

**NINTH ANNUAL  
STUDENT RESEARCH  
POSTER SYMPOSIUM**

**MAY 13, 2005  
1-4 P. M.**

**HOLT HALL**

**DEPARTMENT OF BIOLOGICAL SCIENCES  
CALIFORNIA STATE UNIVERSITY, CHICO**

**POSTERS**

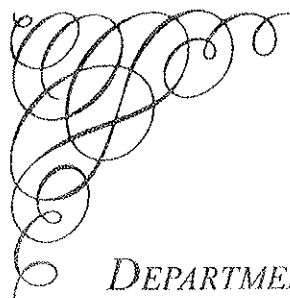
**Lower Division, Upper Division,  
Undergraduate Independent Research**  
*Holt 225*

**Graduate Classes, Thesis Research**  
*Holt 227*

**ENTOMOLOGY CLASS DISPLAY**  
*Holt 235*

**ORNITHOLOGY DISPLAY**  
*Holt 235*

**May 14-15  
GREENHOUSES OPEN TO VIEW  
10 a.m. – 3 p.m.**



DEPARTMENT OF BIOLOGICAL SCIENCES  
CALIFORNIA STATE UNIVERSITY, CHICO

RECIPIENTS OF THE  
TOM RODGERS  
OUTSTANDING RESEARCHER AWARD

1997 Ronald E. Loggins

1998 Maura Eagan

1999 Moaiad A. Kanaan

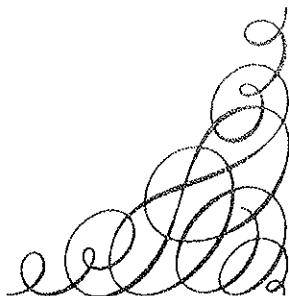
2000 Carina M. Jung

2001 Cary Coburn

2002 Glen Lubcke, Jack Campbell, Gary Lechner

2003 Julia Terry

2004 Colleen Martin, Michelle Sopoliga,  
Michelle Ocken



## Lower Division Class Projects

### EFFECT OF AMMONIA AND ACETIC ACID IN A SERIES OF DILUTIONS UPON SEED GERMINATION IN CABBAGE SEEDS

BIOL 006B -- Travis Barber and John Eymil  
Sponsored by Dr. David Wood

To investigate if, and at what concentration, ammonia, ( $\text{NH}_3$ ) and acetic acid ( $\text{CH}_3\text{COOH}$ ) would inhibit cabbage seed germination. Cabbage seeds were germinated in aqueous solutions of succeeding lesser concentrations of ammonia and acetic acid, with a total of nine dilutions for each, as well as one treatment germinated in demonized water as a control. Both ammonia and acetic acid were found to inhibit seed germination completely up until a dilution of 1/320 for ammonia, and 1/640 for acetic acid, after which seed germination success was greatly increased in the next dilution of ammonia (1/640) from 0% to 50%, and acetic acid (1/1280) from 0% to 80%. It can be concluded that there is a specific range in concentration for both substances in which conditions for seed germination change dramatically.

### INSECT DIVERSITY & TOPOGRAPHY

BIOL 006B -- Ninfa Ramaros, Marni Merrill, Rachae Perkins  
Sponsored by Dr. Michael Marchetti

The object of this experiment was to determine if changes in topography affect insect diversity. Other studies have shown that there is a greater insect diversity in the transitional region between two ecosystems (Brewer 1994). We wanted to see if topographic features played a part in determining insect diversity. We did an eight-day experiment with 25 insect pitfall traps in Upper Bidwell Park. The results showed that topographic differences have little effect on insect diversity.

### EFFECTS OF EUCALYPTUS EXTRACTS ON LACTUCA SATIVA SEED GERMINATION AND SEEDLING LENGTH

BIOL 006B -- Brandy Spaulding and Caitlin Ostrom  
bspaulding@mail.csuchico.edu and caitlinostrom@yahoo.com  
Sponsored by Dr. David Wood

Previous research on allelopathy finds leaf litter, leaf litter extracts, and plant extracts of some species to have inhibitory effects on other species. Eucalyptus is one species found to demonstrate allelopathic effects. Therefore, it was hypothesized that there would be a significant effect of eucalyptus leaf extracts on both *Lactuca sativa* (lettuce) seed germination and seedling growth (as measured by length of seedling). Extracts of 100 percent, 50 percent and 10 percent were tested against the control. Two one-way ANOVAs revealed a significant inhibitory effect of percent concentration of eucalyptus extract on both seed germination and seedling growth, as hypothesized. The higher the concentration the more both germination and growth were inhibited. Hence, the null hypothesis was rejected.

## Upper Division Class Projects

### EFFECT OF SALICYLIC ACID ON DEFENSE GENE EXPRESSION IN TOBACCO AND SUBSEQUENT SURVIVORSHIP OF AN APPLIED BACTERIAL PATHOGEN

BIOL 228 – Danil Abruzzini, Danielle Baker, Christopher Cockrell, Mathew Cox, Michael Fassio, Dhillon Frago, Jessa Guisse, Mark Gustafson, Michael Larson, Barbara Manning, Andrew Petyo, Kristina Short, Elon Steers, Christian Taylor, Glen Thomayer, Ashley Waters, Jeannette Young  
Sponsored by Dr. Kristopher Blee (kblee@csuchico.edu)

Can plant defense genes be artificially induced by spraying them with a solution of salicylic acid (SA)? To answer our question we pretreated plants with SA before inoculating them with the *Pseudomonas syringae* pv. tabaci (Pst).

