

Genetics of Stigma Position in Phaseolus vulgaris x P. coccineus Hybrid  
Materials

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An interest in applying population improvement procedures in common bean breeding led us to investigate the possibility of incorporating the outcrossing flower structure of Phaseolus coccineus into common bean germplasm. The principal feature of this structure is the extrorse stigma, which restricts self-pollination while facilitating cross-pollination. A genetic study of stigma position in the two species and in materials derived from interspecific hybrids was initiated to determine the feasibility of this approach. Lengths of stigmas on internal and external surfaces of styles were measured quantitatively with the aid of a dissecting microscope fitted with a calibrated ocular reticle. Measurements made on 2 to 5 flowers per plant were averaged to arrive at individual phenotypic values. Preliminary studies indicated that stigma length was little influenced by environmental variation. Consequently, measurements obtained at different times during the flowering period, from different locations, or in different seasons were assumed to be directly comparable.

Five different interspecific crosses were made using 2 P. vulgaris cultivars as female parents and 5 P. coccineus lines as male parents. With few questionable exceptions, stigma length distributions in resulting  $F_1$ ,  $F_2$ , and backcrossed populations could best be explained by a quantitative mode of inheritance. Mean internal stigma lengths of  $F_1$  populations were uniform and shifted somewhat toward the P. vulgaris parent from the midparental value. In 3 of the 5 interspecific crosses, the means of  $F_2$  populations were intermediate between the  $F_1$  means and the midparent values, indicating partial dominance of genes contributed by P. vulgaris over those from P. coccineus. Stigma types in  $F_2$  populations were continuously distributed, with one questionable exception which may have had major gene segregation. Skewing of  $F_2$  populations toward the P. vulgaris parent was attributed primarily to partial dominance, although the possibility of some selective elimination of P. coccineus genes could not be excluded. In 4 of the 5  $F_2$  populations, a total of 192 plants, no parental stigma types were recovered. Backcrossed populations were continuously distributed between  $F_1$  means and the respective parental mean, with one exception which yielded a non-Mendelian segregation ratio.  $F_3$  progenies had internal stigma length means which varied between progenies, but all were intermediate between the means of the parental species. Also, variability of  $F_3$  progenies was greater than that of the parental species, but less than in the  $F_2$ , as expected with a quantitative mode of inheritance. Regression of  $F_3$  progeny means upon respective  $F_2$  parents yielded a high correlation coefficient ( $r = 0.93$ ) and narrow sense heritability estimate ( $h = 0.62$ ). The stigma length means of 26  $F_3$ ,  $F_4$  and  $F_5$  progenies which were essentially homozygous for stigma genes did not form clusters, indicating that major gene heterozygotes were not responsible for the continuous distribution. The result of a reciprocal test cross involving an  $F_5$  line homozygous for extrorse stigma indicated that a minimum of 5 to 7 genes were responsible for stigma segregation over the range tested. The complete range of stigma lengths from P. vulgaris to P. coccineus is controlled by an even greater number of genes. The polygenic nature of this character explains our inability to recover extrorse stigma types in large field-grown BC- $F_2$  populations derived from  $F_2$ ,  $F_3$ , and  $F_4$  plants having extrorse, or nearly extrorse, stigma types.