A Key Enzyme in the Biosynthesis of a Plant-Derived Anti-HIV Drug

Rhododendron dauricum (Ericaceae), a native of northeastern Asia, produces unique secondary metabolites, including daurichromenic acid (DCA). DCA has attracted considerable attention as a medicinal resource because this compound is one of the most effective natural products with anti-HIV properties in cell culture. Thus, chemical synthesis of DCA has been extensively studied over the past few years. Previously, a partial characterization has been made of an oxidocyclase, named DCA synthase, using a crude protein extract from young leaves of R. dauricum. DCA synthase is an enzyme that catalyzes the stereoselective oxidative cyclization of farnesyl moiety of grifolic acid to form DCA. Unlike P450-type cyclases involved in glyceollin and furanocoumarin biosynthesis, DCA synthase is a soluble protein and does not need exogenously added cofactors for the reaction. Remarkably, these features are similar to those reported for cannabinoid synthases from Cannabis sativa.

Iijima et al. (pp. 2213–2230) isolated the cDNA of the gene encoding DCA synthase, based on homology search against translated R. dauricum young leaf transcriptome, using cannabinoid synthases as queries. Heterologous expression of the recombinant proteins in a Pichia pastoris system provided evidence that one of the candidate cDNAs is of a gene that encodes an active DCA synthase. Previously, the authors have shown that relevant metabolites as well as DCA synthase activity are predominantly localized to young leaves of R. dauricum that are covered with multicellular trichomes called glandular scales. The authors provide evidence that DCA, a phytotoxic metabolite, is primarily biosynthesized in the glandular scales of young leaves and accumulated extracellularly.

What Limits the Growth of Cyanobacteria?

The commercialization of cyanobacteria-based biomass and biomolecules requires optimization for sustainable economic viability. Many studies identified growth-limiting factors in the model cyanobacterium Synechocystis (e.g., nutrients and light). Understanding the factors controlling the limitation of Synechocystis growth would facilitate the use of this strain as a cell factory for the production of biomass, pigments, secondary metabolite natural products, biofuel, and other high-value compounds. Estevas-Ferreira et al. (pp. 2166–2182) investigated the growth and metabolism of Synechocystis under different nitrogen sources, light intensities, and CO2 concentrations. Cells grown on urea showed the highest growth rates. Under all the conditions tested, however, the daily growth rates in batch cultures decreased steadily over time, and the stationary phase showed similar cell densities. After 4 d of culture, growth was inhibited for all conditions tested, and this inhibition was not related to a metabolic limitation or the availability of photoassimilates. Further physiological investigations indicated that nutrient limitation, quorum sensing, light quality, and light intensity (self-shading) are not the main factors responsible for the decrease in the growth rate and the onset of the stationary phase. Cell division rates in fed-batch cultures, however, were positively correlated with dilution rates. Based on these observations, the authors hypothesize that Synechocystis may be able to sense the gradual increase of cell density occurring in batch cultures via cell-cell interaction, leading to the gradual decrease of division rate until the onset of stationary phase.

Is Root Cortical Senescence Beneficial?

Root cortical senescence (RCS) is a type of programmed cell death found in the Triticeae tribe. RCS is unrelated to the formation of root cortical aerenchyma or the loss of the root cortex due to secondary growth in dicots. Conceivably, RCS may benefit the plant by reducing maintenance respiration in the root or by nutrient reallocation from the senescing tissues. On the other hand, as RCS formation progresses and more cortical cells senesce, the continuity of the cell-to-cell pathway is increasingly disrupted. Additionally, RCS formation and root aging coincide with increased suberization of the endodermis, which may also contribute to reduced hydraulic conductivity. To address the question of if and how RCS benefits plants, Schneider et al. (pp. 2333–2347) used the functional-structural model SimRoot to evaluate the functional implications of RCS in barley (Hordeum vulgare) under suboptimal nitrate, phosphorus, and potassium availability. By the time flowering occurred, RCS was projected to increase simulated plant growth by up to 52, 73, and 41% in nitrate, phosphorus, and potassium limiting conditions, respectively. Nutrient reallocation during RCS had a greater effect on simulated plant growth than reduced respiration or nutrient uptake. Additionally, RCS was quantified in field-grown barley in different nitrogen regimes. Living cortical volume per root length (an indicator of RCS) decreased with depth in younger plants, while roots of older plants had very little living cortical volume per root length. The authors conclude that RCS may be an adaptive trait for nutrient acquisition by reallocating nutrients from senescing tissue and secondarily by reducing root respiration. These simulated results suggest that RCS merits investigation as a breeding target for enhanced soil resource acquisition and edaphic stress tolerance in plants.

