CHAPTER V

CONCLUSION

1. CGTase from *Bacillus* sp. A11 was purified approximately 144 folds with a 36% yield and specific activity of 3,574 units/ mg protein.
2. CGTase activities were lost after modifications of carboxyl, histidine, tryptophan, and tyrosine residues by 1-ethyl-3- (3-dimethylaminopropyl) carbodiimide, diethylpyrocarbonate, *N*-bromosuccinimide, and *N*-acetylimidazole, respectively.
3. Modification of cysteine, lysine, and serine residues with *N*-ethylmaleimide, iodoacetamide, or dithiothreitol, 2,4,6-trinitrobenzenesulfonic acid, and phenylmethylsulfonyl fluoride, respectively, did not affect the CGTase activities.
4. The loss of CGTase activities after the modification of carboxyl, histidine, tryptophan, and tyrosine residues were reduced in the presence of protective substances, α-, β-, γ-CD, or maltotriose.
5. Amino acid residues which were protected by protective substances were two histidine, one tryptophan, and two tyrosine residues.
6. In non-denaturing PAGE, CGTase after modification by EDC move slower than unmodified enzyme. While upon modification of histidine by DEP or modification of tyrosine by NAI, the CGTase bands moved faster. However, modification of tryptophan did not change bands migration.
7. Kinetic parameters for CD coupling activity, K_m values were 1.55, 1.60, and 1.94 mM and V_{max} values were 2.81, 2.50, and 1.40 μmoles/ min for β-CD, G_2- β-CD, and methyl- β -CD, respectively.
8. Kinetic parameters for cyclodextrin degrading activity, K_m values were 3.16, 1.69, 1.42, and 91.63 mM and V_{max} values were 58.96, 13.12, 8.61, and 10.69 μmoles/ min for α-, β-, γ-CD, and maltotriose, respectively.