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.

16 September 1988


1. Taber, R. A. and Strong, M. E., *Mycologia*, 1982, 74, 152.
2. Dwivedi, R. S. and Pathak, S. P., *Indian Phytopathol.*, 1981, 34, 524.
3. Ammani, K., Venkateswarlu, K. and Rao, A. S., *Curr. Sci.*, 1985, 74, 120.
4. Selvaraj, T., Kannan, K. and Lakshminarasimhaim, C., *Curr. Sci.*, 1986, 55, 728.
5. Gerdemann, J. W., *Annu. Rev. Phytopathol.*, 1968, 6, 397.
6. Mosses, B., *Annu. Rev. Phytopathol.*, 1973, 11, 171.
7. St. John, T. V. and Coleman, D. C., *Can. J. Bot.*, 1983, 61, 1005.
8. Phillips, J. M. and Hayman, D. S., *Trans. Br. Mycol. Soc.*, 1970, 55, 158.
9. Gerdemann, J. W. and Nicolson, T. H., *Trans. Br. Mycol. Soc.*, 1963, 46, 235.
10. Trappe, J. M. and Schenck, N. C., In: *Methods and Principles of Mycorrhizal Research*, (ed.) N. C. Schenek, The American Phytopathological Society, USA, 1982, p. 1.
11. Abbott, L. K. and Robson, A. D., *Austr. J. Agric. Res.*, 1982, 32, 389.
12. Menge, J. A., *Can. J. Bot.*, 1983, 61, 1015.
13. Safir, G. R., *Vesicular Mycorrhizal and Crop Productivity*, Academic Press, New York, 1980, p. 231.
14. *F.A.O. Agricultural Services Bulletins*, Manuals on Sericulture, 1987, Reprinted by Central Silk Board, Bangalore.


## FINE STRUCTURE ANALYSIS OF THE GLUTINOUS LOCUS IN RICE

A. K. SARALA and G. M. REDDY
*Department of Genetics, Osmania University, Hyderabad 500 007, India.*

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

endosperm, however. is a triploid tissue and this might account for some variability.

The experimental procedure standardized by Nelson[1,2] in maize is simple. The waxy pollen stained red whereas the normal pollen stained blue with iodine–potassium iodide solution. Crosses were made between waxy mutants which produced low frequency of standard normal (WX) type pollen stained blue with varying frequencies. Data from these crosses ultimately allowed detection of mutants with the waxy locus.

In rice, crosses were made between pure breeding (31) *indica* glutinous varieties in all possible combinations, and the blue-staining pollen from $F_1$ plants were scored. The mutation rate for glutinous to normal was determined by scoring (25 to 75,000) pollen grains in each cross. Pollen from glutinous varieties exhibited red staining with iodine–potassium iodide, while some stained blue. The frequency of 'blue-stained', studied separately for the glutinous varieties, varied from zero to $12.5 \times 10^{-5}$. The frequency of 'blue-stained' in each cross over and above the mutation frequency was taken as the frequency of recombinants.

In the cross MNP-263 × MNP-407, the frequency of normal pollen in $F_1$ was $13.5 \times 10^{-5}$, significantly higher than that in the parents ($1.64 \times 10^{-5}$ in MNP-263; $3.8 \times 10^{-5}$ in MNP-407). This suggests that within the region of the waxy locus, which affects pollen stainability, there are more than one site. Earlier studies[3] with different *indica* varieties suggested the presence of five sites.

The method is useful in the analysis of the fine structure of the glutinous locus. The variation in the synthesis of amylose in glutinous varieties could be exploited through proper breeding programmes to develop lines with desirable quality for various purposes.

6 August 1988; Revised 30 November 1988

1. Nelson, O. E., *Science*, 1959, 130, 794.
2. Nelson, O. E., *Genetics*, 1968, 60, 507.
3. Li, H. W., Wu, H. P. and Chu, M. Y., *Bot. Bull. Acad. Sinica*, 1968, 9, 22.

