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NATURAL OUTCROSSING IN *LATHYRUS SATIVUS* L.

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ABSTRACT

The extent of natural outcrossing was studied in three genotypes of *Lathyrus sativus* L. (grasspea) in November 1992 and 1993 at the Pulses Research Centre, Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh. Individual plots of red, pink and white flowered (all recessive) genotypes were surrounded by a dominant marker line with blue flowers. The number of blue flowered plants in the progeny rows of 30 random plants of each test genotype was recorded. The extent of outcrossing was 27.8% for red, 19.4% for pink, and 9.8% for the white genotypes. Differences among genotypes were significant. It was assumed that these differences were due to brightness of flower colour which attracted bees. Implications of outcrossing to future breeding strategies and maintenance of genetic purity of varieties are discussed.

Key words: Genetic deterioration, genotypic differences, grasspea, *Lathyrus sativus*, natural outcrossing.

Lathyrus sativus L. (grasspea) is widely cultivated in Bangladesh, India, Nepal, Pakistan, Ethiopia and to a limited extent in Algeria, China and Spain [1]. It is grown as a forage crop in Central and Southern Europe and the Mediterranean region [2]. It is a hardy crop which can tolerate adverse environmental conditions like drought and excess moisture. It can be cultivated with little inputs and even as a relay crop. There are no major disease or insect which affect this crop. Its seeds, however, contain a free amino acid known as β-N-oxylylaminoalanine (BOAA), which may cause a neurological disorder called lathyrism in human beings [3].

Although it has been used as a pulse crop for over 8000 years [2], its genetic improvement was not attempted until recently. The improvement work was initiated in India in 1966 [4], in Canada in 1967 [5], in Bangladesh in 1980 [6], and in Nepal in 1986 [7]. Breeding procedures for the self-fertilized crops have been followed for its improvement

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[1]. The floral biology of *L. savitus* favours true self fertilization. However, there are indications that outcrossing occurs in this species at a higher frequency than is acceptable in a truely self-fertilized crop [2]. Valero et al. [8] and Godt and Hamrick [9] reported *L. latifolius*, a related species of *L. sativus*, as a cross-fertilized species. We have observed much bee activity in *L. sativus* plots. Much information is not available on outcrossing in this species. The present study has been undertaken to determine the extent of natural outcrossing in *L. sativus* as influenced by its flower colour.

MATERIALS AND METHODS

It has been reported that blue flower colour is dominant over red, pink and white and the combination of pink x white and red x pink produce blue flower [10] in *L. sativus*. Hence natural outcrossing can readily be identified through scoring the blue flowered plants from within the red, pink and white populations. Four germplasm lines, viz. Charbadna (blue flowers), Jamalpur (pink flowers), LS-NC-8a-100 (red flowers), and LS 84015 (white flowers) were used in this study. The experimental procedure was followed as described by Girithi et al. [11]. Each of the recessive flower colour genotypes (red, pink and white) was planted in a 4 row plot of 4 m length in 3 replications at the Pulses Research Centre of the Regional Agricultural Research Station, Ishurdi, Pabna, Bangladesh, on 3 November 1992. Each plot was surrounded by 6 rows of the blue flowered genotype. In addition, 20 more rows of the blue flowered marker line were planted surrounding the entire experiment. Spacing between rows was 50 cm and between plants 10 cm. At maturity, seeds from 10 random individual plants from each plot of a genotype were harvested. Single plant progenies from these 30 plants of each variety were raised in November 1993. The plot size was one row, 4 m long, with a spacing of 50 x 10 cm. At flowering, the number of total as well as blue flowered plants were recorded to compute percentage of outcrossing. The χ^2 test was done using the 3 x 2 contingency table.

RESULTS AND DISCUSSION

The frequency of hybrid plants (blue flowered) observed in the progenies of red, pink and white flowered genotypes indicates that percentage of outcrossing varied among the genotypes under study (Table 1). The highest outcrossing (27.8%) occurred in the red flowered genotype, followed by pink (19.4%) and white (9.8%) flowered genotypes. Prasad et al. [12] and Byth et al. [13] reported genotypic differences in outcrossing among pigeonpea genotypes. It seems probable that the bright red colour attracts more bees compared to the other two colours in the present study. Similar observation was also reported in pigeonpea [14]. The procedure for estimating the degree of natural outcrossing in this study did not consider the amount of natural outcrossing within the genotypes with recessive and dominant markers and from recessive to dominant genotypes. However, the study provides

Table 1. Natural outcrossing in three flower colour genotypes of *Lathyrus sativus*, at the Pulses Research Centre, Regional Agril. Research Station, Ishurdi, Pabna, Bangladesh in 1993

Flower colour of genotype	No. of plants with parental flower colour	No. of blue flowered plants (outcrossed)	Total	Outcrossing, %
Red	840	324	1164	27.8
Pink	941	226	1167	19.4
White	913	99	1012	9.8

χ^2 (2) = 112.78 ($P < 0.001$).

fairly reliable information that significant natural outcrossing occurs in *L. savitus* although the degree may vary from place to place and depends on the genotype used. *L. sativus*, therefore, can be classified as an often cross- fertilized species. Outcrossing affects varietal purity and breeding procedures. Thus, the present methods of self-fertilized crops followed for breeding *L. sativus* are probably not appreciable. It is also possible to follow population improvement procedures and even develop hybrids in this crop.

The immediate impact of this finding will be on the development and maintenance of low-neurotoxin varieties of this crop which are being bred in about ten active *L. sativus* improvement programmes around the world. The breeders will have to determine isolation distance and other effective ways of controlled pollination and maintenance of varietal purity.

The use of pedigree or SSD method for advancing generations or for genetic studies of the selected plants should be accompanied with proper pollination control. Otherwise the results may be erroneous and the efficiency may be reduced due to selection of vigorous hybrid plants arising out of outcrossing in the previous generations. Hence it may be difficult to achieve homozygosity for a particular character (especially low toxin) after several years of selection.

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