



## Molecular regulation of starch metabolism

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Starch is the second most abundant biomass next to cellulose and composed of amylopectin, a highly branched glucan, and amylose, an essentially linear glucan. The former and the latter glucans usually account for approximately 65–85% and 15–35% of the total starch, respectively. During the last three decades the basic scheme of starch biosynthesis has been established based on numerous biochemical, genetic, and molecular biological approaches worldwide using a variety of higher plants and algae. It is well known that after the synthesis of ADPglucose by ADPglucose pyrophosphorylase (AGPase), amylopectin's fine structure is formed by concerted actions of multiple isozymes from three classes of enzymes, starch synthase (SS), starch branching enzyme (BE), and starch debranching enzyme (DBE), and that amylose is synthesized by mainly granule-bound SS (GBSS). In addition to the roles of starch biosynthetic isozymes, the contributions of  $\alpha$ -glucan phosphorylase,  $\alpha$ -glucan, water dikinase, phosphoglucan, water dikinase, pyruvate, phosphate dikinase,  $\alpha$ -amylase, and carbohydrate-binding modules have been documented. Information on the whole genome sequence and omics analyses are available in main

plant species. All these results revealed the roles of key biosynthetic isozymes of SS, GBSS, BE, and DBE and subunits of AGPase to starch biosynthesis, and presently we know to what extent the fine structure of starch molecules and the internal structure and physicochemical properties of starch granules as well as starch amounts can be modified in accord with the activity levels of these isozymes and subunits.

However, in spite of numerous past investigations, the regulation of the network of enzymatic reactions has not been fully understood. To resolve the complex mechanisms, we need to examine several topics such as redundancy and supplementary functions of multiple isozymes, enzyme-enzyme interaction(s), and regulatory factors controlling catalytic and specific activities of individual isozymes, temporal and spatial co-expression of multiple isozymes, post-translational modification of enzymatic capacities such as phosphorylation, glycosylation, and redox state. There are still lots of uncertainties in the understanding of the initiation of starch biosynthesis.

On the other hand, the present era can be said as the harvest timing for starch science. Accumulation of information on starch metabolism and materials such as mutants and transformed lines having novel starch phenotypes could provide us with great opportunities, including the ability to mitigate the detrimental effect of high-temperature stress on cereal yields caused by global warming, as well as to use these starches for food and industrial applications. For this purpose, plant materials in which multiple starch biosynthetic enzymes are simultaneously modified can be of great use because they frequently exhibit a variety of more interesting starch phenotypes than expected from the sum of contributions of individual enzymes. To make these materials suitable for practical uses, the relationship between the structure and composition of starch molecules and the internal structure of starch granules must be clarified in more detail.

At present, plant species-specific events are still full of secrets. New approaches for comparative studies using a

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number of different plant species might give us invaluable information for agricultural uses and future applications.

The Special Issue entitled “Molecular Regulation of Starch Metabolism” encouraged the active starch scientists worldwide to report their ongoing studies with leading scientists in this field as Guest Editors; Jinsong Bao (Zhejiang University), Christophe Colleoni (Université de Lille), Naoko Fujita (Akita Prefectural University), Alberto A. Iglesias (CONICET-UNL), Yasunori Nakamura (Akita Prefectural University), Martin Steup (University of Potsdam), and Ian Tetlow (University of Guelph). We are honored to present 15 papers belonging to this Special Issue (the paper entitled “Improving rice eating and cooking quality by coordinated expression of the major starch synthesis-related genes, *SSII* and *Wx*, in endosperm”, by Huang et al. has already been published in 2021 in *Plant Molecular Biology* volume 106, pages 419–432).

The Guest Editors thank all contributors for submitting their exciting papers and the invited reviewers for their

critical and helpful comments on the manuscripts. We also thank Prof. Motoaki Seki, Editor-in-Chief of PMB, for his kind and timely invitation to edit this Special Issue, and all staffs of the Editorial Office of PMB for their continuous help during the editing process. The accepted papers cover a wide range of topics related to our aims of this Special Issue. We believe that the new results and ideas presented in these papers will strengthen our understanding of the complexities of starch metabolism and will motivate young students and researchers to work towards the future success of starch industrial and agricultural applications.

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