

## Annual Poster Presentation on November 21, 2008

### 1) **Anurag Gautam, Nobish Varghese, and Max Shpak**

Title: Role of Codon Bias in Influenza-A Host Shift

Abstract:

Codon usage bias refers to differences among organisms in the frequency of occurrence of codons in protein-coding DNA sequences. This bias in codon preference has been reported in most genomes that have been studied so far. In some organisms, highly expressed genes have a strong codon preference that is consistent with the concentrations of corresponding tRNAs, whereas genes expressed at a lower level have a more uniform pattern of codon use. Viruses rely on their host's cell machinery to transcribe and translate their genes and hence the abundance of tRNAs in the host dictates the efficiency with which viral RNA is translated into protein. Consequently, it is hypothesized that host tRNA abundance leads to codon bias in viruses, and that host shift is constrained by codon usage patterns. It is also possible that the viral virulence is at least partially due to this codon bias and most virulent strains would be those that match the codon usage patterns of the respective host genomes. Influenza-A virus strains endemic to both wild and domestic fowl and transmitted to humans with varying degrees of virulence is used as a model system for the present study.

### 2) **Poorva Mudgal and Sara Grineski**

Title: To Create Datasets for Further Studies of Respiratory Health Effects Caused by Dust Storms

Abstract:

Dust storms are regular and frequent occurrences in El Paso, Texas and Ciudad Juarez, Chihuahua, but little is known about their respiratory health effects. We plan to assess the respiratory health effects of dust storms by combining hospitalization data and dust data in time-series statistical models. To investigate the relative risk of respiratory outcomes, data were acquired from the Texas Health Care Information Council, the Texas Commission on Environmental Quality, and the National Weather Service. The data were parsed using the PERL programming language and compiled into two datasets: a patient level dataset and a daily weather and pollution dataset for further statistical studies.

### 3) **Jon Mohl**

Title: The RNAVLab's Graphical User Interface

Abstract:

Secondary structures of RNA can play an important role in replication of viruses and the translation of the RNAs into proteins. The secondary structure can be as simple as a piece of RNA folded back on it self in the form of a stem loop, or it can have complex structure with pseudoknots. Pseudoknots are a complex structure in which a loop from a stem-loop structure will base pair with a region farther down the sequence, and may have multiple structures in between. The prediction of pseudoknots becomes computationally expensive. The RNAVLab research group is working on creating a web service in which secondary structures of RNA sequences can be predicted, and the Graphical User Interface (GUI) is a desktop Java program that interacts with this service. The GUI allows for input of a group of RNA sequences, selection of specific RNA sequences, then selection of different secondary structure prediction algorithms, and finally display of the secondary structure and sequence alignment. It is designed with a "tabbed" workflow layout, making the process simple and intuitive.

#### 4) **Srilaxmi Nerella**

Title: Cancer Biomarkers

Abstract:

Cancer is the leading cause of death in the United States. Traditional diagnostic tests for the detection of cancer have a number of drawbacks like poor sensitivity, lack of specificity, and costly and invasive protocols. The desirable property and utility of a technique lies in its ability to indicate disease progression at an early stage of cancer. Advances in biotechnology and genomics gave a new hope that biomarkers can be used in improving cancer screening and detection to be non-invasive, sensitive, and specific. They can be used to diagnose cancer at different stages—initiation, development, and progression of cancer detection. Advancements in genomic and proteomic technologies, data from gene sequencing projects and the availability of powerful bioinformatics tools have led to promising approaches in the search for cancer biomarkers.

#### 5) **Ana Betancourt**

Title: Malaria: Treatment and Classification Tools

Abstract:

Malaria is a vector-borne disease caused by four types of *Plasmodium* parasites with approximately 200 million new infections every year, almost a million deaths mostly of children, and 3 billion people at risk of infection. Parasites multiply in the liver and infect red blood cells, and unless promptly treated, severe malaria causes renal failure, anemia, pulmonary edema, and death. There is no current vaccine for malaria and prophylactic treatments are usually unaffordable for most people in endemic areas. Following a personal interest in Malaria caused by *Plasmodium*, here I present tools developed by Joubert and Joubert for the identification and classification of malarial proteins into a specialized database, and a tool for identification and classification of candidate vaccines developed by Chaudhuri *et al.* Interests in these two publications results from the evident need of bioinformatics tools in the treatment of diseases.

#### 6) **Ketaki Bhide**

Title: Application of *In Vitro* Transposon Mutagenesis System to Determine Molecular Basis of Hyper-Invasive Phenotype of *Campylobacter Jejuni* Strain 01/51

Abstract:

*Campylobacter jejuni* is a major cause of diarrhea worldwide, especially in USA and UK. It expresses several virulence factors and cause infection by adhesion and invasion of host intestinal epithelial cells. Variation in invasiveness among strains has been determined from previous research work in this area. Lack of suitable genetic tools led to the need of development of both *in vitro* and *in vivo* systems to elucidate hyper-invasiveness among strains. For hyper-invasive strain 01/51, an *in vitro* transposon mutagenesis system was developed which generated an isogenic random transposon mutant library. Screening of mutants available in the library was applied to identify genes responsible for virulence. In previous work, 27 mutants were found hypo-invasive. In 21 of these mutants, genes responsible for virulence were identified by finding transposon insertion locations. Our aim was to find the location of transposon insertions in three hypo-invasive mutants named 1H5, 1H10, 1G5 and to obtain gene sequences of transposon insertion sites followed by sequence analysis. Sequences were obtained for transposon insertion sites in these three mutants. However, due to the poor quality of the sequences, their analysis only gave a brief idea of the genes responsible for hypo-invasion in mutants that are in turn responsible for hyper-invasiveness in strain 01/51.

