Mutation profiling of 100 cerebrovascular disease patients based on targeted exome sequencing

Wei li
Capital Medical University, China

To explore the application value of the high-throughput second-generation sequencing technique in patients with suspected cerebral vascular genetic defects. We select 100 cases with suspected hereditary deficiency of cerebrovascular disease from January 2016 to June 2017 in Beijing Tiantan Hospital. DNA was extracted from the peripheral blood using a blood sample extraction kit. Then the DNAs were interrupted, repaired and connected to build the library. The Agilent capture chip was used to capture the exons and 30bp flanking sequences of exons of the 62 genes associated with hereditary cerebrovascular disease. Using the Illumina X10, the PE150 sequencing platform to sequence, using the BWA software to analysis sequence alignment, using the GATK software to detect the mutations, the artificial analysis is used to judge the mutation pathogenic type. And the pathogenic mutant site is validated by the ABI 3730 sequencing platform for the proband and his parents. There were 60 men (60%) and 40 women (40%) from 12 to 86 years old, the average age was 51 years (SD=13.1). Categorically 39 cases were denied the family histories, 43 cases were family histories, and 18 cases were not clear. 33 cases of known or suspected pathogenic mutations were detected, accounting for 33% of the overall detection rate, including 12 cases of pathogenic mutations and 21 cases of suspected pathogenic mutations. No family history or unclear samples were detected 15 cases with mutation (detection rate 26.32%). The *NOTCH3* gene mutations (CADASIL) were detected in 24 samples (72.73%); the *COL4A1* gene (cerebrovascular disease) mutations were detected in 2 samples (6%); the *KRIT1* gene mutations (cerebral cavernous hemangioma) were detected in 3 samples (9%); and respectively the *PDCD10* (cerebral cavernous hemangioma), PRNP (prnp-related amyloid angiopathy), COL4A2 (Intracerebral hemorrhage, susceptibility to), COL5A1 (Ehlers-danlos syndrome, Classic type) gene mutations were detected in one each (3%). The *NOTCH3* gene had 23 missense mutations and one INDEL mutation, including 16 reported sites and 8 new mutation sites. The target region capture technique in high-throughput second-generation sequencing can be effectively applied to genetic detection of hereditary cerebrovascular disease; and there is a higher mutation defected rate in the family history sample; and the *NOTCH3* gene mutation is an important proportion in hereditary cerebrovascular disease.

Speaker Biography

Li Wei is a Doctor of Neurobiology, Chief Physician and Associate Professor of Neurology. He is specialized in the genes and correlation study of cerebral vascular disease.

e: lwdoctors@sina.com

Notes: