



# IN VIVO

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## 36th Annual Fall MACUB Conference

Saturday, November 1, 2003

Wagner College

Staten Island, New York

Conference Theme: *“When Science Becomes Controversial:  
Professional Ethics and Research Limits”*

**“The Quiet Battleground:  
Environmental Health Issues and the  
Role of Science Ethics”**

will be presented by:

**Dr. Joann M. Burkholder**

PEW Fellow and Director, Center for Applied  
Aquatic Ecology



Dr. Joann M. Burkholder is Professor of Aquatic Botany and Marine Sciences at North Carolina State University. Her research over the past 20 years has emphasized the nutritional ecology of algae, dinoflagellates, and sea grasses, especially the effects of cultural eutrophication on algal blooms and sea grass disappearance. Since co-discovering the toxic dinoflagellate, *Pfiesteria piscicida*, in 1991, she has been working to characterize its stimulation by sewage and other nutrient enrichment, and to determine the range of its impacts on commercially important finfish and shellfish in North Carolina estuaries and aquacultural facilities. Dr. Burkholder is also actively engaged in regional education and outreach efforts on water quality, using *Pfiesteria* as an example of the unanticipated results of coastal water quality degradation. To date she has presented more than 150 outreach seminars to non-scientists, from sixth graders to adults, and she has discussed her findings with industry stakeholders and the media to further spread information. Burkholder has also developed a sampling program as a science education tool for use at children's camps, and she has helped guide and write policy for safe sampling of *Pfiesteria*-related fish kills and disease events, and for closing/opening of affected toxic outbreak areas.

**“What Does Science Really Know About  
The Mind?”**

will be presented by:

**John Horgan, Jr.**

Science Writer and author of “The End of  
Science. Facing the Limits of Knowledge in the  
Twilight of the Scientific Age”



John Horgan is a freelance journalist and author. A former senior writer at Scientific American (1986-1997), he has also written for numerous publications around the world. His latest book is *Rational Mysticism: Dispatches from the Border Between Science and Spirituality*, published by Houghton Mifflin in January 2003. He discusses the hope of some scientists that mysticism could yield knowledge that complements or transcends science. In his first book, *The End of Science: Facing the Limits of Science in the Twilight of the Scientific Age*, Broadway Books, 1996, he interviewed leading physicists, cosmologists, evolutionary biologists, neuroscientists and other scientists. to present an interesting, controversial perspective on the limits of knowledge and of science.

His awards include the American Psychiatric Association Certificate of Commendation for Outstanding Reporting on Psychiatric Issues (1997); the Science Journalism Award of the American Association for the Advancement of Science (1992 and 1994); and the National Association of Science Writers Science-in-Society Award (1993). In 1994 he received an "excellent" rating in the Forbes Media Guide: A Review of the Nation's Most Influential Journalists.

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**Instructions for Authors**

***IN VIVO*** is published three times yearly during the Fall, Winter, and Spring. Original research articles in the field of biology in addition to original articles of general interest to faculty and students may be submitted to the editor to be considered for publication. Manuscripts can be in the form of a) full length manuscripts, b) mini-reviews or c) short communications of particularly significant and timely information.

Articles can be submitted electronically to [invivo@mec.cuny.edu](mailto:invivo@mec.cuny.edu) or mailed as a printed copy (preferably with a diskette that contains the file) to the Editorial Board at Medgar Evers College. All submissions should be formatted double spaced with 1 inch margins. The title of the article, the full names of each author, their academic affiliations and addresses, and the name of the person to whom correspondence should be sent must be given. As a rule, full length articles should include a brief abstract and be divided into the following sections: introduction, materials and methods, results, discussion, acknowledgments and references. Reviews and short communications can be arranged differently. References should be identified in the text by using numerical superscripts in consecutive order. In the reference section, references should be arranged in the order that they appeared in the text using the following format: last name, initials., year of publication. title of article, journal volume number: page numbers. (eg. - <sup>1</sup>Hassan, M. and V. Herbert, 2000. Colon Cancer. *In Vivo* **32**: 3 - 8). For books the order should be last name, initial, year of publication, title of book in italics, publisher and city, and page number referred to. (eg. - Prosser, C.L., 1973. *Comparative Animal Physiology*, Saunders Co., Philadelphia, p 59.). Abbreviations and technical jargon should be avoided. Tables and figures should be submitted on separate pages with the desired locations in the text indicated in the margins.

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# **Save the Date**

## **36th Annual Fall MACUB Conference**

**Saturday, November 1, 2003**  
**Wagner College**

# Employing The GenBank And TIGR Databases For Phylogenetic And Functional Gene Analysis Of Putative ILR1 and IAR3 Hydrolase Homologs In Plants

by

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## ABSTRACT

GenBank is the repository of all DNA sequences available to the scientific community, while the Institute for Genomic Research (TIGR) is a major center of genomic sequencing and functional gene annotation. We have found that we can employ these two sites to obtain DNA sequence data for use in model studies of plant phylogenetics and molecular evolution. Our laboratory studies the ILR1-like family of hydrolase genes initially isolated in the model plant *Arabidopsis*; these gene products control active levels of the plant hormone indole-acetic-acid. We are interested in how this family of genes has evolved in dicot and monocot species genetically distant from *Arabidopsis*. We have employed the GenBank and TIGR databases to retrieve putative homologs for the ILR1 and IAR3 hydrolase genes in selected monocots and dicots. The relationships between these orthologous sequences were then assessed employing phylogenetic analysis programs to examine molecular evolution and phylogeny. Our studies indicated clear evolutionary differences at the DNA and protein sequence levels between the monocots and dicots studied for the ILR1 orthologs. By comparison, the IAR3 orthologs showed less complex evolution in DNA and protein sequences, demonstrating more conservation among dicots and monocots and suggesting the physiological importance of a conserved IAR3 hydrolase.

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## INTRODUCTION

GenBank is a collection of all the publicly available DNA sequences provided by the National Institute of Health's genetic sequence database ([www.ncbi.nlm.nih.gov/80](http://www.ncbi.nlm.nih.gov/80))<sup>1,2</sup>. GenBank databases are utilized to obtain DNA sequences and perform searches to obtain homologous gene sequences. The Institute for Genomic Research (TIGR) is a research institute that focuses on structural, functional and comparative analysis of genomes and gene products<sup>3</sup>. Both GenBank and TIGR contain databases where many gene sequences have been provided in the form of Expressed Sequence Tags (ESTs). These ESTs are DNA sequences that have been derived from cDNA libraries and represent expressed transcripts. They are present in the databases as either partial or full sequences. Many of these sequences have been partly characterized for function by TIGR or GenBank using sequence homology to other genes with known function, but most

have not been isolated or entirely characterized because of the great volume of work involved.

We have found orthologous (i.e. interspecific) members of gene families in the TIGR and GenBank databases that may be of interest to plant physiologists and evolutionary biologists, but which remain uncharacterized and "buried" within the databases. We have attempted here to demonstrate the great value of these forgotten sequences to the study of molecular evolution and gene families.

Molecular phylogenetic methods have become common in recent years to examine the associations between species<sup>4,5,6</sup>. These molecular methods employ examination of the dynamic changes occurring between DNA sequences of organisms and calculation of the statistical significance of those alterations. Initially these DNA changes were examined indirectly. One of the oldest molecular methods compared molecular weight changes in isoenzymes using SDS-polyacrylamide gel

electrophoresis. More recently these types of studies have been refined to more directly examine polymorphic changes in large, highly plastic segments of DNA, such as microsatellite regions; these polymorphisms are investigated using the Polymerase Chain Reaction and gel electrophoresis or Restriction Fragment Length Polymorphism analysis. More accurate phylogenetic methods sequence the DNA and compare altered sequences directly. The most current innovation in phylogenetic analysis employs the massive databases of DNA and protein sequences now available to researchers at GenBank and TIGR.

Our laboratory is interested in the ILR1-like hydrolase gene family that controls free Indole-3-acetic acid (IAA) concentrations in *Arabidopsis thaliana*. Indole-3-acetic acid is an important growth hormone<sup>7,8,9,10</sup> that stimulates cell division, cell elongation, differentiation in plant tissue and gene expression. This hormone also affects vascularization, geotropism, fruit development, flower development, and apical dominance. On average, 95% of all plant IAA is present in a conjugated, inactive form either amide-linked to an amino acid or ester-linked to a sugar.