After SA treatments, we measured the amount of phosphorylated kinase which reacts when stimulated to activate a cascade of defensive responses in plants. The amount of phosphorylated kinase peaked at 30 minutes after SA treatment, which is in direct correlation with the amount of time to trigger plant defense.

Plants in our experiments contained a reporter gene construct, the bacterial  $\beta$ -glucuronidase gene behind a tobacco PR1a promoter. The PR1a promoter is turned on during plant defense, so the amount of  $\beta$ -glucuronidase that acts as an indicator of defense activation in these particular plants. For a second way of determining defense activation we looked for an increase in peroxidase which helps strengthen plant cell walls in the event of a pathogen attack. A combination of increased  $\beta$ -glucuronidase as well as peroxidase in the treated samples 7 days after inoculation supports the assumption that plant defense was turned on by SA treatment.

We found that in SA pretreated plants, there was significantly less survivorship of Pst in leaves. These results support our hypothesis and indicate we had helped these plants defend themselves against the pathogen. While we did this in small applications it is our hope that further research will find ways to do this in ways that would be more suited towards large scale production.

### DO EXTERNAL LEAF RESINS PLAY A ROLE IN DETERRING HERBOVORY IN THE FOOTHILL WOODLAND PLANT SPECIES *ERIODICTYON CALIFORNICUM*.

BIOL 258 – William Gray  
Sponsored by Dr. David Wood

Yerba Santa (*Eriodictyon californicum*) is a significant member of the Sierra Nevada foothill woodland plant community. It produces a variety of external leaf resins and, for this reason, is used as a folk remedy for treating various respiratory complaints. The composition of this resinous extrusion has been well studied and found to contain eleven flavonoids, nine aglycans and two glycosides. The biological function of many of these compounds is not fully understood, though it is assumed that they play a role in plant defense. In this study the external leaf resin quantity was compared between herbivorized and non-herbivorized *Eriodictyon* plants. No significant difference was found to exist between these two groups, indicating that resin quantity and herbivory are not directly related.

### ROLE OF DISTURBANCE ON AQUATIC INSECT COMMUNITIES IN DISTURBED AND UNDISTURBED PORTIONS OF BIG CHICO CREEK

BIOL 259 – Valerie Henry and Greg True  
Sponsored by Dr. Michael Marchetti

Aquatic habitats can be affected by disturbance due to the presence of human activity. Variation in the level of recreational use in Big Chico Creek was used to examine the effect of human disturbance on the aquatic insect communities. A disturbed site was located at the Five Mile Recreational Area, downstream from the foot-bridge. An undisturbed site was located approximately seven miles upstream, at the end of the unimproved road. A standard one square foot Surber sampler was used to collect five samples from each location. Samples were sorted and aquatic invertebrates were separated into functional feeding groups (FFGs). The study examined three questions related to the aquatic insect community: (1) Are there significant differences in the FFG members collected between the disturbed and undisturbed sites; (2) Are there differences in the taxonomic diversity between the disturbed and undisturbed sites; (3) Are there differences in the relative tolerance values for each FFG between the disturbed and undisturbed sites. The results of a t-test ( $\alpha = 0.05$ ) found no difference between sites for all of the FFGs except predators ( $P = 0.0063$ ) and shredders ( $P = 0.0304$ ). Graphical analysis of family level diversity and tolerance values show no significant trends. Our results may be explained through the dynamics of invertebrate communities within stream systems (Gurtz and Wallace 1984; Feminella and Resh, 1990; and Death and Winterbourn 1995) and the intermediate disturbance hypothesis (Connell, 1978).

### COMPARATIVE BIOASSESSMENT OF GRIZZLY CREEK ABOVE AND BELOW GRIZZLY FOREBAY

BIOL 259 – Katie Colleen Price [777@oroville.com](mailto:777@oroville.com)  
Sponsored by Dr. Michael Marchetti

This study was conducted along Grizzly Creek, above Grizzly Forebay and below Grizzly Dam, in Plumas County, CA. Two sample sites were chosen qualitatively by closest similarity of gradient, width, depth, flow, and shoreline vegetation. Three surber samples were taken randomly at each site beginning downstream in the riffle for durations of 3 minutes. Collected invertebrates were put into a jar with 70% alcohol solution. Total invertebrate quantity was determined for each sample and water quality was determined using the invertebrate families within orders Ephemeroptera, Plecoptera, and Trichoptera (EPT), and the dipteran family Chironomidae. Total sample number (mean  $\pm$  SD) was 136.3  $\pm$  11.3 above Grizzly Forebay and 128.3  $\pm$  36.8 below Grizzly Dam. Family biotic index was calculated using EPT families and Chironomidae. The FBI (mean  $\pm$  SD) was 3.33  $\pm$  .19 above Grizzly Forebay, and 4.23  $\pm$  .17 below Grizzly Dam. Water quality above the forebay ranked excellent, while water quality below the dam ranked very good. Percent similarity was 78.7%, indicating slight impairment below the dam. Percent EPT (mean  $\pm$  SD) was 84.3  $\pm$  1.7 above Grizzly Forebay and 55.3  $\pm$  6.9 below Grizzly Dam, and were not significantly different. Percent Chironomidae (mean  $\pm$  SD) was significantly lower above Grizzly Forebay with .01  $\pm$  .009, compared to .38  $\pm$  .08 below Grizzly Dam. Average taxa richness for both sites was 11.3, including EPT families and Chironomidae. Grizzly Dam appears to have an impact on Grizzly Creek downstream, but this impact is not significant enough to cause concern.

