of the cell walls. It could also be a function of the porosity of cell walls and molecular size of the enzymes as suggested by Knee *et al*[9].

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SOMATIC INSTABILITY IN THE POPULATIONS OF *CYPERUS CYPEROIDES* (L.) O. KUNTZE (CYPERACEAE)

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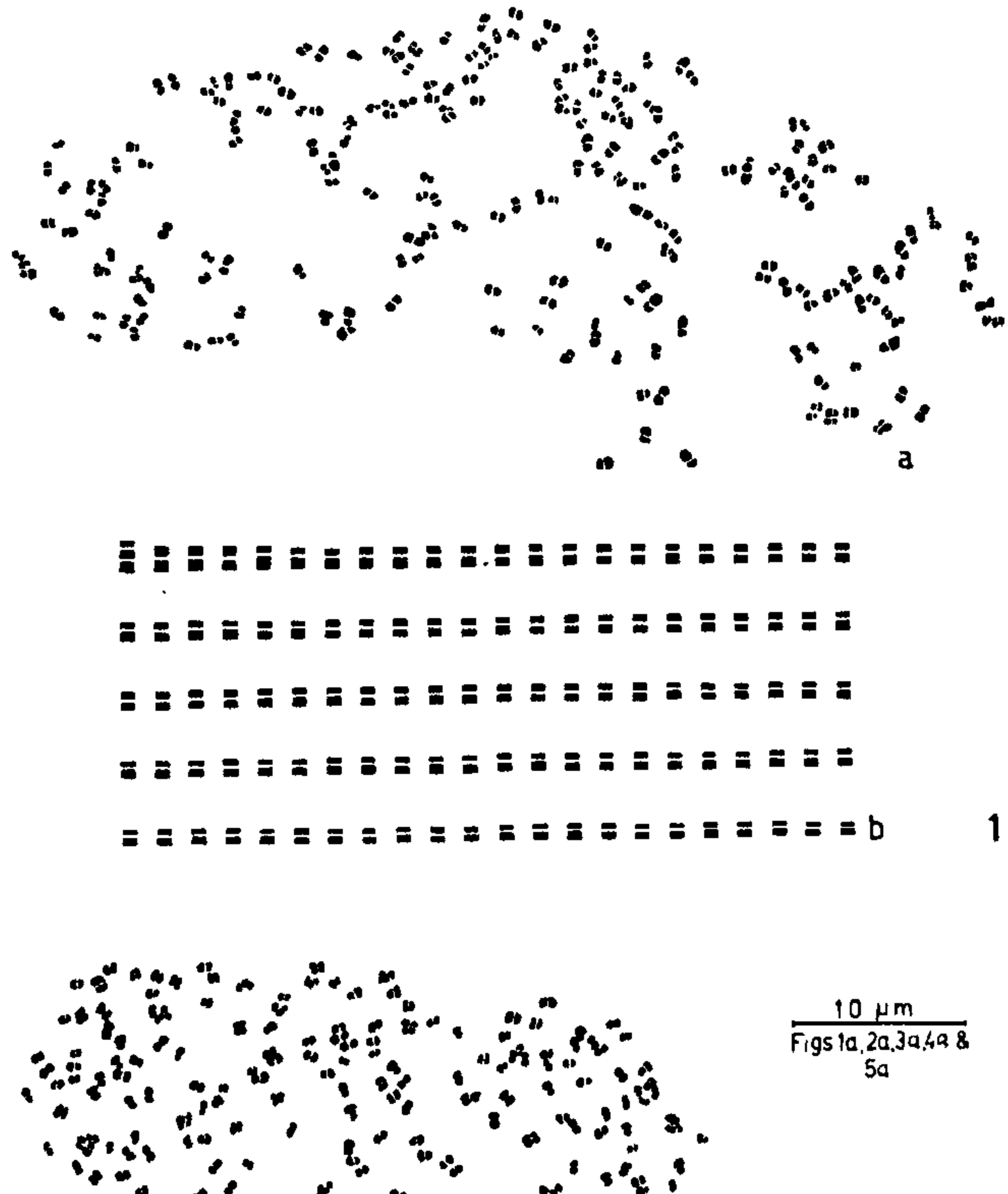
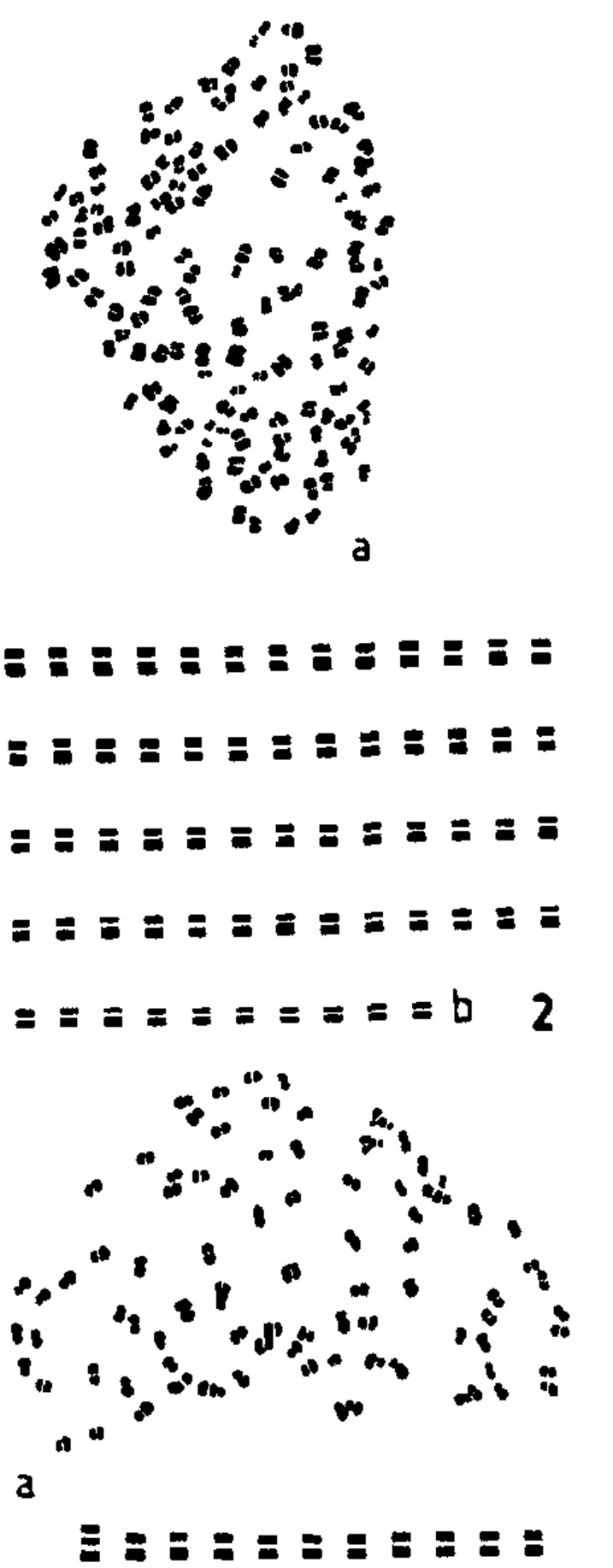
CYPERUS CYPEROIDES is one of the polymorphic sedges widely distributed adapting to different geo-

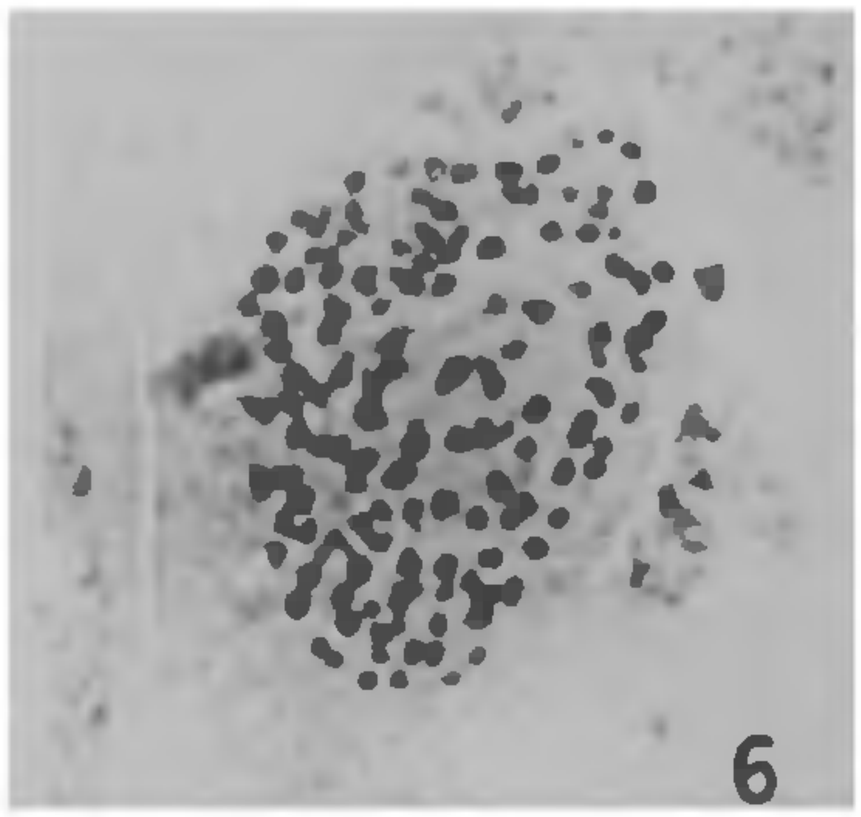
graphical ranges from tropical to subtropical regions. It is a rhizomatous perennial with robust stems.

