

乳头状甲状腺癌差异表达基因的筛选及生存分析

刘中娇 窦龙涛 庄振 刘玲 周永维 刘曼 李晶 张红梅*

(德州学院生命科学学院,山东省功能性生物资源利用高校重点实验室,山东省生物物理学重点实验室,山东 德州 253023)

[摘要] 目的 利用生物信息学方法筛选乳头状甲状腺癌(PTC)的关键基因及其所在信号通路,探讨其致癌机制。方法 从基因表达综合数据库(GEO)的两个测序平台的7个GSE芯片中获得PTC和癌旁组织样本的数据。首先利用R语言分别筛选出两个测序平台样本的差异基因,然后通过Metascape和STRING对差异基因进行生物学功能、信号通路分析和蛋白质-蛋白质相互作用分析,最后利用Cytoscape 3.5.1软件筛选出关键基因。结果 两个测序平台的样本求交集共获得302个差异表达基因,其中149个基因上调,153个基因下调,利用Cytoscape 3.5.1软件筛选出15个关键基因,其中12个关键基因位于细胞外基质受体相互作用信号通路中。利用UALCAN数据库对15个关键基因进行生存分析,其中4个基因的表达水平变化与患者的生存时间紧密相关。结论 利用生物信息学技术对来自7个PTC基因芯片数据集的信息进行分析,弥补了小样本结果的不一致性,提高了结果的可靠性和稳定性,并且筛选出了15个关键基因,发现了细胞外基质受体相互作用信号通路在甲状腺癌的发生发展中的重要作用。

[关键词] 乳头状甲状腺癌;生物信息学;差异基因;生存分析;人

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Screening and survival analysis of differentially expressed genes in papillary thyroid carcinoma

LIU Zhong-jiao, DOU Long-tao, ZHUANG Zhen, LIU Ling, ZHOU Yong-wei, LIU Man, LI Jing, ZHANG Hong-mei*

(College of Life Science, Dezhou University, Shandong Key Laboratory in University of Functional Bioresource Utilization, Shandong Provincial Key Laboratory of Biophysics, Shandong Dezhou 253023, China)

[Abstract] **Objective** Bioinformatics method was used to analyze gene expression microarrays of papillary thyroid cancer (PTC) and adjacent tissues. The key genes of PTC and their signal pathways were screened to understand their carcinogenic mechanisms. **Methods** Data on PTC and paracancerous tissue samples were obtained from seven GSE series on two sequencing platforms in the Gene Expression Omnibus Database (GEO). Firstly, the differential genes of the two sequencing platform samples were screened by R language. Then biological function, signal pathway analysis and protein-protein interaction analysis were performed on differential genes by Metascape and STRING. Finally, the key gene were selected by Cytoscape 3.5.1 software. **Results** A total of 302 differential genes were obtained from the intersection of the two sequencing platform samples, of which 149 genes were up-regulated and 153 genes were down-regulated. Using the Cytoscape 3.5.1 software to screen out 15 key genes, 12 of them are involved in the extracellular matrix receptor interaction signal pathway. Survival analysis of 15 key genes was performed using the UALCAN database, and the changes in the expression levels of 4 genes were closely related to the survival time of patients. **Conclusion** This study uses bioinformatics technology to analyze the data from seven PTC gene chips, making up for the inconsistency of small sample result and improving the reliability and stability of the result. In addition, 15 key genes are screened out and found that the matrix extracellular receptor interactions pathway plays an important role in the development of thyroid cancer. The result of this experiment provides guidance for the further study of PTC molecular mechanism, diagnosis and screening of prognostic molecular markers.

[Key words] Papillary thyroid carcinoma; Bioinformatics; Differentially expressed gene; Survival analysis; Human

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[作者简介] 刘中娇(1998—),女(汉族),山东省临沂市人,大学本科。

* 通讯作者(To whom correspondence should be addressed)

E-mail: dzxy7678@163.com Tel: (0534) 8985840