论著

阴道毛滴虫Rac1蛋白的cDNA克隆和序列分析(英文)

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收稿日期 修回日期 网络版发布日期 接受日期

摘要

目的 获得阴道毛滴虫Rac1蛋白的cDNA克隆,研究其在细胞周期中的调解作用。 方法 提取阴道毛滴虫总RNA,构建cDNA表达文库,随机分离cDNA克隆并测序。用在线生物分析软件NCBIBLAST、ClustalW以及Treeview等程序进行序列分析。 结果 获得一株有714bp的cDNA克隆。序列分析表明,该克隆开放阅读框具600bp,推测肽链具200个氨基酸。该肽链与Rho家族中Rac1鸟苷三磷酸(GTP)酶同源性最高(>60%),并具多种RhoGTP酶的保守基序,如GTP结合部位、GTP酶激活蛋白作用基序、GTP分离抑制因子作用基序、鸟嘌呤核苷酸交换因子作用基序等。进化树分析显示该克隆属于Rac亚家族GTP酶,与原虫Rac1蛋白最接近。 结论 该克隆属RhoGTP酶的Rac亚家族,很可能是阴道毛滴虫的Rac1蛋白。

关键词 阴道毛滴虫 Rac1 GTP酶 cDNA克隆

分类号

Molecular Cloning and Characterization of a Rac1 Homologue cDNA from Trichomonas vaginalis

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Abstract

Objective To clone and characterize a Rac1 homologue from Trichomonas vaginalis for studying cell cycle of the organism. Methods A cDNA library derived from T. vaginalis mRNA was constructed into λ TriplEx2 phage vector. An expression sequence tag program was launched. Sequences of cDNA clones were analyzed using NCBI BLAST algorithms, and ClustalW and Treeview programs. Results A cDNA clone with a length of 714 base pairs was isolated. The sequence analysis showed that the cDNA clone has an open reading frame with 600 bp. The deduced amino acid sequence from the open reading frame contains 200 residuals and is most homologous to Rac1 subfamily of Rho GTPases with >60% identity. The conserved sequence elements of Rho GTPases, such as GTP binding sites, GTPase activating protein (GAP) interaction motifs, GTP dissociation inhibitors (GDI) interaction motifs, quanine nucleotide exchange factor (GEF) interaction elements, etc, were detected in the amino acid sequence. The phylogenetic analysis showed that the cDNA clone is grouped in the Rac subfamily and is more closely related to Rac1 proteins of protozoa. Conclusion The cDNA clone isolated belongs to Rac subfamily of Rho GTPases and is probably a Rac1 protein of T. vaginalis. Key words Trichomonas vaginalis Rac1 GTPase cDNA clone

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