Accession numbers 076 and 079 (Shajapur), 111 (Raisen), 119 and 128 (Mandla), and 142 (Betul) were promising for harvest index, shelling percentage, and grain yield per plant. They also had more racemes and primary branches than other accessions. Accession numbers 076 and 079 were moderately resistant, while 097 (Sehore) and 142 (Betul) were moderately susceptible to seedling diseases.

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Breeding/Genetics

Preliminary Investigation of Microsporogenesis of Genic-cytoplasmic Male-sterile Pigeonpea

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The discovery of three sources of genetic male-sterility (Reddy et al. 1978, Wallis et al. 1980, Dundas et al. 1982) and the prevalence of sufficient natural outcrossing by several insect species (Williams 1977, Onim 1981) led to the development (Gupta et al. 1983) and later on release of the first pigeonpea hybrid in India in 1991. The three sources of male sterility were found to occur due to the failure, at different stages, of male meiosis.

Reddy et al. (1978) reported that male steriles were identifiable by non-dehiscent, flat, translucent anthers. This male-sterile line was designated ms_1. Male meiosis proceeded normally in this male-sterile line up to the formation of tetrads. Then degeneration occurred because of nonseparation of tetrads. The tapetum was found to be intact, whereas in normal cells it disintegrated as meiosis advanced. In the male-sterile line identified by Wallis et al. (1980) which is designated ms_2, the stamens are brown, shrivelled, and arrow-head shaped. Meiotic failure of this source of male-sterility occurs earlier than it does in ms_1. Pollen mother cells degenerate at the tetrad stage with the rupture of the nuclear membrane. The anther morphology of the third source of male-sterility is similar to that found by Wallis et al. (1980). Meiotic failure occurs at the pachytene stage i.e., earlier than the other two male-sterile types (Dundas et al. 1982).

Ariyanayagam et al. (1993) reported the development of gene-cytoplasmic male-sterility. The present report gives preliminary observations of microsporogenesis of the genic-cytoplasmic male-sterile source.

Microsporogenesis

Flower samples of differing growth stages of the genic-cytoplasmic male-sterile line were fixed for 24 h in Cornoy's fluid II, then transferred to Cornoy's fluid I containing ferric chloride for 24 h. Anthers of fixed buds were squashed in 1% acetocarmine for observation.

The development of sporogenous tissue and the progression into pollen mother cells (PMC) were normal in the genic-cytoplasmic male-sterile line. The tapetum showed signs of disintegration (Fig. 1a) suggesting that the development of the PMC had progressed. Figure 1b confirms this, as deeply stained PMCs were present, in contrast to ms_2, where meiotic failure occurs due to the disintegration of PMCs. Continued development of PMCs into tetrads was noticed and at that stage too, deeply stained differentiated PMCs were observed (Fig. 1c). Meiosis proceeded uninterrupted until after the tetrad release stage (Fig. 1d) into the early microspore stage, at which time deep staining of the newly formed pollen grains was noticed. Signs of meiotic failure appeared later when cytoplasm was seen to separate from the wall

