EXPRESSION PROFILE OF MIR-200 FAMILY MEMBERS AND THEIR TARGETS IN PROSTATE CANCER

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Prostate cancer (PCa) shows the highest rate of new cancer cases in male population. Low sensitivity and specificity of traditional diagnostic tests have limited their implementation for early detection of PCa. The differential expression pattern of miR-200 family and their target genes has the potential of being considered as biomarkers for prostate cancer detection in combination with traditional screening. In this study we aimed to investigate changes in the expression profiles of the miR-200 family members/targets in PCa tissue samples. We examined the miR-200 family members and their target genes (TCF7L1, CTBP2, E2F3, CTNNB1, DLC1 and EP300) expression profile using quantitative Real-time PCR (samples n = 24). The results showed decreased mean expression level of miR-200a and miR-429 and DLC1 gene in tumor samples. Also, the expression level of E2F3, CTNNB1, EP300, CTBP2 and TCF7L1 genes was up-regulated in the tumor samples. ROC and AUC analysis showed that the combination of miR-200 family and their target genes expression profile successfully discriminated PCa samples from their non-tumor counterparts (miR-200 family AUC = 0.699, $p < 0.01$ and target genes AUC = 0.899, $p < 0.0001$, respectively). The results of this study indicate that the deregulated expression of the miR-200 family and their gene targets may have a role in the pathogenesis of PCa. We suggest further assessment of the expression profile of miR-200 family and their target genes in comparison with other PCa diagnostic biomarkers.

Key words: *Biomarker, MicroRNAs, miR-200 family, Prostate cancer, Quantitative Real-time PCR.*

ПРОФІЛЬ ЕКСПРЕСІЇ ЧЛЕНІВ СІМЕЙСТВА МІКРОРНК-200 ТА ЇХНІ ЦІЛІ ПРИ РАКУ ПРОСТАТИ

Рак простати (РП) має найвищу частоту серед нововиявлених випадків захворювання на рак серед чоловіків. Низький рівень чутливості та специфічність традиційних діагностичних тестів обмежили їхнє використання з метою раннього виявлення РП. Схема диференційної експресії сімейства мікро РНК-200 та їхніх цільових генів може потенційно розглядатися як біомаркер для виявлення раку простати у поєднанні з традиційним скринінгом. У цьому дослідженні наша мета полягала у вивченні змін у профілях експресії членів сімейства мікро РНК-200/цілей у зразках тканин РП. Нами було досліджено профілі експресії членів сімейства мікроРНК-200 та їхні цільові гени (*TCF7L1, CTBP2, E2F3, CTNNB1, DLC1* та *EP300)* за допомогою ПЛР у реальному часі (зразки − $n = 24$). Результати продемонстрували знижений середній рівень експресії мікроРНК-200a і мікроРНК-429, а також гену *DLC1* у зразках пухлин. Також рівень експресії генів *E2F3, CTNNB1, EP300, CTBP2 і TCF7L1* був позитивно регульований у зразках пухлин. Аналіз ROC і AUC показав, що поєднання профіля експресії сімейства мікроРНК-200 і їхніх цільових генів успішно вирізнило зразки РП від їхніх непухлинних аналогів (AUC = 0,699, $p < 0,01$ сімейства мікроРНК-200; AUC = 0,899, $p < 0,0001$ для цільових генів, відповідно). Результати цього дослідження демонструють, що дерегульована експресія сімейства мікро РНК-200 і їхніх цільових генів може відігравати роль у патогенезі РП. Ми вважаємо, що необхідно проводити подальшу оцінку профіля експресії сімейства мікроРНК-200 і їхніх цільових генів у порівнянні з іншими біомаркерами для діагностики РП.

Ключові слова: біомаркер, мікроРНК, сімейство мікроРНК-200, рак простати, кількісна ПЛР у реальному часі.

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Received January 13, 2020
Received April 13, 2020
Accepted July 18, 2021