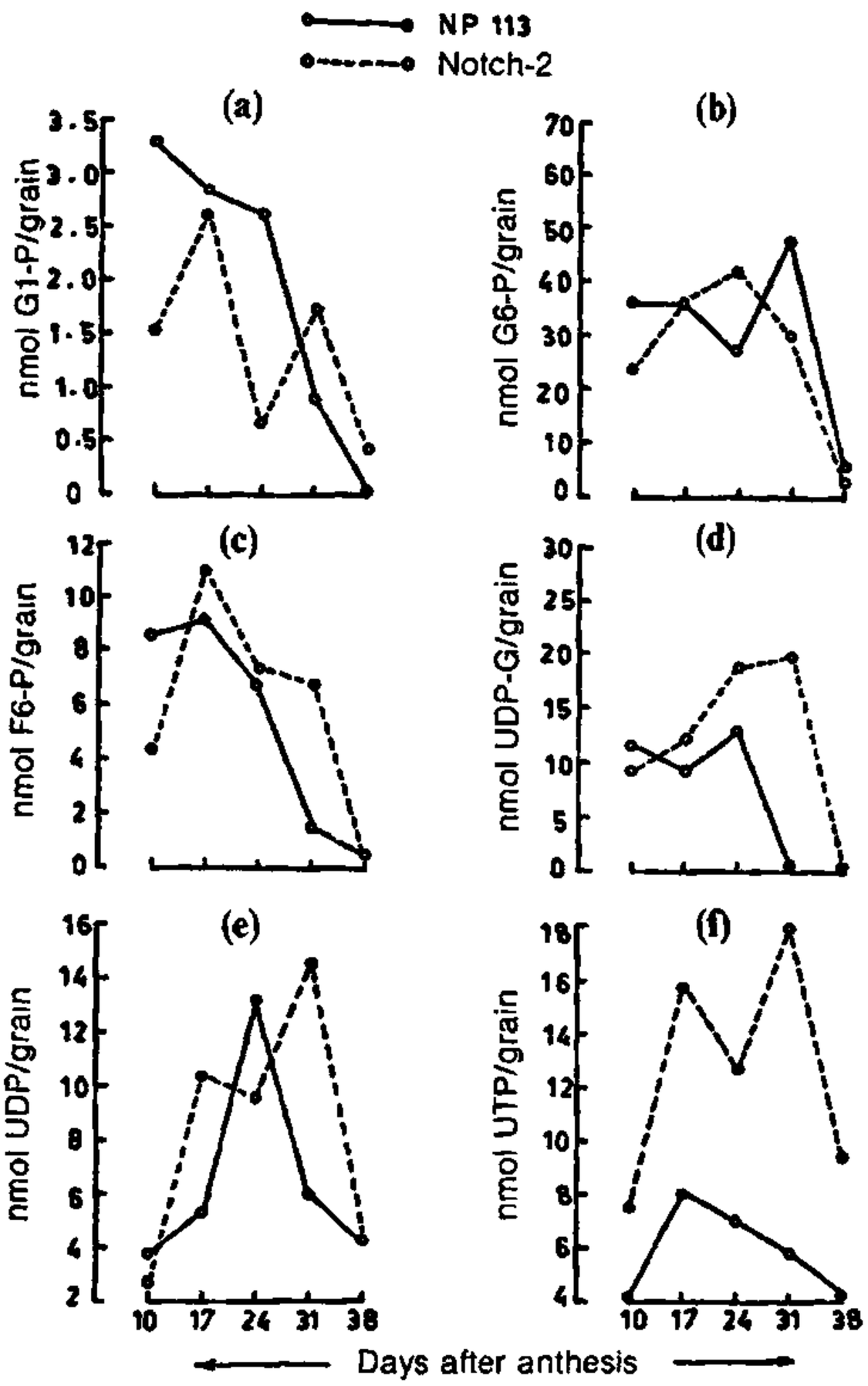

Figure 1. (a) Glucose 1-phosphate; (b) glucose 6-phosphate; (c) fructose 6-phosphate; (d) uridine diphosphate glucose; (e) uridine diphosphate; and (f) uridine triphosphate in developing grains of NP 113 and Notch-2 barley.

