



Genetic analysis of floral organ size in broccoli × cabbage via a mixed inheritance model of a major gene plus polygene

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ABSTRACT. Broccoli and cabbage are important vegetable crops that produce hybrid seeds after insect pollination; the size of floral organs is crucial for this process. To investigate the genetic characteristics of floral organ sizes (corolla width, petal length and width, and lengths of stamen, anther, style, and stigma) and to improve the flower size and breeding efficiency of broccoli, we used multi-generation analysis of a major gene plus polygene model. Six populations obtained from a broccoli inbred line 93219 (small floral organs) and cabbage inbred line 195 (large floral organs) were used for the analysis. Corolla and petal width and stamen and anther length were controlled by the additive-dominance-epistasis polygene model. The heritability of these traits in BC_1 , BC_2 , and F_2 generations was high (72.80-93.76%). Petal and stigma length were governed by the two major genes of additive-dominance-epistasis effects plus additive-dominance polygene model; the major gene heritability in the F_2 generation were 79.17 and 65.77%, respectively. Style length was controlled by one major gene of additive-dominance effects plus additive-

dominance-epistasis polygene model; the major gene heritability in BC₁, BC₂, and F₂ were 40.60, 10.35, and 38.44%, respectively; the polygene heritability varied from 41.85 to 68.44%. Our results provide important genetic information for breeding, which could guide improvement of flower-related traits and lay the foundation for quantitative trait loci mapping of the flower-size traits in *Brassica*.

Key words: Broccoli; Floral organ; Polygene; Genetic analysis