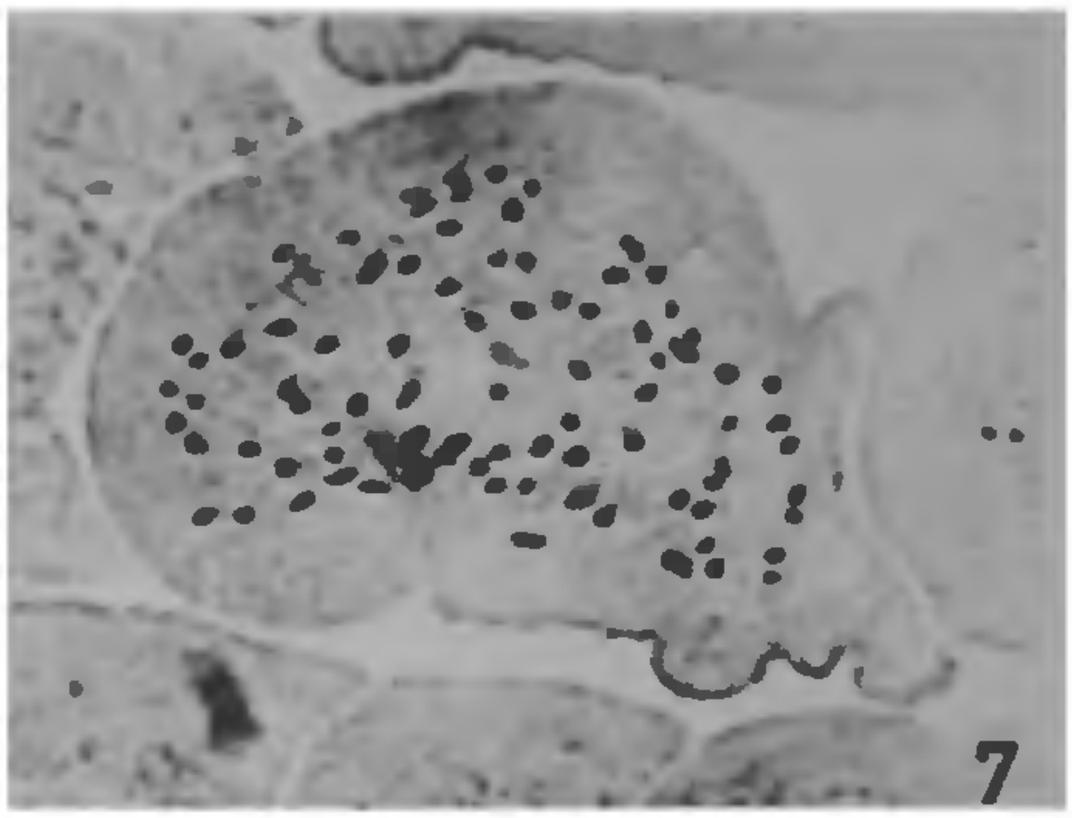
Since no previous cytological work is available on this species, five populations collected from Nandi Hills, Kemmangundi, Yercaud and Bangalore, were subjected to karyotypic analysis. To study the somatic chromosomes, the root tips were pretreated with *p*-dichlorobenzene and stained in Feulgen.