## EFFECTS OF FIRE ON THE REGENERATION OF *PINUS PONDEROSA* SEEDLINGS IN A MIXED-CONIFER FOREST

GEOS 275 – Katie Colleen Price [777@oroville.com](mailto:777@oroville.com)  
Sponsored by Dr. Tal Nahir

Density and distribution patterns associated with the post-fire generation of Ponderosa Pine in a mixed-conifer ecosystem, located between the Sierra Nevada and Cascade Ranges of Northern California, were compared to seedling density and distribution in an unburned area. A 150 m baseline transect was designated in each study site, from which 3 transects for Point-quarter sampling were used. From Point-quarter sampling data, densities and distribution patterns of mature trees was determined. *P. ponderosa* was determined to have the greatest density in both the burned and unburned sites, with 97.0 trees/ha and 177.6 trees/ha, respectively. Distribution of all species of mature trees was determined random with 95% confidence. Three quadrats at each site, 10 x 10 m with 2 X 2 m grid squares, were used to determine mean density and distribution of seedlings. Mean density ( $\pm$  SD) was found to be greater in the unburned area than the burned area, with 10.3 ( $\pm$  8.7) seedlings/ha and 99.3 ( $\pm$  129.9) seedlings/ha, respectively. Using pooled standard deviations for significance, densities were determined significantly different with 99.9% confidence. Spatial distribution patterns of the seedlings were determined to be random in the burned area and contagious in the unburned area, with 95% confidence.

## Undergraduate Independent Research

### ENRICHMENT AND CULTURING OF CYANIDIUM-LIKE ALGAE FROM BOILING SPRINGS LAKE, CA

BIOL 199 – Mary Ellen Sanders, [marvebear9@yahoo.com](mailto:marvebear9@yahoo.com)  
Sponsored by Dr. Gordon Wolfe, [gwolfe2@csuchico.edu](mailto:gwolfe2@csuchico.edu)

P. Brown recently found 18S rRNA sequences of the rhodophyte *Cyanidioschyzon* from Boiling Springs Lake (BSL) at Lassen Volcanic National Park, CA\*. This pH 2.2, 55°C lake has ideal conditions for this taxon, as well as its sister taxa *Cyanidium* and *Galderia*. Therefore, we sampled water from BSL and environs to see if we could enrich and isolate *Cyanidium*-like algae. We set up enrichment cultures in SAG medium at 55°C with light and carbonate as a carbon source, and monitored growth by fluorimetry and visual observation. We found *Cyanidium*-like algae in almost all samples that grew after 4-6 weeks to high densities, and appeared morphologically to be *Cyanidium*. However, we have had difficulty extracting DNA for genetic analysis or isolating pure clones for further study.

\*P.B. Brown, 2005. A Survey of Protist Genetic Diversity in the Hydrothermal Environments of Lassen Volcanic National Park. M.S. Thesis, CSU Chico.

### BORRELIA COMPARATIVE GENOMICS

Rebecca Torres- [rtorres7@mail.csuchico.edu](mailto:rtorres7@mail.csuchico.edu)  
Undergraduate Summer Project, The University of Utah  
Faculty Mentor – Dr. Sherwood Casjens, Department of Pathology.

Lyme disease is one of the leading vector borne diseases in the U.S.A. It is known to be the result of infection caused by a tick bite and the transmission of the bacteria *Borrelia burgdorferi* into the blood and tissues. Studying its genomics allows scientists to gain a better understanding of the molecular biology and of the mechanisms used by *B. burgdorferi* concerning plasmid exchange in the wild. In this study we investigated two aspects of the genome sequences of strains N40 and 297 of *B. burgdorferi*. It was found in many cases that non-homologous rearrangements among *Borrelia* plasmids have occurred. One example is seen in the DNA sequences of the linear plasmids of lp36 from the strains 297 and B31. There is a deletion in B31, which yielded the lp36 plasmid of 297. In our second investigation, we discovered that the DNA sequence from the linear plasmid lp27 in strain N40 is comprised of 27 kbp instead of the predicted 22 kbp. With the use of restriction enzymes and southern analysis we were able to determine that there is approximately 2.5 kbp of undetermined DNA missing from each side of the plasmid. This undetermined sequence, in turn, will have to be determined by more direct methods.