Amide conjugates account for the bulk of conjugated IAA in dicots studied to date. IAA-Aspartate (IAA-Asp) and IAA-Glutamate (IAA-Glu) have been identified as natural conjugates in cucumber<sup>11</sup> and soybean<sup>12</sup>. IAA-Alanine (IAA-Ala) has been detected in *Picea abies*<sup>13</sup>. IAA-Ala, IAA-Asp, IAA-Leucine (IAA-Leu), and IAA-Glu have been detected in *Arabidopsis thaliana*<sup>14,15,16</sup>.

Sugar ester conjugates dominate in monocots and include IAA-inositol, IAA-myoinositol, and IAA-glucose<sup>17,18,19</sup>. These sugar conjugates have been identified in many grain species for the last 60 years<sup>17</sup>, though the IAA-ester hydrolase enzymes controlling the free-IAA concentrations have not yet been isolated.

Conjugation of IAA has been shown to act as a homeostatic control to rid plants of excess auxin, a protective mechanism against overproduction of auxin, and as a possible aid to transport during germination<sup>7,8,9,20</sup>.

Several IAA amidohydrolases have been isolated from *Arabidopsis thaliana*<sup>21,22</sup>. The enzymatic activities of these enzymes allow cleavage of various amino acid-type conjugates. Each enzyme has a different IAA conjugate specificity. The ILR1, ILL1, ILL2, ILL3 and ILL5 enzymes are able to cleave IAA-Phenylalanine and IAA-Leucine, while the IAR3 enzyme is able to cleave IAA-Aspartate. Another ILR1-like family member, sILR1, with an IAA-Glycine substrate specificity has also been isolated from the related species *Arabidopsis suecica*<sup>20</sup>.

We have employed the ILR1-like family of genes as a model to study molecular evolution. Specifically, we have used DNA and protein homology to examine molecular change among various dicots and monocots.

Studies of molecular change can give us an indication of how important genes are to the plant kingdom and how much change species tolerate in genes that are required for species survival. Additionally, this type of study can be used as an analytic tool in the functional assignment of genes and proteins<sup>2</sup>. Enormous amounts of sequence data are presently available through GenBank and TIGR and more will be forthcoming in the future. Many of these genes have been putatively assigned functions based on simple homology. More in-depth phylogenetic comparisons of orthologs of unknown function against characterized gene products can give genomics researchers greater confidence in assignment of protein function.

In this study we used TIGR and GenBank databases to identify ten monocot and dicot species having homologous DNA and protein sequences to the *Arabidopsis* sILR1, ILR1 and IAR3 genes. This study is designed to give us a better understanding of how genes

**Table 1. Plant species used in this study**

Species	Accession Number	Homologous to
<i>Arabidopsis thaliana</i>	AY-081499	ILR1
<i>Arabidopsis suecica</i>	AF-468012	ILR1
Barley	TC-36547	ILR1
Maize	TC-113408	ILR1
Potato	BG-598945	ILR1
rice	TC-91825	ILR1
sorghum	TC-42893	ILR1
tomato	TC-107732	ILR1
wheat	TC-48711	ILR1
wheat	TC-55038	ILR1
wheat	TC-49296	ILR1
<i>Arabidopsis thaliana</i>	AF-081067	IAR3
<i>Lotus japonicus</i>	TC-966	IAR3
<i>Medicago truncatula</i>	TC-43941	IAR3
<i>Medicago truncatula</i>	TC-43940	IAR3
<i>Medicago truncatula</i>	BE-123972	IAR3
potato	TC-50186	IAR3
potato	TC-47432	IAR3
potato	TC-50170	IAR3
rice	TC-83230	IAR3
soybean	TC-120817	IAR3
soybean	TC-121750	IAR3
tomato	TC-105095	IAR3
tomato	TC-99719	IAR3
wheat	TC-52572	IAR3

change over time between large populations of plants that are more closely or distantly related.

## MATERIALS AND METHODS

### Sources of ILR1 and IAR3 sequence data.

The GenBank ILR1 DNA sequences used for ortholog searches were *Arabidopsis thaliana* (Accession #AY081499), *Arabidopsis suecica* (Accession #AF468012) (Table 1). DNA Ortholog searches were conducted using the resident BLAST search engine on the TIGR website ([tigrblast.tigr.org/tgi](http://tigrblast.tigr.org/tgi))<sup>23</sup>.

Homologous ILR1 sequences found on TIGR included corn (*Zea mays*) (Accession #TC113408), barley (*Hordeum vulgare*) (Accession #TC36547), wheat (*Triticum aestivum*) (Accession #'s TC48711, TC55038 and TC49296), sorghum (*Sorghum bicolor*) (Accession #TC42893), tomato (*Lycopersicon esculentum*) (Accession #TC107732) and potato (*Solanum tuberosum*) (Accession #BG598945) (Table 1).

The *Arabidopsis thaliana* DNA sequence (GenBank Accession # AF081067) was employed to search for IAR3 orthologs using the TIGR BLAST engine as previously stated. Homologous IAR3 sequences found on TIGR

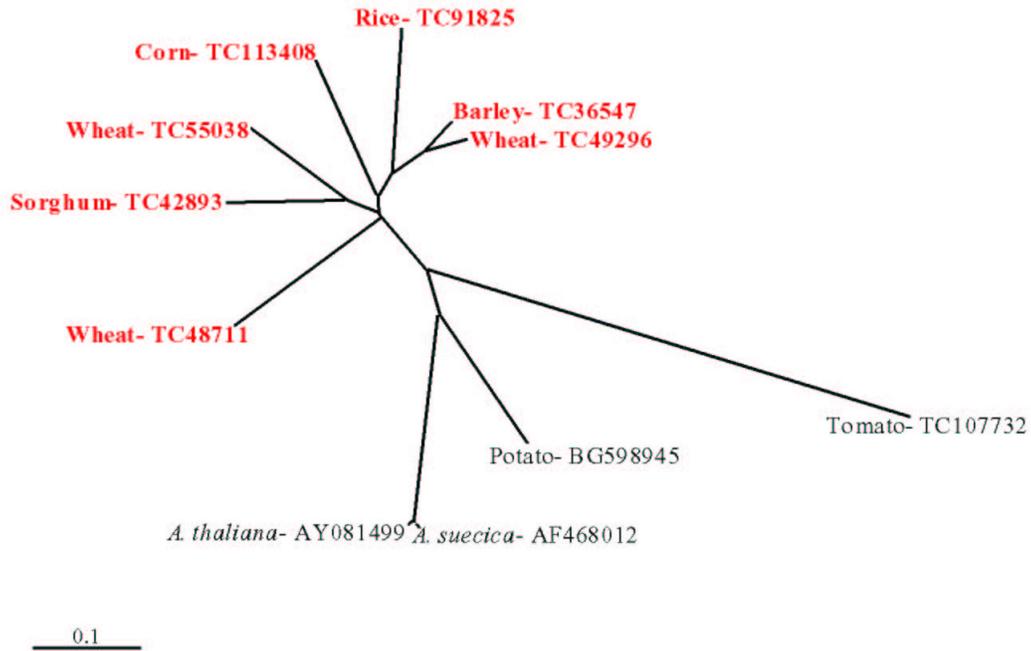


Figure 1. Unrooted radial tree of 9 species constructed analyzing orthologous ILR1 DNA by neighbor-joining method using CLUSTAL X. The trees were generated by the TREEVIEW program. Monocot species are in red.

