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Identification of distribution of human endogenous retroviruses K (HML-2) by PCR-based target enrichment sequencing

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Abstract

Human endogenous retroviruses (HERVs), suspected to be transposition-defective, are more likely to reshape the transcriptional network of the human genome by regulatory elements distributed in their long terminal repeats (LTRs). HERV-K (HML-2), the most preserved group with the least accumulation of mutations, has been documented to be involved in tumorigenesis and autoimmune diseases. Because of the high sequence similarity between different HERV-Ks, current methods have limitations in providing genome-wide mapping specific for HERV-K (HML-2), a major barrier in delineating HERV-K (HML-2) function. While trying to acquire itemized appropriation data of HERV-K (HML-2), we used a PCR-based objective advancement sequencing convention for HERV-K (HML-2) (PTESHK) loci, which maps the nearness of reference loci, yet additionally distinguishes non-reference loci, empowering assurance of the genome-wide dissemination of HERV-K (HML-2) loci. Here we report on the genomic information got from three people (3 imitates each). We distinguished an aggregate of 978 loci utilizing this technique, including 30 new reference loci and 5 non-reference loci. Among the 3 people in our examination, 14 polymorphic HERV-K (HML-2) loci were recognized, and solo-LTR330 and N6p21.32 were distinguished as polymorphic just because. Strikingly, PTESHK gives a way to deal with the ID of the genome-wide dispersion of HERV-K (HML-2) and can be utilized for the distinguishing proof of polymorphic loci. Since the reconciliation polymorphism of HERV-K (HML-2) is associated to be unified with the purposes behind their pathogenicity, PTESHK can enhance other developing methods in getting to polymorphic HERV-K (HML-2) components in malignancy and immune system illnesses.

Biography:

Bei Xue is a PhD student of Shantou University Medical College (SUMC), majoring in immunology. Now she is performing part of her PhD project in Dalhousie University as a visiting research student.

Speaker Publications:

1. "Human Endogenous Retrovirus K (HML-2) in Health and Disease" July 2020Frontiers in Microbiology 11
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2. "Identification of the distribution of human endogenous retroviruses K (HML-2) by PCR-based target enrichment sequencing
December 2020Retrovirology 17(1) DOI: 10.1186/s12977-020-00519-z
3. "2019-nCoV (Wuhan virus), a novel Coronavirus: Human-to-human transmission, travel-related cases, and vaccine readiness" January 2020The Journal of Infection in Developing Countries 14(01):3-17 DOI: 10.3855/jidc.12425

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