

Host Response to *Xanthomonas campestris* pv. *vesicatoria* Wild-Type and *hrp* Mutants,

The goal of this project was to examine the response of tomato to *Xanthomonas campestris* pv. *vesicatoria* (*Xcv*) wild-type pathogen and the *hrpG* and *hrpE1* mutants. Specifically, to determine which genes are up- or down-regulated in response to inoculation with *hrpG* and *hrpE1* mutants versus inoculation with the wild-type pathogen. Tomato leaflets were sampled at time intervals following inoculation and total RNA was extracted. The total RNA was used as a template for multiplex RT-PCR using glyceraldehyde phosphate dehydrogenase (GAPDH) primers as an internal control and gene-specific primers for the host response genes. The genes examined included: pathogenesis-related (PR) protein genes PR-1a1, PR-1b, PR-2b, and PR-5; plus β -1,3-glucanase (B-1,3-G), chitinase (CHT), lipoxygenase (LOX), phenylalanine ammonia lyase (PAL), and phospholipase D (PLPD). These genes have previously been observed to be up- or down-regulated in response to infection by viruses, fungi, or bacteria, and could be involved in the host response to *Xcv*. Initial results show that PR-1b was down-regulated in response to both mutants compared to the water control and wild-type pathogen. Both CHT and B-1,3-G were also up-regulated in response to *hrpE1* compared to the water control and wild-type. Future RT-PCR studies will be used to identify additional differentially expressed genes, which then will be examined by Northern analyses.

Regional climatic drivers of wildfire regimes in northern Idaho,

Wildfire plays an important role in ecosystem processes of many forest types. Dendrochronological techniques can be used to examine the relationship between climatic events and fire patterns. Previous studies in South America and the southwestern United States have concluded that climate is an important driver of fire regimes. These studies have found significant relationships between La Niña events and/or significantly dry years and fire events in these regions. Such investigations are beginning in the Northern Rocky Mountains, but little is known about the regional drivers of fire regimes in this area. Preliminary studies indicate a relationship between dry years and/or El Niño years and fire events in the region. I investigated the climatic drivers of historical fire regimes in northern Idaho to add to the understanding of these forces in the Northern Rockies region. Using crossdating and other dendrochronological techniques I determined the historical fire regime on the University of Idaho Experimental Forest. I used superposed epoch analysis (SEA) to demonstrate a significant relationship between fire years and historical drought periods. I found that mean precipitation was significantly lower in regional fire years than in other years. Additional analysis showed a relationship between fire years and El Niño events. Synchrony among the fire histories established on my site and sites in the Blue Mountains of Washington and Oregon also suggests that climatic events are drivers of the regional fire regime. These findings are consistent with other results from studies in the Northwest, Southwest, and South America.

Encapsulation In Neotropical Caterpillars;

Encapsulation is an internal immune response some species of caterpillar are able to use in defense against parasitoids. Often preventative toxicity, morphology, and behavior are not enough defense against natural enemies, thus internal response provides a distinct benefit to an individual. Upon detection of a foreign body, hemocyte concentration is increased, and individual hemocytes adhere to the surface of the object. The accumulation of the hemocytes creates a thick capsule, which smothers the object. Encapsulation is an understudied process that I hypothesized to influence overall parasitism rates for a species. I conducted a survey over 18 species of Costa Rican caterpillars, to test for encapsulation ability in each. Each individual was injected with glass beads that mimic parasitoid eggs and are shown to induce proper immune response in the literature. From these experiments I determined which species displayed encapsulation ability and correlated the encapsulation data with parasitism rates for the species. My data showed a weak, but significant correlation between the ability to encapsulate and a lower parasitism rate.

Nutrient Selection and Foraging Behavior of the North American Pika (*Ochotona princeps*).

