Clinical Prognostic Factors and Genomic Alterations of Cholangiocarcinoma in Thai Population

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Background: Cholangiocarcinoma in Western and Eastern population has the different genetic features, frequency, and prognosis. Most of Thai patients present with the advanced disease and the prognosis is very poor in advanced stage. Effective chemotherapy is limited. The aim of this study was to determined natural history, prognostic factors, and explored the genomic alterations of cholangiocarcinoma in Thai population.

Method: A computerized search of tumor registry and tissue archive database of Ramathibodi Hospital from November 2007 to December 2013 identified the patients who had the diagnosis of cholangiocarcinoma and having adequate tumor tissue for DNA extraction. Data on the natural history and clinical behavior were collected. The association and predictive ability of patient and tumor characteristics with overall survival (OS) and progression-free survival (PFS) outcomes were examined, respectively. The optimal cut points of baseline CEA and CA19-9 were analyzed based on ROC curve which provided the best median OS discrimination. The genomic alterations was explored for EGFR, KRAS, BRAF and PIK3CA in 81 samples. Immunohistochemistry(IHC) staining for HER2, ALK and Ki-67 expression was tested in 74 samples.

Results: 270 patients’ medical records were reviewed. Median follow up time was 6.68 months. The median OS(mOS) and median PFS(mPFS) were 6.5 and 6 months, respectively. There were 5 significant poor prognostic factors for OS including advanced staging, poor ECOG performance status, inoperable case, hepatitis C virus (HCV) infection and CEA pretreatment level of >15μg/L. The incidence of EGFR, KRAS, and PIK3CA mutation in Thai population were 21%, 12%, and 16%, respectively. No BRAFV600 mutation was found. Strongly positive for HER2 expression was found in only 1 patient whereas ALK expression was not found. Median Ki-67 expression was 42.5%.

Conclusion: Our study demonstrated 5 strong prognostic factors in cholangiocarcinoma (staging, ECOG, surgery, HCV infection, CEA level). The presence of mutation in EGFR, KRAS and PIK3CA may produce a potential clinical implication in order to apply targeted drugs in the future of cholangiocarcinoma treatment.