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Sample Abstracts for Undergraduate Research Day

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Cloning of Human Herpesvirus-6 gp105 Varients into a Baculovirus Vector for Study of Heparin Binding (1999)

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Abstract

Human Herpesvirus 6 (HHV-6) is a T-lymphotropic §-herpesvirus that was initially isolated from peripheral mononuclear cells from patients with various lymphoproliferative disorders including AIDS. More than 90% of the population are seropositive for HHV-6 by age two. This virus has been shown to be the causative agent of exanthem subtum (ES, roseola infantum), which is characterized by a high fever and skin rash. The virus has also been associated with diseases such as autoimmune disorders (multiple sclerosis), chronic fatigue syndrome, malignancy (Hodgkin's and non-Hodgkin's lymphoma) and complications associated with tissue transplantation.

Individual isolates of HHV-6 differ in certain properties such as cell tropism, antigenicity, restriction enzyme profiles, nucleotide sequences and disease association. The isolates can be assigned to one of two groups, HHV-6A and HHV-6B. HHV-6B infection is more common and has been identified as the causative agent of ES. HHV-6A is less prevalent and has not been associated with disease. HHV-6A, however, has a wider variety of cell tropism invitro than HHV-6B.

Both HHV-6A and HHV-6B encode for a major envelope glycoprotein, gp105 that is a target of neutralizing antibodies and therefore believed to be important in viral infection. Gp105 from HHV-6A contains three putative heparin binding domains which are absent from HHV-6B. For these studies we cloned gp105 from HHV-6A and HHV-6B into a baculovirus expression vector. Current and future work will examine the ability of these glycoproteins to bind heparin in attempt to explain in part the biological and epidemiological differences observed between HHV-6A and HHV-6B.

Cloning and Sequencing of a Divergent β-Tubulin in *Tetrahymena pigmentosa*

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Abstract

Tubulins are a family of proteins essential to cell function. Two of the three major types of tubulins, α and β, heterodimerize to form microtubules, the major building blocks of many cellular structures, including cilia, flagella and mitotic spindles. The third major type of tubulin, γ-tubulin, functions to organize various microtubule systems, and is found in the basal bodies from which cilia and flagella originate.

A β-like tubulin, or *BLT*, was originally identified in *Tetrahymena thermophila.* The *BLT* sequence is 68% homolous to conventional β-tubulin. The major difference between the two genes comes from an additional 27 amino acids at the C-terminus of *BLT*. The C-terminus is a common site for post-translational modifications such as polyglycylation, polyglutamylation and detyrosination. *BLT* is unique among tubulins because although it is similar in sequence to β-tubulin, immunofluorescence studies have shown that it localizes around the base of the ciliary basal bodies of *Tetrahymena thermophila.* The extended C-terminus may be the key to understanding the unique function and localization of *BLT*.

The goal of this project is to clone and sequence the *BLT* gene in another ciliated protozoan, *Tetrahymena pigmentosa*. The cloning is being done by library cart method (see diagram). Cloning will enable us to find out if *BLT* is present in other species, or is unique to *T. thermophila*. Knowing the sequence of another *BLT* gene will also allow us to compare the amino acid sequences and determine which amino acids are important to the unique function of this protein.