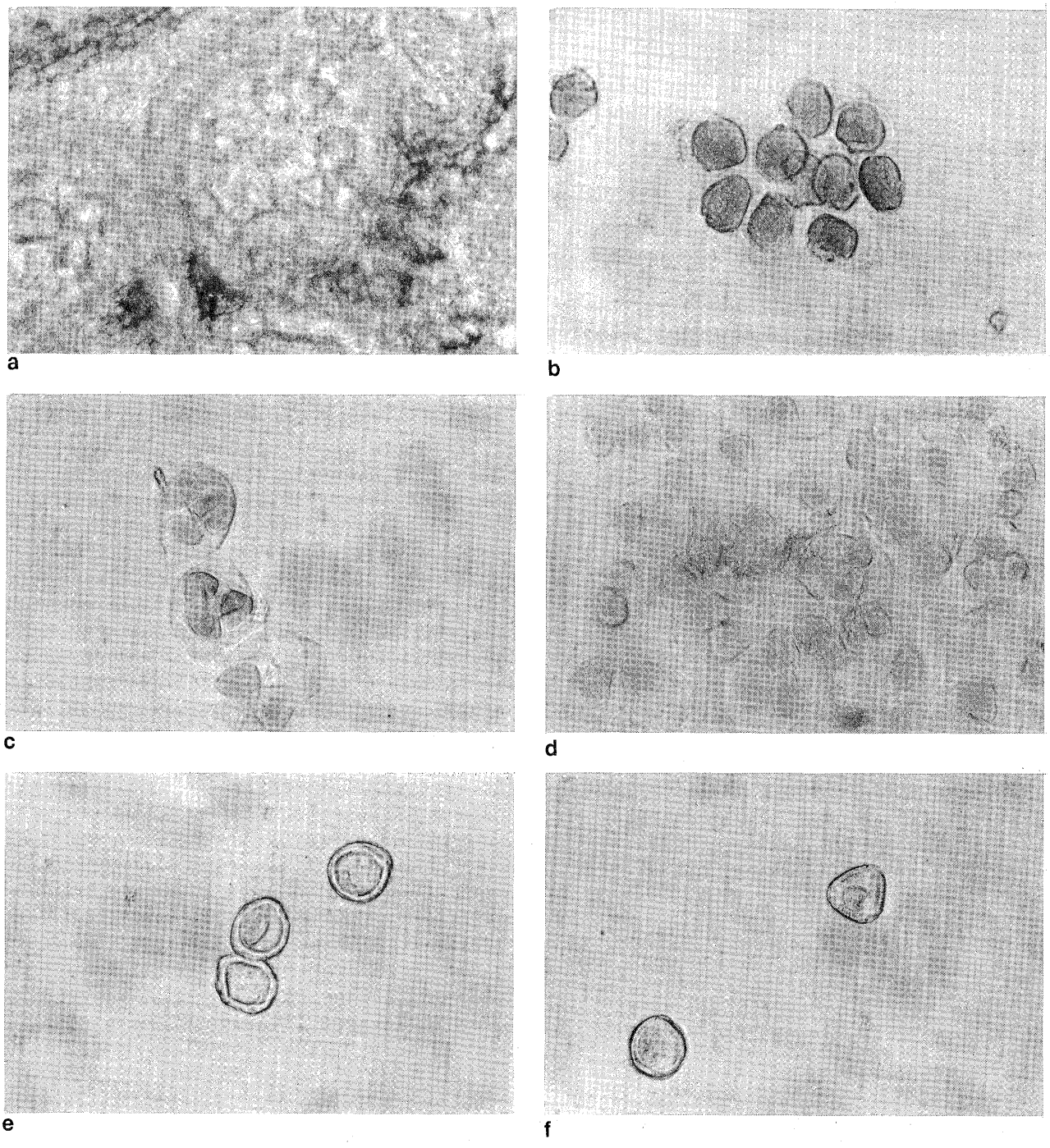

Figure 1. Stages of microsporogenesis in genic-cytoplasmic male-sterile pigeonpea: a. sporogenous tissue, b. normal pollen mother cells of CMS, c. tetrad stage, d. release of microspores from tetrads, e. variation of pollen grains, and f. clear sterile pollen grains.

(Fig. 1e). Vacuolation then occurred and eventually the pollen become clear and unstained (Fig. 1f).

Meiotic failure of the genic-cytoplasmic male-sterile line hence occurs at a later stage than that reported for the genetic male-sterile sources. Failure of meiosis at late microspore stage was reported in alfalfa (Bradner and Childers 1968). Since genic-cytoplasmic male-sterility results from interactions of genomic and cytoplasmic genetic factors of cells, the late appearance of sterility symptoms suggests that either the interaction does not begin until the pollen grains differentiate, or that the time lapse for the interaction to take effect is long. Detailed studies are needed to confirm these observations.

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Correlation Studies in Segregating Generations of Pigeonpea

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Assessment of the genetic variability in the base population is the first step in any breeding program. Analysis of the various characters contributing to yield, and their interrelationships can be of immense help to breeders in selecting desirable genotypes. This papers reports the results of such a study in short-duration pigeonpea.

Ten short-duration pigeonpea cultivars; ICPL 269, Pusa Sweta 2, ICPL 87, GAUT 82-99, H 76-208, ICPL 312, ICPL 151, ICPL 8306, BDN 31, and BWR 245 and their half-diallel F_2s were grown in a randomized-block design with four replications at the Main Pulse Research Station, Gujarat Agricultural University, Sardar Krishinagar, Gujarat, India during 1989. Each entry was grown in a plot containing 4 rows each 4-m long. Spacing was 60 × 20 cm. For each entry, agronomic characters were recorded for 10 randomly selected plants. For protein analysis, grain of the selected plants was bulked replication-wise, and a composite sample taken from each replication. The nitrogen content was determined using the micro-Kjeldhal method (Jackson 1967). Crude protein content was estimated as nitrogen value × 6.25.

Table 1. Range for different characters in pigeonpea.

Characters	Ranges
Days to 50% flowering	83.75 – 115.25
Days to maturity	128.50 – 160.75
Plant height (cm)	74.28 – 147.05
Branches plant^{-1}	4.63 – 10.43
Pods plant^{-1}	101.30 – 236.43
Pod length (cm)	3.48 – 5.15
Seeds pod^{-1}	3.30 – 5.15
Seed yield plant^{-1} (g)	25.51 – 62.38
100-seed mass (g)	6.57 – 11.57
Protein content (%)	14.13 – 18.95