This study focused on determining selection and food preferences in the North American pika (*Ochotona princeps*) in Colorado and Montana populations. Specifically this was done in the Indian Peaks Wilderness of Boulder County, Colorado, and the Gallatin Range of Gilpin County, Montana in July and August of 2003. Pikas are non-hibernating, plant-caching animals that inhabit high-alpine talus slopes where vegetation is not always abundant and often contains toxic compounds called phenolics. Phenolics are a type of secondary plant metabolite that inhibits the digestive processes of most mammals, but they provide antibacterial and antifungal properties to plants in an herbivore's cache, and also may have other benefits. The main objective of this study was to examine nutrient selection in pika by comparing the abundance of high phenolic plants in ridge-top conditions to canyon conditions. I hypothesized that haypiles in ridge-tops would have higher concentrations of phenolics due to a stronger demand for them, and that pikas in canyon areas would select fewer of these nutritive plants due to less demand. I recorded available vegetation and percent composition of species in haypiles from 10-20 sites at each of four study sites, consisting of two canyon sites and two ridge-top sites, and I performed biochemical nutrient tests on the plant matter at each site, including an assay for total phenolics, a protein precipitable phenolics assay, and a carbon and nitrogen percentage analysis. My results indicated that haypiles on ridges contained higher concentrations of nutrients than what was available, suggesting that pikas selected for these nutrients on ridges, and that haypiles in canyons contained lower concentrations of nutrients, suggesting that there was relatively no selection for phenolics despite their high availability. On certain nitrogen-dense ridges where phenolics were not available, pikas tended to select for highly nutritive nitrogenous material, but did not select for this in canyons where plants contained relatively similar levels of nitrogen. This suggests that where nitrogen is present, pikas will select for it only in harsher

conditions. Differences between what was available for each habitat reflected soil quality, concluding that pikas selected for more nutritious material in harsher climates but that the type of nutrient selected for varied. These data indicate that herbivores have a higher demand for nutritious material in harsher climates and that pikas and possibly other plant-caching herbivores are specialist species.

Diversity and Conservation of *Teagueia* Species (Orchidaceae) in the High Elevation Cloud Forests of the Ecuadorian Andes,

This study set out to establish the conservation status of the orchid genus *Teagueia* through an assessment of the limits to its geographical range, and the abundance of individuals of each species within the known populations. The study took place in the high elevation cloud forests of the Rio Pastaza watershed, near the village of Baños, in the eastern Andes Mountains of Ecuador. The α , β , and γ diversities of the region and of each site were assessed. A method for sampling cloud forest orchids was developed and used to assess the abundance and species richness of each study site. Results showed most species of *Teagueia* to be locally abundant, yet restricted to isolated populations typically above 3000 meters. The geographic and altitudinal ranges of the genus are greater than previously believed, although *Teagueia* can still be considered narrowly endemic in the context of the Ecuadorian Andes. Conservation concerns about rarity were alleviated for some species, but remain prominent for others. A basal knowledge of the genus *Teagueia* was established, and methods were developed which can be adapted in future studies on Andean orchids in general, and on this highly diverse genus in particular.

Investigating the IL-27 Paradox

IL-27 is a heterodimeric cytokine consisting of EBI-3, a p40 related protein, and p28, a poorly secreted IL-12 p35-related polypeptide. The ligand binds to the WSX-1/gp130 receptor complex and induces the secretion of IFN- γ , which is necessary for cell differentiation to a Th1 phenotype. Recent studies using animals deficient in the individual components of the IL-27/IL-27 receptor system have shed light on the role of each component in relation to Th1/Th2 responses. Animals deficient in WSX-1 fail to produce IFN- γ at the early stages of infection and hence have a compromised Th1 immune response. However, EBI-3 deficiency resulted in a relative increase in IFN- γ production. These data leave us with a puzzle – specifically, how can eliminating the receptor for a cytokine give a phenotype that is essentially the exact opposite of the phenotype noted when one component of the cytokine is eliminated? One possible explanation is that EBI-3 also pairs with another poorly secreted partner to form a unique cytokine that modulates Th2 responses. The premise for the following study attempts to answer this paradox by examining possible candidates for a novel EBI-3 heterodimeric cytokine.

DNA Fingerprinting of South Pacific Populations.

