allied academies

Annual Congress on

ONCOLOGY AND BIOMARKERS SUMMIT

November 27-28, 2017 | Atlanta, USA

Analysis of small fragment deletions of the APC gene in Chinese patients with familial adenomatous polyposis

Senqing Chen
Jiangsu Institute of Cancer Research, China

Statement of the Problem: Familial adenomatous polyposis (FAP) is an autosomal dominant inherited disease mainly caused by mutations of the adenomatous polyposis coli (APC) gene with almost complete penetrance. These colorectal polyps are precancerous lesions that will inevitable develop into colorectal cancer at the median age of 40-year old if total proctocolectomy is not performed. So, identification of APC germline mutations has great implications for genetic counseling and management of FAP patients.

Methodology & Theoretical Orientation: In this study, we screened APC germline mutations in Chinese FAP patients, to find novel mutations and the APC gene germline mutation characteristics of Chinese FAP patients. The FAP patients were diagnosed by clinical manifestations, family histories, endoscope and biopsy. Then patients peripheral blood samples were collected, afterwards, genomic DNA was extracted. The mutation analysis of the APC gene was conducted by direct DNA sequencing for micromutations and MLPA for large duplications and/or deletions.

Findings: We found 6 micromutations out of 14 FAP pedigrees, while there were no large duplications and/or deletions found. These germline mutations are c.5432C>T (p. Ser1811Leu), two c.3926_3930delAAAAG (p.Glu1309AspfsX4), c.3921_3924delAAAA (p.Ile1307MetfsX13), c.3184_3187delCAAA (p.Gln1061AspfsX59) and c.4127_4126delAT (p.Tyr1376LysfsX9), respectively and all deletion mutations resulted in a premature stop codon. At the same time, we found c.3921_3924delAAAA and two c.3926_3930delAAAAG are in AAAAG short tandem repeats, c3184_3187delCAAA is in the CAAA interrupted direct repeats and c4127_4128 del AT is in the 5'-CCTGAACA-3', 3'-ACAAGTCC-5 palindromes (inverted repeats) of the APC gene. Furthermore, deletion mutations are mostly located at codon 1309.

Conclusion & Significance: Though there were no novel mutations found as the pathogenic gene of FAP in this study, we found nucleotide sequence containing short tandem repeats and palindromes (inverted repeats), especially the 5 bp base deletion at codon 1309, are mutations in high incidence area in APC gene.

e: chensenqing2008@126.com