Decreased miR-320 and increased AQP1 in patients with breast cancer and the clinical significance

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Abstract

Background: Our previous studies have demonstrated overexpression of AQP1 in breast cancer, but the mechanism of its overexpression and the clinical significance were not clearly identified. MiR-320 has been reported down-regulated in various types of cancer and downregulation of miR-320 promotes overexpression of its target gene AQP1. The aim of this study was to investigate the role of miR-320 and its target gene AQP1 in breast cancer and to assess their clinical significance.

Methods: QRT-PCR was used in the detection of miR-320 and AQP1 mRNA expression both in breast cancer tissue and in adjacent normal tissue. Immunohistochemistry and western blot were used in the detection of AQP1 protein expression. The clinicopathological implications of these molecules were analyzed statistically. Survival analysis was also performed to assess their prognostic significance.

Results: Down-regulation of miR-320 was associated with overexpression of AQP1 mRNA in breast cancer tissue with a negative correlation (r = -0.698, P < 0.05). MiR-320 expression was significantly associated with pathological stage (P = 0.004) and lymph node involvement (P = 0.024). Overexpression of AQP1 was associated with histological grade (P = 0.033). Survival analysis indicated that reduced expression of miR-320 versus overexpression of AQP1 is associated with a poorer prognosis (P < 0.05).

Conclusions: Our results suggest that down-regulation of miR-320 may result in enhanced expression of AQP1 in breast cancer, which consequently favored tumor progression. MiR-320 and AQP1 may play important roles as biomarkers for prognosis and therapeutic targets in breast cancer.

Key words: miR-320; AQP1; breast cancer; prognosis