effective use of changes in salinity to trigger auxospore formation: in short, synchronizing its life cycle to changes in the hydrology of the habitat.

Amphora coffeaeformis (Agardh.) Kütz. isolated from a particular salinity grew best only at that salinity and differences in their behaviour seem to be related to the place of origin (cf figure 1 showing the typical behaviour of the diatom isolated from mid salinity range). Thus, there seem to be races differing in their salinity responses, as indicated for other species[5,6]. Cells when transferred from freshwater to very low salinity or from high to low salinity did show significant increase in length of apical axis of valves showing a response similar to *C. meneghiniana* Kütz.

Studies on salinity tolerance of diatom species isolated from freshwater, brackish water and marine environments confirmed the existence of races in many diatoms exhibiting optimum growth at low, mid or high salinity ranges, although the species as a whole may be classified as euryhaline. These can be conveniently called micro-, meso- and macro-euryvalent species. Occurrence and abundance of individual species may depend on conditions most favourable for their optimum development (figure 2).

In nearshore waters that are influenced by rivers, phytoplankton blooms often follow marked decreases in salinity. Dominant diatoms of such blooms, are in many cases, estuarine. During monsoon seasons both the Cooum and the Adyar estuaries deliver an influx of nutrients into the sea along with euryhaline diatoms, which play an important role in phytoplankton abundance both in estuaries and in nearshore waters. When phytoplankton from the sea are inoculated into the media of low salinities/freshwater, euryhaline diatoms such as *Cyclotella meneghiniana* Kütz., *Skeletonema costatum* (Grev.) Cleve, *Amphora coffeaformis* (Agardh) Kütz., *Navicula halophila* (Grun.) Cleve and *Nitzschia closterium* (Ehr.) Wm. Smith occur in sufficient numbers to be recognizable. These euryhaline diatoms may survive in coastal waters in non-monsoon season and may multiply in the estuary, its low salinity favouring their growth. They may also multiply in nearshore waters during monsoon season, when there is a decrease in salinity of the waters. While a small decrease may favour macrovalent species, a large decrease may favour meso- and even microvalent species. Rivers during this period will add more euryhaline diatoms to nearshore water and together they may produce a coastal bloom of euryhaline diatoms.

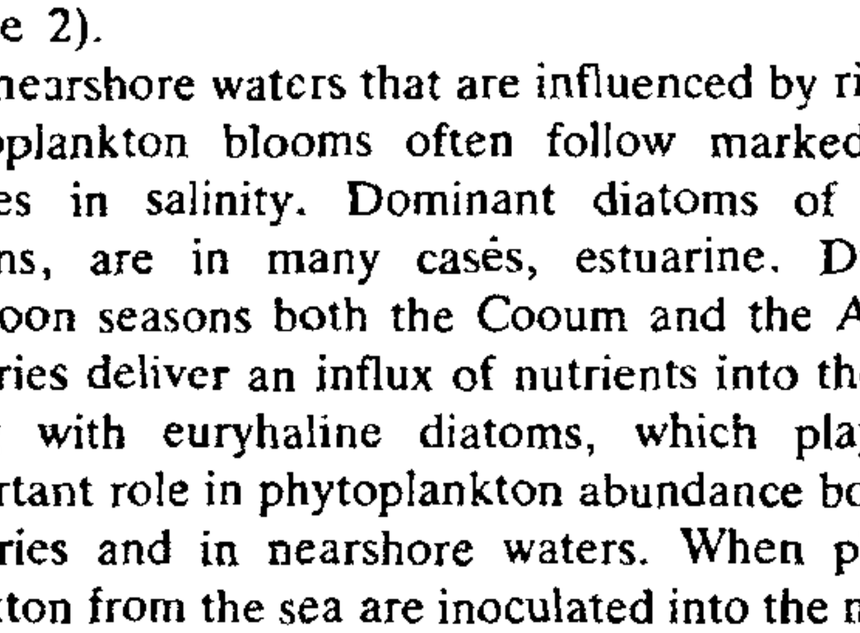

Figure 2. Hypothetical curves explaining the growth behaviour of euryhaline diatoms (after Desikachary and Rao[6]).

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SEED-BORNE INFECTION OF *FUSARIELLA HUGHESII* IN MUNGBEAN

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DURING the seed health testing of mungbean, seed samples received from Directorate of Pulses Research, Kanpur for screening against various diseases under natural conditions in spring and summer seasons showed the occurrence of 10% *Fusariella hughesii* infection in mungbean cultivar UPM 82–4 under standard blotter method test[1]. The fungus was isolated from untreated as well as treated seeds with 1% sodium hypochlorite for 5 min. In most cases the fungus did not allow the seed to germinate but it covered the whole surface of the seed with greenish black stromatic conidial masses (figure 1a). Conidia taken directly from the seed surface were fusoid, conicotruncate at the base, smooth, mostly 3 septate, 14–26 × 4.6 μm (figure 1C, D).