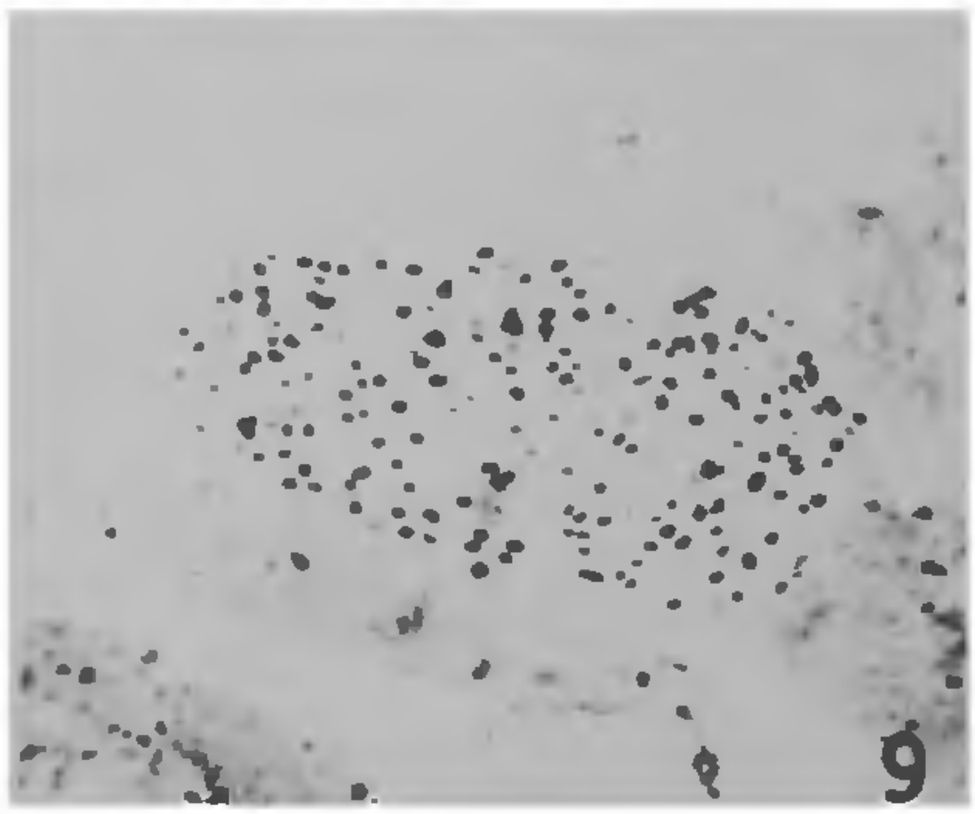


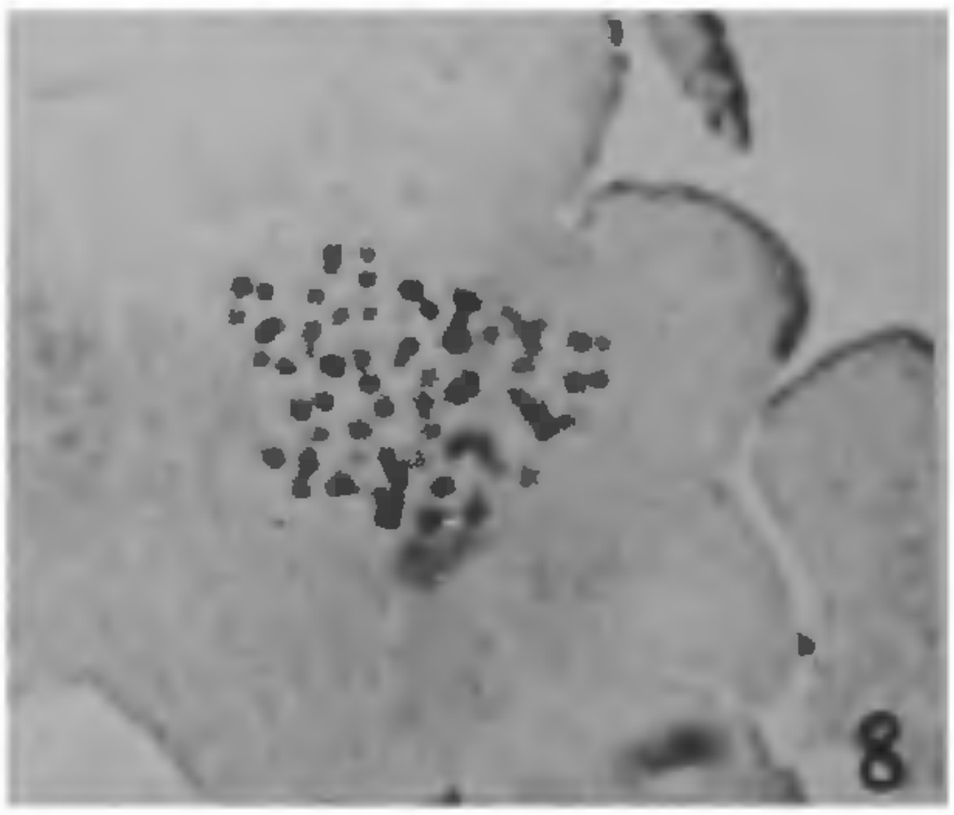


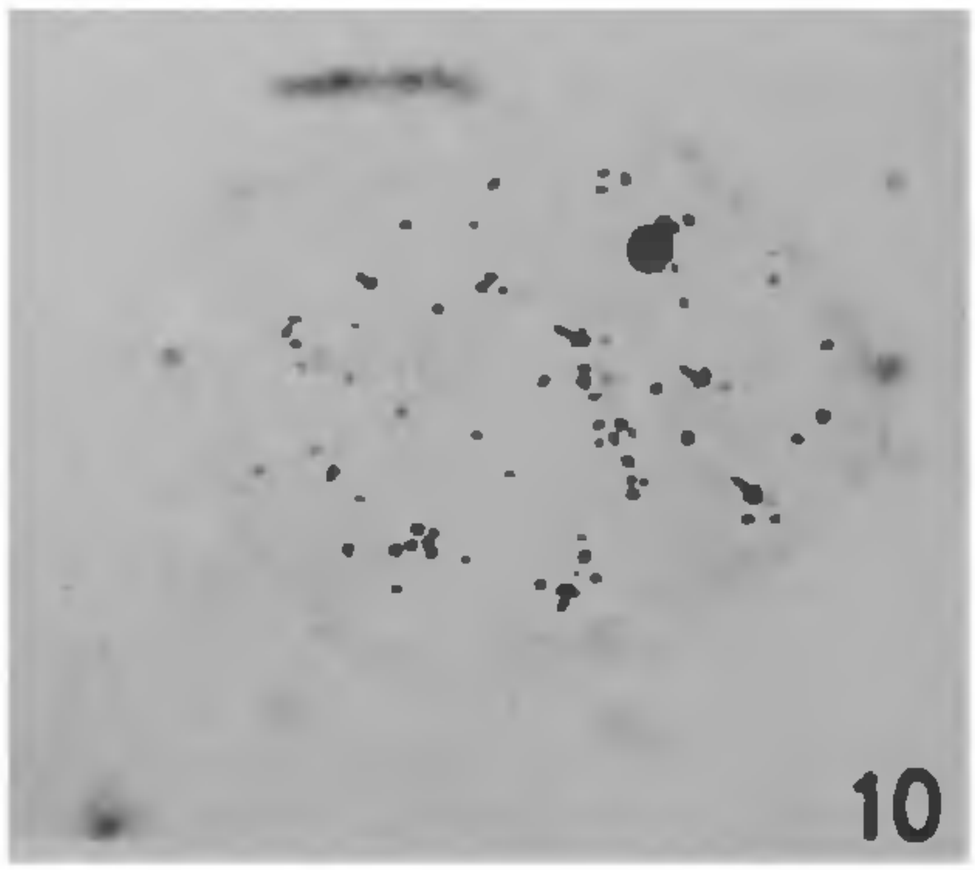
Figures 1–5. Coll. Nos. 96, 92, 119, 97 and 122 respectively. **a.** represents somatic metaphase, and **b.** idiogram of the same.