### POINT MUTATIONS OF THE SEMAPHORIN 3C AND CONNEXIN 43 GENES CAUSE ABNORMALITIES IN SKELETAL DEVELOPMENT

Jeffery B. Holland<sup>a</sup>, Amanda T. Boyce<sup>a</sup>, Cecilia W. Lo<sup>a</sup>, Bishwanath Chatterjee<sup>a</sup>,  
Qing Yi<sup>a</sup>, Heather E. Price<sup>a</sup>, and Rocky S. Tuan<sup>b</sup>  
Sponsored by Dr. John Mahoney<sup>b</sup>

The goal of this project is to examine the skeletal phenotypes of two mouse lines with mutations in the Semaphorin 3C and Connexin 43 genes, which code for a chemoattractant/repellent and a gap junction protein, respectively. The mutant lines show obvious skeletal and vascular defects. Both Semaphorin 3C and Connexin 43 are important for the functions of neural crest cells, some of which migrate dorsolaterally and produce the craniofacial mesenchyme, which in turn differentiates into the cartilage and bone of the face. In addition, Connexin 43 is involved in condensation of limb bud mesenchyme, a process that is a prerequisite for the formation of the early cartilage anlagen, the shape of which determine the final shape of the skeleton. Due to the fact that Semaphorin 3C can act as a chemoattractant, it may be involved in the vascularization of the early cartilage anlagen, a process that transports bone forming osteoblasts into the developing skeleton. In order to examine the roles of Semaphorin 3C and Connexin 43 in the development of the skeleton, histological analysis and scoring procedures were used. Wild type and homozygous mutant embryos are paraffin imbedded, sectioned, and stained with dyes specific for cartilage and bone. Measurements were taken to determine the relative amounts of bone and cartilage in the tibia, radius and ulna long bones. Data gathered from these preliminary experiments have laid out the groundwork for determining the molecular mechanisms responsible for these phenotypic defects.

<sup>a</sup> National Institute of Arthritis and Musculoskeletal and Skin Diseases  
National Institutes of Health  
Department of Health & Human Services

<sup>b</sup> Department of Biological Sciences, CSUC [Jeffery1Holland@gmail.com](mailto:Jeffery1Holland@gmail.com),  
[JMahoney@csuchico.edu](mailto:JMahoney@csuchico.edu)

## Graduate Class Projects

### ARE ROOT-ASSOCIATED BACTERIAL COMMUNITIES INFLUENCED BY PLANT DEFENSE?

BIOL 331 – John Hein [jhein1@mail.csuchico.edu](mailto:jhein1@mail.csuchico.edu), Amber Abbott, Katsunori Kichise, Kylene Klevinghaus, Arthur Laganowsky, Alan Raetz, Bernie Pletschet  
Sponsored by Dr. Kristopher Blee, [kblee@csuchico.edu](mailto:kblee@csuchico.edu) and Dr. Gordon Wolfe, [gwolfe2@csuchico.edu](mailto:gwolfe2@csuchico.edu)

Here we investigate the potential for using plant defense to alter microbial communities in rhizosphere soil. Effects of plant defense on bacterial communities were examined using terminal restriction fragment length polymorphism (T-RFLP) analysis of rhizosphere soil DNA from wild type (wt) and selected mutant *Arabidopsis thaliana* (ecotype Col-0). *Cpr1* constitutively expresses the defense response systemic acquired resistance (SAR) as defined by abundant expression of PR1 mRNA. *Npr1-1* mutants were also used, in which SAR is non-inducible.

Antisense PR1/PDF1.2 probes were used to measure transcript abundance in *A. thaliana*. Bacterial rDNA's from the rhizospheres of wt, *npr1-1*, and *cpr1*, were amplified with 27-FAM and 534-HEX primers for T-RFLP, which was performed with an ABI 310 genetic analyzer.

PR1 was expressed in shoots of all three plant types, but not in the roots. Though not statistically significant, there were measurable differences in PR1 transcript abundance between *npr1-1* and *cpr1* plant types, with *cpr1* showing greater expression. T-RFLP fingerprints for the three plant genotypes (wt, *npr1-1*, *cpr1*) showed minor differences, but cluster analysis did not support a dominant pattern based on plant defense gene expression.

Our data provide little support for plant defense gene expression effecting rhizosphere microbial community diversity. However, expression of PR1, a widely utilized marker of SAR, could not be detected in root tissues of our experimental plants, including *cpr1*. In future studies we can apply additional markers for defense and/or defense stimulatory compounds in combination with additional statistical evaluation of T-RFLP data sets.

### COMPARISON OF POTASSIUM-SELECTIVE ION CHANNELS IN *PARAMECIUM* AND *PLASMODIUM*

BIOL 333B – Nicole J. Huber ([njhuber@sbcglobal.net](mailto:njhuber@sbcglobal.net))  
Dr. G.V. Wolfe ([gwolfe2@csuchico.edu](mailto:gwolfe2@csuchico.edu))  
Sponsored by Dr. Jeffrey R. Bell ([jbell@csuchico.edu](mailto:jbell@csuchico.edu))

Potassium-selective ion channels (K<sup>+</sup> channels) have been found in organisms representing all domains of life, but little is known about their diversity in unicellular eukaryotes. In the ciliate *Paramecium*, which is thought to have more K<sup>+</sup> channel genes than humans, K<sup>+</sup> channels play a role in ciliary movement, particularly during avoidance response. To begin investigating whether similar trends exist in other protists, I searched the recently sequenced genomes of the apicomplexans *Plasmodium falciparum*, *P. vivax*, and *P. yoelii*, sister alveolates to ciliates. Using keyword searches, I obtained 11 sequences coding for hypothetical K<sup>+</sup> channel

proteins, but comparison of these sequences to three different groups of *Paramecium* K<sup>+</sup> channel (PaK) proteins indicated no highly conserved regions. Searching the database with known PaK protein sequences, I found three hypothetical K<sup>+</sup> channel proteins in *P. falciparum*, *P. vivax*, and *P. yoelii*, which I aligned with three groups of PaK proteins, as well as known K<sup>+</sup> channel proteins from representatives of diverse phyla. Comparison of the protein sequences shows that *Paramecium* and *Plasmodium* have significant similarities in a stretch of 30-40 amino acids comprising the pore-loop region of the K<sup>+</sup> channel, but that they are no more similar to each other than they are to K<sup>+</sup> channel proteins from other organisms.

