School of Science and Mathematics

Student Research Poster Display

Caputo Hall Lobby

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- BIOLOGY •
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Note: The names of Millersville University faculty advisors are designated by an asterisk (*) in the abstracts.

Biology

1. Insight into the Evolutionary Relationship between Short-chain Isoprenyl Diphosphate Synthases, Terpene Synthases and Triterpene Synthases.

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Short-chain isoprenyl diphosphate synthases (IDS), members of prenyltransferases, catalyze the synthesis of the key intermediates for the biosynthesis of various terpenes. Terpene synthases (TPS) catalyze the synthesis of monoterpenes, sesquiterpenes and diterpenes, while triterpene synthases (TTPS) synthesize triterpenes. So far the evolutionary/phylogenetic relationship between these three mechanistically related families remain unclear. Also unclear is the evolutionary relationship of plant and microbial IDS, TPS and TTPS. A genome-wide identification of IDS, TPS and TTPS genes, their detailed structural analysis and chromosomal localization/gene clustering as well as phylogenetic analysis of these three gene families were conducted in both Arabidopsis and cyanobacteria. An evolutionary model has been developed as a result of these analyses. Our results suggest that the three gene families appear to have evolved in parallel from a common ancestor in both Arabidopsis and cyanobacteria, via tandem duplication and divergence, domain deletion, and domain fusion. Each family appears to have a common proximate ancestor in Arabidopsis, as well as in the IDS and TPS (but not TTPS) of cyanobacteria. Cyanobacteria TTPS have likely evolved from two different but related proximate ancestors. Arabidopsis and cyanobacteria GGPPS exhibit higher homology to each other than to the other IDS in the same species as the most conserved group among the three families. Most other subfamilies exhibit species-specific homology to each other in this study. Our results provide novel insight into the evolution, relatedness and function of short-chain IDS, TPS and TTPS.

2. A Preliminary Study on the Nesting Ecology of Broad-winged Hawks (*Buteo platypterus*) at Hawk Mountain Sanctuary

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The Broad-winged Hawk (*Buteo platypterus*) is a small raptor that breeds in mixed- deciduous forests in northeastern North America and migrates each winter to Central and South America. Although the Broad-winged Hawk (BWH) population is continuing to expand, little information has been recorded on their nesting and breeding behavior. A pilot observational study was conducted on a pair of BWH's nesting at Hawk Mountain Sanctuary (HMS) in Kempton, PA, from April – August, 2013. The objectives of this study were to quantitatively and qualitatively describe the nesting ecology of adult BWH and juveniles. Approximately 27.5 hours were spent searching for BWH nests. Nest site data, e.g., tree type, height, nest size and nest site habitat were characterized. Adult/juvenile nesting behaviors were observed and catalogued over 67.72 hours from a ridge about 50 meters away from the nest tree. Nest-building behaviors that were recorded included sprig delivery, prey delivery and adult attentiveness. We found one nest

located in a Chestnut-Oak (*Quercus prinus*) tree. The nest was located approximately 17.06 meters from the base of the tree. We estimated the nest dimensions to be approximately 71.12 cm (length) x 30.48 cm (width) x 22.86 cm (depth). Nest-site habitat that included distance to water and distance to forest opening, supported previous findings and indicated that BWH adults were selective in choosing nest sites. We found that adult BWH delivered more bark than any other nest material. Of the prey taxa delivered to the nestlings, more rodents were delivered to the nest than other prey observed. Adult attentiveness was characterized as time spent at the nest during the total time of observations. Approximately 13.9 % of the time adults were attending to the nest or juveniles during the observational period. This preliminary study has provided valuable nesting ecological/behavioral information that will aid in the conservation of Broad-winged Hawks.

