

SL204

Carbon Partitioning in Transgenic Plants

한지학

Food Science Department, Rutgers University

Photosynthesis in plants represents the main machinery of energy production used to support all biological processes in living organisms ranging from bacteria to humans. Net energy flows from photosynthetically active tissues such as leaves, representing the source, to photosynthetically inactive tissues such as tubers and seeds, representing the sink. Carbon assimilates, the final products of photosynthesis, are partitioned in leaves in the form of sucrose, and in tubers, seeds and leaves in the form of starch.

Starch plays a key role in the world's economy, generating an estimated \$50 billion per year in the U. S. alone, and has long been a source for sweeteners and numerous other food ingredients, as well as for pharmaceuticals, textiles, alcohol-based fuels, adhesives and biodegradable packaging materials. Sucrose, a natural sugar and also a major food ingredient, is the only carbon source for starch biosynthesis. Therefore, the regulation between sucrose and starch biosynthesis in plant cells should be well coordinated. In addition, these two carbohydrates are the major biochemical components stored and utilized for the growth and development of plants. In order to synthesize these carbon assimilates, carbon metabolic enzymes such as fructose 1,6-bisphosphatase, sucrose-phosphate synthase, ADP-glucose pyrophosphatase, starch synthase and branching enzyme in plant cells are believed to be coordinated with each other along with metabolites under biochemical and genetic regulation.

The primary objectives of the recent and future research in the biotechnology of carbon partitioning are to clone the cDNAs encoding the major enzymes associated with the metabolic pathway of starch and sucrose biosynthesis and to introduce those genes into plant tissues, thereby generating transgenic plants. The proposed end result is the achievement of marked improvements in the level of starch and sucrose in plant cells increasing total crop yield. Although early progress has been made in this area with the aforementioned enzymes, starch synthase, which catalyzes the stepwise addition of glucan from ADP-glucose to an elongation glucan chain of starch, has not yet been well characterized at the molecular level. We have identified a 76 kDa polypeptide from corn as starch synthase and cloned a 2.3 kb cDNA. In future work, the cDNA clone of starch synthase will be expressed in transgenic plants to see whether it can influence the partitioning and metabolism of carbohydrates.