Population and evolutionary genetics are used in conjunction with linguistic and anthropological studies to trace the evolution and migratory patterns of early man. One significant question that still remains is the migratory path of South Pacific populations in Polynesia. Through DNA fingerprint techniques and genetic data sets, scientists are finding conflicting answers of which population migrated to these islands. The large diversity of the Austronesian languages has led to the belief that ancestral Taiwanese farmers migrated southward to Polynesia. Comparisons between DNA from present day indigenous tribes in Taiwan and DNA from populations in Indonesia were made and used to examine this theory. Colleagues and I analyzed nine short tandem repeats were analyzed from DNA samples taken from two Taiwanese aboriginal tribes (Ami and Atayal) and one Indonesian population (Balinese). William Richardson and I compared the microsatellite data with other data from surrounding and worldwide groups to look at historical migratory patterns. After calculating the allelic frequencies of the different populations, we performed Hardy-Weinberg equilibrium testing, centroid analysis, principal component maps to analyze the data from the microsatellites. We then created phylogenetic trees to map the evolutionary history of the South Pacific.

Effects of global and local strain on enzymatic activity of endothelial cells,

Tumor growth is dependent on many factors, including angiogenesis, or the growth of new capillaries from pre-existing blood vessels. Families of metal-dependent ectoenzymes that facilitate angiogenesis include the matrix metalloproteases (MMPs). The endogenous substrates of MMPs include the collagen-based basement membrane and extra cellular matrix (ECM) surrounding existing capillaries. In the simplest description, new capillaries are formed when stimuli induce locally elevated levels of MMPs; ECM degradation proximal to the capillary then allows migration of endothelial cells to form new capillaries. It has been shown qualitatively that capillary formation correlates with local strain (capillary wall defects) and global strain (tumor compression). Therefore it is possible mechanical stimuli impact MMP activity independently of chemical stimuli. This work attempts to correlate the expression of MMPs with marked increases in the magnitude of local and global tensile strain. First, we will discuss efforts to quantify the relationship between applied global strain and enzyme activity from bovine capillary endothelial cells. Next, we will outline the development of a new in vitro platform for quantification of applied strain effects on adherent cells. Our results indicate that the activity of MMP-2, a gelatinase, correlates inversely with applied global strain.

Deletion Analysis of HilA Transcription Factor Function in *Salmonella enterica* sv. Typhimurium,

HilA is a transcription activator that regulates the expression of two large operons for the Type III Secretion System (TTSS) found encoded on *Salmonella* Pathogenicity Island I. The DNA-binding domain of HilA is located at the N-terminal of this 553 amino acid protein, and it shows sequence similarity to the CadC family of transcription activators. The 400-plus amino acids of the HilA C-terminus have yet to be characterized for function, but the protein sequence suggests evidence of a tetratricopeptide repeat (TPR) along with a Tad D domain in this region. We have employed a deletion mutation strategy in order to study possible function in the HilA C-terminus. Five *hilA* deletion mutations were constructed by crossover PCR, and were inserted into a vector that placed the modified *hilA* under control of a pBAD promoter. Each construct was expressed in *E. coli* reporter strains where HilA activation or binding activities would affect *lacZ* expression. This allowed us to independently measure the effect of specific deletions upon activation or DNA-binding. Analysis of mutant *hilA* function in the reporter strains indicates that C-terminal regions of HilA are required for effective transcriptional activation.

Montane rainforest succession on landslides at Lake Thompson, Fiordland, New Zealand,

The focus of this study was plant succession of Fiordland montane rainforest on five parallel north-facing slip faces. Changes in soil depth and pH over time, vascular plant diversity, and mean height of the highest layer of vegetation were examined in fifty 100 m² random plots distributed on slips aged 5, 56, 90 and 119 years, and in mature forest. The growth rate of the mean height of the top tier of vegetation was shown to decrease through time. Other landslides in this region can be aged directly from mean height measurements. The rate of soil formation following a landslide decreased through time. More than half of the soil found in the mature slip was formed in the first 56 years after a landslide. Simpson's diversity and equitability indices were used to quantify the diversity and dominance of vascular plants. Contrary to the typical pattern of forest regeneration, species richness was highest in the 5-year-old slip and decreased consistently through the other four slips. The deviation from the usual trend can be attributed to the location of the study site and its unusually close proximity to the tree line. Alpine species typically restricted to habitats above the tree line tend to be the primary colonizers following a disturbance. This study is important because the observed deviations from typical patterns of succession are a result of habitat location and altitude.