3. Chemical Detection of Human Baiting Activity for White-tailed Deer

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Due to the potential negative impacts of baiting on white-tailed deer, and the philosophy of fair chase, many of the United States have outlawed or restricted the use of hunting over bait. In addition, the issue of illegal take of wildlife (i.e., poaching) has been increasing in the United States as well as internationally. The objective of this study was to determine whether baiting activity on white-tailed deer can be determined by analyzing the chemical composition of deer feces and to determine if unique chemical signatures are left by commercial baits (i.e., baits purchased at a local retailer). We implemented a variety of experiments to determine if there are any unique chemical markers in either soil or deer feces that would enable a conservation officer to determine whether an area has been illegally baited. Our experiments have indicated that a variety of experimental techniques do not provide adequate support for determining a baited area, including the use of an Advanced Agricultural Soil Testing kit by LaMotte®, Atomic absorption spectrophotometry, Gas Chromatography-Mass Spectrometry, Thin Layer Chromatography (TLC), chloride ion probe, and carbon dioxide probe. However, when we reacted acetic acid with a plot of soil saturated with deer bait we identified that a bubbling reaction occurs due to the production of carbon dioxide. This simple test could be used to identify areas where illegal baiting for white-tailed deer has occurred. However, results from the other tests were inconclusive.

4. Uncertainty in Population Estimates for Endangered Animals and Improving the Recovery Process

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United States recovery plans contain biological information for a species listed under the Endangered Species Act and specify recovery criteria to provide basis for species recovery. The objective of our study was to evaluate whether recovery plans provide uncertainty (e.g., variance) with estimates of population size. We reviewed all finalized recovery plans for listed terrestrial vertebrate species to record the following data: (1) if a current population size was given, (2) if a measure of uncertainty or variance was associated with current estimates of population size and (3) if population size was stipulated for recovery. We found that 59% of

completed recovery plans specified a current population size, 14.5% specified a variance for the current population size estimate and 43% specified population size as a recovery criterion. More recent recovery plans reported more estimates of current population size, uncertainty and population size as a recovery criterion. Also, bird and mammal recovery plans reported more estimates of population size and uncertainty compared to reptiles and amphibians. We suggest the use of calculating minimum detectable differences to improve confidence when delisting endangered animals and we identified incentives for individuals to get involved in recovery planning to improve access to quantitative data.

5. Regulation of Neural Crest Cell Emigration in Turtle (*Trachemys scripta*) Embryos Smith, Matt; Gochnauer, Heather and Cebra-Thomas, Judith*

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The plastron is the portion of the turtle shell that covers the turtle's belly. The development of the turtle plastron continues to be controversial. The plastron bones appear to be formed from a specialized cell type known as trunk neural crest, which has not previously been shown to form bone. Neural crest precursor cells stay at the neural plate border during neurulation and after neural tube closure, come to reside in the dorsal neural tube. Neural crest development is controlled by a gene regulatory network. This premigratory neural crest precursor population expresses characteristic transcription factors including Snail2, FoxD3, Sox9, and Sox10.

The period of time over which trunk neural crest cells emigrate from the neural tube appears to be much longer in turtle embryos than in other amniote embryos. There appears to be a second, late emigrating skeletogenic group of trunk neural crest cells in turtle embryos that are not found in chicks or mice. At this time, it is not known whether the region of premigratory cells in the dorsal neural tube persists in a dormant phase during the period when neural crest cells are not emigrating, or whether the ability to generate neural crest cells is re-induced in the older turtle embryos. To address this question, we investigated the expression of a premigratory neural crest marker, the *Snail2* gene, in the neural tube of turtle embryos at different stages of development. If the expression of this gene persists throughout all stages, this will suggest that the premigratory region is maintained, and that the lack of neural crest cell migration could be due to the lack of a supportive environment. In contrast, if this gene is only expressed during the periods of neural crest cell migration, then the second wave of neural crest cell migration would require a second inductive signal not found in chick embryos.

