Software Tool for Predicting Sequences in a Genome that are Subject to Restriction or Other Surveillance Mechanisms

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BACKGROUND

Many genomes encode Restriction-Modification systems (RMs) that act to protect the host cell from invading DNA by cutting at specific sites (frequently short 4-6 base reverse complement palindromes). RMs also protect host DNA from unfavorably being cut by modifying sites within the host DNA that could be targets by the host's own surveillance enzymes. It is also not unusual to find that these enzymes are adjacent to each other in the host genome. Traditional approaches to understanding these sites involve finding a methylase that is typically adjacent to a restriction enzyme, and then extracting DNA, expressing protein and then testing DNA sequence for evidence of cutting. In certain laboratory research (e.g., programs that involve transforming DNA/RNA) it may be desirable to more comprehensively understand the sequences being surveilled by the host. Moreover, it may be desirable in certain laboratory research to know/predict which surveillance enzymes are present in a genome in order to affect cell transformation efficiency through evasion of those sequences.

TECHNOLOGY DESCRIPTION

To help address these challenges in RMs, investigators at UC Santa Cruz (UCSC) have developed a new approach to detection of surveillance targets (RM sites, for example) by a thorough examination of possible targets. By evaluating short sequences that are statistically under-represented in a genome, UCSC's approach can more holistically predict the potential for surveillance activity. Conversely, by removing the statistically under-represented surveilled sequences from a transforming DNA/RNA, it's possible to avoid the surveillance. By using UCSC's "Stealth" technology, researchers could more effectively transform an otherwise recalcitrant cell type, or efficiently predict presence of novel surveillance enzymes (RMs for example) in a host genome.

APPLICATIONS

- bacterial research
- gene editing
- proteomics
- drug discovery
- software

ADVANTAGES

- modular and fast to develop with
- no custom hardware or specialized computer
- can be used with a broad range of cell types

RELATED MATERIALS

ADDITIONAL TECHNOLOGIES BY THESE INVENTORS

- Salt-Tolerant Dna Polymerases
- Trna Handles

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OTHER INFORMATION

KEYWORDS

genomes, genome, genomic, genomics, restriction-modification, restriction, surveillance, enzymes, DNA, RNA, sequences, sequence

CATEGORIZED AS

- **Biotechnology**
  - Bioinformatics
  - Genomics
  - Proteomics
- **Computer**
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  - Research Tools

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