How Wheat Root Tips Break through Tough Soil

Soils exhibiting high mechanical impedance as a result of soil compaction or drying, limit root elongation and adversely affect soil exploration and resource uptake. When soil mechanical impedance is increased, root elongation rate decreases within hours and may entirely cease, leading to significant yield losses. Root thickening is one of the most common responses of roots when growing through soil with higher mechanical impedance. This adjustment of roots to increased soil strength reduces the risk of root buckling and decreases the mechanical stress acting on the root during penetration. The geometry of the root tip can also influence a root system’s penetration of the soil. Colombi et al. (pp. 2289–2301) explored how root diameter and root tip geometry influence root elongation under different levels of soil strength in 14 wheat (Triticum aestivum) varieties. Under moderate and high soil
strength, smaller root tip radius to length ratio was correlated with higher genotypic root elongation rate, whereas root diameter was not related to genotypic root elongation. It was found that smaller root tip radius-to-length ratio reduced penetration stress, thus enabling higher root elongation rates in soils with greater strength. Furthermore, it was observed that roots could only partially adjust to increased soil strength. Root thickening was bound by a maximum diameter, and root tips did not become more acute in response to increased soil strength. The results obtained demonstrate that root tip geometry is a pivotal trait governing root penetration stress and root elongation rate in soils of greater strength. The integration of functional root traits, which enable for resource acquisition at minimum energetic costs, into breeding programs is a promising approach to improve agricultural productivity under limited soil fertility.

A MicroRNA Switch That Controls Lateral Root Growth and Nodulation

Legume roots form two types of organs, lateral roots and symbiotic nodules, which participate in the uptake of water and mineral nutrients and in nitrogen fixation, respectively. Since both organs have considerable impacts on plant growth, understanding the mechanisms underlying the development of lateral roots and nodules is crucial to improve agronomical traits in legumes. MicroRNA390 (miR390) is an evolutionarily conserved miRNA that targets non-coding Trans-Acting Short Interference RNA3 (TAS3). Cleavage of TAS3 by ARGONAUTE7 results in the production of tasiRNAs, which target mRNAs encoding AUXIN RESPONSE FACTOR2 (ARF2), ARF3, and ARF4. The miR390/TAS3 pathway plays key roles in plant development. tasiARFs suppress the juvenile-to-adult phase transition in Arabidopsis (Arabidopsis thaliana) and are required for leaf patterning and leaf polarity in different plant species, including the two model leguminous plants Lotus japonicus and Medicago truncatula. The miR390/TAS3 pathway also defines a network that quantitatively controls lateral root growth in Arabidopsis. Hob Becker et al. (pp. 2469–2486) now show that the activation of the miR390/TAS3 regulatory module by overexpression of miR390 in M. truncatula promotes lateral root growth but prevents nodule organogenesis, rhizobial infection, and the induction of two key nodulation genes. Accordingly, inactivation of the miR390/TAS3 module, either by expression of a miR390 target mimicry construct or mutations in ARGonaute7, enhances nodulation and rhizobial infection, alters the spatial distribution of the nodules, and increases the percentage of nodules with multiple meristems. These results reveal a key role of the miR390/TAS3 pathway in legumes as a modulator of lateral root organs, playing opposite roles in lateral root and nodule development.

Auxin Biosynthesis and Wheat Yield

In plants, there are two biosynthetic pathways for the production of the plant hormone indole-3-acetic acid (IAA), namely, the Trp-dependent and the Trp-independent pathways. Shao et al. (pp. 2274–2288) performed a genome-wide analysis to identify a key gene in wheat (Triticum aestivum) that functions in the Trp-dependent pathway of IAA biosynthesis, namely, Trp Aminotransferase of Arabidopsis/Tryptophan Aminotransferase-Related (TAA1/TAR).

TAR converts Trp to indole-3-pyruvic acid, an intermediate that is then converted by other enzymes to form IAA. Unlike other IAA biosynthesis genes, the overexpression of TAA1/TAR genes does not result in growth defects. By sequence mining together with gene cloning, the authors have identified 15 TatAR genes in wheat. TaTAR2.1 had the most abundant transcripts among the TatAR2 genes and was expressed mainly in roots and up-regulated by low nitrogen (N) availability. Knockdown of TaTAR2.1 caused vegetative and reproductive deficiencies and impaired lateral root growth under both high- and low-N conditions. Overexpressing TaTAR2.1-3A in wheat enhanced lateral root branching, plant height, spike number, grain yield, and aerial N accumulation under different N supply levels. In addition, overexpressing TaTAR2.1-3A in Arabidopsis elevated the accumulation of IAA in the primary root tip, lateral root tip, lateral root primordia, cotyledon, and hypocotyl. Overexpression of TaTAR2.1-3A also led to an increase in primary root length, lateral root number, and shoot fresh weight under high- and low-N conditions. These results suggest that TaTAR2.1 is critical for wheat growth and shows potential for genetic engineering with the goal of improving the grain yield of wheat.

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