基于数据挖掘分析NETO2基因在头颈鳞癌中的表达及临床意义

Title:	Expression of NETO2 and its prognostic role in head and neck squamous cell carcinoma:Evidence from data mining

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摘要: 目的:通过对相关数据库数据分析，探究头颈鳞癌组织中NETO2基因的表达情况和临床意义。方法：应用cbioprotal在线分析平台分析TCGA 数据库中528例头颈鳞癌RNA-SEQ 数据，并结合患者的完整生存期信息，采用Kaplan-Meier法分析NETO2变异与头颈鳞癌患者生存之间的关系。利用UALCAN数据库网站搜索NETO2在头颈鳞癌组织及癌旁组织中的表达情况，以及NETO2的相关蛋白。结果：528例头颈鳞癌样本中有32例发生NETO2 基因变异，变异率为6%，其中扩增5例（0.9%），错义突变2例（0.4%），节段突变1例（0.2%），缺失1例（0.2%），mRNA上调23例（4.4%）。NETO2变异组总生存时间短于无变异组（P=0.009 21）。NETO2变异组无病生存时间与无变异组差异无统计学意义。NETO2 mRNA 在头颈鳞癌组织中的表达明显高于相应癌旁组织，差异有统计学意义（P＜0.001）。S100A8、S100A9表达与NETO2表达呈负相关。结论：通过分析表明，NETO2基因在头颈鳞癌组织中表达上调，与头颈鳞癌患者预后相关，提示该基因在头颈鳞癌的发生发展中起到了一定作用，将为后续的肿瘤研究提供重要理论依据。

Abstract: Objective:To explore the expression and clinical significance of Neuropilin and tolloid-like 2 (NETO2) gene in head and neck squamous cell carcinoma (HNSCC) based on relative database analysis.Methods:Data of 528 patients with HNSCC in the TCGA database were analyzed by cbioprotal online analysis platform.Kaplan-Meier method was used to analyze the relationship between the NETO2 genetic alteration and HNSCC survival.The NETO2 gene expression level in HNSCC and paracancerous tissues,and NETO2 related proteins were obtained from UALCAN database.Results:In 528 patients,mutation of NETO2 gene was found in 32 patients with a mutation rate of 6%,amplification in 5 cases (0.9%),missense mutations in 2 cases (0.4%),truncating mutations in 1 case (0.2%),deletion in 1 case (0.2%) and mRNA upregulation in 23 cases (4.4%).Kaplan-Meier curve showed that the total survival ofpatients with NETO2 genetic alteration was significantly shorter than that in patients without NETO2 genetic alteration (P=0.009 21).There was no significant difference in the disease-free survival time between the two groups (P=0.085 4).The expression of NETO2 in HNSCC was higher than it in paracancerous tissues.The expression of S100A8 and S100A9 were negatively related with NETO2.Conclusion:Analysis showed that the expression of NETO2 gene in HNSCC was up-regulated，and its expression is associated with the prognosis of HNSCC,suggesting that this gene played an important role in the development and progression of HNSCC.It would be an important theoretical support for the further research．

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