production costs, high price, seasonal changes, and other environmental impacts associated with utilization of these brown sea weeds. These reasons have made researchers to look out for different sources for the production of alginic acid. In later years, it was Linker and Jones [42] and Gorin and Spencer [43] who found that bacteria *Pseudomonas aeruginosa* and *Azotobacter vinelandii* respectively produces polyuronic compounds that resemble alginic acid. After this identification, improvisation in production of alginic acid by these bacterial species has been explored. It has also been found that several other bacterial species, such as *Pseudomonas mendonica, Pseudomonas putida, Pseudomonas phaseolicola, Pseudomonas savastanoi, Pseudomonas glycinae*, and *Pseudomonas fluorescens* produce alginic acid [44–47].

14.3 Synthesis of Alginate

As described earlier, alginate is a linear exopolysaccharide comprising D-mannuronic acid and L-guluronic acid linked by β (1→4) and α (1→4) glycosidic bond. These mannuronate and guluronate units of alginate are called M and G blocks, respectively [10] (Figure 14.1).

Alginate biosynthesis has been divided into four stages, viz., synthesis of precursor substrate, polymerization and cytoplasmic membrane transfer, periplasmic modification, and export through the outer membrane. The biosynthesis of alginates initiates with mannose in sea weeds, which is then converted to mannuronate and then alginate. Whereas in bacteria, the precursor of alginate biosynthesis is fructose–6–phosphate, which is converted to Guanosine diphosphate (GDP) mannuronic acid. It is then

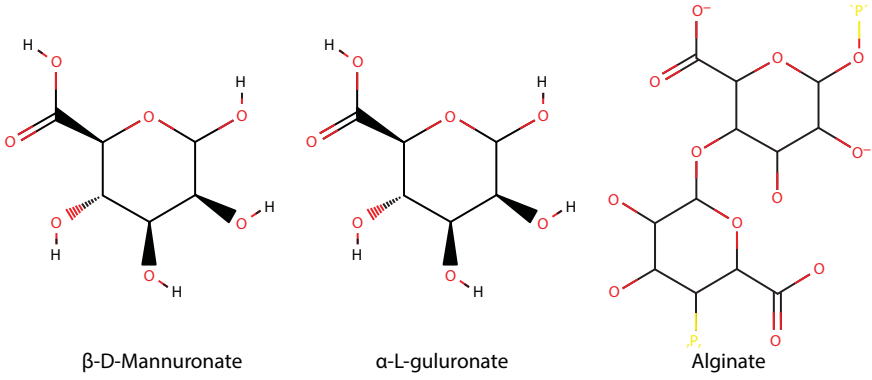

Figure 14.1 Structure of mannuronate, guluronate, and β (1→4) mannuronic acid and α (1→4) guluronic acid.