TABLE I

Pathogenicity-pattern of the physiologic race IC 17 Pyricularia oryzae *Cav.*

Raminad str. 3	Zenith	N.P. 125	Usen	Dular	Kanto–51	CI 8970 (S)	Caloro
R	R	S	R	S	S	S	S

R = Resistant, S = Susceptible.

identification of physiologic races of the pathogen. The highly susceptible variety, Co. 13 was utilised as a check for detecting the success of inoculation and the identity of the physiologic race of the pathogen which may not produce any visible symptoms on the plants of the eight differentials[2]. The method of identification of the physiologic races of *P. oryzae* was the one described by Padmanabhan *et al.*[7]. The classification of Ling and Ou was adopted[5].

The data revealed that the one hundred and ten isolates of the pathogen belonged to the race IC 17[5]. The pathogenicity-pattern of this race is presented in Table I.

The physiologic race IC 17[5] was reported to be the most prevalent one in India since 1962[2,4]. The predominant prevalence, survival and succession of the race IC 17 over the other races indicates that this is a very stable race.

Miura and Ito[8], have reported the 'prosperity and decline of the race C in Japan'. Goto[9], stated "a certain delay is expected in the increase of adapted (or severe) races as compared with the increased cultivation of the varieties with new resistance; for instance, a delay lasted about ten years in the case of the variety, Futaba". The time lag between the introduction of a resistant variety and the break-down of resistance in the plants of the variety—obviously by the appearance of a new physiologic race of the pathogen—denotes a phase of host-pathogen equilibrium in the area. This phenomenon is evidenced by the monoracial succession brought about by the elimination of less stable biotypes of the pathogen and non-appearance of new races of the pathogen in the area. During the period under report no instance of break-down of resistance in a rice variety on a field scale has come to the notice of the authors, which has been known for its resistance in that locality.

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SALT TOLERANCE OF COTTON AND POTENTIAL USE OF SALINE WATER FOR IRRIGATION

A SATISFACTORY stand of cotton crop on saline soils and/or under saline water irrigation is a serious problem of common occurrence. Crop failures are due to the accumulation of salts which results in the reduction of seed germination and plantgrowth. Cotton, being recognised as the most salt tolerant of all the field crops, has not received the salinity study. The present work deals with the relative salt tolerance of some important cotton varieties and hybrid Varalaxmi at germinatios stage with different levels of salinity under field conditions.

The experiment was conducted in bottomless coal tar drums embedded in medium black clay soil (vertisol). Bhagya, Hampi, Laxmi and hybrid Varalaxmi were used in the present investigation. Saline water used for irrigation (conductivity values of 4, 8 and 12 mmhos/cm) was prepared by dissolving sodium chloride, sodium sulphate, sodium bicarbonate and calcium chloride on weight proportions (w/w) so as to obtain Na : Ca in the ratio of 4 : 1 and C_1 : SO_4 : HCO_3 in the ratio

of 2 : 1 : 1[1]. Two replications were maintained for each treatment. Saline water was added and the soil was incubated for 15 days prior to sowing. Ten seeds were sown in each drum and the germination counts were recorded till 30th day. Plant samples were then drawn and dried at 70° C and used for chemical analysis. The leaf samples were analysed for sodium and potassium[3].

The data on germination recorded on 10, 20 and 30th day after sowing reveal that hybrid Varalaxmi had better germinability. At the salinity level of 12 mmohs/cm, per cent germination recorded on 30th day was 40 and 25 in the case of Varalaxmi and Bhagya and 15 in the case of both Hampi and Laxmi. These differences may have greater impact, if cotton has to be grown on a salt affected land and/or under saline water irrigation. Thus, selection of a climatically adopted salt tolerant variety and/or hybrid rather than one of lower salt tolerance may mean the difference between a good to a fair stand.

The effect of presowing salinization on cationic composition of cotton leaves are presented in Table I.

Varalaxmi and Bhagya was much lower than in Hampi and Laxmi in relation to its abundance and availability in the applied saline waters. This strongly suggests that Varalaxmi and Bhagya exclude sodium absorption by some selective mechanism. This exclusion of sodium may partly be responsible for the relatively high tolerance shown by Varalaxmi and Bhagya and this is common to many salt tolerant plants[4,6-8].

In the present study K : Na ratios as high as 1·6 in Varalaxmi and Bhagya as compared to a lower K : Na ratio of 0·63 in Hampi and 0·45 in Laxmi at the salinity level of 12 mmhos/cm provide support to the opinion that K : Na ratio has a role[5,10] in determining salt tolerance in plants (Table I).

