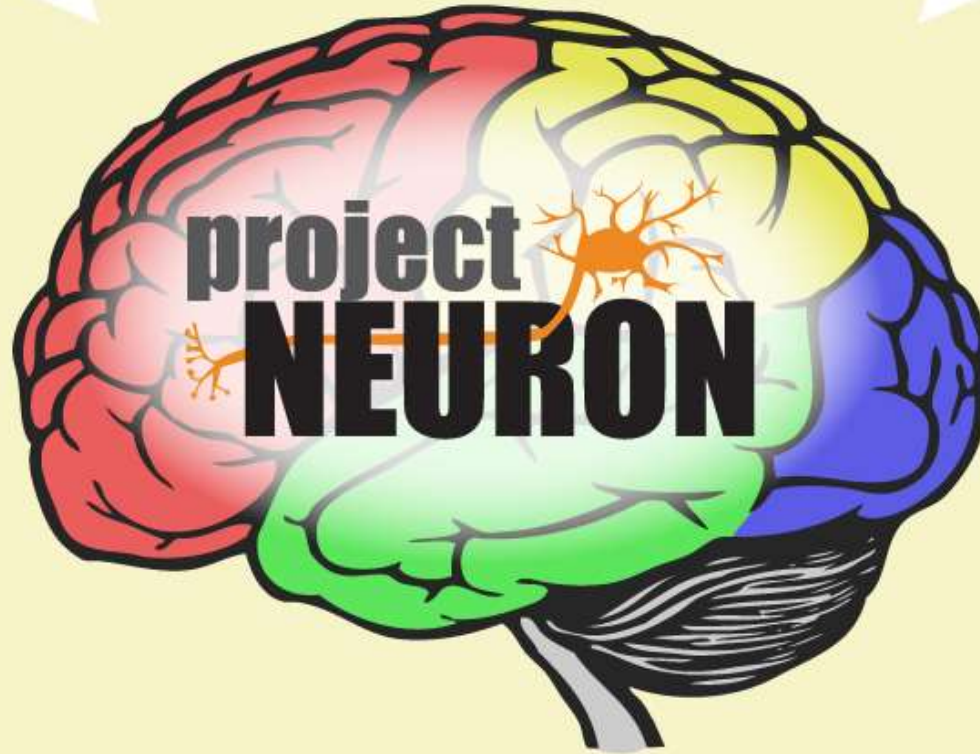


Branch Out with Software to Create Phylogenetic Trees



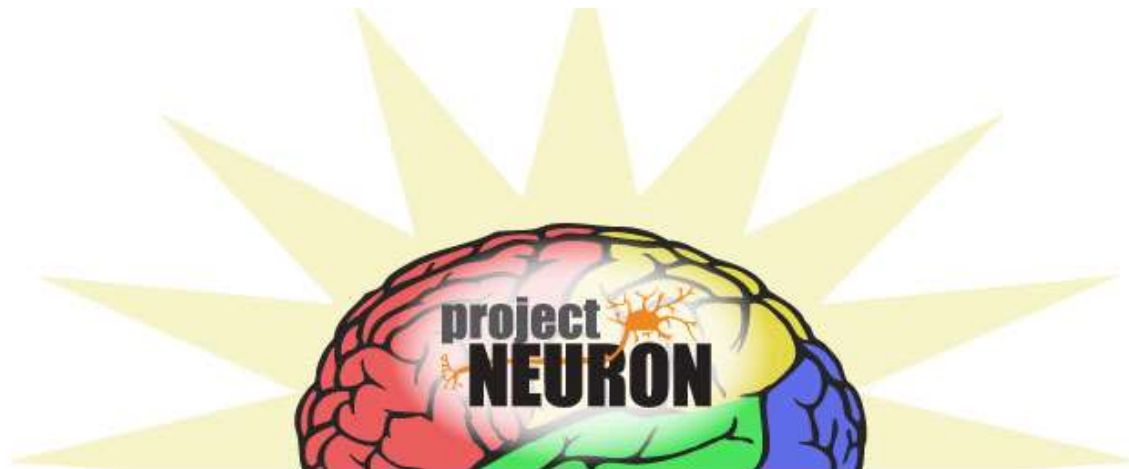
Robert Wallon, Claudia Lutz, & Barbara Hug
University of Illinois



