In vitro CRISPR/Cas9 assisted targeting scheme (CATsCH) for low-cost, ultra-deep and high throughput region of interest genomic analysis (Ramot)

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Abstract

CRISPR/Cas9 assisted targeting scheme (CATsCH) is an in vitro method that targets long sequence specific genomic regions of interest. The RNA-guided Cas9 digestion system was adjusted to in vitro conditions in combination with cloning technique to facilitate the integration of long genomic region to a vector in a single step.

In combination with sequencing methods as next-generation sequencing, optical mapping and bisulfite sequencing CATsCH can overcome the need of whole genome sequencing and allow fast and efficient analysis of large and repetitive genomic regions.

Advanatges

A successful outcome of this project may dramatically change the utility of sequencing and other genomic analysis in the clinical setting. As an illustrative example, a 1Mbp region of interest associated with a common disease comprises 1/3200 of the genome. This implies that for the cost of a single whole genome run that is required today in order to analyze this 1Mbp region, 3200 individuals may be analyzed. Alternatively, this region may be sequenced at ultra-deep coverage, identifying rare genomic aberrations. Both applications may open new and exciting avenues for preventive population screening and personalized medicine.

Potential Applications

Broad range of application in fields including Genomics, Epigenomics, Molecular Pathology, Gene Molecular Biology, and Diagnoses of Genetic Diseases. There are broad range users that can apply this method, it can be used in the lab for cloning large genomic regions and for researchers that peruses sizable genomic regions. There is also a need for specific diagnostic tool that uses the advantage of zooming in to arears of interest in the genomic map.

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