Interspecific competition between *Formica podzolica* Francoeur and *Formica planipilis* Creighton at sugar water baits in Ponderosa Pine forests,

The intent of this research was to elucidate the role of competition in influencing the foraging patterns of two sympatric species, *Formica podzolica* Francoeur and *Formica planipilis* Creighton in a Colorado montane forest, in June and July of 2003. The primary objective of this study was to gain an understanding of the foraging patterns of *F. podzolica* and *F. planipilis*. To do this I first devised a method for estimating a colony's allocation of foragers to sugar resources. I hypothesized that a niche-shift occurred between the species and compared the forager allocation feeders, next to mounds, to tall and short feeders placed between the mounds. I hypothesized that the competition between *F. podzolica* foragers and *F. planipilis* foragers would result in a different proportion of ants found at short and tall treatment feeders. However, this was not found to be the case. The data gathered showed a greater total abundance of ants at tall feeders, suggesting an evolutionary adaptation to forage in canopies. Additionally, while *F. podzolica* foragers appear to be more abundant in number, *F. planipilis* foragers occupied the feeder holes more than expected, suggesting a dominance hierarchy between the species. These results lead to hypotheses concerning how *F. podzolica* can survive and compete for resources, through exploitation competition.

Identification and Determination of Variation in DNA sequences on the Preble's Meadow Jumping Mice (*Zapus hudsonius preblei*) Genome. Kristin Hintz and Dr. Rob

The Endangered Species Act requires ongoing conservation efforts for listed species. Preble's Meadow Jumping Mouse was listed in 1998 as a "threatened" species due to habitat loss caused by development, agriculture, and other forms of human disturbance along the Front Range. Since the listing, more scientific evidence has been collected which suggests that the species is not a unique evolutionary unit (Ramey et al 2003). Mitochondrial DNA testing of samples obtained from the Denver Museum of Nature and Science and samples collected from Halligan Reservoir (situated on the north fork of the Cache La Poudre River) suggest that *Zapus hudsonius preblei* are not genetically distinct from *Zapus hudsonius campestris*. This needs to be clarified with further research, such as corroboration by skull morphometry in order to support a delisting of the Preble's Meadow Jumping Mouse. These same results refute the original qualitative basis of Krutzsch 1954. Overall, this situation suggests that national standards for genetic evidence are needed prior to Endangered Species listings. These standards should be more stringent than the current review process and require: a modern conceptual basis for taxa and distinct population segments, peer review outside of the USFWS, publicly available data, validating the data with required standards of repeatability, individually verifiable data and genotype determination. Through implementation of higher standards, scarce money for research efforts will be directed towards those species with the highest need of protection and conservation and based on the best available science.

Investigating the Genetic Diversity Within and Among Populations of a Rare Plant: *Mimulus gemmiparus*,

Mimulus gemmiparus is one of Colorado's rarest plants. Endemic to the state, it has historically been described in eight populations although only six have recently been found to be extant. This species is a member of a diverse genus of plants that have become model systems for the study of evolution. *M. gemmiparus* is extremely unique, both within this group and with respect to all other plants. This species is clonal and is the only known species to reproduce in the manner described. *M. gemmiparus* produces asexual propagules that are formed at leaf nodes and then drop off the plant to form its overwintering structures. Being a rare, clonally reproducing species, *Mimulus gemmiparus* may be susceptible to extinction caused by a changing environment or by human disturbance. This study is the first step in preserving this plant. Our findings will be used in conjunction of those from future studies to develop a management plan for *M. gemmiparus*. We employed the techniques of Applied Fragment Length Polymorphism (AFLP) analysis to investigate patterns of genetic diversity within and among the six populations. Although asexually reproducing populations have traditionally been thought to have low levels of genetic diversity, our findings confer with those of other more recent studies that indicate otherwise. Using eight primer combinations, we recovered 272 polymorphisms, with an average of 34 per gel. From a distance matrix based on neighbor joining, we found that populations form natural groups and that different populations maintain different levels of diversity. Further patterns of diversity were explored using a wide range of statistical inferences.