### REGULATORY ELEMENT ENHANCER CONSERVATION OF *Msx2*

BIOL 333B – Darren Bertagnolli - [dbertagnolli@gmail.com](mailto:dbertagnolli@gmail.com)  
Dr. Jeffrey R. Bell - [jbell@csuchico.edu](mailto:jbell@csuchico.edu)

Recently, an enhancer was discovered for *Msx2* that appears to be highly conserved amongst mammals<sup>1</sup>. This study is a continuation of this research, with the goal of illuminating the nature and extent of conservation amongst a more evolutionarily broad range of species, including birds, drawing upon modern bioinformatic tools. Findings illustrate that the enhancer is not only conserved sequentially, but spatially as well, with all of the regions occurring between 3-4kbp upstream of *Msx2*. Sequence alignment also indicates that the enhancer is many-fold more conserved than would be expected for cis-regulatory elements separated by such significant evolutionary time. Interestingly, the enhancer appears to be more widely conserved than the gene for *Msx2* itself. Results are suggestive of a developmentally important mechanism whose uniqueness warrants further investigation.

### A PHYLOGENY OF *ORYZA*, *HORDEUM*, AND *TRITICUM* USING WAXY PROTEIN SEQUENCE DATA

BIOL 333B – Kylene Lang  
Sponsored by Dr. Jeffrey R. Bell

Grasses are known to have high ploidy levels, which makes phylogenetic analyses difficult due to potential increased numbers of variant alleles. Recent studies have used the nuclear gene waxy (granule-bound starch synthase I) as the comparative gene of choice, due to its low copy number. Typically, portions of the nucleotide sequence are amplified using PCR and then used to generate phylograms. I have investigated the evolution of the waxy gene in grasses with multiple polyploid events to determine the affect of ploidy in waxy evolution. My analysis shows waxy has a complex history, particularly in *Triticum*, with many separate duplication events, probably of both chromosomes and genes. Branching within the phylogram indicates duplication events prior to polyploid events, as well as an increased rate of evolution in some copies. Several *Hordeum* and *Triticum* species show higher numbers of alleles than others. Future research includes isolation and sequencing of the complete gene for suspected *Triticum* ancestors.

## AUTOMATING THE ASSEMBLY OF A CONTIGUOUS DNA SEGMENT FROM TRACE ARCHIVE FRAGMENTS

BIOL 333B – Alan Raetz [al\\_raetz@yahoo.com](mailto:al_raetz@yahoo.com)  
Sponsored by Dr. Jeffrey Bell [jbell@csuchico.edu](mailto:jbell@csuchico.edu)

The Trace Archive is part of the National Center for Bioinformatics Information (NCBI) website that contains single read DNA fragments that have not yet been assembled into a complete genome. Each fragment is typically 600-800 base pairs of DNA and corresponds to a single sequencing read from a DNA sequencing machine. Currently there are over 360 organisms in the Trace Archive. Although it is possible to do a web-based BLAST search against this data to find a conserved sequence of interest, the matching results display a single fragment, which is unlikely to be the entire gene region. Although enough data may exist to assemble a region of interest into a contiguous segment, this requires a significant amount of manual work. To address this problem, I have created a prototype tool that attempts to assemble a contiguous DNA sequence from the Trace Archive based on an initial BLAST search. The goal is to create a web-based software application that automates the iterative BLAST searches and fragment assembly process using Web BLAST and Clustalw. Researchers could use this tool to search for genes in organisms that have not had their entire genomes assembled, but have enough genomic data available in the Trace Archive to assemble small regions of interest. I present a test case example search for a region of the gene Shaker on the malaria mosquito *Anopheles gambiae*, which has both preliminary genome data available as well as Trace Archive fragment data, allowing me to test and validate the software algorithm.

## DESIGN OF AN INDUCIBLE MITOCHONDRIAL PROTON UNCOUPLER IN *CHLAMYDOMONAS REINHARDTII*

BIOL 333B – Reed Sorenson ([rsorenson2@mail.csuchico.edu](mailto:rsorenson2@mail.csuchico.edu))  
Dr. Jeffrey R. Bell ([jbell2@csuchico.edu](mailto:jbell2@csuchico.edu)),

Hydrogen gas is a potential energy supply supplement to petroleum based energy. Hydrogen gas is produced in the green alga *Chlamydomonas reinhardtii* via ferredoxin electron donation to Fe-hydrogenase. This process is oxygen sensitive. Two hypotheses explain the oxygen sensitivity. One, the hydrogenase enzyme active site is inhibited by oxygen as evidenced by site directed mutagenesis of the gas evolution channel [1] and, two, the electron supply of photosynthetic proteins is consumed during ATP dependant photorespiration. Lee et al. demonstrated that addition of the proton uncoupler carbonyl cyanide-p-trifluoromethoxyphenylhydrazone (FCCP) decreased the oxygen sensitivity dependence and proposed designing an inducible thylakoid proton channel or ATPase subunit CF<sub>1</sub> inhibitor to effectively block thylakoid ATP synthesis [2]. A proton channel peptide or a leaky ATPase would effectively accomplish this objective. Here we report the gene design of two potential proton uncoupler protein genes targeted to the thylakoid membrane.

