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青海柯柯盐湖16株细菌的ARDRA筛选及系统发育初步分析

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A primary study of 16 strains in Keke Salt Lake by ARDRA and phylogenetic analysis

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摘要 从青海柯柯盐湖泥样中分离的16株细菌,用2种限制性内切酶酶切进行ARDRA分析,其中12株菌的酶切带谱有较大差异。根据这12株菌的16SrDNA序列进行系统发育分析结果表明,12株菌有11株分布于芽孢杆菌科中的*Halobacillus*,*Gracilicoccus*,*Amphibacillus*,*Virgibacillus*,*Bacillus*,*Salicibacillus*和1个潜在的新属中,另1株属于Proteobacteria的Gamma亚群*Halomonadaceae*科,*Halomonas*属。而且16SrDNA系统发育分析提示这些菌株中存在3个新种和1个新属的可能。本研究得出的结论为:应用ARDRA来初步筛选菌株是可行的;青海柯柯盐湖这一极端环境中存在较丰富的新的芽孢菌种类。

关键词: 柯柯盐湖 ARDRA 系统发育分析

Abstract: Sixteen bacteria strains were isolated from Keke Salt Lake, Qinghai, China. Their amplification of 16S rDNA and sequencing were performed. The 16S rDNA PCR products of the tested strains were digested by two restriction enzymes (*Afa*I and *Hae*III) and the results showed that 12 strains of them displayed great diversity with their restriction patterns. Phylogenetic analysis revealed that most of these strains belong to six genera of the family *Bacillaceae*: *Halobacillus*, *Gracilicoccus*, *Amphibacillus*, *Virgibacillus*, *Bacillus* and *Salicibacillus*. In addition, from the phylogenetic analysis KN4 may be a new genus and KN2, KN3 and KN16 are probably three new species. The results showed that there are probably many new microorganisms in the extreme environments and Keke Salt Lake harbours a diverse of microbials.

Key words: Keke Salt lake ARDRA phylogenetic analysis

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