Transcriptional Regulatory Elements and Transcription Factors that Control Kaposi’s Sarcoma Human Virus Genes.

Manjula Kasoji1,2, Dr. Bino John1
1 Bioengineering & Bioinformatics Summer Institute, Dept. of Computational Biology, University of Pittsburgh, 15260
2 Bioinformatics Department, Georgia Institute of Technology, 30332

Abstract

- Kaposi’s sarcoma human virus (KSHV) is a tumor developing agent
- Its genes interfere with tumor suppressor pathways and modify the host cellular environment
- Goal: identify the transcriptional sites and factors that are involved in regulating the KSHV genome.
- In reaching this goal we have:
  - characterized the upstream regions of all the protein coding genes.
  - These upstream sequences were loaded into a web program, CLOVER to identify transcription factors.
  - With the identification of these transcription factors we hope to better understand the regulation and infection of the Kaposi virus.

Method

1. Identification of transcription factors and motifs
   - obtaining the KSHV genome
   - identifying all of the protein encoding genes
   - finding the upstream regions of up to one thousand nucleotides of the protein coding genes
   - using programs to identify the factors and motifs that are involved in these upstream regions

2. Validation of these findings
   - random sequences will be generated by a simple Perl script.
   - these random sequences will act as reference or control sequences to which the upstream sequences will be compared against.

Results

- Transcription factors and respective regulated genes.
- With the identification of these transcription factors we hope to better understand the regulation and infection of the Kaposi virus.

Future Research

- Find out which transcription factors regulate miRNAs
  - miRNAs are a class of endogenous, small RNAs that are thought to negatively regulate protein production.
  - aberrant expression of miRNAs is linked to cancer and other diseases

Acknowledgements

The national BBSI program (http://bbsi.eeicom.com) is a joint initiative of the NIH-NIBIB and NSF-EEC, and the BBSI @ Pitt is supported by the National Science Foundation under Grant EEC-0234002.

1) Dr. Bino John
2) University of Pittsburgh

References