**7) Prasanna Kolli**

Title: Biodegradation of Organic Matter

Abstract:

To avoid pollution, organic waste can be degraded naturally using microbes, which have many applications in biofertilizers and organic manure. Gram's staining technique and other biochemical tests are used to find these microbes. *Pseudomonas*, *Bacillus*, and *Aspergillus* are a few microorganisms isolated from different organic wastes and are found to have high degrading capacity of organic wastes.

**8) Sravya Tamma**

Title: Isolation and Biochemical Characterization of Extremophiles (Thermophile).

Abstract:

Extremophile is an organism that thrives in and may even require physically or geochemically extreme conditions. Extremophiles are a unique group of microbes, mainly archaea and bacteria, which thrive in harsh environments previously considered uninhabitable. Thermophiles are a category of extremophiles that are suited to temperatures greater than 45°C. Thermophiles and hyperthermophiles not only have great practical applications, they are also considered as possible links to the origin of life and extraterrestrial life. As a prerequisite for their survival, thermophiles contain enzymes that can function at high temperature. The enzymes produced by thermophiles are DNA polymerases, lipases, amylases, and gelatinases. Our proposed work deals with the isolation and characterization of thermophiles.

**9) Clemente Aguilar**

Title: Distribution of Inverted Repeats in Different Types of Papillomaviruses

Abstract:

An inverted repeat (IR) is a nucleotide string followed closely by its inverted complement, and is present in secondary structures including both stem-loops and pseudoknots. We are interested in the genomic distribution and abundance of IRs, since these data might imply functional roles of biological significance for the corresponding structures. Statistical analysis of the genomic distribution of IRs in 10 types of papillomaviruses (PVs) showed that they are overrepresented in non-coding sequences (Cox *et al.*, 1996; Pearson *et al.*, 1996).

**10) Naresh Prodduturi and Dedeepya Vaka**

Title: P90 Sequence and Functional Analysis

Abstract:

In a study by Junttila *et. al.* (*Cell* 130:51–62, 2007), a high chance for tumor growth was shown when protein phosphatase 2A (PP2A) activity was inhibited. Cancerous Inhibitor of PP2A (CIP2A) was the protein that interacted directly with an oncogenic transcription factor c-Myc, inhibited PP2A activity towards c-Myc serine 62, and caused proteolytic degradation. CIP2A supported anchorage-independent cell growth and the formation of *in vivo* tumor. CIP2A was over expressed in head and neck squamous cell carcinoma and colon cancer, two common human malignancies. The study focused on determining the function of CIP2A as well as the sequence and phylogenetic analysis of this protein by using several proteomic tools. The protein function was inferred at several levels such as amino acid sequence, biological process, subcellular location, pathway, organ, and organism.

### 11) **Kuldeep Matharasi**

Title: Spectral Lib: A Graphical User Interface built on Plone for Spectral Library to Assess Different Vegetation and Land cover Types for Arctic, Antarctic and Chihuahua Desert Ecosystem

Abstract:

We present the Spectral Lib as an assessment tool for different vegetation and land cover types for Arctic, Antarctic, and Chihuahua Desert ecosystems. It is an easily accessible and user-friendly tool providing data to users for their research. It provides different types of functionalities like browsing, searching, and downloading data for different levels of users where the user could be an administrator, a registered user, or a general user. The tool implements the technology of Plone, which has Zope server as the backend. This server incorporates all the methods and forms responsible for interaction between the GUI and Database. The current version is well suited to raise awareness and provide information about various types of data available.

### 12) **Xin Mu**

Title: Detecting Evolutionary Forces of HoxA1 Genes in Primates and Rodents

Abstract:

Homeobox genes, and the proteins they encode, the homeodomain proteins, have turned out to play important roles in the developmental processes of many multicellular organisms. HOXA1 is the first HOX gene that governs very early embryonic development and the making of the body plan. By estimating the force of selective pressures (positive and purifying selections) across various regions of the HoxA1 gene, we can gain a general understanding of how it evolves. The ratio of non-synonymous to synonymous substitutions, known as the Ka/Ks ratio, is used to estimate selective pressures. From the comparison of results, we find that the selective force in rodents and primates are purifying selection, as well as the human with rodents.

### 13) **Amit K Ray**

Title: Polymerase Chain Reaction Based Detection of Human Papilloma Virus (HPV)

Abstract:

HPV is double-stranded DNA virus causing genital warts and cervical cancer. The virus mainly attack cutaneous or mucosal epithelial cells. To date, more than 100 types of HPV have been identified and categorized as high and low risk type viruses. High-risk types HPV 16, 18, 31, 33, and 35 are linked to cervical cancer. HPV types 16 and 18 together cause about 70% of cervical cancers. Polymerase Chain Reaction (PCR) was used to analyze 21 samples of HPV types 6, 11, 16, and 18 in a study by Manos *et. al.* (1998) for their US Patent #5705627. The work provided the basis for all the concurrent studies for optimizing structure-based inhibitor of the HPV E6 protein, responsible for viral genome amplification. HPV DNA sequences were amplified using L1 consensus primer MY09/1. The primers amplified on approximately 450 bp region located in the L1 ORF of more than 40 types of HPV. HPV positive frequency by MY09/1 primers was found to be 80.9%, 4 out of the 21 samples were negative for HPV infection and 15 out of 21 were positive for high-risk HPV type 16. The data in their study suggested that HPV 16 was predominant.