SEPA SCIENCE EDUCATION
PARTNERSHIP AWARD
Supported by the National Institutes of Health

Goals for Session

- Introduce Project NEURON
- Create and analyze a phylogenetic tree based on adapted primary literature
- Connect and apply ideas to your classroom practice



What is Project NEURON?

- Curriculum development
 - Inquiry
 - Connect to standards
- Professional development
 - Summer institutes
 - Conferences

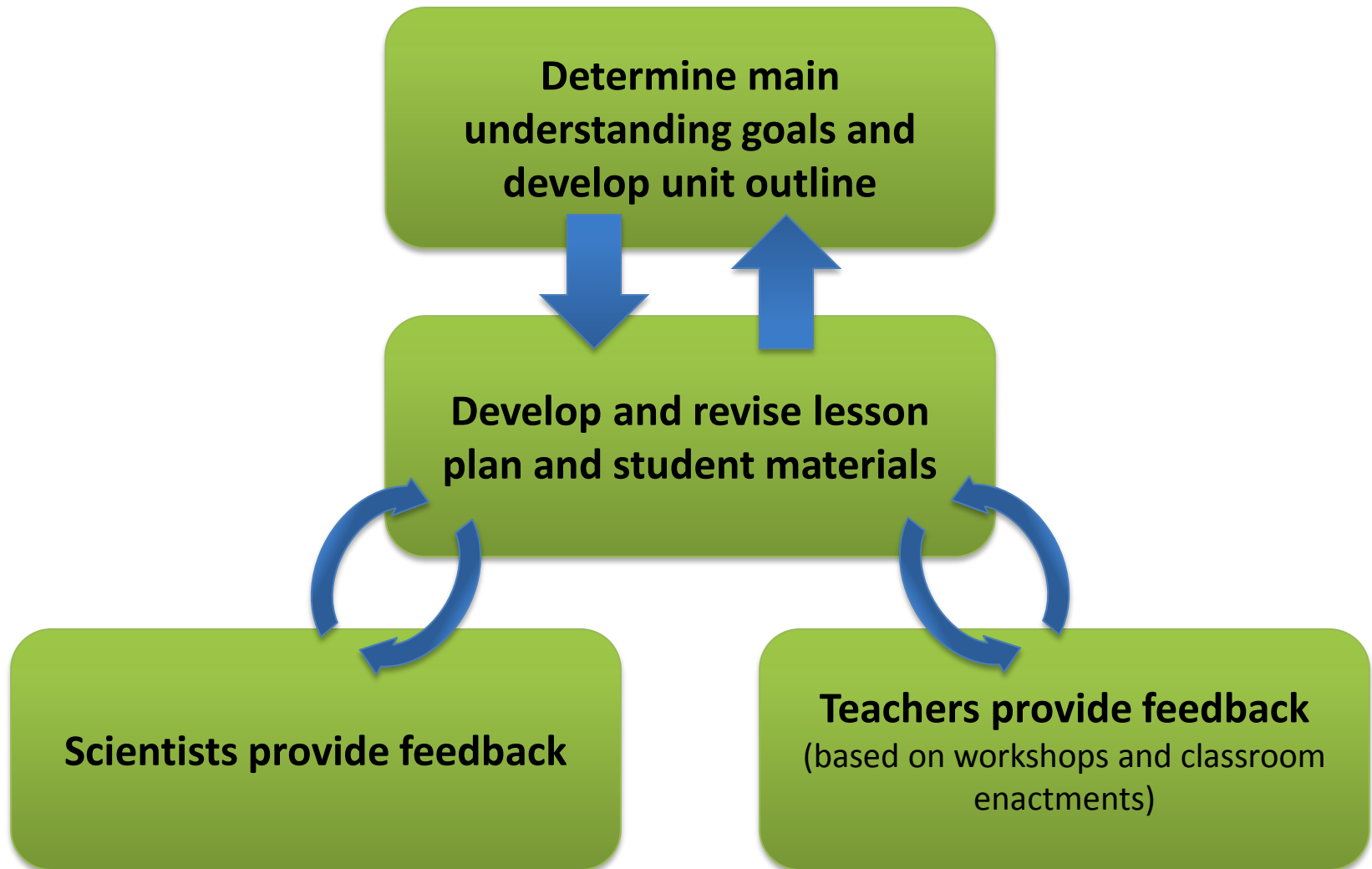


Project NEURON Curriculum Units

- **Do you see what I see?**
 - *Light, sight, and natural selection*
- **What can I learn from worms?**
 - *Regeneration, stem cells, and models*
- **What makes me tick...tock?**
 - *Circadian rhythms, genetics, and health*
- **What changes our minds?**
 - *Toxicants, exposure, and the environment*
 - *Foods, drugs, and the brain*
- **Why dread a bump on the head?**
 - *The neuroscience of traumatic brain injury (TBI)*
- **Food for thought: What fuels us?**
 - *Glucose, the endocrine system, and health*
- **What makes honey bees work together?**
 - *How genes and environment affect behavior*
- **How do small microbes make a big difference?**
 - *Microbes, ecology, and the tree of life*

Available at:
neuron.illinois.edu

Iterative Development



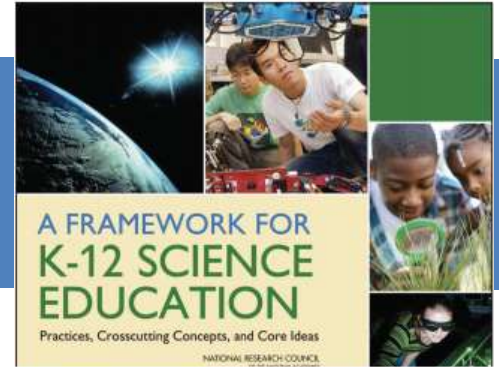
What makes honey bees work together?

- Lesson 1:
What do honey bees do?
- Lesson 2:
Why do honey bees have different jobs?
- Lesson 3:
How do honey bees heat the hive?
- Lesson 4:
