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From Molecular Level to the Whole Plant

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ABSTRACTS

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A COMPREHENSIVE REVIEW OF DORMANCY STATUS IN LEAFY SPURGE CROWN BUDS IN RESPONSE TO REAL WORLD ENVIRONMENTAL AND PHYSIOLOGICAL CUES

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Dormancy in underground adventitious buds (crown and root buds) is an important determinant in the life cycle of perennial weeds like leafy spurge (*Euphorbia esula* L.). Over-wintering crown buds of leafy spurge break eco-dormancy as spring temperatures rise, resulting in new shoot growth. A new set of crown buds usually becomes visible in June. These crown buds enlarge throughout the active growing season but are kept in a state of para-dormancy by both apical meristem- and leaf-derived signals that appear to interact with signaling pathways involved in cell cycle progression. Although apical dominance is clearly an auxin-derived signal, the leaf-derived signal is not yet fully understood but has been shown to require light and photosynthesis for its mode of action. Studies done using plants grown under a controlled environment indicate that the leaf signal could result from synergistic interplay between leaf-derived sugar and gibberellic acid perception in the crown buds. To gain a better understanding of this model under field conditions, we monitored crown bud carbohydrate content and leaf photosynthesis in relation to dormancy status during the seasonal development of leafy spurge crown buds. Sucrose levels increased slowly in para-doramant crown buds (10-22 mg g^{-1} FW) but showed a rapid 4-fold increase during endo-dormancy (October through November). In contrast, an inverse relationship was observed for starch content in para- and endo-dormant crown buds. Hexose levels remained relatively constant (~10 mg g^{-1} FW) in para- and endo-dormant crown buds. Leaf photosynthetic levels were greatest in May (~19 μmol m^{-2} s^{-1}) and remained relatively stable from June to August (~16-14 μmol m^{-2} s^{-1}, respectively) but declined ~3-fold between August and October. As part of our comprehensive study, we also used micro- and macroarrays developed from a leafy spurge database containing ~1800 Expressed Sequence Tags (ESTs) to screen for differentially expressed genes that might serve as molecular markers for dormancy status in developing crown buds. Some of the identified markers, including cell cycle and hormone-responsive genes, have provided additional insight into signaling mechanisms linking environmental and physiological cues affecting dormancy status. A comprehensive review of the data obtained from this study and its significance to the existing model for root bud dormancy will be presented.