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Functional Analysis of Starch Metabolism in Plants

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Message from the Guest Editors

Starch is the major storage carbohydrate in higher plants, and has many important functions. Its major site of accumulation is in storage organs, including seeds, fruits, tubers, and storage roots. Starch has been identified as a major integrator in the regulation of plant growth to cope with continual changes in carbon availability.

Characterization, expression, enzyme activity, and functional analysis in starch metabolism are very important in order to fully understand their function and roles in the carbohydrate production in plants. In addition, the functions of genes and transcription factors have been studied in order to understand their roles and functions in the starch biosynthesis in plants. Recently, there have been more chances to improve our understanding through advanced scientific tools such as GWAS, MABc, gene pyramiding, overexpression, knock-out, RNAi, and gene editing.

This Special Issue will highlight the identification, function, roles, and relationships of genes and transcription factors in starch biosynthesis, and their interactions through the processes in starch synthesis pathway in plants.



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Special Issue



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Message from the Editor-in-Chief

Plants is an open access journal which provides an advanced forum for research findings in areas related to plant function, its physiology, biology, taxonomy, stresses, and its interactions with other organisms. It publishes original research articles, reviews, reports, conference proceedings (peer reviewed full articles) and communications. In original research papers, it is important that full experimental details are provided. We also encourage timely reviews and commentaries on topics of interest to the plant research community.

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