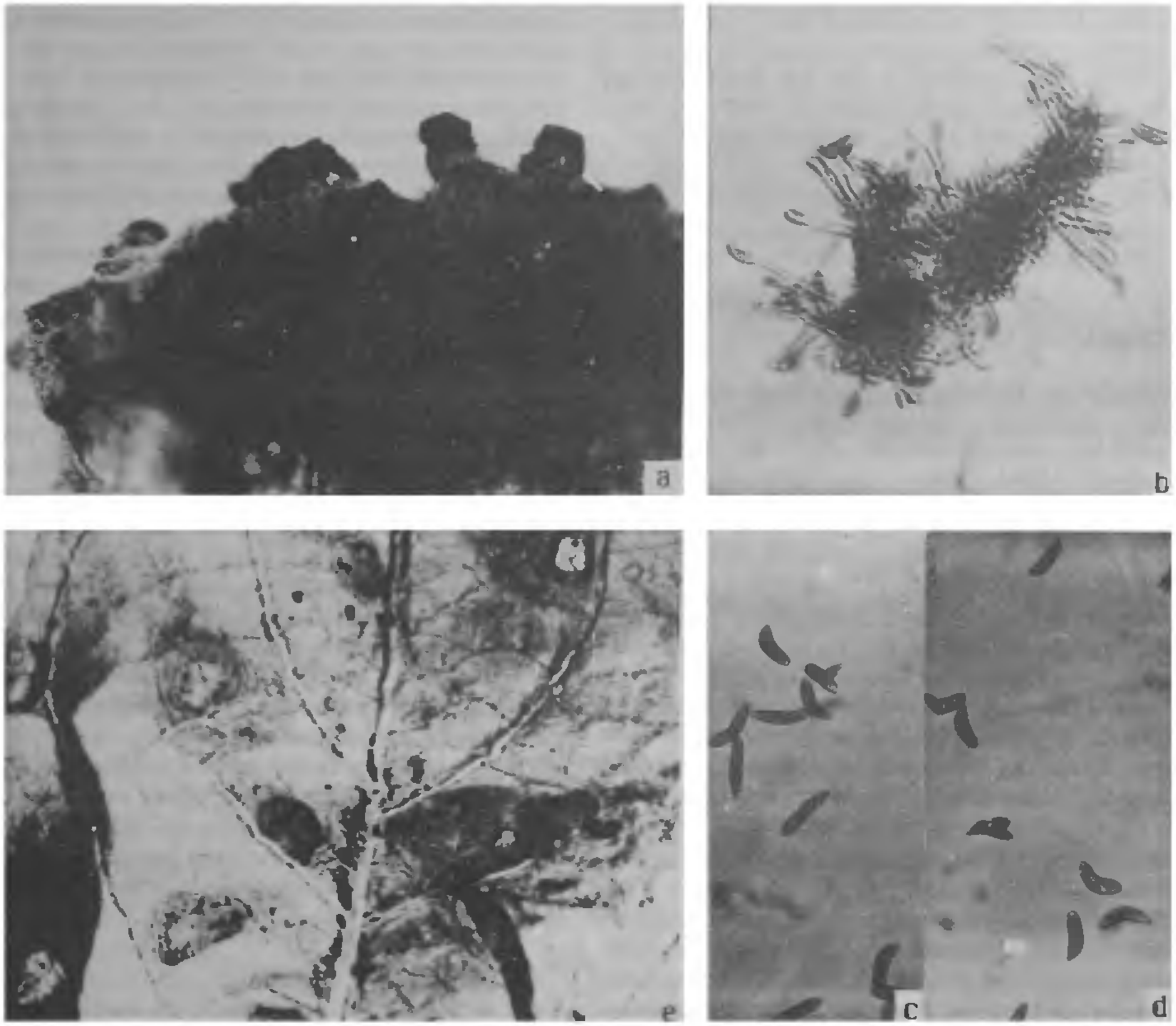

Figure 1a–e. *Fusariella hughesii.* **a.** Growth on incubated seed of mungbean (×400); **b.** Conidia and conidiophores (×1000); **c, d.** Conidia; **e.** Spots on leaf (×400).

On potato dextrose agar, the fungus forms whitish-tan colony which later turns greenish gray due to the formation of conidial mass in concentric rings or in zonation. Mycelium hyaline, septate, smooth and branched. Conidiophores arise as lateral branches of superficial hyphae, 24–36 × 4.0–4.3 μm, smooth. Conidia develop in basipetal succession from the apex of conidiophore (figure 1b), 14–26 × 4–6 μm, 1–3 septate, mostly fusiform. The colony does not bear three kinds of conidia as in the case of *F. indica* reported earlier[2]. But the present isolate is closely related to the *F. hughesii* reported from Israel by Favrman[3].

