

JCK Oral

JCK Oral 4 (II-JCKO4)

Kawasaki Disease/General Cardiology 1

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Sat. Jul 8, 2017 3:30 PM - 4:20 PM ROOM 3 (Exhibition and Event Hall Room 3)

3:30 PM - 4:20 PM

[II-JCKO4-02]Identification of susceptibility genes associated with Kawasaki disease by targeted enrichment of genomic region sequencing technique

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Objective

To discover susceptibility genes associated with Kawasaki disease (KD) and coronary artery lesion (CAL) through targeted enrichment of genomic region sequencing technique.

Methods

114 KD patients and 45 outpatients for health examination were recruited from Shanghai children's hospital between November 2015 and November 2016. Patients were divided into two groups on the basis of echocardiography, one is KD with CAL and another is KD without CAL. 472 single nucleotide polymorphisms associated with KD susceptibility genes and 512 genes in T cell receptor signaling pathway, toll-like receptor signaling pathway, Cytokine receptor interaction, TGF-beta signaling pathway were selected as targeted genes, and target exome capture sequencing chip were customized. Then use Illumina HiSeq X10 for high-throughput sequencing. The sequencing data were used to find out susceptibility genes associated with KD and CAL.

Results

There are 26 susceptibility genes associated with KD and 21 with CAL. *RPS6KB*, *VAV1*, *ACVR2B* and *CXCL14* are significantly associated with KD. *CCL4*, *TNFRSF12A*, *IFIH1* and *IL26* are significant genes of CAL formation. *CXCL14*(rs1046092) T allele(OR=11.455, 95%CI=1.531-85.736), *CXCL14*(rs2547) G allele(OR=11.070, 95%CI=1.477-82.972) increased the risk of KD. *CCL4*(rs1719144) G allele(OR=4.132, 95%CI=1.655-10.316), *CCL4*(rs1049807) A allele(OR=4.132, 95%CI=1.655-10.316), *CCL4* (rs1719152) T allele (OR=3.756, 95%CI=1.495-9.437) increased the risk of CAL (P <0.05).

Conclusions

Targeted sequencing technology can be used in children to evaluate the risk of KD and CAL.