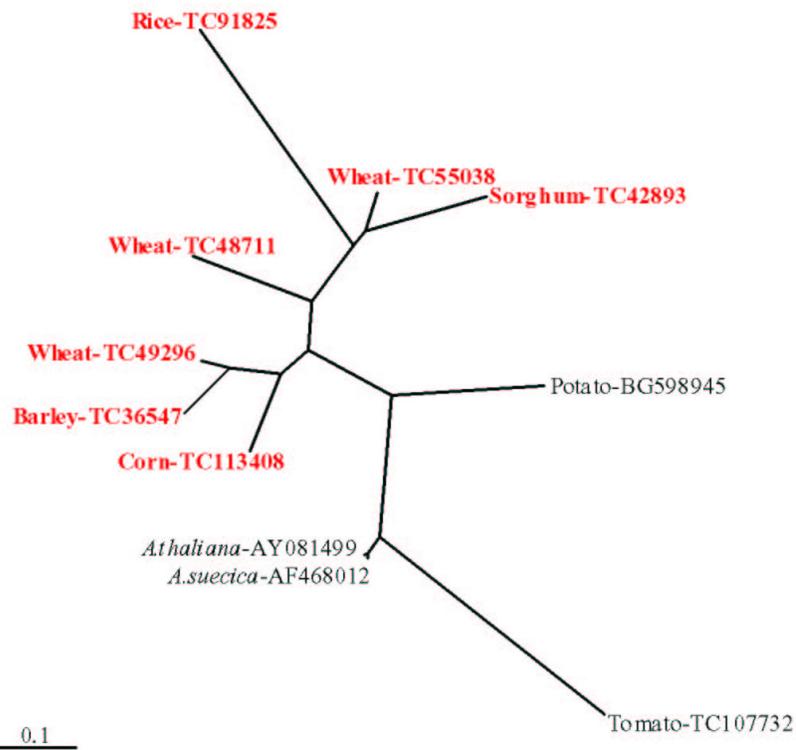


Figure 2. Unrooted radial tree of 9 species constructed analyzing orthologous ILR1 proteins by neighbor-joining method using CLUSTAL X. The trees were generated by the TREEVIEW program. Monocot species are in red.

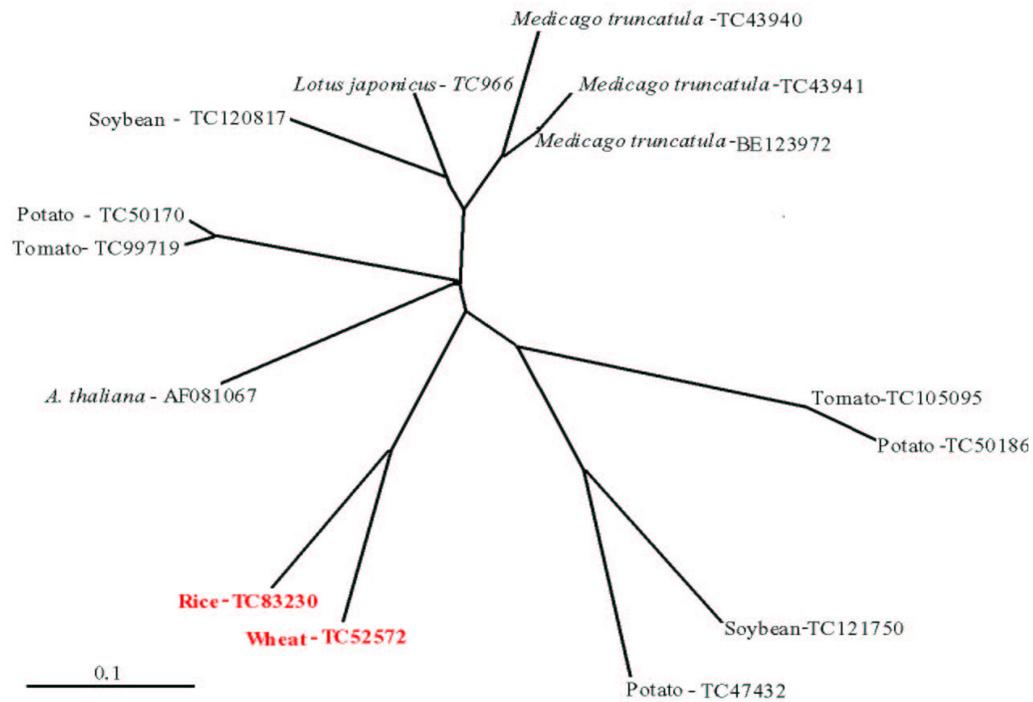


Figure 3. Unrooted radial tree of 8 species constructed analyzing orthologous IAR3 DNA by neighbor-joining method using CLUSTAL X. The trees were generated by the TREEVIEW program. Monocot species are in red.

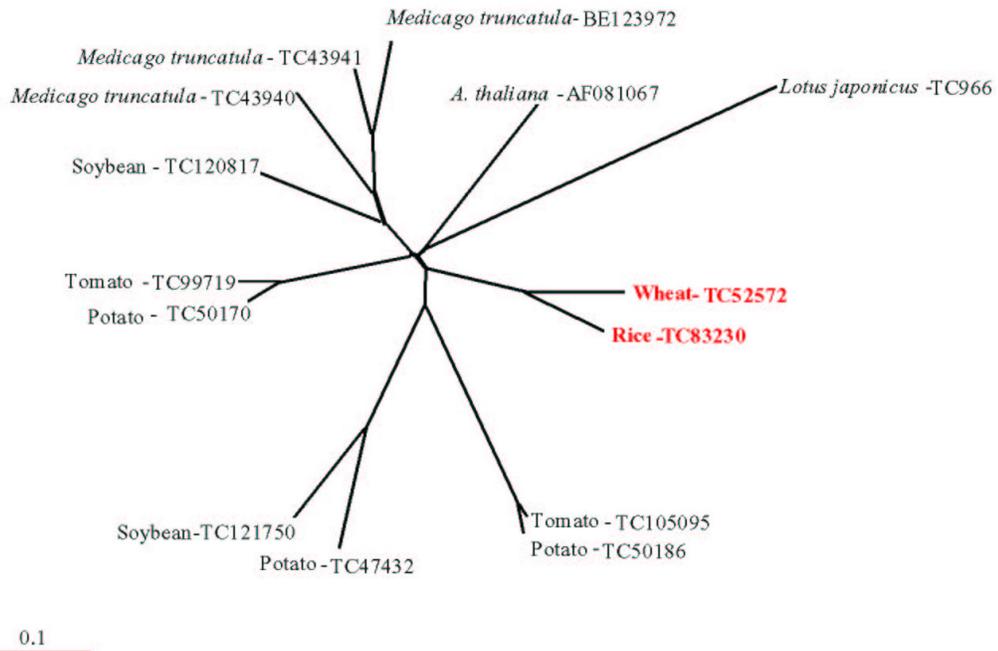


Figure 4. Unrooted radial tree of 8 species constructed analyzing orthologous IAR3 proteins by neighbor-joining method using CLUSTAL X. The trees were generated by the TREEVIEW program. Monocot species are in red.

included clover (*Medicago truncatula*) (Accession #'s TC43941, TC43940, BE123972), lotus (*Lotus japonicus*) (Accession #TC966), wheat (*Triticum aestivum*) (Accession #TC52572), rice (*Oryza sativa*) (Accession #TC83230), soybean (*Glycine max*) (Accession #TC120817), tomato (*Lycopersicon esculentum*) (Accession #'s TC105095, TC99719) and potato (*Solanum tuberosum*) (Accession #'s TC50170, TC50186 and TC4732) (Table 1).

Protein sequences were generated by first determining the correct reading frame of each EST using the GenMark ORF-finding program (M. Borodovsky and A. Lukashin, Georgia Tech University, unpublished). The 5' and 3' untranslated regions (UTRs) of each EST were removed by hand, and the DNA sequences translated to amino acid sequences by application of the Transeq program ([www.ebi.ac.uk/emboss/transeq](http://www.ebi.ac.uk/emboss/transeq))<sup>24</sup>.

#### Sequence alignments and phylogenetic tree construction.

Multiple alignments of ILR1 and IAR3 DNA and amino acid orthologs were constructed using the CLUSTAL X v1.8 algorithm<sup>25</sup> employing the following matrix parameters: IUB for all DNA sequences and Gonnet for all protein sequences. The settings adopted for IAR3 and ILR1 proteins and ILR1 DNA were "Opening 70, Extension 0.75." The settings employed with IAR3 DNA were "Opening 65, Extension 0.1." All other settings were placed at the default level.

Phylogenetic trees were generated from the distances provided by the CLUSTAL X analysis using the neighbor-joining method<sup>26</sup>. The neighbor-joining trees were constructed with the TREEVIEW program<sup>27</sup>.