The pathogenicity of the fungus was determined by inoculating the healthy leaves of mungbean seedlings by spraying the conidial suspension (1000 spores/ml of sterilized water) from 15-day-old culture of *F. hughesii* with atomizer. Dark brown spots of varying size and shape (figure 1e) were developed on leaves after 12 days of inoculation. In nature similar symptoms were also developed on leaves of mungbean plants.

The fungus was recorded on dispersal units (seeds) of *Phalaris minor* and *Trigonella arabica*[3] but its role as a seed-borne pathogen has not been reported on these host seeds. On mungbean (*Vigna radiata* L.) this pathogen is recorded for the first time as seed-borne which also causes leaf spots in the field.

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PHYSIOLOGICAL BLOCKS UNDERLYING DORMANCY OF RICE

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THOUGH dormancy in rice had been described earlier[1,2] the underlying mechanism remains elusive. Specifically, the presence of rudimentary and physiologically immature embryo[3], germination inhibitors[4] and supra-optimal level of IAA[5] has been implicated. Removal or puncture of seed covering structures in rice was reported to improve the germination[6–9]. Recently, Lascorz and Drapron[10] demonstrated in dormant oats that the hulls generally considered as dead tissue are enzymatically active. In the present studies, the possible involvement of hulls and embryo in controlling the dormancy of rice has been elucidated.

Freshly harvested seeds of superfine variety (Basmati-370) were collected on 25 November 1986 immediately after harvest from the Ludhiana and Ropar Farms of the University. The seeds were dried to a moisture level of 12% before storing in cloth bags under ambient conditions. The germinability of the two lots was recorded at 15 day interval in the dark at 25±1°C (petri dishes 10 cm in diameter, 25 caryopses per dish) with four replications. Interestingly, after 75 days of harvesting, the seed lot from Ludhiana became non-dormant (88% germination) while the seed lot from Ropar remained dormant (20% germination). These non-dormant and dormant seeds were studied to understand the mechanism of dormancy. The hulls from the seeds were removed using fine tweezers. The peroxidase activity in the hulls was measured[11] and α-amylase activity was estimated[12].

Germination was studied in hulled (with lemma-palea), dehulled (without lemma-palea) dormant and non-dormant caryopses. In the dormant caryopses, a large difference in germination was observed between dehulled (70%) and hulled (20%) grains. Contrary to this, the difference in germination of non-dormant hulled and dehulled caryopses was very little (88% and 100%) respectively. These differences indicate a dormancy block in the hulls, which probably kept the embryo in hypoxic state and prevented germination. This block is perhaps removed during the dry post maturation period or by dormancy breaking treatments[13].

A high hull peroxidase activity was observed in the dormant caryopses whereas in the non-dormant caryopses, the hull peroxidase activity was feeble (table 1). Considering the findings of Lascorz and Drapron[10], the hulls in rice appear to absorb oxygen due to enzymatic activity and devoid of the embryo of oxygen. Kuo[14] reported high peroxidase activity in hulls of dormant rice caryopses and speculated its role in α-oxidation of fatty acids. Sircar[5] speculated that probably the supra-optimal level of IAA is responsible for the dormancy in rice. Due to high oxidative activity in hulls, the high level of IAA in the embryo does not get oxidized due to non-availability of oxygen.

Presoaking of seeds in water for 24 h did not improve germination nor it had any effect on hull peroxidase activity. Contrary to earlier results[15], the dormancy inhibitor in the present studies was not leachable by water. Presoaking of rice caryopses in GA_3 (500 μg/ml) and KNO_3 (0.2%) for 24 h completely removed dormancy and resulted in significant reduction in peroxidase activity in hulls (table 1).

Table 1 *Germination, peroxidase and α-amylase activities in dormant and non-dormant rice caryopses*

Treatment	Germination %		Peroxidase activity in hulls 10^{-3} A units min^{-1}		α-amylase activity μg starch hydrolysed grain^{-1} 10 min^{-1}	
	ND	D	ND	D	ND	D
Hulled caryopses	88	20	10	40	35.83	7.17
Dehulled caryopses	100	70	–	–	–	–
Water soaking 24 h	98	35	1	38	27.50	7.17
GA_3 soaking 24h (500 μg/ml)	98	92	1	5	28.60	28.60
KNO_3 soaking 24 h (0 2%)	98	82	1	8	30.70	26.50

ND – Non-dormant; D – Dormant.