What is the genetic basis for the evolution of eusocial behavior?

AP Biology Curriculum Framework

- **Big Idea 1: The process of evolution drives the diversity and unity of life.**
 - Enduring understanding 1.B: Organisms are linked by lines of descent from common ancestry.
 - Essential knowledge 1.B.2: Phylogenetic trees and cladograms are graphical representations (models) of evolutionary history that can be tested.
- **Science Practice 5: The student can perform data analysis and evaluation of evidence.**

A Framework for K-12 Science Education



Dimension 1: Scientific & Engineering Practices	Dimension 2: Crosscutting Concepts	Dimension 3: Disciplinary Core Ideas
<ol style="list-style-type: none">1. Asking questions2. Developing/Using models3. Planning/Carrying out investigations4. Analyzing & interpreting data5. Using math, information and computer technology, and computational thinking6. Constructing explanations7. Engaging in argument from evidence8. Obtaining, evaluating, communicating information	<ol style="list-style-type: none">1. Patterns2. Cause and Effect3. Scale, Proportion, and Quantity4. Systems and System Models5. Energy and Matter6. Structure and Function7. Stability and Change	<ol style="list-style-type: none">1. Physical Sciences2. Life Sciences3. Earth and Space Sciences4. Engineering, Technology and Applications of Science

NGSS



Practices

Crosscutting Concepts

Core Ideas



What is the genetic basis for the evolution of eusocial behaviors?