## RESULTS

### ILR1 Ortholog Analysis.

The ILR1 coding sequence appears to be in a state of evolutionary change for the studied monocots and dicots, based on the radial tree topology (Figure 1), which is highly branched and "tree-like". This result suggests that the ILR1 group, although conserved, has experienced sequence alteration over time. Furthermore, this tree demonstrates a clear separation into monocot and dicot clades. All the monocots (red) fall together with shorter branches at one end of the tree (Figure 1), suggesting relatively little mutation of the ILR1 sequence *within* this clade. The dicots in the other clade (Figure 1) demonstrate a greater level of change based on the longer branch-lengths.

The ILR1 protein sequences (Figure 2) show the same monocot-dicot clade separation observed in the coding sequence analysis. The monocot (red) ILR1 protein orthologs have clearly diverged from the dicots. Although this divergence may indicate a basic change in the ILR1 at an enzymatic or functional level, it is important not to be too speculative with the limited number of species examined.

The topology of the ILR1 protein analysis reflects that of the DNA analysis, but shows a more asymmetric "tree-like" structure. This tree-like structure strongly supports divergence of the ILR1 protein in both the monocots and dicots. The amino acid substitutions within the dicots support the observation that even between closely related species, such as *A. thaliana* and *A. suecica*, there are variations in ILR1 structure and function<sup>20</sup>. Substrate specificity may not be highly conserved in orthologs of ILR1.

## IAR3 Ortholog Analysis.

The IAR3 cDNA sequences diverge in dicots into two separate clades, with the monocots forming a third clade (Figure 3). The tree has a general “bush-like” shape that again suggests minimal phylogenetic change. This lower level of change may signify that IAR3 is more highly conserved than ILR1 with fewer changes in its primary coding sequence between orthologs. The two monocots (rice and wheat) in this tree diverge onto a separate, but short branch, suggesting their division into another clade, but not a distant one. Although the results are suggestive, we must be careful not to speculate too much on monocot-dicot evolution based on this limited data set.

The IAR3 protein tree (Figure 4) is more symmetrical and “bush-shaped” than its companion cDNA tree. The protein tree’s topology supports the hypothesis that the amino acid sequence of IAR3 is more conserved than its primary coding sequence. The same two dicot clades and single monocot clade are reflected in Figures 3 and 4, although the protein tree (Figure 4) has a more compact topology than the cDNA tree (Figure 3).

Note that the IAR3 sequences for potato (TC50170, TC50186) and tomato (TC105095, TC99719) are closely conserved in these Solanaceae family members (Figures 3 and 4). However, the ILR1 sequences do not reflect this conservation between potato and tomato (Figures 1 and 2). Again, despite the small sample size, this result supports the hypothesis that IAR3 is a more highly conserved gene than ILR1 and hence, potentially of more physiological importance to dicots and monocots.

## **DISCUSSION**

### The Discipline Of Phylogenomics.

GenBank has approximately 15 million DNA sequences in its database and the number of sequences in GenBank has increased by five orders of magnitude since its founding in 1982. The Institute for Genomic Research, by the end of 1998, had completed sequencing seven microbial genomes, half of the world total at the time. Today, TIGR is in the process of sequencing and characterizing many of the major genomes of the world, including 19 animal, 17 plant, 13 protist, 7 fungal and over 100 bacterial species ([www.tigr.org](http://www.tigr.org)).

All this new information is obviously a great boon to scientists, since there is constantly additional data to be employed in genomic, physiologic and genetic research. The main drawback is that the sheer amount of this new information is becoming overwhelming. So much information is becoming accessible that high-quality, functional gene analysis and categorization is becoming a paramount goal.

Both homology and non-homology methods of computational analysis have been developed over the last 10 years to predict gene function<sup>28</sup>. The homology method is performed in a pairwise fashion comparing DNA or amino acid sequences and basing predictions of function on similarity to genes of known function. Non-homology methods analyze similarity between origins of replication, gene distribution patterns in various species, or even arrangements of neighboring genes. Both methods of analysis are comparative in nature, and thus are limited in creating connections that will allow researchers to discern how and why similarities and dissimilarities arise within gene families<sup>28</sup>.

It has been recently proposed that functional genomics lacks an evolutionary

perspective<sup>28,29,30</sup>, and because genes are compared based on homology, functional analyses are often misleading and not a reliable indicator of evolutionary relatedness or function. Therefore, phylogenetic analyses have begun to be applied to functional gene predictions so as to give measures of relatedness and not simply similarity<sup>28,29,30</sup>. This new analytic method has been dubbed Phylogenomics, the study of relatedness between gene families in a phylogenetic and evolutionary context.

We believe that functional predictions can be improved through evolutionary analysis; the use of GenBank and TIGR databases allows a structured phylogenetic analysis of gene families whose sequences are available. This method is valuable because it allows us to examine how groups of genes from various species have altered through time in an evolutionary context. Additionally, as physiologists<sup>9,20</sup>, this phylogenetic method of analysis allows us to choose the best candidate genes for cloning and characterization from the EST databases, based on their phylogeny, as well as gene homology.

#### ILR1 and IAR3 molecular evolution.

Our studies indicate that the DNA sequence of the ILR1 gene appears less conserved than the IAR3 coding sequence. This conclusion is based on the relative topology of the two phylogenetic trees (Figures 1 and 3). Overall the IAR3 tree appears more "bush-like", that is more branches of equal lengths. This result suggests that for the monocots and dicots studied the coding sequence of IAR3 has undergone fewer changes than ILR1 across plant families. This may imply that IAR3 is under greater selection to be conserved than ILR1.

The IAR3 amino acid sequences also appear to be highly conserved, while there is less conservation in the ILR1 protein sequences. Again, this conservation appears to support the greater relative importance of IAR3 versus ILR1 in the evolution of the physiological framework of plant growth.

Monocots are generally agreed to have diverged from dicots approximately 200-300 million years ago<sup>31,32,33</sup>. The IAR3 and ILR1 genes must pre-date this point of divergence, since they are conserved in both types of species. This result suggests that the role of the ILR1-like family is quite important to plant growth and development in angiosperms. Since our conclusions are based on a limited analysis, we will repeat our experimental studies with a larger number of monocot and dicot plant species as they become available on the GenBank and TIGR databases in the future.

We are further interested in determining whether gymnosperms share this gene conservation as well. Unfortunately gymnosperm genomes are still in the process of being sequenced and characterized. The loblolly pine has been partially sequenced by the University of Minnesota Center for Computational Genomics and Bioinformatics (CCGB), but a search for ILR1 or IAR3 orthologs on the EST database of CCGB turned up no homologous genes (pinetree.ccgb.umn.edu).

One physiological question that arises from the conservation of ILR1 and IAR3 is what the actual role of ILR1 and IAR3 may be in monocot growth. Monocots store IAA conjugated to sugars by ester bonds and not to amino acids. The two ILR1 orthologs that have been isolated from *A. thaliana* and *A. suecica* have high activity against IAA conjugates bound to amino acids, but no activity at all against sugar-bound conjugate substrates<sup>9,20</sup>. None of the monocot ILR1 orthologs have yet been cloned and characterized. One question of interest is

what the substrate specificity of the IAR3 and ILR1 monocot orthologs may be. Are these monocot orthologs able to cleave amino acid-conjugates, sugar-conjugates, or neither? Do these enzymes harbor some other substrate specificity?

Our goals for the future are to clone and characterize monocot orthologs of ILR1 or IAR3 genes. Since amino acid sequence conservation in these genes seems to be high in the orthologs, the question of whether function and activity are also conserved must be answered. We would like to determine whether our computer predictions for functional homology, based on phylogenomic analysis, prove to be correct.

**ACKNOWLEDGMENTS.** The Authors wish to thank Lisa Campanella for her generous help in editing this article. This work was supported primarily by a Sokol grant for undergraduate research from Montclair State University.

