



# Understanding dormancy release in raspberry buds

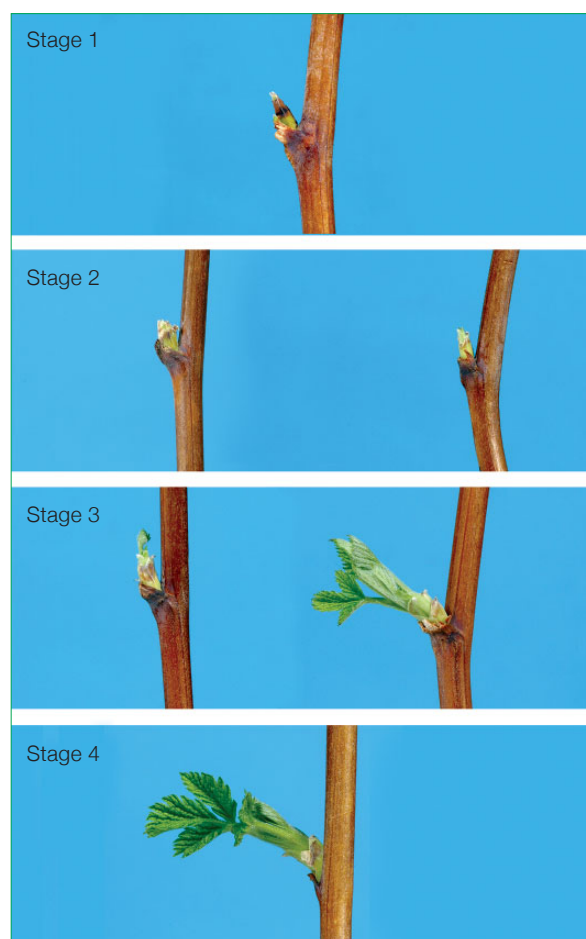
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The control of bud break through a temperature-dependent mechanism is a key ecological factor in woody perennial plant survival. Additionally, important aspects of plant architecture and development are regulated by the coordinated regulation of bud growth. Thus bud dormancy is fundamental to the study of plant developmental processes. Regulation of bud break is also of significant economic importance to fruit and horticultural industries. Bud break in protected raspberry crops is often poor and uneven, with many lateral buds failing to break at all. In order to extend cropping, current practice uses heated glasshouses, and therefore the ability to predict dormancy release becomes a major factor in early fruit production. Furthermore, such concerns are likely to become increasingly important for field production in a period of rising global temperatures.

Bud break of raspberry is dependent upon exposure to a particular duration of cool temperatures (chilling) to release dormancy followed by an appropriate temperature to permit growth in the spring. Usually, before and after the endodormant period (that is, when growth inhibition is regulated from within the bud itself) growth can be arrested at any time by unfavourable growth conditions. This physiological state is known as ecodormancy. Current theories of dormancy suggest that endodormancy is followed by a period of ecodormancy, where buds are held in a dormant state until temperatures rise in the spring allowing growth resumption. Raspberry also exhibits a high degree of paradormancy caused by apical dominance, which is manifested in the typical unbranched form of the canes. Although endodormancy and paradormancy both prevent visible signs of active growth of the cane, the two types of dormancy can be distinguished

experimentally by growth comparison of buds on whole canes with buds on isolated nodal cuttings.

An understanding of the molecular and cellular basis of signals that control dormancy release in woody perennial plants remains elusive. Thus, this study aimed to unveil insights into the overall dormancy processes. Analysis of gene expression patterns, from the onset of dormancy in raspberry buds until the period when plants have accumulated sufficient chilling to permit bud break, provides the basis for a better understanding of the physiological processes within bud tissues. Important tools developed in this study include the generation and analysis of two dormancy stage-specific complementary DNA (cDNA) libraries constructed from endodormant and paradormant buds, expressed sequence tag (EST) analysis, and the development and



Four stages of raspberry bud development. Stage 1 – no development; stage 2 – bud swelling; stage 3 – growth of leaves extending away from the bud scales; stage 4 – second flush of leaves pushing through.



utilisation of a cDNA microarray. By combining these technologies, it was possible to monitor the activity of a large number of genes simultaneously and to identify differentially expressed genes encoding dormancy-associated proteins. Some of the selected genes with interesting expression patterns represent candidate markers for understanding the complex dormancy transition mechanisms. It is possible that key gene sequences identified could prove useful for future molecular breeding programmes, as molecular markers to aid the selection of desirable traits in commercial raspberry lines. The identification of dormancy stage-specific genes will also facilitate the isolation of promoter sequences conferring tight gene regulation during dormancy phase transition. Together with other ongoing raspberry investigations, including physical mapping and QTL analysis, the EST sequences and arrays developed in this project enable for the first time the large scale exploration of the raspberry transcriptome, making this

plant a suitable model system for dormancy studies in woody perennials, especially other members of the Rosaceae. In particular, the array analysis has enabled gene expression profiling during a dormancy time course in a plant that has worldwide economic relevance for production of soft fruit and so we are able to draw conclusions about the metabolic activities taking place during dormancy release in bud meristems, providing the basis for the development and testing of hypotheses concerning dormancy release processes.

#### Reference

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#### Acknowledgement

This work was funded by the Department for Environment, Food and Rural Affairs, project code HH203 NSF.