- [1] Seibert M, King P, Liping Z, Mets L, Ghirardi M. Molecular engineering of algal H<sub>2</sub> production. Proceedings of the 2002 U.S. DOE Hydrogen Program Review, NREL/CP-610-32405.
- [2] Lee JW, Greenbaum E. A new oxygen sensitivity and its potential application in photosynthetic H<sub>2</sub> production. Appl Biochem Biotechnol 2003; 105-8:303-13.

## SURVEY OF PROTIST GENETIC DIVERSITY IN THE HYDROTHERMAL ENVIRONMENTS OF LASSEN NATIONAL VOLCANIC PARK, CALIFORNIA

Patricia B. Brown  
Committee Chair: Dr. Gordon V. Wolfe

**Background:** Recent discovery of novel microbial eukaryote genetic diversity in acidic or anoxic environments suggests that protists are more adaptable and diverse than previously thought. We surveyed the hydrothermal environments at Lassen Volcanic National Park (LVNP) in Northern California for 18S rDNA diversity. **Methods:** We collected biofilms, sediment and water from Bumpass Hell, Sulfur Works and Devil's Kitchen. All sites had diverse pools, streams and mud pots with temperatures 15-85 C and pH 1.7-5.8. Many contained visible algal mats and biofilms. We compared community DNA extraction with a modified CTAB-chloroform purification and the UltraPure soil extraction kit (MoBioLabs). Extracted DNA was amplified with eukaryal 18S rRNA primer sets. We used denaturing gradient gel electrophoresis (DGGE) to compare community complexity and extraction techniques, and sequenced rRNA genes from clone libraries for phylogenetic analysis. **Results:** DGGE showed that DNA extraction methods gave similar community fingerprints. We were able to amplify eukaryotic SSU rRNA genes from almost all samples up to 68° C. Cloning and sequencing showed a diverse collection of eukaryotic rDNA genes dominated by chlorophytes and stramenopiles, with some sequences similar to those found in other acidic environments. **Conclusions:** Molecular characterization shows eukaryotic SSU rRNA diversity at LVNP hydrothermal environments is dominated by autotrophic acidophilic protists.

## CELLULAR LOCALIZATION OF POLYUNSATURATED LONG-CHAIN NEUTRAL LIPIDS IN *EMILIANIA HUXLEYI* AND *ISOCHRYSIS GALBANA* (HAPTOPHYTA)

Matthew Eltgroth ([eltgroth@hotmail.com](mailto:eltgroth@hotmail.com)) Gordon V. Wolfe  
Committee Chair: Dr. Gordon V. Wolfe ([GWolfe2@csuchico.edu](mailto:GWolfe2@csuchico.edu))

A number of prymnesiophyte algae are known for their ability to produce polyunsaturated long-chain (C31-39) alkenones, alkenoates, and alkenes (PULCA). Long used for paleothermometry, the physiological and ecological roles of these unique neutral lipids remain largely unknown, as does their biosynthesis and cellular location. Using the lipophilic dye Nile Red and OTO-TEM, we show that *Emiliania huxleyi* and *Isochrysis galbana* possess neutral lipid bodies that also associate with chloroplasts. Spectrofluorimetric quantification of these vesicles shows a strong correlation to the amount of PULCA as measured by thin layer chromatography (TLC). Lipid vesicles purified by ultracentrifugation consist predominantly of PULCA. PULCA are associated with other cell fractions as well, suggesting a role for other organelles in the metabolism of these molecules. Our results support recent work showing that PULCA function analogously to other algal storage lipids such as triacylglycerides.

## EXPRESSION OF GLUTAMATE RECEPTOR NMDA 2A/2B SUBTYPE AFTER HIPPOCAMPAL DEAFFERENTATION

Jennifer J Evans

Committee Chair: Dr. Jonathan R. Day

Neurodegeneration induced by entorhinal cortex (EC) lesion induces reactive synaptogenesis in the ipsilateral hippocampus. The remaining afferent projections undergo extensive sprouting similar to that seen in the degeneration of the Alzheimer's type. Studies of synapse associated protein immunoreactivity and growth factor receptor expression suggest the loss of afferent projections from the basal forebrain via the fornix and the entorhinal cortex induces an exaggerated synaptogenic response. However, glutamate receptor reorganization after combined entorhinal cortex and fimbria fornix (EC/FF) lesion has not been compared to reorganization after EC alone. To address this, adult Sprague-Dawley rats received combined EC/FF lesion, EC lesion, or fimbria fornix (FF) lesion, and were sacrificed 4 to 42 days post lesion. Sucrose embedded sections were cut at 30  $\mu$ m with a sliding microtome and immunolabelled for glutamate NMDA 2A/2B subtype receptors. Preliminary results for the combined EC/FF lesion show differential NMDA 2A/2B expression compared to the EC and FF lesions alone. The pyramidal cells of the CA1 showed increased immunoreactivity 21 days after EC lesion to EC/FF or FF lesions. The CA3 and DG showed similar increases. However, after 42 days NMDA 2A/2B receptor immunoreactivity in EC/FF lesion was greatly increased in the CA1, CA3, and DG compared to control lesions. The EC and FF lesions displayed limited immunoreactivity in these same regions. This suggests that the combined EC/FF lesion showed a robust, albeit delayed, synaptogenic response that might have important pathological consequences.