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**Birds' Brains: Studies This Past Year Which Used Avian Subjects and Enriched our Scientific Knowledge**

by **Anthea M. Stavroulakis**

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Over the years birds had not only fascinated artists, engineers and scientists, but also me. As a young girl I heard my canary sing with passion and gusto, and wondered how deep a breath he must have taken to sustain his song. Why didn't he collapse? There were annual song variations added to his unique song, a composer! My mother told me of canaries' vital gas-detecting role in coalmines, so a greater appreciation of their remarkable respiratory abilities was gained. Years later I began to read about birds and more fully appreciate my little songster. Initially, their songs and ability to fly fascinated me, but when I purchased a parrot, their talents for imitation and learning intrigued me. Now, as a college professor and research scientist, any articles relating to avians are read with great interest. We gain a great deal of information relating to flight, navigation, neurobiology, respiration and cognition (intelligence) from scientific studies which use avian study subjects. In this article I will briefly discuss a few articles in the literature this past year which studied avian subjects. Not only do birds enrich our knowledge of avian physiology and evolution, but they augment and link to on-going research on higher animals including humans, giving us insight to mechanisms of perception, learning memory and disorders. The topics are varied and include vision, flight, development, neurogenesis, cognition, and conservation, but have one commonality: avian research subjects.

“Ornithologists once assumed that birds perceive the world the same way as people do. The sensory experience of birds, however, extends beyond the

sensory experience of humans. The highly developed color vision of birds reaches into the near ultra-violet range of the spectrum. The broad hearing range of birds encompasses sounds of very low frequencies – called infrasounds – and some owls can track prey in complete darkness by their hearing alone. Birds can navigate by means of patterns of the Earth's magnetism and can orient themselves in flight “automatically” because of their extreme sensitivity to miniscule shifts in gravity and barometric pressure. Recent research reveals that birds have well-developed brains and are more intelligent than is implied by the familiar and in appropriate slur “bird brain”.<sup>1</sup>

We see birds everywhere. An eagle is our National Symbol, doves and hawks are used to symbolize peace and war, carrier pigeons transmitted messages during wars, falcons are used in sport and in mythology the Phoenix symbolizes immortality, resurrection and life after death. Their eggs are an integral part of human diets; we even see references in Science Fiction, the Klingon Bird of Prey spaceship. They have long been favorite subjects of artists, appearing in paintings and sculpture, and companion animals<sup>2,3</sup>. Birds are visually remarkable, possessing abilities to see a wide range of visual cues, including some not visible to our naked eyes, fluorescent pigments.<sup>4,5</sup> Examination of the organization of collagen fibers of the velvet asity, a rare Madagascar bird, under the electron microscope revealed a light

modulation was responsible for the colors we observe.<sup>6</sup> Specifically, the different colors observed were caused by variations in skin collagen fiber arrangement. Arnold<sup>4</sup> studied color perception in budgerigars (*Melopsittacus undulates*) as a sexual signal. Females showed a significant sexual preference for males with fluorescent plumage. This information could suggest a directed evolutionary origin of colors in which females preferred (selected) males with purer colors.

Birds can soar, dive and hover; they are aerodynamic and display an extraordinary range of flight modes. Artist Leonardo da Vinci had modeled wings for humans to be able to fly.<sup>7</sup> Their lightweight skeleton, powerful attached muscles and metabolism are suited to this task. Flight speeds, aerial agility and oxygen consumption are related to wing size and shape.<sup>8</sup> Researchers at the University of Portland, Oregon flew cockatiels (*Nymphicus hollandicus*) and doves (*Streptopelia risoria*) in a variable speed wind tunnel to study the relationship between mechanical power output and forward velocity.<sup>9</sup> Their pectoral muscles (primary flight muscles) tension and length were measured. The work output per wing beat significantly varied with flight speed in both bird species which indicates that variation in wing motion may alter power requirements at different speeds. Differences in their morphology (e.g.: tails) compared to other species could also affect their power requirements. Perhaps these aerodynamic models and power curves may one day be useful to our knowledge of propulsion, lift, drag and thrust. "No aircraft yet approaches the average bird's acrobatic maneuverability. About 50 different muscles control the wing movements. Some muscles fold the wing, others unfold it. Some pull the wing upward, others pull it down, and still others adjust its orientation."<sup>10</sup>

Consideration of the evolution of avian flight has included the origin of feathers and

the origin of flight. Feathers are avian skin structures, which not only assist flight, but also help insulate and camouflage birds, as well as playing a role in assisting communication between individuals. Wing assisted incline running (WAIR) in chukar partridges (*Alectoris chukar*) was studied by Dial<sup>11</sup> who proposes a scenario for adaptive plateaus that feathered theropod dinosaurs reached, which assisted them in developing aerial flight. The birds' wing (flight) feathers were unmodified, trimmed to one half the surface area or completely removed. A decreased flight performance (the maximum slope the birds could ascend) correlated with greater trimming. These results supported the wings role in actively assisting the legs during ascension. The author proposes a WAIR hypothesis to explain how bipedal "proto-birds" could have been an intermediate stage in the development of aerial flight. Fossil discoveries in China suggest the most recent common ancestor of birds and dromaeosaurs had four wings, two on forelimbs and two on legs, which preferentially glided rather than flapped.<sup>12,13</sup> Xu, *et al.*<sup>14</sup> said the animal probably used the four wings to glide in a manner similar to a flying squirrel. The fossil specimen, *Microraptor gui*, was younger than Archaeopteryx. This discovery, they said, represented a previously unknown intermediate stage in the evolution of birds and flight prior to Archaeopteryx. Discovery of aerodynamic function supports an arboreal-gliding hypothesis for bird flight, originally proposed by William Beebe in 1915, and has implications for reexamination of flight originating from the ground up (e.g.: reptiles flapping their feathered forelimbs).

The origin, evolution and physiological development of unique avian features have been studied extensively over the years. Much of what we've learned through these experiments has advanced our understanding of embryology and development in more advanced organisms including human.

During the 19th century Hans Spemann conducted experimentation that analyzed the behavior (interactions) of interspecific embryonic transplants. Since that time embryogenesis studies, which included salamanders and frogs in the 1950's, have advanced to provide us with detailed cellular and molecular analyses of cells and tissues in early development. A recent experiment at the University of California at San Francisco studied the effect of the host environment on the initiation and cessation of neural crest cells.<sup>15, 16</sup> The authors transplanted quail and duck embryonic neural crest cells, which give rise to beaks. Quail cells were transplanted to a duck and duck cells to quails. The ducks grew quail beaks and vice versa. The resulting morphology was determined by the neural crest cells, not by the host into which they were placed. The beak transformations also altered host beak tissues. Our understanding of the molecular and cellular mechanisms of beak diversity is broadened by this study, but also may lead to a better understanding of human craniofacial development, possibly the cause of human defects (e.g.: cleft palate, a human facial birth defect), which may some day be corrected before birth by transplanting appropriately programmed mouth cells.

In relation to body mass, birds have large brains. The main divisions of their brain include the forebrain, olfactory bulbs and cerebral hemispheres, which are typical of all vertebrates. The cerebral cortex, which is the origin of higher thought in mammals including humans, is small and poorly developed in birds' brains. Instead of relying on their cortex, birds have another developed area in the forebrain called the hyperstriatum as their primary origin of intelligence.<sup>17</sup> Studies on how male birds learn and produce their song were published this past year, providing insight into neural mechanisms of learning and motor control. Neuroscientists learned that a song-learning pathway in the avian

brain has significant similarities to a crucial motor-control circuit in mammals, a finding which could give insights into higher brain evolution.<sup>18</sup>

