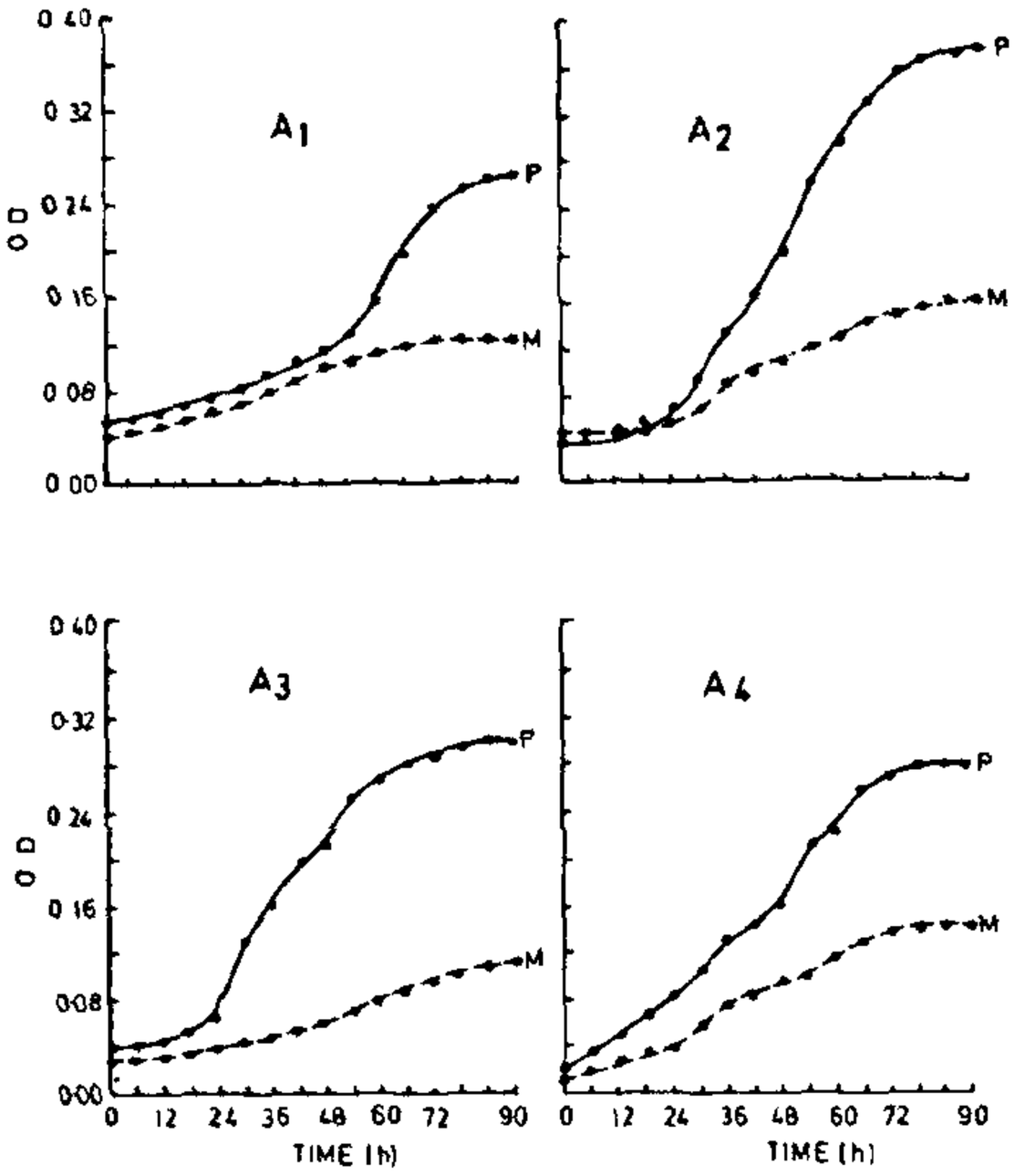

Figure 2. Growth pattern of the parent (P) and the mutant (M) strains of Pigeonpea *Rhizobium*.

phase. The growth pattern of both the parent and the mutant of the A_1 strain up to 54 hr was almost similar; however, later on, the parent culture exhibited a sharp rise in the growth. Strain A_2 showed the characteristic lag phase. The mutant of this strain was relatively slow in growth and showed the lag phase of 18 hr. The maximum difference in the cell density of the mutant and the parent type occurred on the last day of observation. The growth pattern of strain A_3 was almost similar to the strain A_2 and the maximum difference of 173 percent in the optical density of the parent and the mutant cultures was recorded on the final day of observation. Both the mutant and the parent cultures of A_4 did not show the characteristic lag phase. The parent culture of this strain was growing faster than the mutant from the beginning and the difference went on increasing, leading to the highest difference at 78 hr of growth. Pigeonpea rhizobia mutants were comparatively slow in growth rate than chickpea rhizobia mutants.

