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# GENETIC VARIATION IN PIGEONPEA GERMPLASM

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Germplasm is the raw material for crop improvement and its utility depends upon the useful genetic diversity it contains (Mengesha 1984).

The effort given to improve traditional pigeonpea types has been less than that given to major cereals and therefore relatively large genetic gains can be achieved rapidly in pigeonpea (Byth et al. 1981). Though many improved lines have been developed since the 1920s, yield levels have remained virtually static. A major reason for this is the limited use made by breeders of the genetic resources available to them (Ramanujam and Singh 1981). The key to rapid improvements, therefore, lies in greater exploitation of the wide genetic diversity available in pigeonpea (Byth 1981, ICRISAT 1982).

The world collection of germplasm assembled at ICRISAT contains a wide range of the variability existing in all important traits (Table 1). Examples are days to maturity, plant type, seed size, number of seeds per pod, and resistance to environmental and biotic stresses. Future pigeonpea improvement will depend largely upon the effective utilization of this diversity.

Table 1. Range of variability in the pigeonpea germplasm.

| Character | Minimum | Maximum | No. of lines evaluated |
|---|---|---|---|
| 50% flowering (days) | 55.0 | 210.0 | 8582 |
| 75% maturity (days) | 97.0 | 260.0 | 8561 |
| Plant height (cm) | 39.0 | 385.0 | 8526 |
| Primary branches (no.) | 2.3 | 66.0 | 5812 |
| Secondary branches (no.) | 0.3 | 145.3 | 5793 |
| Racemes (no.) | 6.0 | 915.0 | 5812 |
| Seeds per pod | 1.6 | 7.6 | 8413 |
| 100 seed weight (g) | 2.8 | 22.4 | 8475 |
| Harvest index (%) | 0.6 | 62.7 | 5772 |
| Shelling ratio (%) | 5.8 | 86.6 | 5759 |
| Protein percentage | 12.4 | 29.5 | 8206 |

Based on genetic variation, the germplasm has been classified into a number of well defined sections and a catalogue will soon be published. The germplasm maintained at ICRISAT is available to anyone who wishes to use it, and depending upon the need of the user a search for genotypes with the desired combination of traits can be efficiently done now with the aid of our computer.

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