## A COMPARISON OF THE AQUATIC MACROINVERTEBRATE COMMUNITIES OF RESTORED AND NATURAL WETLANDS OF THE SACRAMENTO VALLEY, CALIFORNIA

Mariah Garr [mariahgarr@yahoo.com](mailto:mariahgarr@yahoo.com)

Committee Chair: Dr. Michael Marchetti, CSU, Chico

There has been an increasing awareness of the loss of freshwater wetland habitat and recognition of the need for restoration of this dwindling resource. However, it is not clear whether restored wetlands function like the natural systems they are intended to replace. One of the first steps to quantifying restored wetland function is to examine the aquatic community structure between natural and restored sites. Aquatic macroinvertebrates are one of the most appropriate biological indicators of ecosystem function because they are directly affected by the physical and chemical integrity of their surrounding environment, and therefore likely indicators of restoration success or failure. To compare the macroinvertebrate communities of natural and restored wetlands, I sampled the aquatic macroinvertebrates quarterly across a chronosequence of four restored and one natural freshwater wetland in Butte and Colusa counties. Results suggest the aquatic macroinvertebrate communities in restored wetlands vary according to age and that the older a restored wetland is, the more closely it resembles a natural wetland community.

## PROTEOMIC ANALYSES OF THYLAKOIDS USING LIQUID CHROMATOGRAPHY MASS SPECTROMETRY REVEAL CHANGES IN PROTEIN EXPRESSION PATTERNS AND POST-TRANSCRIPTIONAL ALTERATIONS IN FE DEFICIENT *ARABIDOPSIS THALIANA*

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High pressure reverse-phase liquid chromatography coupled with electrospray-ionization mass spectrometry (LCMS) was used to separate and identify thylakoid membrane proteins from *Arabidopsis thaliana* plants grown under iron deficiency. Provisional identity of the gene products (proteins) was based upon coincidence of measured intact masses with the calculated masses from the genomic sequence. Use of intact masses allows post-transcriptional changes, such as RNA-editing, oxidations, phosphorylations, glycosylations, and cleavages to be identified. Significant differences in protein expression patterns and post-transcriptional alterations between control and iron deficient samples were identified. Intact chloroplasts from iron deficient plants were isolated with percoll and optiprep osmoticum density gradients. Percoll has been suggested to be toxic to cells; however, measurements of oxygen evolution were similar in thylakoids from intact chloroplasts isolated by the two methods. The hydroponic system developed for the nutritional studies will also be discussed.

## ISOLATING AN OLFACTORY-RELATED GENE IN *DROSOPHILA MELANOGASTER*

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DEET (Diethyl-meta-toluamide) is a commonly used topical insect repellent, but its molecular mechanism of action is unknown. Researchers previously created a mutant strain of *D. melanogaster* that is largely insensitive to the repellent effects of DEET, yet has normal responses to other odorants. We have used recombination mapping to locate a region on the X chromosome likely to be involved in the DEET repellency by crossing the DEET-insensitive strain to flies with the visible X chromosome markers yellow, singed, garnet, and forked, and used a simple behavioral assay to score the response of the F2 recombinant male offspring to DEET. Our recombination data shows strong linkage of this trait to the forked marker, and we present preliminary data on the candidate gene Shaker, which is one map unit away from forked. Shaker is a voltage-gated potassium channel that has previously been determined to be involved in olfactory responses. Shaker mutants display the DEET-insensitive phenotype in our assay. When we use the potassium ion channel blocker triethylhexylammonium bromide as a repellent odorant, we found that the DEET-insensitive mutant is also insensitive to this odorant compared to control strains. We present our preliminary DNA sequencing data of the pore region of Shaker in both the mutant and wild-type strains, as well as F1 cross data of female Shaker knockout mutants with the DEET-insensitive mutant.



## DISTRIBUTIONAL AND SPATIAL COMPARISONS OF FISH LARVAE AND JUVENILES IN THE LOWER FEATHER RIVER, CALIFORNIA

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This study provides a comparison of fish larvae and juveniles sampled with a surface net and a benthic net and provides insight into how gear types affect perceived assemblage structure and species abundance. In addition, the unusual design of flow-release structures from the Oroville-Dam Thermalito Complex into the California Central Valley's lower Feather River provided a unique setting to evaluate the relative importance of flow regime for fish larvae. My objectives were to (1) determine which species/taxa were sampled by surface and benthic gear types and in what numbers; and (2) evaluate whether there were distributional and compositional differences among species between flow regimes. A total of 4,207 specimens (3,337 fish and 870 eggs) were sampled at three sites in the lower Feather River over a 26-week period in 2003. The surface net caught 2.7 times more individuals than the benthic net. Prickly sculpin *Cottus asper*, Sacramento sucker *Catostomus occidentalis* and wakasagi *Hypomesus nipponensis* were the most abundant species in both gear types. The surface net sampled four species that the benthic net did not while the benthic net sampled six species that the surface net did not. The most upstream site had 11 species, the middle site had nine species (and the highest total number of individuals) while the most downstream site had eight species. Notably, even though more fish were obtained with the surface net, the combination of both sampling gears provides a more accurate picture of fish larvae and juvenile composition, distribution, and abundance.

