Microarray-based gene expression studies of dormancy phase transition in raspberry (*Rubus idaeus* L.) buds

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The prevention of bud break through a temperature-sensing mechanism is a key ecological factor in temperate perennial plant survival. Failure to receive the required amount of chilling results in poor lateral bud break in the spring and reduced yields, whereas the breaking of buds after minimal amounts of chilling could leave the developing buds liable to subsequent frost damage. This project aimed to characterise bud dormancy in woody perennial plants at the molecular level. To resource this, a total of 5,300 cDNAs were generated from endodormant (true dormancy) and paradormant (apical dominance) raspberry meristematic bud tissue. Expression patterns of these cDNAs during the endodormancy – paradormancy transition were determined using microarrays, comprising spotted PCR products. Furthermore, the effects of ethylene treatment on gene expression during the chilling process, which resulted in increased consistency of bud burst and enhanced rates of development when canes were returned to glasshouse or field conditions, were profiled. Approximately 400 cDNAs exhibited significant differential expression patterns and included several transcription factors, hormone-responsive proteins, and genes associated with cell expansion and oxidative stress response. Two differentially expressed MADS box genes, which belong to a family of transcription factors that control multiple developmental processes in flowering plants, were utilised to screen a raspberry BAC library and positively identified

approximately 60 BAC clones, which are currently being fingerprinted and mapped. The potential roles of these differentially expressed genes in dormancy regulation and ethylene-response will be discussed.

Keywords:
Rubus idaeus, dormancy, ethylene treatment, Microarray, transcript profiling

Topic areas:
Microarrays and microarray validation