While reviewing scientific studies published this past year, I found several papers written about avian cognition and neuronal plasticity. For the most part, prior to the mid 1980's it was believed adult brains were unable to make new neurons. However, at Rockefeller University (New York City) evidence of newborn neurons was seen in canaries (*Serinus canarius canarius*). [should there be a reference here?] These neurons were seen in a brain area know as the High Vocal Center (HVC), a region of the forebrain that helps produce their song. Subsequent studies in canaries and back-capped chickadees confirmed this as neurogenesis, and it was proposed the new neurons played an important role for song learning (in canaries) and memory (in chickadees). Further experimentation expanded the aforementioned neurogenesis research to include rats and mice. Olfactory neurogenesis results paralleled the learning and memories results previously reported. Gage<sup>19</sup> seeks to identify correlations between neurogenesis-blocking drugs and learning. Hence, from avian subject pioneers we continue to gain insight into neurological functions and a possible role in learning and memory. Studies of songbird forebrain robust nucleus of the archistriatum (RA) by Hahnloser, *et al.*<sup>20</sup> suggest occurrence of a sequential precise neuronal burst in this area just before a particular note is sung. They suggest an alteration of song, including error correction, could depend on the pattern of activation in these synapses which is consistent with observations of neuronal plasticity. The authors described how changes in synaptic connectivity would affect song output. Additional RA research reported that a specific set of neurons (HVC) actually sends commands to the RA. This may refine

our thinking on how male birds learn to produce their song through an increased understanding of the significant role the HVC plays in learning by conveying neural signals. Further, it is proposed this brain pathway is "wired up much like the mammalian basal ganglia [which] plays a key role in controlling movement and has been implicated in learning skilled movements".<sup>21</sup> The basal ganglia are the brain nuclei which malfunction in Parkinson's disease. In earlier studies, gene expression and protein synthesis in the songbird forebrain caudomedial neostriatum (NCM) were required for longer lasting habituation (a decreased neural responsiveness to repeated presentation of the same stimulus).<sup>22, 23</sup> Chew, *et al.*<sup>22</sup> demonstrated decrease single neuron firing rates in the caudal NCM upon repeated (unreinforced) presentation of the same conspecific song. Based on their findings, the authors proposed that one form of learning occurs in the absence of reinforcement, and may differ from other kinds of memory such as associative learning. They proposed a method (model?) for testing the relation between neural properties and behavioral levels. Male song intensity and dance displays are important in bowerbird sexual selection.<sup>24</sup> How mating choices are influenced by the aforementioned, could be better understood by a more in depth understanding of avian neural circuitry. Dr. Erich Jarvis at Duke University (North Carolina) has published on vocal learning in birds, and argues that humans have brain structures similarities to vocal learning birds which can be used as a model for human language.<sup>25</sup> Studies in finches (*Taeniopygia guttata*) may serve as an animal model for human stuttering.<sup>26</sup> These finches are commonly used in bird song research. In a recent experiment one half of normal baby finches raised by stutterers grew up stuttering. When tutored stutterers were put among normal zebra finches for several months, their

diction improved suggesting that the stuttering trait can be both learned as well as unlearned. Perhaps further studying this trait in these birds can help us develop and tailor treatments for different kinds of human stuttering.

How do birds cope with intellectual challenges? They must understand, process information, learn and remember to survive and reproduce. Birds build incredible and diverse nests. Many are engineering marvels, built on trees, in cliffs, in sand and even in our homes.<sup>27</sup> They display adaptive architecture, which protect the eggs, nestlings from adverse weather and predation.<sup>28</sup> As flock members' birds must recognize their mates, other members of the cohort and to interpret any alterations in their appearance and behavior that signal moods and intentions. Cooperative behaviors facilitate the aforementioned interactions as well as procurement of food by cooperative hunting, shelter and protection. Animals' reproductive success is enhanced with information regarding the success of the breeding site as well as their neighbors breeding success. Doligez, *et al.*<sup>29,30</sup> studied collared flycatchers (*Ficedula albicollis*) choices to emigrate or immigrate manipulated breeding plots. The number of fledglings per breeding pair per plot and condition correlated with adult emigration rates. Their study suggests adults used both fledgling quantity and quality to assess the hospitability of the breeding plots. The result indicates the use of "public information" by this species in breeding habitat choice, and suggests complex cognitive processes are involved in this decision. These studies provide beneficial information for conservation biology strategies as introduced species reproductive success may be influenced. Breeding success of other individuals in a population is used in deciding where to breed the following year. This finding is supported by avian infidelity studies in the western sandpiper conducted by van Noordwijk.<sup>31</sup>

Use of tools is observed in many animals, with the most extensive use observed in primates. Tool use in birds, which has been reported, is not a sole method of foraging, but rather is supplementary. Usually many birds exhibit anatomical modifications for procuring their food. Weir, *et al.*<sup>32</sup> reported on how New Caledonian crows (*Corvus moneduloides*) purposely modified a straight wire into a hook and successfully lifted a bucket containing meat. The birds did not have previous experience with a hooked wire, and only one-hour experience with pliant material (flexible pipe cleaners) a year before the experiment. This experiment suggests that these birds may have tool-related cognitive capabilities associated with primates. Crows and ravens are members of the Corvidae, a diverse family present on every continent, except Antarctica. Corvids have demonstrated abstraction, memory and creativity, giving them a reputation of mischief and destruction.<sup>33</sup> Subsequent experimentation on this group of birds and others can increase our awareness of non-human comprehension.

Parrots use of human language and relative longevity make them favorable study subjects for avian intelligence. Dr. Irene Pepperberg<sup>34</sup> has been working with African Grey parrots (*Psittacus erithacus erithacus*) studying cognition. Alex, one of the parrots in her lab names and identifies more than one hundred items and can distinguish categorical similarities and differences. He was first taught the names of various objects. After acquiring this language he was taught their attributes (color, texture), and then his awareness of wants and concepts (e.g.: categories) was tested. Alex was able to distinguish which objects were similar or whether there was no difference, a concept of "absence".<sup>34,35</sup> Dr. Pepperberg's work has shown higher levels of mental ability in these birds, the ability to acquire a concept. This interspecific communication based on human language allowed the bird's mind to be more

accessible to study. Her methods are currently used in additional bird species study subjects.<sup>36,37</sup> Dr. Pepperberg's work has "shattered traditionally held views that birds are nothing more than talented mimics. They have proven, instead, that parrots possess intelligence surprisingly to that of a young human child. This discovery has contributed to continued efforts in conservation and encourages bird owners and bird breeders to respect the animal in their care".<sup>38</sup>

Avian species were discovered and rediscovered in 2002. Brazilian researchers discovered a new kind of parrot (*Pionopsitta vulturina*) in Amazonian forests (Brazil), and another group rediscovered another after ninety-one years (Fuertes's parrot) in trees atop a volcano in the Columbian Andes.<sup>39,40</sup> A concern that environmental threats from loggers and ranchers could hinder further finds was expressed. Conservation biologists have successfully influenced offspring sex ratio and fledgling success of an endangered New Zealand parrot, the kakapo by timing food supplementation.<sup>41</sup> These parrots were once common on three New Zealand islands, but suffered extinction on one, and severe reduction on the others due to introduction of non-native species (e.g.: feral cats and stoats). Additional behavioral and conservation studies included a recent article which studied testosterone-enhanced red grouse (*Lagopus lagopus scoticus*) and the role aggressiveness plays in population growth. Older males defending their turf kept away younger birds seeking mates; a decline in the density of males in this population that had been growing was observed.<sup>42</sup> Perhaps sociologists will wish to note this? In a study by Whitfield<sup>43</sup>, wild great tits (*Parus major*) offspring that were bolder dispersed farther than the timid ones. Therefore, the geographic distribution of genes for boldness and other genes would be affected. The boldness trait seemed to correlate with the genetic structure of the birds populations.

Historically, our relationships with birds included symbol, myth, art and science. Birds were admired and imitated from Ancient times in Greek mythology (Icarus wax wings), to present day aircraft design. Scientific studies have enriched our appreciation and understanding of these non-human creatures that share the earth with us. Not only are birds a bioengineering marvel, they are a valuable tool that we use to learn about animal physiology and cognition which may be overlooked as being such. They are useful in so many areas as model systems that can be used more extensively in the future. Certain avian characteristics, such as their sensitive respiratory system, were used as indicators for coal miners early last century. By studying their cognitive abilities, we have gained more insight into the more complex human brain. Their high metabolic rates push the limits of physiology. As science and engineering advanced our knowledge and understanding of their unique physiology, visual acuity, versatility, diversity, flight and song help us further our scientific knowledge. The aforementioned studies give us a glimpse of how unique these animals are, and continue to impress us while augmenting the breadth and depth of our scientific knowledge.

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## The Fall 2002 Conference Member Presentation Abstracts



**Promoting Self-Regulated Learning in Human Physiology: A Pilot Study.** Maureen N. Gannon, Department of Biology and Medical Laboratory Technology, BCC.

