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• 临床研究 •

四种长链非编码RNA在乳腺癌中的表达及与患者预后的关系

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Expression of Four Long Non-coding RNAs in Breast Cancer and Their Relation with Patient's Prognosis

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Abstract: Objective To investigate the expression of EGOT, MEG3, KCNQ10T1 and NEAT1 in breast cancer tissues and their correlation with clinicopathologic features and prognosis of breast cancer patients.

Methods Expression of four lncRNAs in 1097 breast cancer samples and 114 normal samples in the TCGA database were analyzed using UALCAN website. Survival curves were described by Kaplan-Meier Plotter website to analyze the relation between lncRNAs and the prognosis of breast cancer patients. The main functions of the proteins related to their expression were analyzed by LinkedOmics and ClueGO tools.

Results The expression of EGOT and MEG3 in breast cancer tissues were significantly lower than those in normal tissues ($P < 0.05$). Expression of KCNQ10T1 was significantly lower in HER2-positive breast cancer ($P < 0.05$). The NEAT1 expression in stage IV breast cancer, HER2-positive and triple negative breast cancer tissues were significantly lower than that in normal tissues ($P < 0.05$). The expression levels of the four lncRNAs were significantly correlated with the relapse-free survival time (RFS) of breast cancer patients ($P < 0.05$), and the RFS and prognosis of breast cancer patients were relatively poor when lncRNA expression was low. The functional enrichment analysis results showed that all the proteins related to the expression of four lncRNAs were related to important biological processes or pathways. **Conclusion** The four lncRNAs (EGOT, MEG3, KCNQ10T1 and NEAT1) are down-regulated in breast cancer or some subtypes. They may be potential tumor suppressor factors in breast cancer and biological indicators for the prognosis of breast cancer patients.

Key words: Long non-coding RNA; Breast cancer; Prognosis

摘要: 目的 探讨EGOT、MEG3、KCNQ10T1和NEAT1四种LncRNA在不同亚型乳腺癌患者中的表达及与患者临床病理特征及预后的关系。**方法** 利用UALCAN网站挖掘TCGA数据库等大数据,分析四种LncRNA在1 097个乳腺癌组织样本和114个正常组织样本中的表达,用Kaplan-Meier Plotter法绘制生存曲线,分析四种LncRNA与乳腺癌患者预后的关系。通过LinkedOmics网站和ClueGO工具分析与它们表达相关的蛋白质的主要功能。**结果** EGOT、MEG3在乳腺癌组织中的表达显著低于正常组织 ($P < 0.05$); HER2阳性乳腺癌中KCNQ10T1显著低表达 ($P < 0.05$); NEAT1在IV期、HER2阳性和三阴性乳腺癌中的表达显著低于正常组织 ($P < 0.05$)。四种LncRNA的表达水平与乳腺癌患者的无复发生存时间 (RFS) 均有显著相关性 ($P < 0.05$), 且LncRNA低表达时乳腺癌患者的RFS和预后较差。通过功能富集分析发现与四种LncRNA表达相关的蛋白质均与重要生物过程或通路相关。**结论** 四种

LncRNA在乳腺癌或部分亚型中表达下调,它们可能是乳腺癌中潜在的抑癌因子,且可成为判断乳腺癌患者预后的生物学指标。

关键词: 长链非编码RNA; 乳腺癌; 预后

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