biological functions (for example, insect repellents, UV protectants, and cryoprotectants) in response to environmental stimuli. Hence, secondary metabolism is presumably regulated so as to respond dynamically to environmental changes. Our omics-based study using Arabidopsis revealed the genes involved in methionine-derived glucosinolate biosynthesis. Modulation of the expression of these genes affected the amino acid contents, suggesting complicated relationship between amino acid metabolism and secondary metabolism. In this presentation, our recent results on amino acid metabolism will be introduced.

Glutamate: glyoxylate aminotransferase (GGAT) functions as a regulator of amino acid content in *Arabidopsis*

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In photorespiration, peroxisomal glutamate:glyoxylate aminotransferase (GGAT) catalyzes the reaction of glutamate and glyoxylate to produce 2-oxoglutareate and glycine. In other words, the GGAT reaction links the photorespiratory carbon and nitrogen cycles and may function as a plant-specific regulator of amino acid content. However, the gene encoding GGAT has not been identified. Here, I intended to identify the GGAT gene and to examine the importance of the GGAT gene product. Based on the analysis of knockout line of alanine:2-oxoglutarate aminotransferase like gene, we succeeded to identify the *GGAT* gene. A phenotypic analysis indicated that the knockout line (*ggat1-1*) exhibited a well-known photorespiratory-deficient mutant phenotype; growth repression was observed and plants recovered under high CO_2 or low light conditions. To understand the role of GGAT in the regulation of amino acid levels, we generated and characterized plants overexpressing the *GGAT1* gene. The pool size of serine and glycine—products of the GGAT reaction—increased markedly in all *GGAT1* overexpression lines. Further, the levels of these amino acids were strongly correlated with the levels of *GGAT1* mRNA and GGAT activity. Air (CO_2 concentration), light, and nutrient conditions affected the amino acid profiles in the *GGAT1* overexpression lines. These results suggested that the photorespiratory aminotransferase reaction catalyzed by GGAT is an important regulator of amino acid content.

Transporters for amino acids and peptides in plants

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Nitrogen is an essential nutrient for plant growth and productivity. Following uptake from the soil or assimilation within the plant, organic nitrogen compounds are transported within and between cells as well as over long distances in support of plant metabolism and development. Research mainly focused on amino acids that represent in most plants the principal transport form for organic nitrogen, but transport of small peptides and other organic nitrogen forms has also been investigated.

Transporters for amino acids and peptides have been identified and characterized using heterologous expression systems, i.e. *Saccharomyces cerevisiae* mutants and *Xenopus laevis* oocytes. These studies identified transporters belonging to different gene families that mediate low and high affinity transport of amino acids or peptides. Results from different labs revealed differential expression of the respective genes and elucidated the importance of individual transporters for uptake of amino acids or peptides from the soil, for long distance transport and translocation to seeds, respectively.

An overview of current knowledge and recent findings will be presented.

Metabolomics-based functional genomics and network analysis for plant amino acid metabolism

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Metabolomics is a powerful approach to decipher genes' function and elucidate metabolic networks in plants. We have investigated the metabolic profiling of the mutants of serine acetyltransferase genes and β-substituted alanine synthase (BSAS) genes, which encode cysteine synthase (CSase) [O-acetylserine (thiol) lyase] and β-cyanoalanine synthase (CASase) of Arabidopsis thaliana. This analysis concluded mitochondrial BSAS3;1 is a genuine CASase, and β-cyanoalanine is present as a conjugated form as γ-glutamyl-β-cyanoalanine. We also investigated the metabolic network of two mutants (methionine-over accumulation 1 [mto1] and transparent testa4 [tt4]). Although the mutants showed no apparent morphological abnormalities, the overall metabolite correlations in mto1 were much lower than those of the wild-type and tt4 plants, indicating the loss of overall network stability due to the uncontrolled accumulation of methionine. In the tt4 mutant, several new correlations were observed, suggesting an adaptive reconfiguration of the network module. Gene-expression correlations presumably responsible for these metabolic networks were determined using the metabolite correlations as clues.

Function of glutamine synthetase and glutamate synthase in rice plants

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A major source of inorganic nitrogen for rice plants grown in paddy soil is ammonium ions. The ammonium-ions, actively taken up by the roots, are assimilated into the amide-residue of glutamine (Gln) by the reaction of glutamine synthetase (GS) in the roots. The Gln is converted into glutamate (Glu), which is a central amino acid for synthesis of a number of amino acids, by the reaction of glutamate synthase (GOGAT). Although a small gene family for both GS and GOGAT is present in rice, ammonium-dependent and cell-type specific expression suggest that cytosolic GS1;2 and plastidic NADH-GOGAT1 are responsible for the primary assimilation of ammonium ions in the roots. In the plant top, approximately 80% of the total nitrogen in the panicle is remobilized through the phloem from senescing organs. Thus, nitrogen remobilization determines productivity of rice. Since the major form of nitrogen in the phloem sap is Gln, GS in the senescing organs and GOGAT in developing organs are important for nitrogen remobilization and re-utilization, respectively. Our recent work with a knock-out mutant of rice clearly showed that GS1;1 and NADH-GOGAT1 are both responsible for the remobilization processes. Since the integration of the functions of many genes is required for the overall process of nitrogen utilization in plants, it is not easy to draw the whole picture from studies on an individual gene. Recent studies obtained from the profiling of metabolites in the *OsGS1;1* mutants, together with transcriptome analysis, will be discussed in this symposium.