

研究报告

SARS冠状病毒S蛋白结构预测及表达初探

孙美玲, 朴锦华, 尹长城, 杨公社, 黄华樑

西北农林科技大学动物科技学院, 杨凌 712100;

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摘要 利用生物信息学的工具和方法, 对SARS病毒基因组中预测的S蛋白 (spike protein) 的编码序列进行了分析, 预测了其结构特征和可能的功能域。选择其中最有可能参与受体识别及产生主要免疫原性的区域 (S401~659) 作为待表达区域。将通过PCR获得的此段S蛋白片段的编码序列克隆至大肠杆菌载体pET28a(+) 和酵母表达载体pPIC9K中, 分别构建了pET28a(+)-S和pPIC9K-S表达质粒, 转化至大肠杆菌菌株BL21 (DE3)-star和毕赤酵母中表达。产物的蛋白电泳和蛋白印记结果表明, S蛋白片段获得成功表达。采用镍离子螯合层析法纯化变性的包涵体样品, 纯度达90%以上。

关键词 [SARS](#) [冠状病毒](#) [S蛋白](#) [表达](#)

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A Preliminary Study of the Structure Prediction and Expression of SARS-CoV Spike Protein

SUN Mei-Ling, PIAO Jing-Hua, YIN Chang-Cheng, HUANG Hua-Liang

College of Animal Science and Technology, Northwest Sci-Tech University of Agriculture and Forestry, Yangling, Shaanxi, 712100, China

Abstract

In this study, the encoding sequences of SARS-CoV spike protein were analyzed by bioinformatics methods, the structural characteristics and functions were forecasted based on available data. It suggests that the fragment of spike glycoprotein (S401~659) may be crucial for viral attachment and may be a major immunodominant epitope. Then the fragment was amplified and subcloned into expression vector pET28a(+) and pPIC9K. These two plasmids pET28a(+)-S and pPIC9K-S were transformed to E.coli strain BL21(DE3)-star and Pichia pastoris, respectively. SDS-PAGE and Western blot analysis showed that the recombinant protein was successfully expressed. The denatured inclusion bodies were purified with Ni-NTA chelate agarose and its purity can reach 90%.

Key words [SARS](#) [coronavirus](#) [spike protein](#) [expressing](#)

DOI:

通讯作者 孙美玲 lisasun78@yahoo.com.cn

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