HBP SURGERY WEEK 2019
& The 50th Annual Congress of the Korean Association of HBP Surgery
Beyond Excellence Toward the Best!
APRIL 5-6, 2019
Seoul, Korea

BP OP 4-6

Clinical genetic analyses for patients with bile duct cancer

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Introduction : To search for therapeutic drug candidates, our hospital has operated MSK-IMPACT, a cancer clinical sequencing assay from November 2016, which was developed at the Memorial Sloan Kettering Cancer Center. We report on the results of the clinical sequencing analyzed in patients with bile duct cancer in our department.

Methods : We examined genetic analysis of 468 cancer gene for nine cases of bile duct cancer using MSK-IMPACT from 2017 to 2018.

Results : Nine cases consisted of four cases of intrahepatic cholangiocarcinoma, three cases of hilar cholangiocarcinoma, and two cases of gall bladder cancer. In eight out of nine cases (88.9%), genetic mutation was detected for any of 468 cancer genes analyzed. In five out of nine cases (55.6%), the genetic mutations can be expected to have candidate drugs with effect in evidence level of a clinical trial. Among the five cases, Two cases have Tumor Mutation Burdon-high (one with BRCA 2 gene mutation), two cases FGFR 2 fusion gene,and one case MDM 2 amplification. Two of five patients for whom candidate drugs were identified are currently in remission in the image after the multidisciplinary therapy and have observed without the need for candidate drugs. Three patients could not treated with the candidate drug, because two patients had cancer progression and one could not obtain the investigational drugs.

Conclusions : The clinical sequencing for bile duct cancer can identify genetic mutations that can be therapeutic targets in about half of cases, even though the number of case is small, suggesting the possibility of clinical usefulness.

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