Abstract

Pyrazines (1,4-nitrogen substituted benzenes) have near ubiquitous biological distribution and are also anthropogenic. Despite their wide occurrence and vast applications, their bacterial degradation studies are limited and hence, it was of interest to isolate a bacterium and study its potential to catabolize pyrazine-2-carboxylate, which was the objective of the thesis.

A bacterium (strain HCU1) capable of metabolizing pyrazine-2-carboxylate was selected from the 50 screened isolates and its affiliation to the genus *Stenotrophomonas* was indicated by its polyphasic characterization. The 16S rRNA gene sequence of strain HCU1 closely clustered with the type strain of *Stenotrophomonas maltophilia* (98.7% sequence similarity). Growth of *Stenotrophomonas* sp. HCU1 and ring reduction of pyrazine-2-carboxylate was demonstrated when pyrazine-2-carboxylate was used as a sole source of carbon, nitrogen and supplement. Ring reduction of pyrazine-2-carboxylate was observed with both growing and resting cells of *Stenotrophomonas* sp. HCU1. Out of 4 metabolites isolated from the culture supernatant of *Stenotrophomonas* sp. HCU1; two (1,2,5,6-tetrahydropyrazine-2-carboxylate, 2-amino-2-hydroxy-3-(methylamino) propanoic acid were characterized based on UV, IR, $^1$H, $^{13}$C NMR and mass spectroscopic analyses. Based on the masses of the identified metabolites a putative reductive pathway of pyrazine-2-carboxylate catabolism is proposed. A ~65kDa enzyme catalyzed the reduction of pyrazine-2-carboxylate to 1,2,5,6-tetrahydropyrazine-2-carboxylate and the enzyme also had a broad substrate specificity for other N-heterocyclic compounds.