glucose (UDP-glucose) and amylose primer in reactions catalysed by ADP-glucose (UDP-glucose) pyrophosphorylase and starch phosphorylase[3]. The Notch-2 grain is known to have higher activities of phosphoglucomutase[8], UDP-glucose pyrophosphorylase and starch phosphorylase[9] compared to NP 113. The two genotypes had almost similar activities of ADP-glucose pyrophosphorylase[9]. It may therefore be inferred that the lower level of G1-P in Notch-2 mutant is not the result of reduced production; rather, it might be due to its higher utilization in Notch-2 amyloplasts compared to that in NP 113. Starch biosynthesis in Notch-2 is therefore also unlikely to be limited at the level of G1-P.

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OCCURRENCE OF VESICULAR-ARBUSCULAR MYCORRHIZAL FUNGI IN ROOTS OF *MORUS ALBA* L.

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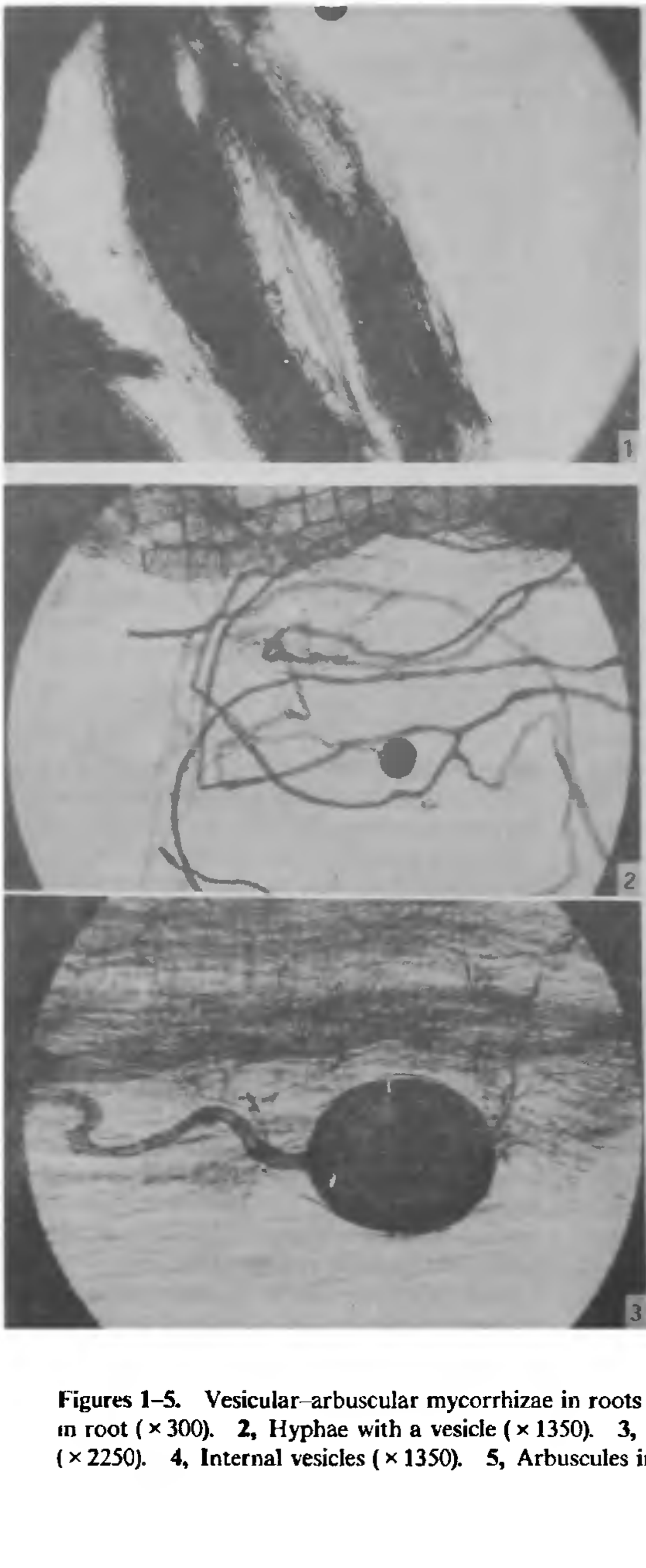
VESICULAR-ARBUSCULAR mycorrhizal (VAM) fungi have been reported in several crop plants and ornamentals[1-4]. The anatomy and distribution of mycorrhizae and their influence on plant growth is well established[5,6]. In recent years studies on the ecophysiology of VAM associations have gained much attention[7]. This paper reports the occurrence of VAM in *Morus alba* L. K_2 variety. *Morus alba* L. is a cultivated plant and has great economic importance as the food of mulberry silkworms.