## NO APPARENT BENEFIT OF LOW GLYCEMIC INDEX MEALS ON THE POSTPRANDIAL LIPID RESPONSE IN WOMEN WITH OBESITY OR INSULIN RESISTANCE

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The goal of this study was to determine if the type of carbohydrate [low vs. high glycemic index (GI)] influences the postprandial lipid response in obesity or insulin resistance. Subjects ( $27 \pm 9$  years) were 15 normal weight (lean) and 26 abdominally obese women. Using a randomized cross-over design, subjects consumed two breakfast meals, high (66) and low (45) GI, after fasting on two occasions. Blood samples were collected prior to each meal and 1, 3, and 5 h after and analyzed for total triglyceride (TG), chylomicron-TG (CM-TG), HDL-cholesterol (HDL-C), insulin, and apoprotein C-3. The insulin area under the curve (AUC) after the high GI meal was significantly ( $p < 0.04$ ) greater for both obese and lean subjects. The GI did not affect the total TG AUC or CM-TG AUC in obese or lean subjects. Subjects were separated into insulin sensitive [ $<10 \mu\text{IU/ml}$ ] and insulin resistant [ $>14 \mu\text{IU/ml}$ ] groups based on average fasting insulin levels. The average insulin AUC was nearly 2.5 fold higher; total TG/HDL-C ratio was 2.5-fold higher; the average total TG AUC was 2-fold higher; and the average apo C-3 was slightly higher ( $p=0.08$ ) in the resistant group. However, the insulin sensitive group had a significantly ( $p < 0.02$ ) reduced postprandial total TG response after the high GI meal, most likely due to the greater insulin response. In conclusion, subjects with insulin resistance have an exaggerated postprandial TG response which may be partially due to elevated apo C-3, a known inhibitor lipoprotein lipase. But, these data do not support a benefit of low GI meals in obese or in those with insulin resistance.

## PRESCHOOLERS IN RURAL NORTHERN CALIFORNIA

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The purpose of this study was to explore ethnic differences in dietary patterns among low income preschoolers (3-5 years) in rural Northern California. Subjects were 458 children enrolled at the Yuba Sutter Head Start Program. A dietary evaluation instrument was completed by staff and a parent or guardian. Ethnic distribution was 41% Hispanic, 36% White, 12% Asian, 5% Black and 6% other. 38% of children had a BMI  $> 85^{\text{th}}$ %. 89% of households were at or below poverty level, 12% of the families reported running out of food at times, and 8% lacked cooking equipment. Significant ( $p < 0.05$ ) ethnic differences in dietary patterns are as follows: Blacks consumed more "other" milk products than Asians and more meat and nuts and seeds than Hispanics and Whites. Asians ate more rice than Blacks, Hispanics and Whites. Even though a majority (= 76%) of all ethnicities reported meeting 5 servings of fruits and vegetables per day, Asians had the highest consumption of vitamin C-rich fruits and vegetables than other ethnic groups. Asians also consumed more vitamin A-rich foods than whites or "other" and more of the other fruits and vegetables than whites. In agreement, more Asians met or exceeded the recommendation for bread group foods (49%), fruits and vegetables (92%) and vitamin A-rich foods (90%) than other ethnic groups. Hispanics consumed more sugary-foods like doughnuts and cookies than Whites. Sugary-foods were associated with BMI. A better understanding of dietary patterns can help nutrition educators design ethnically appropriate programs to improve health and well being.

## FOOD INSECURITY AMONG NORTHERN CALIFORNIA ELDERLY

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Rural Northern California is experiencing rapid growth in the elderly population as baby boomers approach retirement age and urban retirees migrate to rural communities. Elderly in rural areas tend to experience more health problems, reduced access to services, and higher rates of poverty which is the main cause of food insecurity. The objective of this study was to assess food insecurity among rural Northern California elderly and identify within or between county differences based on demographic variables and participation in food assistance programs. A convenience sample of 266 male and female seniors ( $77 \pm 8.9$  years) was recruited from senior nutrition sites and health fairs. Subjects completed a survey assessing demographics, health status, and indicators of food insecurity. 86% of subjects were Caucasian, representative of rural Northern California demographics. 42% of subjects reported annual incomes of less than \$15,000. Eight percent of subjects reported not always having enough money to buy the food they need. Nine percent of subjects reported worrying whether their food would run out before getting money to buy more and having to choose between buying food and paying rent, utilities and/or medications in the last twelve months. Three percent of subjects reported experiencing hunger in the last 12 months but did not eat because of financial constraints. Food insecurity may exist among rural Northern California elderly, especially among low-income seniors. Further research is warranted given the anticipated graying of the Northern California population in order to ensure adequate access to nutrition services in this at-risk population.