Effective student-learning requires students to independently extract information and monitor their own performance. This study describes attempts to determine if increased student performance can be achieved through the use of open note quizzes. Different sections of the physiology component of Human Anatomy and Physiology (BIO 23) were randomly assigned to experimental and control groups. The same instructor taught all sections, which received identical unit exams, course content and materials. The experimental groups were given open note 20 minute quizzes, approximately once every three weeks, while the control groups received instructor-based review of the material covered. Preliminary analysis of test results indicates that students given open note quizzes performed better than students in the control group, as reflected in their higher unit exam scores (range 6-10%), and an improvement in the final course grade distribution. However, the percentage of students that failed to complete the course was not significantly different between the two groups (40% control versus 36% experimental). Results from formal and informal student assessment surveys suggest that students in the experimental groups increased their ability to study independent of formal instruction, and felt more confident of monitoring their own performance. While the extent to which this technique can be incorporated into the curriculum is limited by the necessity to cover course content, this study suggests a way to promote student-based learning in the biological sciences,

This work is an extension of the Reading, Learning and Thinking Across the Curriculum Workshop, part of the Faculty Excellence Center funded under a Title V grant to BCC.



**Histochemical and Ultrastructural Details of Endosperm in *Alyssum maritimum* and *Iberis amara*.** Kumkum Prabhakar, Nassau Community College.

Flowering plants, being the most advance category in the plant kingdom, exhibit special embryological features. Other than traditional fertilization, the fusion of sperm nucleus with the polar nuclei by double fertilization results in the formation of primary endosperm nucleus. The primary endosperm nucleus in *Alyssum maritimum* is surrounded by a large number of polysaccharide grains. The grains are utilized during the nuclear development of the endosperm. The nuclear endosperm stains intensely for the proteins, DNA, and RNA but the concentration of these metabolites declines during cellularization. The concentration of polysaccharide, however, increases with cellularization. Finally, the single layer of cellular endosperm, in mature seeds, stores insoluble polysaccharides in the form of cell walls. Prior to cellularization, metabolically active endosperm surrounding suspensor and embryo proper shows some interesting ultrastructural details such as variation in the size and shape of polyploid nuclei and extrusion of nucleolar material. This presentation will discuss significant histochemical and ultrastructural features in *Alyssum maritimum* that confirm nutritive role of endosperm and the route of nutrition to the embryo sac through absorptive wall ingrowths at micropylar and chalazal ends and the suspensor.



**Molecular characterization of a cDNA encoding a four-and-a-half LIM domain protein in sea scallop.** Mohsin U. Patwary<sup>1</sup>, Terrence Y. Bissoondial<sup>2</sup>, Timothy W. Short<sup>2</sup> and Ellen L. Kenchington<sup>3</sup>. <sup>1</sup>Biology Department, Medgar Evers College, CUNY, <sup>2</sup>Biology Department, Queens College, CUNY, <sup>3</sup>Science Branch, Bedford Institute of Oceanography, Dartmouth, N.S., Canada.

LIM proteins have unique cysteine-rich domains composed of two zinc fingers that are separated by two amino acids found in over sixty distinct proteins. Each LIM domain coordinates binding of two zinc ions and shows striking structural similarity to zinc fingers believed to stabilize tertiary folds of the protein. These domains are involved in a variety of functions including protein-protein interactions mediating specific functions, erythroid cell development, and muscle cell differentiation. A cDNA encoding a LIM- domain-containing protein has been isolated from a sea scallop adductor muscle-specific cDNA library and sequenced from both directions. An additional 24 base pair (bp) truncated 5' untranslated portion of the cDNA was obtained using 5' RACE. The full-length 2038 bp-long cDNA includes a 163 bp untranslated region at the 5'end, an 852 bp open reading frame (ORF) and a 1023 bp 3' untranslated region including an 18 bp polyA tail. The ORF encodes a 32.8 kDa four-and-a-half LIM domain protein with 283 amino acids. This cysteine-rich protein has 35 cysteine residues followed by 31 lysine residues. There are 100 non-polar, 92 polar uncharged and 91 polar charged amino acids in this protein. Several amino acids show a bias for codons with C at their third position. Southern blot hybridization indicates that this LIM gene belongs to a family of 1-4 genes of unknown function in sea scallop. Genomic DNA from several sea scallops when hybridized with LIM cDNA probe revealed RFLPs at several loci indicating its potential use as a genetic marker in sea scallop.



**Urea Uptake Rates Respond to Changing Food Urea Concentrations in Urea-Resistant and Susceptible *Drosophila* Populations.** Valerie Pierce and Jeanine Mangogna, College of Staten Island, CUNY.

We are using laboratory-selected *D. melanogaster* populations to investigate physiological mechanisms of toxin resistance. Larvae from replicate fly populations selected for resistance to 300 mM urea take up urea more slowly during development than susceptible wild-type larvae. We have characterized the relationship between food urea concentration and initial urea uptake rates. We fed resistant and wild-type larvae foods containing 0, 200, 400, 650 and 900 mM urea and then assayed the urea concentration of hemolymph from all groups. Urea uptake rates in mM urea/hr were calculated from hemolymph urea concentrations and feeding time. Analysis of variance indicates urea uptake rates are significantly affected by the interaction between replicate number and food urea concentration ( $p < 0.001$ ), selection treatment ( $p < 0.003$ ), replicate number ( $p < 0.001$ ) and food urea concentration ( $p < 0.001$ ). We interpret the significant interaction term and main effect of replicate number as a block effect because replicate populations were assayed on different days. Increasing urea concentration in the food significantly increased the rate of uptake, as expected for a system where urea entry is likely to be diffusion-dependent. Graphically, rates appear to level off between 650 and 900 mM urea for both types of larvae, suggesting it may be a saturable process. The significant selection term indicates that resistant and wild-type larvae differ in their response to increasing urea concentrations.



**Preliminary Analysis of Bacterial and Genetic Risk Factors for Periodontal Disease Among Asian Indians.** Subramaniam, Raji and Patricia Schneider, Department of Biological Sciences and Geology, Queensborough Community College, Bayside, N.Y.



Periodontal disease results from a complex interaction between bacteria infection and immune response. Studies of Caucasian populations have shown that risk of tooth loss increases 1.6 times with the presence of *Porphyromonas gingivalis*, and 6.8 times with a specific IL-1 genotype. This study investigated the significance of these factors in the Indian population. Subjects in good general health with periodontal alterations were selected from the patient pool at a private dental clinic in Jamaica, Queens, N.Y. Patients were excluded based upon the following criteria: presence of systemic disease, smoking in the past 5 years, history of antibiotic therapy in the previous 3 months, and pregnancy or lactation. Clinical and radiographic criteria were used to classify subjects into "mild", "moderate" and "severe" categories. Those with "mild" classification served as controls. Increased BANA (bacterial enzyme test) intensity was observed with increasing pocket depth. The significance of *P. gingivalis* remains unknown because it could not be isolated from the clinical specimens. Twenty percent of the subjects tested positive for the IL-1 composite genotype consisting of allele 2 of the IL-1A and allele 2 of the IL-1B. The high prevalence of positive genotypes is approximately 10 times the number reported for Chinese (2.3%) and close to that observed in Northern Europeans (29.1%). Preliminary results suggest that BANA testing and genotype analysis may be of clinical value in this ethnic group.

This project was funded by PSC-CUNY grant 62293-00-31.



**The Vascular Flora of Sable Island, Nova Scotia.** Richard Stalter, Affaf Munir, Natalie Atarion, Milena Bonilla, Peter Gangione, Nicolleta Marianna and Natalie Khvostovaya, Department of Biology, St. John's University, Jamaica, New York.

Sable Island, comprising 3400 ha, is located 44 N 60 W approximately 160 km east of the mainland of Nova Scotia, Canada. Five floristic inventories were conducted on Sable Island from 1899 to 1981, a sixth floristic survey was undertaken by Stalter in August, 2002. The vascular flora of Sable Island consists of 235 species in 150 genera in 59 families. The largest families in the flora were Poaceae, 26 species, and Asteraceae, 24 species. Together they compose 21.3% of the flora. Other large families were the Cyperaceae (15 species), Polygonaceae (14 species), Rosaceae (11 species), Caryophyllaceae (10 species), and Juncaceae (10 species). The largest genera were Polygonum and Juncus, each with nine species. Seven species of Carex were identified. One hundred fifty four species, 65.5% of the flora are native to the region.

