INTRODUCTION

This chapter reviews starch synthesis in higher plants, with special reference to the steps that can be manipulated to advantage by genetic manipulation. Thus, the enzymology and biochemistry of the various enzymes in the plant, algal and cyanobacterial systems will also be described as these are the potential sites for manipulation of both starch quantity and quality. Regulation of starch synthesis at the enzymatic and cellular levels will also be discussed with emphasis on its relevance to genetic engineering.

The reactions of glycogen synthesis in the cyanobacteria are similar to those observed in the higher plants and particularly at the regulation of cyanobacterial glycogen synthesis at the ADP-glucose synthesis step and therefore they will be discussed. Since the properties of the starch biosynthetic enzymes and the effects of certain mutants on starch structure are known, a pathway for starch synthesis can be proposed which postulates specific functions for the starch synthases and branching enzymes. Recent results indicating how starch content has been increased in certain plants will also be described. Recent reviews on starch biosynthesis (1-12) discuss a number of the areas presented in this chapter.

Essentially two polymers can be found in the starch granule: amylose, which is mainly linear, and amyllopectin, highly branched. Amylose is mainly a linear chain of about 840 to 22,000 units of α-D-glucopyranosyl residues linked by α-(1→4) bonds (molecular weight around 136,000 to 3.5 x 10⁶). The number of anhydroglucose units varies quite widely with plant species and their stage of development. Some of the amylose molecules are branched to a small extent (α-1→6-D glucopyranose; one per 170 to 500 glucosyl units). Amylopectin, in contrast, which usually comprises about 70% of the starch granule, is more highly branched with about 4 to 5% of the glucosidic linkages being α-1→6.

Starch content in many plant seeds or reserve tissue is 65 and 90% of the total dry matter and the patterns of starch accumulation during development of the tissue are specific to the
species and related to the pattern of organ development. Many models of amylopectin structure have been proposed based on much experimental data and those currently accepted are those postulated by Robin et al. (13), Manners and Matheson (14) and Hizukuri (15; Figure 1). The model is described as the cluster model. The chemical and physical aspects of the starch granule and its components amylase and amylopectin have been discussed in recent excellent reviews by Morrison and Karkalas (16) and Hizukuri (17).

ENZYME REACTIONS OF STARCH SYNTHESIS IN PLANTS AND ALGAE

Presently, synthesis of starch requires six reactions. First, synthesis of a glucosyl donor and in the case of starch it is adenosine diphosphate glucose. ADP-glucose synthesis is catalyzed by ADP-glucose (synthetase) pyrophosphorylase (reaction I, E.C. 2.7.7.27; ATP:α-D-glucose-1-phosphate adenylyltransferase). Reaction II is catalyzed by starch synthase (E.C. 2.4.1.21; ADP-glucose;1,4-α-D-glucan 4-α-glucosyltransferase). Reaction III is catalyzed by branching enzyme (E.C. 2.4.1.18; 1,4-α-D-glucan 6-α-(1,4-α-glucano)-transferase).

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\begin{align*}
\text{ATP} + \alpha-\text{glucose-1-P} & \Leftrightarrow \text{ADP-glucose} + \text{PPi} \\
\text{ADP-glucose} + \alpha-1,4 \text{ glucan} & \Rightarrow \alpha-1,4-\text{glucosyl-} \alpha-1,4 \text{ glucan} + \text{ADP} \\
elongated \alpha-1,4-\text{oligosaccharide chain} & \Rightarrow \alpha-1,4-\alpha-1,6 \text{ branched-glucan} 
\end{align*}
\]

The differences in the catalytic properties of the starch synthases and branching enzymes isolated from different plant sources, such as chain elongation by the synthases, size of