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

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Kaposi's sarcoma-associated herpesvirus (KSHV)

- A virus that causes <u>Kaposi's sarcoma</u>, a cancer
- It was originally described by Moritz Kaposi, an Austro-Hungarian dermatologist
- Commonly occurs in <u>AIDS</u> patients
- Fourth most common cancer caused by an infectious agent worldwide following gastric, cervical, and hepatic cancers.





KSHV

- causes abnormal tissue growth under the skin and leads to lesions.
- usually not life threatening unless it reaches to the internal organs
- Functional studies of KSHV indicate that
 - its genes interfere with established tumor suppressor pathways
 - modify the host cellular environment



Goal

The goal of this experiment is to identify the transcriptional regulatory sites and factors that are involved in the transcriptional regulation of the viral genome.

Methods

- Find a good web program that predicts transcription factors based on a <u>database of known transcription factor</u> <u>motifs.</u>
 - <u>TRANSFAC*</u>
 - <u>JASPER</u>
 - Chosen web program: <u>CLOVER</u>
 - http://biowulf.bu.edu/MotifViz/

CLOVER

- CLOVER predicts transcription factors based on a database of known transcription factors and motifs.
- The database used was TRANSFAC.
- Takes in 3 files:
 - Target sequences (upstream/promoter regions of all protein coding genes)
 - Background sequences
 - TRANSFAC (.dat) file

Methods cont...

Obtain genome and protein coding genes

 <u>http://www.ncbi.nlm.nih.gov/</u>

 Obtain 1000 nucleotides (nt) upstream of all protein coding genes
 generate random sequences of 2000 nt from same genome. These are used as

background sequences.

5. Obtain TRANSFAC data file (.dat)

CLOVER Output

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CLOVER Output



CLOVER Output

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Conclusion

With the identification of these transcription factors we hope to better understand the regulation and infection of the Kaposi virus.

Future Work

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

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