Abstract

MicroRNA-200C Expression in Cholangiocarcinoma Patients at King Chulalongkorn Memorial Hospital

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Background: Cholangiocarcinoma (CCA) is a common cancer in Thailand, where it was uniquely associated with *Opisthorchis viverrini* (OV) infection. MicroRNA-200c (miR-200c) is a microRNA involving in carcinogenesis especially epithelial mesenchymal transition. Its prognostic value has been demonstrated in several cancers. Previous study reported the aberration of miR-200c expression in CCA.

Objective: The aim of this study is to explore miR-200c expression and its clinical correlation in Thai CCA patients.

Method: 31 archival formalin-fixed paraffin embedded tissues (FFPE) CCA and 6 normal bile duct samples in King Chulalongkorn Memorial Hospital from January 2007 and November 2013 were collected. After, RNA extraction using miRNeasy FFPE kit, quantitative reverse-transcription polymerase chain reactions (RT-qPCR) using Taqman MicroRNA Assay were performed to quantitate the miR-200c expression. Using the $2^{\Delta\Delta C_{t}}$ of 2.0 as the cut off for miR-200c overexpression, we analysed the clinical correlation by chi-square test or Fisher exact test and Kaplan Meier method.

Results: Of 31 CCA samples, the miR-200c overexpression was shown in seven (22.5%) samples. The miR-200c overexpression was found in four from eight (50.0%) patients with T3-4 compared to three from 23 (13.0%) patients with T1-2, p= 0.053) Similarly, five (33.3%) from 15 patients with nodal metastasis compared to two (12.5%) from 16 patients without nodal metastasis, p= 0.17. However, the overall survival was not difference between the patients with and without miR-200c overexpression, p=0.923.

Conclusion: About one fifth of Thai CCA patients had miR-200c overexpression in our study. There were the trends toward the association of miR-200c expression with tumor extension and nodal metastasis. Further study of miR-200c expression in a larger CCA population with functional validation is warranted.