UP-Regulation of Dicer and Drosha Expression in Ovarian Cancer Tissues

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Research Article

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Abstract

BACKGROUND: miRNAs show to play fundamental roles in diverse cellular processes and associate with a variety of cancers. DROSHA and DICER are two major enzymes in the miRNA maturation process.

OBJECTIVE: Dicer and Drosha genes expression investigated Ovarian Cancer and analyzed the impact of clinicopathological characteristics on their expression.

METHODS: The present study has performed on 50 cancer patients (50 tumor tissue samples and 50 marginal tissue samples) overall, 100 specimens referred to Al-Zahra Hospital's surgical department in Tabriz and Motahari Hospital Urmia for identification and treatment during 2018 and 2019. After extracting total RNA and cDNA Synthesis, using the HRM-PCR method, the rate of change in the expression of DROSHA and DICER genes assessed using the 2-ΔΔCT method. Data were analyzed using Paired t-test and Kolmogorov–Smirnov test.

RESULTS: Our study showed a significant difference in the rate of expression changes in DROSHA and DICER genes in tumor tissue compared to marginal tissue. This difference was associated with an increase in DROSHA and DICER gene expression.

CONCLUSIONS: Up-regulated expression of miRNAs biogenesis machinery enzymes (Dicer and Drosha) during ovarian cancer can alter the miRNA expression involved in the pathogenesis of malignancy.

Full-text

Due to technical limitations, full-text HTML conversion of this manuscript could not be completed. However, the manuscript can be downloaded and accessed as a PDF.