POSTERS

***Chromobacterium violaceum* contains a functional homolog of *S. typhimurium* HilA, a key *Salmonella* Pathogenicity Island 1 transcription regulator,**

HilA is a transcription activator of a Type III Secretion System (TTSS) of *Salmonella typhimurium*. While the N-terminal DNA-binding domain of this protein is related to the CadC family of transcription activators, the role of 400 amino acids in the C-terminal region remains to be determined. Recent genomic sequencing of *Chromobacterium violaceum* revealed the existence of a possible *hila* homolog, and other TTSS genes, in this phylogenetically distant bacterium. We have isolated the *C. violaceum hila* (*hila_{Cvi}*) gene by PCR amplification of genomic DNA, and inserted it into a pBAD expression vector that allows us to control *hila* expression using arabinose. The pBAD-*hila_{Cvi}* plasmid was then transformed into *E. coli* reporter strains, PL372 and PH538, that contain HilA binding boxes in positions that will activate or repress expression of a genomic beta-galactosidase gene that is under control of a lac promoter. Using these reporters, we evaluated the activation and repression activities of the HilA_{Cvi} protein relative to *S. typhimurium* HilA (HilA_{Stm}) expressed from the same vector, and relative to null vector control strains. Where HilA_{Stm} shows 300-fold activation over the null vector control, the HilA_{Cvi} is only capable of a 14-fold activation. The HilA_{Stm} represses the expression of the *LacZ* reporter by 62% compared to the null vector strain, while HilA_{Cvi} repressed *LacZ* expression by only 6%. We are currently constructing domain exchanges between the HilA_{Cvi} and HilA_{Stm} proteins by crossover polymerase chain reaction, using the existence of some conserved domains in these proteins as a guide. We found that a hybrid protein containing the HilA_{Cvi} N-terminus and the 400 amino acid HilA_{Stm} C-terminus binds to the HilA box DNA and activates transcription in *E. coli* as well as HilA_{Stm}. The data suggest the existence of important functional domains within the HilA_{Stm} C-terminus.

The Effect of Nest Predation on Flammulated Owl Habitat Selection,

Nest predation is an important factor affecting the habitat quality of birds. The flammulated owl (*Otus flammeolus*) is a sensitive species that reproduces more in forests of primarily open ponderosa pine (*Pinus ponderosa*) as opposed to forests of mostly dense Douglas fir (*Pseudotsuga menziesii*). Determining what factors pressure the owl to nest in open ponderosa pine forests is important in the effort to conserve this species and their habitat. Forests of dense Douglas fir are poor nesting habitats for flammulated owls possibly because red squirrels (*Tamiasciurus hudsonicus*) are more prevalent in dense Douglas fir forests. During the summer of 2003 we collected data to try and determine the effect of squirrel predation on flammulated owl habitat selection. We set up artificial nest boxes to determine predation rates among three different habitat types, and we set up straight line transects to measure squirrel and midden densities among the three habitat types. Because of a small sample size and a scarcity of squirrels, there were no significant results found. This study should be repeated with a larger sample size, and last for more than one year.

Determining the Activation Surface for Transcription Factor HilA in *Salmonella enterica* serovar Typhimurium

Transcription factor HilA is responsible for initiating construction of the Type Three Secretion System I, a key virulence factor of *S. typhimurium* that translocates effector proteins into the host's intestinal epithelial cells. Structurally, HilA is thought to contain a DNA binding/activation domain in its N terminus, and thus far the alpha loop of HilA has been favored to contain this activation surface. All feasible positions of the alpha loop have been tested except position two, at which W65 remains untested. In this study, the tryptophan at position 65 was changed to an alanine using site-directed mutagenesis. The mutant's DNA binding and transactivation properties were measured by beta-galactosidase assay.