## EARLY-MATURING MUTANTS IN GROUNDNUT CULTIVAR PHULE-PRAGATI (JL-24)

CHANDRA MOULI and D. M. KALE
*Nuclear Agriculture Division, Bhabha Atomic Research Centre, Trombay, Bombay 400 085, India.*

EARLY-maturing groundnut (*Arachis hypogaea* L.) varieties are important for rain-fed cultivation, specially in those locations where the rainfall is limited to a short period of three months or less. More than 75% of the groundnut area in India has this type of agroclimate. Groundnut cultivar Phule–Pragati commonly known as JL-24, is suitable for such areas and is also used as a national check in yield trials of All-India Co-ordinated Projects on Oilseeds[1]. It matures between 90 and 110 days in different agroclimatic zones. Therefore it is desirable to develop cultures maturing in 90 days or less, with yield potential similar to JL-24, and with other useful agronomical attributes. Gamma-ray treatment of JL-24 and screening of $M_2$ and succeeding populations led to the identification of mutations affecting maturity, seed size, shelling percentage and oil content[2]. Three mutants, viz. JL-24M-6, JL-24M-

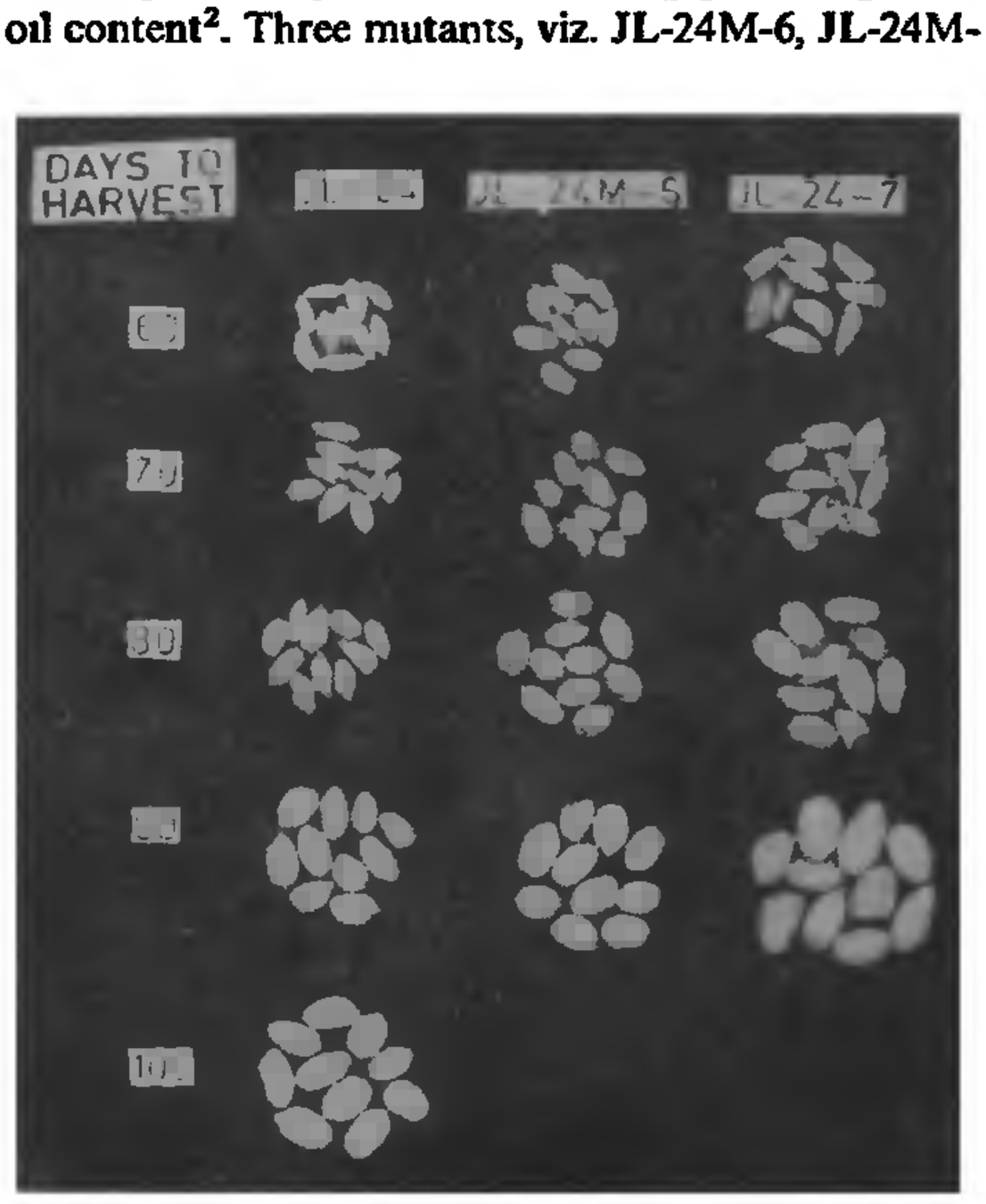


**Figure 1.** Seed development in the mutants and in JL-24 harvested at 60, 70, 80, 90 and 100 days after sowing.