Figures

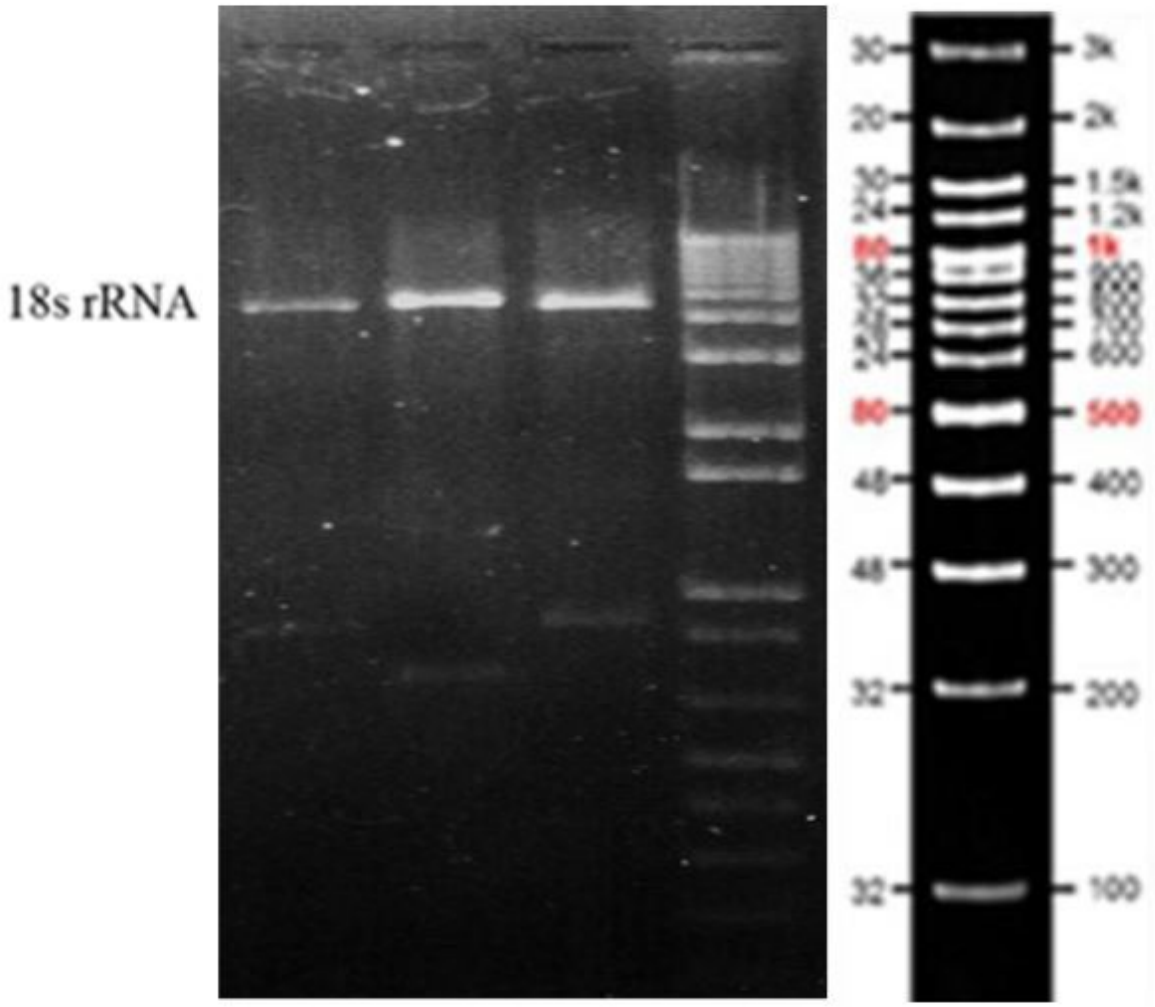

Figure 1

The bands corresponding to the extracted RNA on 2% agarose gel

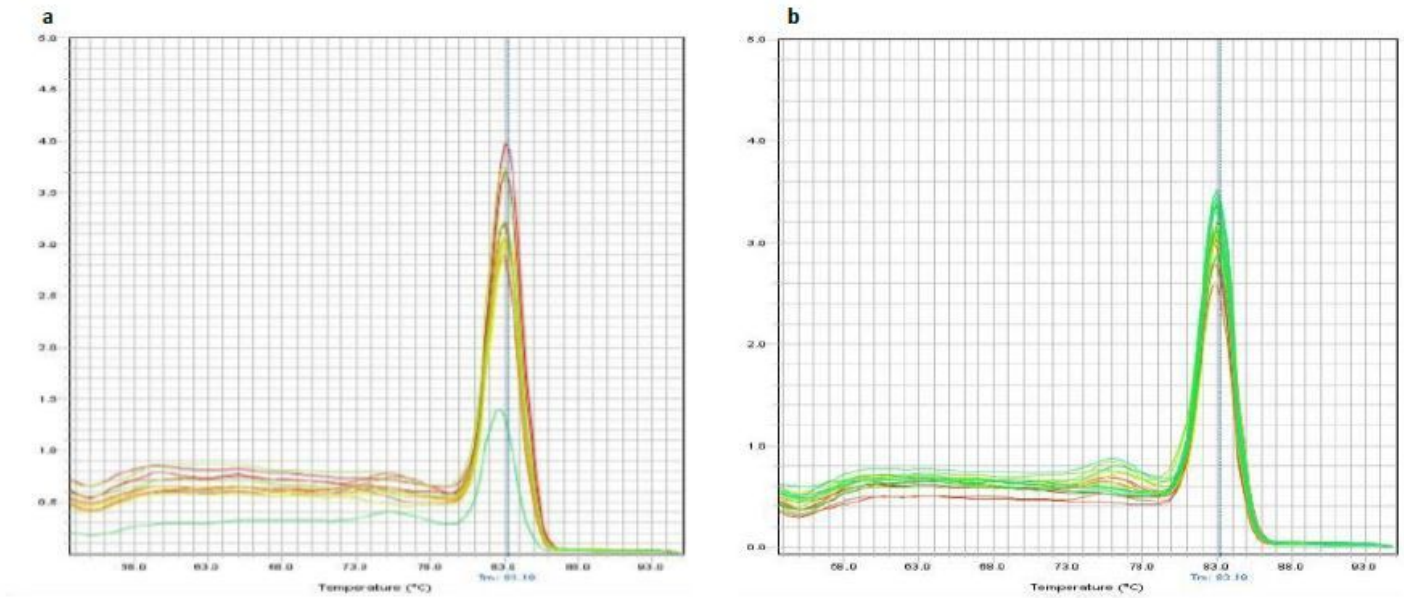

Figure 2

a) DICER gene melting curve b) DROSHA gene melting curve in High-Resolution PCR reaction.

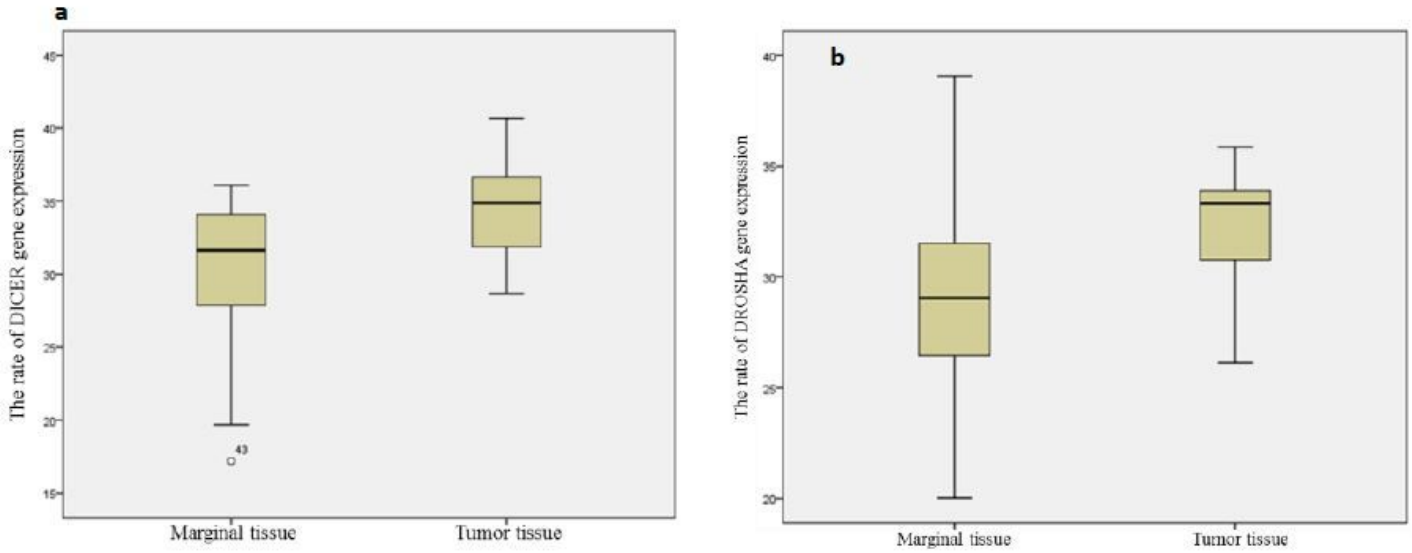

Figure 3

The mean of (a DICER and b DROSHA) genes expression rate in tumor tissue relative to marginal in patients with ovarian malignancy.