Not much work has been done on the physiology of antibiotic resistant mutants. In general, it has been observed that the streptomycin resistant mutants of bacteria are slow in growth[4]. In contrast, Dadarwal *et al.*[5] reported positive correlation between the growth rate and resistance of *Rhizobium* to penicillin and streptomycin. Zelazna-Kowalska[5] reported a spheroplast formation in *R. trifolii* strain B, after mutation to a high level of streptomycin (1000 μg/ml).

In view of the above results there appears a serious danger in the use of antibiotic resistant mutants in ecological studies because such slow growing mutants may be poor competitors for nodule forming sites on roots as well as for the other growth limiting factors. In general, a slow growing culture has poor saprophytic competence[7]. On the other hand, many workers[8-10] have reported that the antibiotic resistant mutants of *Rhizobium* are in no way inferior to the parent types in nodulation and other symbiotic properties. To resolve this point, more work is required on the growth rate in medium as well as in soil.

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MYCELIOPHTHORA VELLEREA (SACC & SPEG) VAN OORSCHOT: A NEW RECORD FROM INDIA

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MYCELIOPHTHORA is one of the most conspicuous and

better known keratinophilic hyphomycete genera, occurring in soil, rich in keratin. This was placed in synonymy with *Chrysosporium*[1] but was reintroduced[2]. Nearly all species of *Myceliophthora* produce ampulliform swellings, a feature absent in *Chrysosporium*.

The type strain of *Chrysosporium asperatum* synonymous to *Myceliophthora vellerea*, is distributed in the soils of Canada[3], Egypt[3] and USA[1] and so far reported only from soil. It is of particular interest that during the survey of keratinophilic fungi and related dermatophytes, *M. vellerea* was recorded from dropped off feathers of a stork, collected from the Zoo at Nagpur, Maharashtra, India. The fungus was obtained in pure culture and identified as *M. vellerea* (IMI 282420).

The colony on Sabouraud's dextrose agar medium is circular, flat, pale brown with white, even margin. The reverse is cream-coloured, racquet hyphae absent, hyphae hyaline 1–2 μ wide and thin-walled. Conidia occur in singles, twos or threes, borne on ampulliform swellings of the hyphae or its short or long narrow branches. They are hyaline, smooth and thin-walled in the initial stage but become pale brown or yellow, thick-walled and spiny or verruculose later. They are pyriform, elliptical or subglobose in shape, measuring 3–9 × 4–13 μ. The diameter of the colony reaches 49 mm in ten days at a temperature of 28°C. The isolate resembles the type description of *M. vellerea* (Sacc and Speg)[3].

Myceliophthora vellerea is reported here for the first time from India.