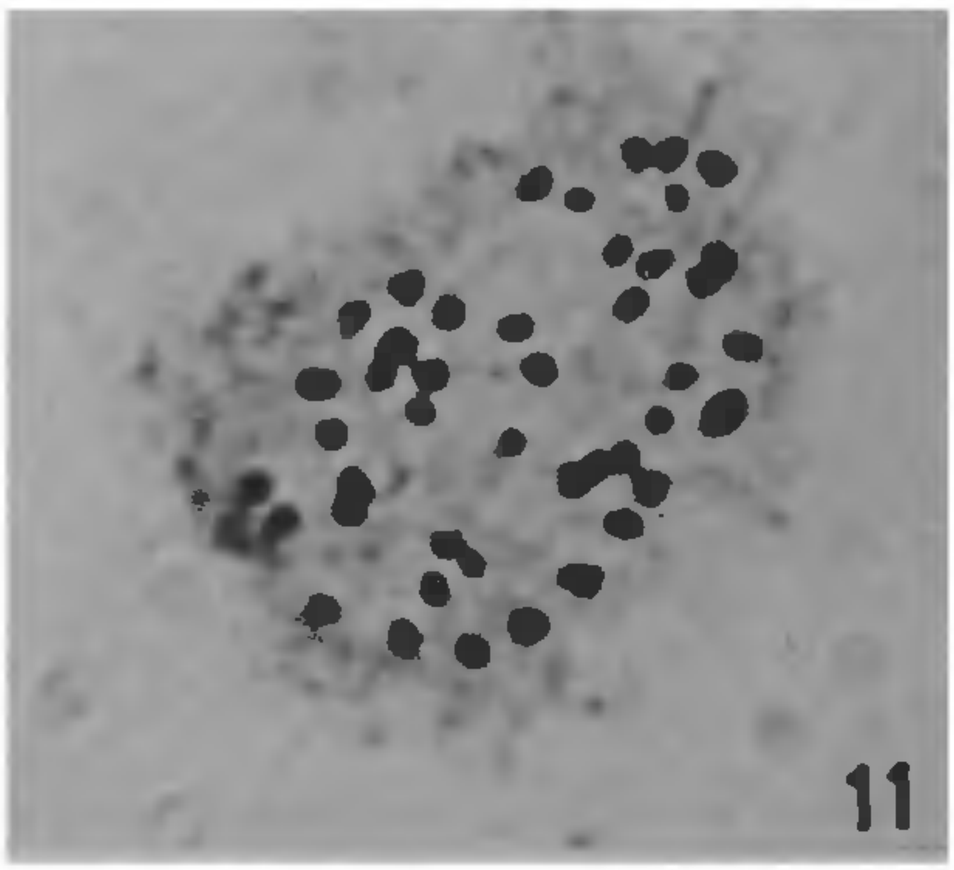












Figures 6–11. 6–9. Photomicrographs of somatic metaphase. Coll. Nos. 92, 119, 97 and 122 respectively. **10.** Coll. No. 92. Diakinesis showing 65 bivalents and 4 univalents (marked), and **11.** Coll. No. 119. Metaphase I showing 44 bivalents.

Well-spread plates of somatic chromosomes were selected for drawing and photomicrography. For meiotic studies, buds of proper stage were fixed in acetic alcohol (1:3) and smears prepared using 2% acetocarmine.

The diploid chromosome numbers vary from 82 to 224. All the five populations exhibit symmetrical karyotypes with a predominance of chromosomes having median and submedian centromeres. The chromosomes are relatively small ranging in length

Table 1 *Karyotype analysis in Cyperus cyperoides*

Taxa populations and locality	Chromosome number ($2n$)	Type of chromosomes		No. of satellited chromosomes	Total length of the diploid component (μm)
		Median	Sub-median		
Coll. No. 97 Nandi Hills	82	27	14	–	50.5
Coll. No. 119 Kemmangundi	88	37	7	–	64.4
Coll. No. 92 Yercaud	134	56	11	–	98.1
Coll. No. 96 Bangalore	220	100	10	2	172.1
Coll. No. 122 Bangalore	224	105	7	–	162.1

No sub-terminal chromosome was found in any of the taxa.

from 0.4 μm to 1.15 μm (figures 1–9). The details of karyotypes are given in table 1.

Meiosis is fairly normal in all the five populations (figure 11). Occasionally, in an Yercaud population, 2 or 4 univalents have been observed in a few pollen mother cells at diakinesis (figure 10).