CHEMISTRY

6. Characterization of Halogenases within the Malbrancheamide Biosynthetic Pathway

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Malbrancheamide is a compound isolated from a fungus, Malbranchea aurantiaca, that has demonstrated chemotherapeutic potential through its use as a calmodulin antagonist. The halogen substituents located on the indole ring differentiate Malbrancheamide from the rest of the bicyclo[2.2.2]diazaoctane family, and they are critical to its biological activity. Consequently, this investigation was aimed at determining and characterizing the enzymes involved in the halogenation step of the Malbrancheamide biosynthetic pathway. It has been hypothesized that a flavin-dependent halogenase, as well as a flavin-reductase are required for the dichlorination of Premalbrancheamide in two sequential steps to form Malbrancheamide. MalA, a halogenase from the fungal gene cluster consisting of seven genes that are responsible for the production of Malbrancheamide, was expressed alongside previously identified putative halogenase, MalHal, and reductase, MalRed. Additionally, phaC, which codes for a known flavin-reductase from Pseudomonas aeruginosa, was also expressed and tested in these reactions in order to determine the halogenase specificity for the reductase that it interacts with. Through testing the isolated enzymes on various substrates (Tryptophan, Premalbrancheamide, Malbrancheamide B, and Isomalbrancheamide B), the details behind the chlorinations in the pathway may be revealed. The product formation was monitored through LC/MS analysis of the reaction solution and it was determined that both MalA halogenases were able to chlorinate and brominate Malbrancheamide B as well as Isomalbrancheamide B.

COMPUTER SCIENCE

7. Exploring the Theory of Algorithmic Self-Assembly

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Self-assembly is a fundamental phenomenon in nature, expressing itself in crystal growth, viral replication, and cell reproduction. It is a process characterized by an automated assembly of subcomponents into a larger structure, often in a highly efficient and effective manner. In recent decades technology has advanced to the point of enabling the construction of arbitrary self-assembling systems on a nanoscale, with a broad potential for practical application. On the theoretical side, a number of models have emerged that have catalyzed advances in practical results, as well as stimulated a wealth of interdisciplinary research combining mathematics, computer science, chemistry and biology. Our research aims at surveying the present state of this field, in particular focusing on the theoretical computer science involved. Some of the topics being explored include the various models in use, the criteria necessary for universal computation, how algorithms manifest as patterns and structures in assemblies, and complexity analysis of assembly systems. An additional aim of this research is to identify some open problems in the field which could serve as candidates for undergraduate level thesis work.

8. Obtaining Real-time Weather Data from a Vehicle's CAN Bus

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The purpose of this project is to develop a system to collect and organize vehicle diagnostic data to be used for weather prediction. The data collected can include windshield wiper status, fog light status, external air temperature, and barometric pressure.

In order to collect the necessary data, we built a vehicle interface device (VI) using a chip KIT microcontroller and network shield to interface with the vehicle's CAN bus network. The VI will use the OpenXC library to read CAN signals and send the data to a host device such as a connected laptop, or over Bluetooth to an Android-powered device.

Because the format of individual CAN messages is proprietary information set by vehicle manufacturers, we initially used the VI to determine the necessary message ID numbers required to select the data we needed. This was done by programming the VI to output the message ID and data segments of all CAN messages it received, along with a timestamp of when the message was read. We then sorted the list of CAN messages by message ID and plotted each data segment against its timestamp, in order to match each recorded message ID to the information it represented. With the necessary CAN message IDs determined, we included the signal information in the VI firmware provided by the OpenXC library, allowing the VI to request what data we needed.

EARTH SCIENCES

9. The Ocean's Surface Optical Properties

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This study is about how sunlight is attenuated through the ocean's suface layer in the North Atlantic Ocean. The attenuation coefficient of light in the 490 nm band (K490) is related to the concentration of the major pigment found in phytoplankton, chlorophyll a ([Chl a]), in the upper ca. 100 meters of the ocean. We make the assumption that [Chl a] in seawater is a suitable proxy for the biomass of the phytoplankton, and test the hypothesis that the main source of K490 variability is phytoplankton biomass (i.e., "Case I waters"). [Chl a] showed a strong non-linear relationship to KPAR, and was similar to published model results developed using much larger datasets over broad regions of the surface ocean is controlled by the distribution of pigmented phytoplankton cells. When higher concentrations of phytoplankton are present, sunlight is attenuated more strongly with depth, thus reducing the thickness of the ocean's productive layer. The nature of other suspended and dissolved materials in seawater that may have also contributed to the patterns in K490, and to the scatter in the [Chl a] vs K490 relationship, is also discussed.

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An asterisk (*) denotes the SCMA Faculty Advisor for the student research