Short Communication

Natural out-crossing in pigeonpea in China

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Natural out-crossing in pigeonpea [Cajanus cajan (L.) Millsp.] is primarily responsible for the deterioration of purity of cultivars and genetic stocks. A variety of insects are responsible for transferring pollen from one plant to another within and across the fields. The major pollinating vectors identified are Apis mellifera, Apis dorsata, Megachile lanata, Ceratina binghami, and Xylocop spp. (2, 6, 10). Onim (6) reported that each insect visit to a flower lasts between 15-55 seconds. Williams (10) counted between 5500 and 107333 pollen grains on the body of each visiting insect and more than 90% of these pollen grains belonged to pigeonpea. The populations of pollinating vectors and local environmental factors that assist in the movement of insects determine the extent of natural out-crossing at a particular location. In India, Howard et al. (4) were the first to report 14% natural out-crossing in pigeonpea. This was followed by a number of reports with a wide range of natural outcrossing at different locations. In Kenya, 12.6-45.9% outcrossing with a mean of 23.8% was reported by Onim (6), while 6.3 - 19.6% natural out-crossing was reported in Sri Lanka by Saxena et al. (9). Wilsie and Takahashi (11) reported 5.9-30.0% out-crossing in Hawaii and in Australia, Byth et al. (3) recorded 2.0-40.0% out-crossing in different pigeonpea cultivars.

Pigeonpea was introduced into China in the 6th century from India and since then it was cultivated sporadically in the southern provinces. In the 1950s, Chinese scientists in Yunnan province identified pigeonpea as a favourable host for lac insect (Kerria lacca Kerr.) because it was found to have useful traits such as easy establishment, fast growth, and high yield of quality lac. Recently, under crop diversification programme in China, many more usage of pigeonpea such as soil conservation, fodder, feed, and fresh vegetable have emerged (7) and specific cultivars for specific purposes have been developed from the breeding materials received from ICRISAT. In order to sustain pigeonpea productivity, it has now become mandatory to maintain the genetic purity of these cultivars, and as a first step it was found essential to determine the extent of natural out-crossing in China and, therefore, this experiment was conducted.

Variety ICPL 87091 with determinate growth habit, was selected for this study. The experiment was conducted at Nanning in Guangxi province. Twenty single-row plots of ICPL 87091 were sown with breeding

line having indeterminate growth habit and matching flowering time. These plots, measuring 5m in length, were scattered at different places in the field. At least 10 pollinator rows on either side of each ICPL 87091 plot were ensured. The inter and intra-row spacing was kept at 100 cm and 50 cm, respectively. Only two insecticidal sprays were done to control Helicoverpa pod borer. From each plot, five individual plants were randomly harvested. The progenies of 66 selections with sufficient quantity of open-pollinated seeds were sown in the subsequent rainy season. Since indeterminate growth habit is dominant over determinate growth habit, counts were made in each plant-progeny row for the self (determinate) and hybrid (indeterminate) plants. The frequency of natural outcrossing in each row was estimated as percentage of the observed hybrid plants.

In spite of two insecticidal sprays, a lot of insect activity was observed during flowering stage in the entire field. More than one type of insects were active, but their

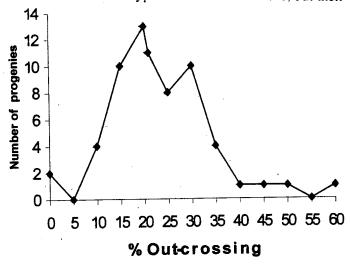


Fig 1. Frequency distribution of natural out-crossing in the openpollinated progenies of ICPL 87091

identification was not feasible. However, among these, the predomiance of honeybees was apparent. The data from the single plant progenies of ICPL 87091 revealed a large plant-to-plant variation (Fig.1) for natural out-crossing in the preceding season with a mean of 24.6%. In two progenies, no out-crossed hybrid plant was recorded, while in four progenies more than 40% hybrid plants were observed. One progeny recorded 60% natural out-crossing. Of the 66 progenies evaluated, 52 exhibited

15-30% natural out-crossing. The inter-plant variation for natural out-crossing observed at Nanning may be due to variation in plant growth or shading from neighbouring tall plants due to which the pollinating vectors were relatively less active on such plants and the insects preferred to land on the well grown tall plants.

The results of present study show that, like in other countries, in China also, the active pollinating vectors are present in large numbers and they are potential danger to the maintenance of genetic purity in pigeonpea. Since pigeonpea is being promoted under a range of environments, the extent of natural out-crossing is likely to vary from place to place. Therefore, it is advisable to determine the extents of natural out-crossing in the representative locations before undertaking the seed production of more than one genotypes at one place. For small-scale pure seed production in the breeding programmes, use of mosquito nets is recommended to maintain purity of seed while for large-scale seed production, a safe isolation distance will be necessary. Since, in a particular environment the population of pollinating vectors and other physical factors are important, effective isolation distances for major pigeonpea growing areas need to be estimated. Pending such study, the sowing in isolated blocks separated by at least 200 m, as recommended by FAO (1) be followed. Besides seed production, there are two other contrasting implications of natural out-crossing in pigeonpea breeding. On one hand, it is detrimental to pedigree breeding programme that involves evaluation and selection of pure genotypes. On the other hand, the phenomenon of natural out-crossing can be used for the genetic improvement of breeding populations (5) and hybrid breeding (8). Since pigeonpea research programme in China is in budding

stage, the information on the extent of natural outcrossing is essential to develop both long and short-term research and development strategies.

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