

Dr. Kristi M. Westover, Associate Professor

Pictures

Old-field Plant Community
Fungal Pathogen
Bacillus Mycooides

HBV Phylogeny - (pdf - 28kb)

Soil Community Dynamics

The interactions between plants and soil microorganisms are the focus of one of my current areas of research. I have been studying the relationships between plants and their rhizosphere microbial associates utilizing a feedback approach. Feedback essentially involves two steps. First, a plant or population of plants changes the composition of the soil community; and secondly, this change in turn affects the growth rate of the plant or population. This research involves examining the influence of plants on rhizosphere bacteria and in turn the importance of different bacterial agents for plants. I have dedicated efforts to studying the influence of plants on bacterial community structure and I am currently investigating the influence of plants on the genetic variability of strains of particular organisms using molecular techniques. To begin understanding the significance of host-specific bacterial strains and communities for individual plants, I am screening bacteria for their effects on plant growth. One bacterium, *Bacillus mycooides*, appears to be important for plant growth and evidence suggests that plant growth is higher when plants are inoculated with strains the plant is normally found in association with. I am currently investigating the effects of host-specific isolates of *Bacillus mycooides* and a fungal pathogen, *Pythium macrosporum*, on plant growth. The results show no indication that an advantage for differentially host-adapted *Bacillus* isolates involves protection from pathogens. However, both organisms may be agents of negative feedback through the soil community, and therefore involved in the maintenance of plant diversity. I am hopeful that future work in this area will include a more comprehensive study of the host-specific genetic variability in *Bacillus mycooides* using sequence analysis. Variability at this level needs to then be incorporated into our current model of negative feedback. In addition, I would like to be involved in the continued search for additional microbes important in this system. Finally, I hope to examine the direct mode of interaction between organisms like *Bacillus* and *Pythium* in systems where there is evidence of their importance for plant interactions.

Feedback through the soil community may exert strong effects on the numerical and spatial dynamics of plant populations and communities. For example, negative feedback between plants and their soil communities may act to maintain species diversity within an ecological neighborhood. While this negative feedback suggests that the dynamics within the soil community can contribute to the maintenance of diversity within plant communities, it does not identify the importance of these feedbacks in plant species coexistence relative to other potential factors, such as interspecific competition. Another component of my current research involves examining how feedback through the soil community influences plant-plant interactions, specifically testing whether soil community feedbacks generate negative frequency dependence between the two perennial plant species, *Anthoxanthum odoratum* and *Panicum sphaerocarpon*. These studies are being conducted in collaboration with Dr. J.D. Bever at the University of Indiana-Bloomington. The generality of the hypothesis that microbes play a role in the maintenance of plant species diversity needs to be addressed with further experimentation, something we hope to pursue in the future.

Host-Viral Evolution

My current research involves the study of the relationships between viruses and their animal hosts in terms of sequence response to host immune pressures. This work employs techniques for isolation and purification of DNA/RNA (molecular microbiology) and theories used to analyze sequences (bioinformatics). Viral proteins encoded for by overlapping reading frames have attracted the attention of evolutionary biologists since their discovery. My research in this area has focused on the question of how natural selection can act simultaneously on two different protein products encoded in different reading frames by the same DNA sequence. This may be of particular relevance for regions of viral genomes coding for cytotoxic T cell-recognized epitopes. If natural selection, including selection by the host, acts to favor amino-acid altering nucleotide substitutions in one reading frame, yet amino acid changes in overlapping reading frames are not favored because of a functional constraint, a kind of within-genome evolutionary conflict arises. By collecting publicly available genetic sequences may be gathered, aligned, and analyzed using comparisons of the rates of synonymous and nonsynonymous amino acid changes and phylogenetic methods to reconstruct evolutionary changes in known epitope regions, we have examined natural selection on simian immunodeficiency virus (SIV) and hepatitis B virus (HBV) proteins to understand how natural selection in one reading frame affects the evolution of a protein encoded by an overlapping reading frame. For both viruses there was evidence of simultaneous positive and purifying selection on overlapping reading frames. Cytotoxic T cells exert positive selection favoring nonsynonymous amino acid replacements of epitopes in such a way as to cause predominantly synonymous amino acid changes in corresponding overlapping reading frames. These results represent one mechanism of viral evasion of the host immune system and suggest considerations for the development of effective vaccination and treatment protocols. In addition, we intend to examine other disease-causing viruses to test the generality as the results of such analyses will increase our understanding of host-virus co-evolution, and thereby lay groundwork for predictive models of the evolution of the immune system and viral evasion strategies. This work is being done with Dr. A.L. Hughes at the University of South Carolina-Columbia. Dr. Hughes and I hope that a successful relationship between our two institutions designed to study evolution of genetic sequences will serve as a step towards developing a regional strength in bioinformatics.