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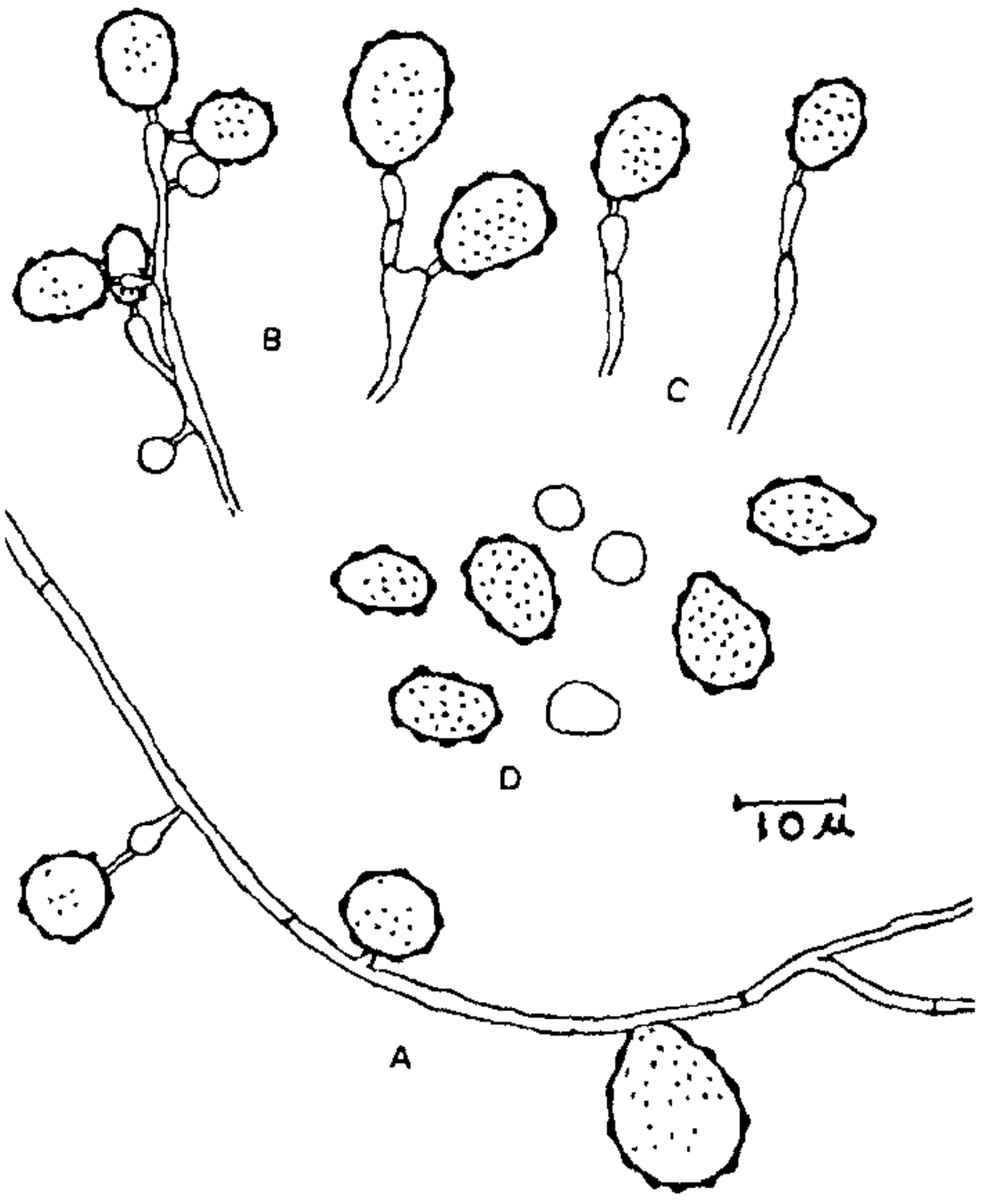

Figures A–D. *Myceliophthora vellerea.* **A.** Mycelium with conidia, **B.** Young and old conidia on the hypha, **C.** Old conidia on ampulliform swellings, **D.** Conidia.

STEROID DEHYDROGENASES IN REGENERATING TAIL OF HOUSE LIZARD *HEMIDACTYLUS FLAVIVIRIDIS*

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INFLUENCE of steroid hormones on the process of lacertilian tail regeneration is apparent from the fact that the rate of growth of the regenerate in the house lizard, *Hemidactylus flaviviridis* is faster in males as compared to females[1]. It is also known that administration of male hormone enhances the rate of regeneration in females[2]. However, apparently no attempt to localize the enzymes involved in steroid metabolism within the regenerating organs has been made. Presently, activities of the two key enzymes of sex steroid metabolism *viz* Δ^5-3β hydroxysteroid dehydrogenase (Δ^5-3β HSDH) and 17β hydroxysteroid dehydrogenase (17β HSDH) were studied histochemically in the regenerating tail of both the sexes of house lizard to elucidate the pattern of steroid hormone utilization within the regenerating organ.

Adult house lizards, *H. flaviviridis* of both the sexes obtained from a local dealer were maintained in the laboratory on a diet of insects. Fifty lizards were used for the present investigations conducted during the breeding season (October to April) when the sex difference in rate of regeneration was most obvious. In