The Cyperaceae is known for a remarkably wide range of chromosome numbers which vary from $n = 3$[1,2] to $n =$ c.108[3]. The present report of $n = 112$ in one of the populations studied, is the highest number reported so far in a family. The suggested basic numbers for the genus *Cyperus* are $x = 8, 9$, 13 and 60[3,4]. Löve *et al*[5] and Mehra and Sachdeva[6] suggested that the original basic number for Cyperaceae is $x = 5$ and other numbers are derived from this number through aneuploidy. Ramakrishnan and Ramachandran[7] while discussing the original basic number of the genus *Fimbristylis* categorically stated that the higher basic numbers may not be true in the phylogenetic sense as they might have been secondarily derived from the original basic number of 5. However, the basic number for the present species is difficult to decide because of somatic instability. The five different chromosome numbers observed in the five populations are in the multiples of 5, 8, 41 and 67.

The extensive series of chromosome numbers found in the inter-related populations are reported in *Carex*[8] and *Eleocharis*[9–11]. This range of chromosome numbers is attributed to the diffuse nature of the centromeres *in* those particular genera. However, the present observations reveal the presence of chromosomes with localized centromeres in all the populations studied. Stebbins[12] suggested two reasons for the wide variations in chromosome numbers within a single species. This range is attributed to the hybridizations and inter-crossings between races and subsequent doubling of chromosomes. Secondly, the loss and gain of individual chromosome pairs will have less deleterious effects, because of the higher degree of chromosome duplications. The variations in chromosome numbers within a single species indicate the role of aneuploidy in speciation.

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XANTHOMONAS CAMPESTRIS PV. *JUGLANDIS* —A NEW REPORT FROM INDIA

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THE walnut is an important fruit crop of hills of India. The bacterial blight of walnut (*Juglans regia*) caused by *Xanthomonas campestris* pv. *juglandis* is recorded from India. The disease, observed in the orchard of the Govt. Fruit Research Station, Pithoragarh during May and June, was noted in all the ten varieties of walnut. The fruit infection (%) was Xenia 47.16; Tutle 31 25; Tutle 16 16.23; RX Giant 20; Hartley 42.85; Franquette 39.39; Conveymytle 16.15; Payne 39; G. Seedling 37.50; and Blackmore 33.73.

No infection was found on local varieties of walnut. In Switzerland the fruit infection was reported[1] to be very high i.e. Esterhazy 70–90% and Franquette 50%.

The young leaves seem to be most vulnerable to infection during mid May. The water-soaked translucent spots appear on the leaves along the midrib and sometimes on the leafsheath. These spots gradually increase in diameter, turn brown to black and form circular to irregular patches. The disease spreads to new leaves and sometimes large areas are formed due to the coalescence of a number of small spots leading to the death and shedding of leaves. Symptoms also appear on petiole and fruits (figure 1). Infection causes considerable reduction in the fruit size and premature fall of fruits. During the advanced stage dry spots become rougher, raised, cracked and the entire fruit decays. The bacterium is rod-shaped (0.2–0.5 × 1.2–2 μ in size), forms no spores and capsule, and is gram-negative and aerobic. Colonies on beefagar are circular, straw yellow to pale yeliow and slightly raised.

Figure 1. Infected fruits of walnut by *Xanthomonas campestris* pv. *juglandis*.

The pathogen has been identified as *Xanthomonas campestris* pv. *juglandis* (IMI 317492 and 317493).

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TRANSFER OF BIOLOGICALLY FIXED NITROGEN FROM SOIL TO RICE PLANT

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PADDY soils favour the activities of free-living nitrogen fixers significantly contributing to nitrogen economy[1,2], $^{15}N_2$ incorporation studies on rice plants under water culture conditions reveal that less than 10% of the fixed nitrogen was translocated to the plant tissues[3]. However, a total of 19–25% of the nitrogen fixed in the rice rhizosphere was transferred to the roots, leaves, stems and ears of the rice plant during $^{15}N_2$ exposure[4]. Considerable losses of nitrogen can also occur in waterlogged rice soils than in aerobic soils[5,6]. Evidently, information regarding the availability, transfer and distribution of biologically fixed nitrogen to rice is limited and conflicting. The present study was, therefore, aimed at demonstrating the transfer and distribution of biologically fixed nitrogen to the rice plant employing ^{15}N-tracer technique.

The transfer of biologically fixed nitrogen to the