Molecular studies of flowering in *Metrosideros excelsa (Myrtaceae)*

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Abstract

Molecular and anatomical studies were conducted on *Metrosideros excelsa* to determine if the current genetic models for flowering with regard to inflorescence and floral meristem identity genes in annual plants applied for a woody perennial. Microscopy studies revealed that floral initiation as cymule primordia began in May. Cymules began to develop by August and by October all the floral organs were fully differentiated. *MEL, MESAP1* and *METFL1*, the partial orthologues of *LEAFY*, *APETALA1* and *TERMINAL FLOWER1* respectively, were then isolated from *M. excelsa* buds through RT-PCR. RT-PCR analysis and expression Southerns showed that *MEL* and *MESAP1* were present at low levels as early as March, and that they were both upregulated at the time cymule primordia were initiated and again during floral organogenesis. As *AP1* is considered an indicator of floral determination, the expression of both *MEL* and *MESAP1* as early as March indicated that floral commitment had occurred by then. The results from microscopy studies supported this conclusion. Studies on juvenile *M. excelsa* plants revealed that GA_3 application caused upregulation of *MEL* but not *MESAP1* indicating that meristem competence was also probably required to promote flowering in *M. excelsa* as has been suggested for *Arabidopsis* (Weigel and Nilsson, 1995).

In situ hybridisation studies revealed that *MEL* expression shifted from the apex of the distal axillary bud in May to cymule primordia in early June and subsequently to the sepals, petals, anthers and the gynoecium and ovules in the later stages of floral development. *MESAP1* expression was seen in young floral meristems, but during the later stages of floral development it was confined to the sepals, petals and the perianth region, which is typical of a Class A gene. *METFL1* was expressed throughout the period of inflorescence development. It was expressed in the inflorescence meristem and not in the floral meristems, as is the case with *TFL1* in *Arabidopsis*. Thus the key floral and inflorescence meristem identity genes in the woody perennial *M. excelsa* showed similar spatial expression patterns as their equivalents in herbaceous plants. However, there were differences in temporal expression patterns such as the bimodal pattern of expression seen with *MEL* and *MESAP1*.

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