NATURAL OUTCROSSING RATES OF BEAN CULTIVARS.

Francisco Ibarra-Perez and Giles Waines, Department of Botany and Plant Sciences, University of California, Riverside, CA 92521.

A high frequency of offtypes in the progeny of bean plants grown at Irvine, CA was observed over several years. Recently, Wells et al. (1988) reported high rates of outcrossing from 0.0 to 85% at Irvine, in 1985; the rate varying with cultivar and time of flowering. Experiments were conducted in 1989 which repeated those of Wells et al. (1988) at Irvine and extended them to the campus of the University of California, Riverside. Two experiments were conducted at each location, with May and July planting dates. The main objectives were to determine the rate of outcrossing among common bean cultivars grown at Irvine and Riverside, and to determine whether or not genetic variability exists for this character.

Hypocotyl color was used as a marker for outcrossing events. The allele purple hypocotyl color is dominant to that for green hypocotyl color (Leakey, 1988). The six white-seeded, green hypocotyl, cultivars evaluated were: FM 53, Sal, Comtesse de Chamborde, 80BP-30, PI 164778 and PI 345576. A bulk of black seeded, purple hypocotyl, bean cultivars was created to provide a constant source of pollen. The bulk consisted of equal amounts of seed from the following cultivars: Turtle Soup 39, BAT 424, G4459, G4524, PI 151027, PI 312254, PI 313526, PI 345574 and PI 353497.

For each planting date, each white-seeded cultivar was randomly assigned to six five-row plots, 3-m long, with rows on 0.76 m apart, arranged as a completely randomized design. The center row of each plot was planted with a sample of five seeds from the assigned white-seeded cultivar interspersed every 0.50 m among the 25 seeds from the black-seeded bulk. The four outer rows of each plot were each planted with 30 seeds from the bulk.

All white-seeded plants were considered as potential female parents and were individually harvested from the middle rows of the plots. All pods produced by each plant were handled separately. In order to determine the outcrossing rate, seeds from the female plants were sown in flats in such a way that seeds from a single pod formed one line. Moreover, seeds were sown in the order in which they occurred in the pod. Seedlings that developed purple hypocotyls from white seeds were scored as outcross events while seedlings with green hypocotyls were scored as selfs.

The results of two of the six bean cultivars (FM 53 and PI 164778) harvested from the May planting date at Irvine, CA are reported here; the results of the other bean cultivars, and from the other planting dates have yet to be fully analyzed.

Analyses of variance were performed on several variables related to natural outcrossing. The number of pods produced by these two bean cultivars was significantly different, as was the number of outcrossed pods. Among the 1353 pods scored 903 belonged to FM 53 and 448 to PI 164778; this large difference could be due to the fact that even though both cultivars have indeterminate growth habit, FM 53 has a semivine type while PI 164778 was a bush type.

Furthermore, the analysis of variance indicated significance in the number of hybrid seeds, the percentage of hybrid seeds, and the estimated outcrossing rate, t (Jain, 1979). More than six thousand white seeds were scored, 4321 of them from FM 53. Among these, 344 produced seedlings with purple hypocotyls. The rest of the seeds scored (2116) were from PI 164778 but only 92 of these produced hybrid seedlings (Table 1). These numbers influenced the percentage of outcrossed seed and the estimated outcrossing rate The semivine cultivar, FM 53, had almost a two-fold higher outcrossing rate than the bush type, PI 164778, 9.96% vs. 5.44%, respectively, thus confirming the results of Wells et al. (1988).

Table 1. Natural outcrossing in two common bean cultivars grown at South Coast Field Station, Irvine, CA.

Cultivar	# of seeds scored	# of hybrid seeds	% of hybrid seeds	estimated outcrossing rate (t)*
FM 53	4321	344	7.96	9.95
PI 164778	2116	92	4.35	5.44
Total	6437	436	6.77	8.46
LSD 0.05	251	30	3.40	4.30

* t=H/p*100 where H= a/(a+b); a= heterozygotes & b= homozygotes
p= pollen allelic frequency

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