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MTA1 在卵巢癌中的表达及其对卵巢癌细胞侵袭转移影响的研究

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Expression of Metastasis-associated Gene 1 in Ovarian Carcinoma and Its Effects on the Invasion and Migration of Ovarian Carcinoma Cells

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摘要

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摘要 目的：研究转移相关基因1（metastasis-associated-gene1，MTA1）表达与卵巢癌发生发展转移的关系，研究MTA1 对卵巢癌侵袭转移能力的影响，并探讨抑制卵巢癌侵袭转移的潜在靶点。方法：免疫组织化学法检测110 例卵巢癌组织中MTA1 的蛋白表达水平，分析MTA1 蛋白表达与卵巢癌分化程度、临床分期及与腹腔转移的关系。并通过脂质体介导方法，将特异性siRNA表达载体psilencer 2.0-MTA 1-siRNA转染入人卵巢癌细胞系HO- 8910PM，采用RT-PCR 以及Westernblot检测特异性siRNA 对MTA1mRNA及蛋白表达的抑制效果。应用划痕损伤实验及Transwell 实验检测MTA1 对卵巢癌细胞侵袭转移能力的影响。结果：MTA1 随卵巢癌组织学分化程度的升高而降低，呈负相关，MTA1 的表达随着FIGO分期期别的增加而增加，呈正相关，MTA1 的表达随卵巢癌腹腔转移而增加，呈正相关。RT-PCR 及Westernblot结果显示，siRNA 成功抑制卵巢癌细胞系HO- 8910PM中MTA1的表达。划痕损伤实验显示转染后划痕损伤愈合明显减慢，迁移率明显降低，Transwell 体外侵袭实验结果显示，转染后穿膜细胞百分率显著降低（P<0.05）。 结论：MTA1 表达水平的增高与卵巢癌的分化程度、临床分期及远处转移密切相关，体外研究显示抑制MTA1 在卵巢癌细胞中的表达，使细胞生长、侵袭及转移能力均受到抑制，提示MTA1 在卵巢癌的远处侵袭转移过程中发挥重要作用，可能成为卵巢癌基因治疗的潜在靶点。

关键词： MTA1 卵巢癌 siRNA 侵袭 转移

Abstract: Objective:This study aims to investigate the relationship between the protein expression of metastasis-associated gene 1 (MTA 1) and the pathogenesis and progression of ovarian carcinoma. The effects of MTA 1 on the invasion and migration of the ovarian carcinoma cell line HO- 8910 PM were determined using interfering RNA (siRNA)-targeting MTA 1. Methods:The protein expression of MTA1 in 110 cases of ovarian carcinoma was determined by immunohistochemistry. Differences in MTA 1 protein expression among the clinical features (e.g., pathological grades, clinical stages, and metastasis) of ovarian carcinoma were explored. Data were analyzed using chi-square test. The specific siRNA expression vector psilencer2.0-MTA 1-siRNA was transfected into the HO-8910 PM cells through liposome. The mRNA and protein expressions of MTA1 were detected using RT-PCR and western blot assay, respectively. The invasion and migration abilities of MTA 1 were evaluated using the scrape wound healing assay and transwell assay.Results:The protein expression of MTA1 in ovarian carcinoma was negatively associated with pathological grades and positively associated with clinical stages and metastasis. RT-PCR and western blot analyses showed that the mRNA and protein expressions of MTA 1 were depressed effectively. In the siRNA-transfected group, the scrap wound healed more slowly, and the relative percentage of HO- 8910 PM cells cut through a Matrigel decreased. Conclusion: MTA1 was closely correlated with the pathological grades, clinical stages, invasion, and metastasis of ovarian carcinoma. In vitro experiments showed that MTA1 plays an important role in the invasion and migration of ovarian carcinoma and may become a new potential target in ovarian carcinoma therapy.

Key words: Metastasis-associated gene1 Ovarian carcinoma siRNA Invasion Migration

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