

T H E  
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ON THE COVER



The *Rosea1*, *Rosea2*, and *Venosa* genes encode MYB-related transcription factors active in the flowers of *Antirrhinum majus*. Schwinn et al. (pages 831–851) show that these genes control the intensity and pattern of anthocyanin pigmentation in flowers. Despite the structural similarity of these proteins, they influence the expression of target genes encoding the enzymes of anthocyanin biosynthesis with different specificities. Different *Antirrhinum* species show striking differences in their patterns and intensities of floral pigmentation due to variations in the activity of the *Rosea* and *Venosa* loci. The resulting patterns of pigmentation may provide visual guides for bees, attracting them to enter and pollinate the closed flowers. Cover photograph by Vernon Clarke shows the floral phenotype of the *Venosa*<sup>+</sup> allele of *A. majus*.

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<sup>W</sup> Online version contains Web-only data.

<sup>OA</sup> Open Access articles can be viewed online without a subscription.



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