Designing a Robust RT-PCR Protocol for Examining Host Response to *Xanthomonas campestris* pv. *vesicatoria* (Xcv) Wild-Type Pathogen and the *hrpG* and *hrpE1* Mutants

The goal of this project was to design a robust RT-PCR protocol that can be used to examine the response of tomato to *Xanthomonas campestris* pv. *vesicatoria* (Xcv) wild-type pathogen and the *hrpG* and *hrpE1* mutants. This project aimed to identify inherent variables that may obscure the RT-PCR results. The finished protocol should be able to determine which genes are up- or down-regulated in response to the *hrpG* and *hrpE1* mutants and to compare this response to that observed following inoculation with the wild-type pathogen. Since RT-PCR would be used to qualitatively examine the expression state of different host response genes, variables that would alter the efficacy of the RT-PCR process were looked at. Optimal number of PCR cycles and annealing temperatures were determined so that RT-PCR would operate at a higher efficiency for the genes of interest, which included pathogenesis-related (PR) protein genes PR-1a1, PR-1b, PR-2b, and PR-5; plus β -1,3-glucanase (B-1,3-G), chitinase (CHT), lipoxygenase (LOX), phenylalanine ammonia lyase (PAL), and phospholipase D (PLPD). In addition, RNase and DNA contamination caused problems in the test runs of the RT-PCR, but was effectively eliminated through modifying the the protocol. Further research may be helpful in determining the accuracy of our set parameters and also to check for any additional variables.

Thermodynamic Analysis of Domain II of the Hammerhead Ribozyme,

The hammerhead ribozyme is a tertiary folded RNA sequence that has catalytic properties. Catalytic RNAs are being used as templates for the design of de novo ribozymes to cleave desired foreign nucleotide sequences. The structure of the hammerhead ribozyme has been studied extensively and crystal structures have been obtained of this molecule in the presence of a multitude of metal ions. Mg²⁺ is necessary for catalysis to occur and has been identified in the crystal structure of hammerhead. These structures do not correlate with the catalytic properties of this molecule. The catalytic domain is a junction of three helices where non-canonical base pairs are seen in the structure. Type and stability of the bonds in domain II between A14-U7, A13-G8, and G12-A9 are of particular interest to this study. Mimics of domain II employ an 18 atom ethylene glycol linker to simulate the three helix junction in order to isolate and study the small region of interest.

Effects of invasive species on tract gas emissions and soil nutrient cycling in a nitrogen-limited ecosystem

The invasion of *Myrica faya*, a nitrogen (N) -fixing tree dominates many native ecosystems in the Hawaii Volcanoes National Park where primary production is known to be limited by N. Previous studies have shown that *M. faya* increases rates of N cycling, giving *M. faya* a competitive advantage over slow-growing native *Metrosideros polymorpha* (Ohi'a). We examined the effects of *M. faya* on N cycling and soil trace gas emissions in seven paired *M. faya*- Ohi'a plots during the summers of 2001 and 2002. Stands of *M. faya* doubled rates of soil nitrogen cycling and trace gas emissions compared to Ohi'a stands, significantly altering nutrient availability and atmospheric chemistry. Future studies will assess winter fluxes as well as variations caused by plant morphology in order to scale plot-level fluxes to the region.

Inhibition of Interleukin-7 Signaling is not required for Allelic Exclusion

A functional, membrane-bound pre B cell receptor (pre-BCR) starts a signaling cascade resulting in allelic exclusion at the immunoglobulin heavy chain locus. It remains unknown how the signal sent by the pre-BCR results in allelic exclusion. One model proposed by Chowdry and Sen is that the pre-B cell receptor sends a signal that down-regulates IL7R signaling (Immunity 2003; vol. 18, 229-241). This model predicts that allelic exclusion imposed by HEL transgenic mice can be broken if IL7R signaling is not down regulated. To test this prediction, HEL transgenic mice were crossed with mice expressing a constitutively active form of STAT5 (called STAT5b-CA). We have previously demonstrated that STAT5 signals are sufficient to functionally replace the IL7R during B cell development. In STAT5b-CA mice, STAT5 signals cannot be inhibited and therefore their B cells behave as if no down regulation of the IL7R has taken place. Therefore, if down regulation of IL7R signaling is sufficient to cause allelic exclusion, HEL x STAT5b-CA transgenic mice should not show allelic exclusion. Our flow cytometry data shows there is not a significant increase in cells expressing both the IgM^a and IgM^b allotypes in HEL x STAT5b-CA transgenics. In conclusion, our results demonstrate that IL7R down-regulation is not sufficient to cause allelic exclusion and hence the pre-BCR must enforce allelic exclusion via an alternate mechanism.