Since this crop is grown primarily for its seed cotton, the effect of presowing irrigation with saline water on seed cotton yield is of importance. The per cent drop in seed cotton yield at the salinity level of 12 mmhos/cm compared to the yield obtained under best available water (conductivity of 1 mmhos/cm) used for irrigation was 9. 45, 59 and 75 in the case of Varalaxmi, Bhagya, Laxmi and Hampi respectively.

TABLE I

Ionic composition of cotton leaves as affected by presowing salinization

Ionic constituents, meq/100 g of dry matter	Salinity level, mmhos/cm	Varieties/Hybrid			
		Varalaxmi	Bhagya	Hampi	Laxmi
Na	0	4·17	3·83	7·48	6·87
	4	6·96	19·14	26·53	23·49
	8	26·97	29·58	28·70	41·33
	12	28·72	16·53	59·16	65·25
K	0	48·58	44·74	42·51	34·80
	4	46·02	35·74	28·38	35·79
	8	54·97	42·19	38·99	42·19
	12	48·24	27·29	37·07	29·12
K : Na ratio	0	11·66	11·68	5·68	5·06
	4	6·61	1·87	1·07	1·52
	8	2·04	1·43	1·36	1·02
	12	1·68	1·65	0·62	0·44

Presowing salinization affected the uptake of Na and K. Leaf samples of all the varieties revealed a sharp increase in Na content with increasing salinity of the water and support the findings of other workers[1,4,6,8]. Sodium uptake by

The ability to exclude sodium in relation to its relative data availability in the applied saline waters, the data on germination and seed cotton yield indicate the salt tolerance potential of Varalaxmi and Bhagya.

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DEXTRANASE PRODUCTION BY CERTAIN PLANT PATHOGENIC FUNGI

DEXTRANASE, which hydrolyses α-1, 6 glucosidic linkages in dextran, is of common occurrence in moulds and bacteria[1,2]. Though amylases are secreted by fungi they are reported not to hydrolyse any bonds in dextran even though the type of glucosidic linkage in dextran and starch is similar. Three soil-borne plant pathogenic fungi, *viz.*, *Rhizoctonia bataticola*, root-rot fungus of peanut, *Sclerotium oryzae*, stem-rot fungus of rice and *Fusarium oxysporum* f. *melonis*, the muskmelon wilt fungus were tested for the production of extra cellular dextranase and the results are reported here.

Czapek's medium containing dextran at 3% level as carbon source was dispensed in 50 ml quantities into 250 ml Erlenmeyer flasks, sterilized at 15 lb psi and inoculated with 8 mm disc of the fungi. Replicates were maintained for each organism. After 15 days of inoculation the biomass was filtered through previously oven dried and weighed filter-paper, dried at 105° C for 24 hr and reweighed. The dry weights of the biomass were recorded separately. The culture filtrates were retained for enzymes assay. The assay method described by Tsuchiya *et al.*[2], was followed with a modification for determining the dextranase activity. The reaction mixture contained 4 ml of 1% dextran suspended in sodium acetate-acetic acid buffer (pH 5·1), 2 ml of the buffer and 2 ml of the enzyme source. The release of the reducing sugar was estimated at 0 and 2 hr[3]. The activity of the enzyme on starch was also investigated.

The biomass production and enzyme activity of the three fungi are reported in Table I.

TABLE I

Effect of dextran on growth and dextranse production of the three fungi

Fungus	Biomass (mg)	Enzyme activity* (mg/ml)	
		On Dextran	On Starch
Rhizoctonia bataticola	250·0	0·223	0·295
Sclerotium oryzae	104·5	0·017	..
Fusarium oxysporum f. *melonis*	200·5	0·038	0 030

* Expressed as glucose equivalents.

Although Bourdu and Quilet[4] have reported the occurrence of dextran in the roots of *Anchusa sempervirens*, the substance, however, has not been located on most plant species[5]. Dextranase production by plant pathogens has not so far been reported. In the present study, of the three pathogens *R. bataticola* exhibited a marked dextranase activity and recorded a higher biomass followed by *F. oxysporum* f. *melonis* and *S. oryzae*. Interestingly, the culture filtrate from *R. bataticola* hydrolyzed starch effectively while that of *F. oxysporum* f. *melonis* showed only traces of activity. However, the enzyme from *S. oryzae* failed to act upon starch. Repression or inhibition of pathogen's enzyme(s) by fungitoxicants of the host, such as phenols was reported earlier[6 7 8]. The ability of *R. batatiola* and *F. oxysporum*. f. *melonis* to elaborate dextranase that can also act upon starch might therefore be of importance in pathogenesis as the dextranase might be active in case of amylase inhibition or repression by fungitoxicants of the host. Extracellular dextranase production by certain saprophytic fungi is well known[2]. All the three plant pathogens in the present study are soil-borne. Dextran is present in soil through the synthesis by soil bacteria[9]. Production of dextranase by these soil-borne plant pathogens