Roots of *Morus alba* L. K_2 were collected from mulberry plots in RRL campus. The roots were washed thoroughly with tap-water and distilled water, cleaned in 1 N KOH, bleached with 3% H_2O_2, and stained with trypan blue in lactophenol[4] and examined under a Leitz microscope. Spores, isolated from the infected roots and soil around the



Figures 1–5. Vesicular–arbuscular mycorrhizae in roots of *Morus alba* L. K_2. **1,** VAM infection in root (× 300). **2,** Hyphae with a vesicle (× 1350). **3,** External vesicle with a subtending hypha (× 2250). **4,** Internal vesicles (× 1350). **5,** Arbuscules in the root tissue (× 1350).

roots using the wet seiving method[9], were inoculated in pots containing sterile soil. VAM were allowed to grow in the susceptible host *Sorghum*. After sufficient growth of VAM, i.e. at the mycelial stage, the shoots of *Sorghum* were cut off and mulberry cuttings were planted in the same pots. Sprouting and growth of the cuttings were recorded. Sorghum roots grown without VAM were used as controls.

Microscopic examination revealed that in natural conditions the roots were heavily infested with VAM (figure 1). The hyphae appeared knobby (figure 2) and interwoven closely. The hyphae in figure 2 were separated from the mycelium by gentle treasing with a fine-tipped needle. The vesicles were globose, with simple, knobby and undulated subtending hyphae (figure 3). Vesicles were observed both internally and externally. External vesicles were scarce and spread over the surface of the roots (figure 3). Internal vesicles were more in number and showed differential staining and size variation (figure 4). Figure 5 shows the arbuscules in the root tissue. The infection pattern indicates that the fungus belongs to the genus *Glomus*[10].

Sprouting and growth rates were high in the cuttings planted in the pots with VAM inoculum. Enhanced nutrient uptake by VAM symbionts and subsequent higher growth rates of host plants have been reported earlier and this has great potential for improving agriculture[11–13]. Cultivation of high-quality mulberry is a significant aspect of silk production and it is estimated that 60% of the cost of silk is due to mulberry cultivation[14]. The VAM–mulberry symbiosis can be explored further for commercial utilization.

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FINE STRUCTURE ANALYSIS OF THE GLUTINOUS LOCUS IN RICE

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FINE structure studies of genes in higher plants are difficult owing to difficulty in detection of recombinants. Pollen grains provided an opportunity for such a study in the case of the waxy locus in maize[1]. Nelson[2] identified 24 alleles at the waxy locus in maize. Li *et al*[3], suggested the presence of five sites at the waxy locus in some varieties of rice.

In the ptesent study, 31 *indica* glutinous varieties obtained from the Central Rice Research Institute, Cuttack, were screened for amylose content and endosperm/pollen stainability in iodine–potassium iodide solution. Normally glutinous varieties have less than 6% amylose and have opaque kernels with red-staining endosperm and pollen grains. In the present study, pollen grains of the glutinous varieties stained red and had an amylose content ranging from 2 to 15.8% and with opaque or less opaque (milky-white) kernel. Some of the milky-white kernels stained dark brown in iodine-potassium iodide solution. This independence between amylose content (endosperm stainability) and stainability of the pollen of glutinous varieties suggests that perhaps the endosperm and pollen phenotypes are governed by different genes. It is also known that amylose content is influenced by modifier genes. The