Genetic Diversity of *Quercus gambelii* as Determined by Inter-simple Sequence Repeats (ISSR)

As part of a larger ecological study to examine the spatial and temporal patterns in seed production by *Q. gambelii* (Gamble's oak), the clonal identity of several Gamble's oak stems were analyzed using inter-simple sequence repeats. Leaf samples from four different stems were collected from individual clones at various geographic locations in Colorado. DNA was extracted from these leaf samples and then analyzed with a series of six inter-simple sequence repeat primers. The SSR primers were used to generate any variation in the DNA from the four different stems. With this analysis, the four stems could be confirmed as clones or as genetically different individuals. Nine clones were analyzed with SSR primers 813, 866, 872, and 873. Primers 869 and 861 were never successfully optimized during the research period. The genetic variability of Castle Rock clone #71 was concluded as stems 1 and 3 being similar and stems 2 and 4 being similar. All other clones need further primer analysis in order to confirm clonal identity among stems.

Examining Biofilm Formation of *Vibrio fischeri* Induced by Different Carbon Sources

Biofilms are complex communities of microorganisms attached to surfaces or associated with interfaces. Despite the focus of modern microbiology research on pure culture, planktonic (free-swimming) bacteria, it is now widely recognized that most bacteria found in natural, clinical, and industrial settings persist in association with surfaces. *Vibrio fischeri* is best known for its symbiotic role with *Euprymna scolopes* (Hawaiian bobtail squid). Though *V. fischeri* was one of the pioneering models for quorum-sensing, the conditions under which it forms a biofilm are still undefined. We hypothesized that *V. fischeri* would have to be functional in the following areas to form and/or accelerate growth of a biofilm: flagellar motility, exopolysaccharide synthesis, and pili formation, which induces a twitching motility. A correlation between nutrient availability and pili formation had been established in *P. aeruginosa*, thus we tested *V. fischeri* on a variety of carbon sources. Initially, four strains of *V. fischeri*, one dark (ES114), three light producing (CG101, WH1, and VLS2), were tested on four different minimal media: CAS amino acids, N-acetyl glucosamine, glucose, and glycerol. It was determined that *V. fischeri* grown on a minimal media with CAS amino acids yielded the most proficient biofilm formation. Another experiment compared the biofilm formation of the ES114 and WH1 strains on CAS amino acids. It was found that WH1 was about twice as efficient in biofilm formation.

A study on cavity nesting birds and aspens at Catamount Institute

Two different studies were carried out at the Catamount institute during the summer of 2003. One study focused on the effects of forest thinning in the upper montane forests of the Southern Rockies while the other studied the importance of *Phellinus tremulae* for the cavity-nesting birds of the area. For the forest-thinning project, the land was divided into five different plots, each plot being comprised of a control and thinned plot of similar slope and aspect. To determine rates of nest predation, sixty nests were hid in each plot and two eggs were placed in each. The nests were checked every other day for ten days. No significant difference was found between predation rates in the two sections of each plot. Inventories of vascular plants and lichens were collected in each plot and canopy closure was measured. Small mammals were trapped in each plot and the thinned plots were found to contain up to twice as many small mammals as the control plots.

To prove the importance of *Phellinus tremulae* to cavity nesting birds a certain aspen grove was selected and the number of trees above 15 cm that had visible conks and cavities was recorded. Seventy-eight percent of trees in selected grove showed visible signs of infection. Twenty-four ¼ hectare plots were chosen from the forest at large and found using a GPS. Each snag and aspen tree in the plot was measured and it was recorded whether they had cavities and/or conks. The results of this study are being submitted to the Ecological Society of America's "Frontiers of Ecology" journal.