论文

脑缺血再灌注损伤后小分子RNA的分析

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摘要：

目的　检测假手术和脑缺血再灌注大鼠脑组织小分子RNA的差异表达。方法　选取假手术组(F)和脑缺血再灌注组(B)大鼠海马脑组织，提取小分子RNA，应用Solexa高通量测序技术进行深度测序，通过信息分析获得miRNA的表达情况。结果　F组和B组分别获得6833331和6407399个序列，平均长度均为22nt。将原始数据与miRbase、Genbank和Rfam(9.1)数据库进行比对和分类注释。在F组和B组，miRNA总数分别占小分子RNA总数的76.77%和75.22%，两组间共有32种差异表达的miRNA，预测出新的候选miRNA 130条。结论Solexa测序是一种快速、全面地研究和发现小分子RNA的重要手段，筛选出的差异表达及候选miRNA可能参与脑缺血再灌注的发展。

关键词： 高通量测序；脑缺血再灌注；小分子RNA

Analysis of small RNAs induced by cerebral ischemia reperfusion injury

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Abstract:

 Objective　To detect small RNAs and identify those differentially expressed between sham operation (F group) and cerebral ischemia reperfusion (B group) in rats. Methods　Total RNA was extracted from the hippocampus tissue from the two groups. Solexa high-throughput sequencing was used to obtain miRNA expression profiles and bioinformatics analyses were performed. Results　6833331 and 6407399 reads were obtained in the F and B groups, respectively, with a average length of 22 nucleotides in either group. All reads were examined against the miRBase15.0, Genbank and Rfam (9.1) databases, and were annotated into different categories. For groups F and B, MiRNA sequences account for 76.77% and 75.22%, respectively, of the respective total reads. It was found that there were 32 differently expressed miRNAs between the two groups. In addition, 130 novel miRNAs were predicted by the Mireap Software. Conclusion　Solexa sequencing is a rapid and effective method for discovering small RNAs and screening differentially expressed species. These miRNAs may function as regulators of many key genes during the development and reconstruction of brain injury.

Keywords: High-throughput sequencing； Cerebral ischemia reperfusion； Small

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