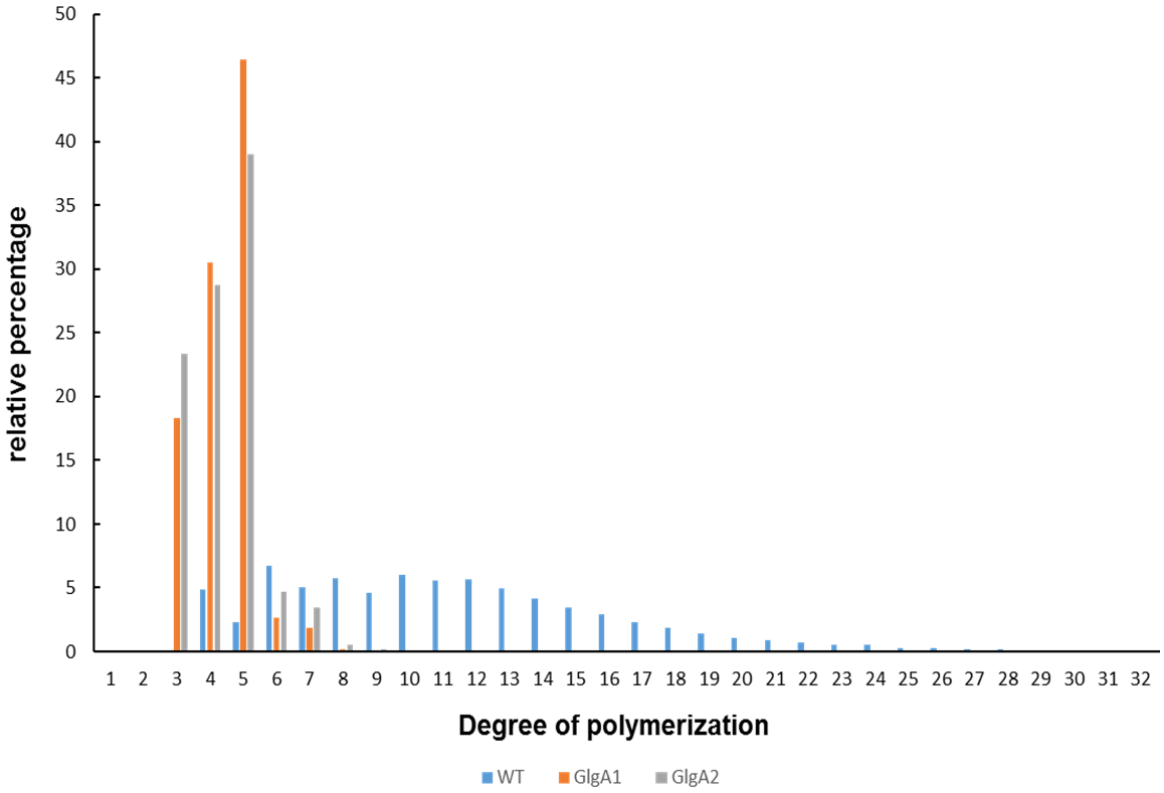

Supplemental Figure 6. Structural analysis of the glycogen accumulated by the *Escherichia.coli* wild type strain and the mutant strain ΔglgA deleted in glycogen synthase complemented with GlgA1 or GlgA2. The mutant strain ΔglgA was complemented with pET-glgA1 or pET-glgA2, the cells were cultivated overnight in M9 medium at 37°C then harvested by centrifugation at 4000g during 10 minutes at 4°C. The cells were disrupted through a French Press then centrifuged at 16000 g for 10 min at 4 °C. Water-soluble polysaccharides present in the supernatant were purified from the wild type or the Δ*glgA* mutant complemented with pET-glgA1 or pET-glgA2. After complete digestion with commercial isoamylase, glucan chains were separated according to their degree of polymerization (DP) by FACE (Fluorescence anisotropy capillary electrophoresis). The wild type strain produces short and long chains, no difference was observed between the mutant strains complemented with GlgA1 or GlgA2, both produce a polysaccharide with very short chains (DP3 to DP8). This surprising result could be due among others to ineffective interaction of the cyanobacterial enzyme with the *E. coli* branching enzyme leading to misleading modification of the elongation to branching ratio.