## MACUB Gears Up for Spring with an Environmental Biology Mini-conference by Kathleen A. Nolan, Ph.D., St. Francis College, Brooklyn, NY

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No, I did not get my Prince Charming when I kissed the frog! Wood frogs and green frogs, hawks and owls, ropes and canoes were all part of our "PEEC Into Spring" mini-conference held at the Pocono Environmental Education Center/Fernwood Resorts May 2-4, 2003. Over 70 people, including faculty and students from many colleges attended this event. Students were from Medgar Evers College, Kingsborough College, and St. Francis College of Brooklyn. Six students were from the inaugural National Science Foundation Undergraduate Mentoring in Environmental Biology grant that is a collaboration among St. Francis and Medgar Evers colleges and the American Museum of Natural History.

Friday evening began with a buffet dinner in the spacious A Frame at the Fernwood Resorts. We later adjourned to a conference room and were treated to a performance by Bill Streeter, "Live Birds of Prey". Bill covered more ground in an hour with his "flying tongue" than I can normally cover in three. He did a very thorough job of enrapturing us with "raptor talk" that included viewing live birds - an American Kestrel, a red-tailed hawk, a harred owl, the diminutive saw whet owl, and a golden eagle. Bill and his wife live at the Delaware Valley Raptor Center where they rescue damaged birds of prey that are brought to them. Unfortunately, many of these birds are shot for sport and then left to die, as it is illegal to shoot birds of prey. The most magnificent bird was the golden eagle, which could not fly because of a damaged wing. We learned that the feathers on the back of the golden eagle, called hackles, are "raised" when this eagle is excited--hence the expression "raising one's hackles."

George Danno, our DJ, taught us how to do line and square dancing back in the A Frame. "I didn't think it would be this much fun", was one of the remarks I heard from a student. George expanded the repertoire with dances such as the "Hokey Pokey", "My Achy Breaky Heart", "The Electric Slide", and, my personal favorite, the "Pizza Dance". This was an activity that was enjoyed by the whole group which ranged in age from 18 to 60-plus!

The Saturday and Sunday breakfasts were superb, and I ate much more than I would have eaten at home. We had a choice of cold cereal, sausages, eggs, bacon, home fries, bagels, Danishes, juice and coffee--definitely enough to carry us through the not so strenuous activities that lie ahead.

On to the Pocono Environmental Education Center (PEEC) which is a private, non-profit organization that specializes in environmental programming for families and groups. PEEC also has cabins with bunk beds, bathrooms with showers, tubs and hot water, and desks, bureaus and lamps. Definitely more luxurious than tenting, but too much like dorm rooms for our eclectic

tastes--hence our decision to bunk in the Fernwood Resorts that was eight miles away.

One of the keys to the success of this program was, besides perfect weather, that there was some flexibility involved. One had a choice of activities over three different hour and a half intervals. Choices throughout the day included: a geology walk complete with fossils, an ecology walk on the Two Ponds Trail, canoeing in a pond with a beaver lodge, a herpetology walk with David Karmann from the American Museum of Natural History, pond water study and a confidence trail that tested one's balance by walking on low ropes and logs suspended from trees, and from swing to swing! A hearty lunch was served at PEEC in between morning and afternoon sessions.

The two activities that I was the most involved in were the confidences course and the herp walk. I enjoyed watching the competition between Medgar Evers and Kingsborough students as they tried to see who could win the balance contest. David Karmann had me chuckling as he was romping around in a muddy pond, determined to catch the elusive painted turtle. He actually caught two--the larger female and the male with the "sexy" long forepaws, and a couple of water snakes, frogs and a salamander.

All in all, people enjoyed the day's walks and activities (the canoes were also a big hit), and headed back to Fernwood for a little R& R before our banquet. I actually snuck in a swim and a little whirlpool! We feasted on shrimp, soup and salad, and our choice of chicken, fish, or prime rib, and had cheesecake for desert. No, it wasn't Juniors or S & S, but it wasn't bad! Dave Karmann gave us a spirited slide show of snakes from New York State and New England, and entertained questions for quite a while after the talk was over.

Sunday saw the dawn of another perfect day weather wise, and a few hardy souls joined Carol Griffiths and Jim Remsen, our ornithologists, for "birding". I saw a cardinal and two swallows - others saw and/or heard robins, vireos, orioles, grosbeaks, banded kingfishers, catbirds, crows and various warblers.

After the weather had warmed up a tad, we were ready to head to Child's Park, which is in the national park system. Beautiful boardwalks made for non-treacherous, fairly easy hiking along a stream that drained from Silver Lake, which was broken up by a series of beautiful waterfalls. River otters may have been present, we were told, but we didn't see them. It was back to PEEC for a lunch of Italian sandwiches, and then on home.

Many thanks go to Gary Sarinsky, Gary Spory, Paul Russo and Ed Catapane, for all their behind-the-scenes activities that made this weekend something to be remembered for a long time.



# PEEC Highlights



# CALL FOR NOMINATIONS

The terms of office for the following positions will be up for re-election to serve on the Year 2004 Executive Board:

- ♦ Vice-President
- ♦ Treasurer
- ♦ Recording Secretary
- ♦ Members-at-Large (2 positions)

The duties of these officers will involve attending all Executive Board meetings in addition to specific duties as describe below:

**Vice-President:** Will establish and serve as chairperson of the Advisory Council. In the event the President is no longer able to serve, the Vice-President will automatically succeed to the presidency for the remainder of the term.

**Treasurer:** Is responsible for the preparation of an annual fiscal report, processing of dues, preparing regular financial reports for the Executive Board meetings, income tax reports, and other duties usually pertaining to this office.

**Recording Secretary:** Shall record Board Members who are present, absent or excused from Executive Board meetings and shall distribute the minutes of the Executive Board meetings, the annual business meeting, and any other officially sanctioned meetings as advised by the Executive Board. The Recording Secretary is responsible for Election Committee duties as described in Article VIII of the Bylaws.

**Member-at-Large:** Chairs committees (Articulation, Exhibition, etc.) and handles other assignments as directed by the Executive Board.

Normally, each candidate for Vice-President, Treasurer, and Recording Secretary should have been a Member-at-large for at least one term and each candidate for Member-at Large should have attended at lest one Annual Conference.

**DEADLINE FOR NOMINATIONS is SEPTEMBER 15, 2003**

If you are interested in running for office (or wish to nominate anyone else) please send a letter of nomination to:

Dr. Paul Russo  
Division of Natural Sciences and Math  
Bloomfield College  
467 Franklin Street  
Bloomfield, NJ 07003-2726

You are invited to participate in the 36th Annual Fall MACUB Conference. Proposals are now being accepted for member paper presentations and poster presentations.

#### Member Paper Presentations

Proposals are now being accepted for member paper presentations. If you wish to make a paper presentation (20 minutes) which will discuss the results of research or share ideas, please send an abstract to Professor Carla Beeber, Kingsborough Community College, Department of Biological Sciences, 2001 Oriental Boulevard, Brooklyn, NY 11235 (718- 368-5265)

#### Poster Presentations

If you or any of your students wish to make poster presentations, please send an abstract and notify Prof. Mary Ortiz, Department of Biological Sciences, Kingsborough Community College, 2001 Oriental Boulevard, Brooklyn, NY 11235 (718- 368-5724) or Prof. Anthea Stavroulakis, Department of Biological Sciences, Kingsborough Community College, 2001 Oriental Boulevard, Brooklyn, NY 11235 (718-368-5095)

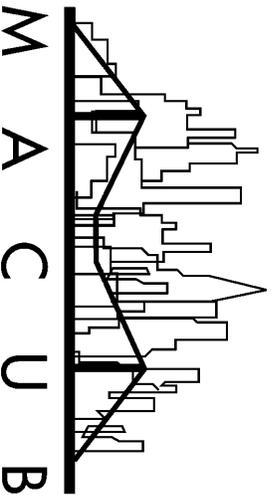
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Dr. Edward J. Catapane  
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Brooklyn, New York 11225

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