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關鍵字(中)	耐熱菌 菌種鑑定 綠島 微小桿菌
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摘要(中)	台灣擁有許多地熱資源，而這些高溫環境中蘊含著豐富的嗜熱性微生物。本研究自台東縣綠島鄉柚子湖地區的高溫海水水樣中，分離純化出耐熱性細菌。根據 16S rDNA gene sequence 定序比對結果篩選出 4 株序列比對較接近的菌株 NTU-1329、NTU-1330、NTU-1331 及 NTU-1337 進行本實驗。 本研究菌株在 modified Thermus mediume 固體培養基上培養兩天後，呈現直徑 2-3 mm 的橘黃色、凸面具有光澤的菌落。經分析皆為格蘭氏陽性菌，有周鞭毛具移動性，不產孢子的好氧菌。在對數成長期呈現桿狀，穩定期時會變成球狀，細菌長約 1.16-1.45 μm 寬約 0.65-0.82 μm。最適生長條件為 30 oC，pH 7-11；在生化分析方面，4 株菌皆具有

	alkaline phosphatase、esterase、leucine arylamidase 、acid phosphatase、α-glucosidase 、β-glucosidase、catalase、oxidase 等酵素活性以及具有 skim milk 與 starch 水解的能力。在碳源利用上，主要可利用 citrate 、D-mannose、D-xylose、L-glutamate、malate、pyruvic acid、L-proline、L-alaline、L-ornithine。脂肪酸組成主要為 C16:0、isoC16:0、aiC17:0 以及 C18:0。 由 16S rDNA 結果分析顯示此 4 菌株與 Exiguobacterium aestuarii 的相似度在 97.9 ~ 98.7 % 之間，在 DNA G+C 組成上為 60.3 ~ 62.9 mol %。根據形態、生理生化以及遺傳特性分析的結果發現，本研究的 4 株菌株與比對最相近的菌株 E. aestuarii 確實有差異，在酵素活性測試部分，最相近菌種 E. aestuarii 無 oxidase 與 starch 水解能力，本研究菌株皆有活性。本研究菌株 DNA G+C 組成皆大於 60 % 以上，而 Exiguobacterium 菌屬中目前無發現高於 60 % 的菌種。本研究菌株生長溫度最高可達 50 oC，為目前此屬中最高溫，而耐鹽度最高可達 15 %。因此推測本研究的四株菌株可能成為 Exiguobacterium 菌屬中的新菌種。
摘要 (英)	There are many geothermal areas which include variable microorganisms in Taiwan. The study is aimed to isolate the thermophiles from the sample of warm sea water located on Lyudao Township, Taitung County. According to the results of 16S rDNA sequences analyses, four isolates, NTU-1329, NTU-1330, NTU1331, and NTU-1337 were selected for further investigation. Colonies are 2-3 mm in diameter after incubation for 2 days on modified Thermus agar at 40 oC and yellow-orange convex with entire margin and glossy. Cells are Gram positive, non-spore forming, motile with peritrichous flagella. Cells are short rods (0.73 μm x 1.23 μm) in the early stationary phase. Growth occurs at 30 oC and 50 oC, with optimal growth at 30 oC. The optimal pH for growth is pH 7-11 and growth does not occur in the presence of 16 % NaCl. All strains hydrolyze skim milk and starch. They show alkaline phosphatase, esterase, leucine arylamidase, acid phosphatase, α-glucosidase, β-glucosidase, catalase and oxidase activity. All strains utilize citrate, D-mannose, D-xylose, L-glutamate, malate, pyruvic acid, L-proline, L-alaline and L-ornithine. Major fatty acids are C16:0, isoC16:0, C18:0 and anteisoC17:0 . The 16S rDNA sequence similarities of NTU-1329, NTU-1330, NTU1331, and NTU-1337 to Exiguobacterium aestuarii are between 97.9 ~ 98.6 %. The DNA G+C contents of the isolates are between 60.3 ~ 62.9 %. On the basis of morphological, physiological and genetic data, there are differences between the four strains and E. aestuarii. It is found oxidase-negative and no hydrolysis of starch in E. aestuarii but not in four strains. The maximal growth temperature and pH of four strains are the highest in the genus of Exiguobacterium. As a result, the four strains might be a novel species in the genus of Exiguobacterium.
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