- **Activity 1: Read adapted primary literature**
 - Identify components of a research article
- **Activity 2: Construct a phylogenetic tree**
 - Provide a rationale for selecting a gene to compare between honey bees and other organisms based on adapted primary literature
- **Activity 3: Compare phylogenetic trees**
 - Compare the phylogenetic tree for a gene of interest to an established phylogenetic tree

Adapted Primary Literature

Genes involved in convergent evolution of eusociality in bees

S. Hollis Woodard¹, Brielle J. Fischman^{1*}, Aarti Venkat², Matt E. Hudson³, Kranthi Varala³, Sydney A. Cameron¹, Andrew G. Clark⁴, and Gene E. Robinson^{1,5,6,7,8}

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Contributed by Gene E. Robinson, March 12, 2011 (sent for review February 17, 2011)

Eusociality has arisen independently at least 11 times in insects. Despite this convergence, there are striking differences among eusocial lifestyles, ranging from species living in small colonies with overt conflict over reproduction to species in which colonies contain hundreds of thousands of highly specialized sterile workers produced by one or a few queens. Although the evolution of eusociality has been intensively studied, the genetic changes involved in the evolution of eusociality are relatively unknown. We examined patterns of molecular evolution across three independent origins of eusociality by sequencing transcriptomes of nine socially diverse bee species and combining these data with genome sequence from the honey bee *Apis mellifera* to generate orthologous sequence alignments for 3,647 genes. We found a shared set of 212 genes with a molecular signature of accelerated evolution across all eusocial lineages studied, as well as unique sets of 173 and 218 genes with a signature of accelerated evolution specific to either highly or primitively eusocial lineages, respectively. These results demonstrate that convergent evolution can involve a mosaic pattern of molecular changes in both shared and lineage-specific sets of genes. Genes involved in signal transduction, gland development, and carbohydrate metabolism are among the most prominent rapidly evolving genes in eusocial lineages. These findings provide a starting point for linking specific genetic changes to the evolution of eusociality.

social evolution | social insects | sociogenomics | molecular phylogenetics

The evolution of eusociality, the phenomenon in which female offspring forego personal reproduction to care cooperatively for their siblings, is one of the major transitions of life on Earth (1). This evolutionary transition has occurred multiple times, but only in a small number of lineages, primarily in the insects (1) or more times; ref. 2). The evolution of eusociality has long fascinated biologists because it requires that the balance between cooperation and conflict shift in favor of cooperation, despite strong selective pressure for individual reproductive success (3).

Despite a rich history of theoretical work on the evolution of eusociality (4, 5), relatively little is known about the molecular changes associated with eusocial evolution (6). These molecular changes have the potential to inform us about the evolutionary processes involved in the evolution of eusociality, such as types and levels of selection (7). Some insights have been gained about molecular mechanisms underlying eusociality in individual eusocial lineages (6), but a broad comparative framework for exploring common principles of the molecular basis of eusocial evolution is lacking. One major unresolved question is whether independent evolutionary trajectories of eusociality involved similar or different genetic changes.

We explored the genetic basis of eusocial evolution in bees, an ideal group for comparative studies of social evolution. There is a wide diversity of social lifestyles within this group, from solitary to intermediately social to elaborate eusociality (8). Additionally, eusociality has been gained independently at least six times (9–12) in the bees, more than in any other group. These features make it possible to compare multiple, independent origins of

different social lifestyles among relatively closely related species. Furthermore, the extensive knowledge of bee natural history (8, 13, 14) provides a valuable framework for developing hypotheses about the adaptive significance of genetic changes detected in eusocial bee lineages.

To study patterns of molecular evolution associated with eusociality in bees, we generated ~1 Gbp of expressed sequence tags (ESTs) from a set of nine bee species (Table S1). This set of species reflects the remarkable social diversity in bees by including eusocial and non-eusocial species; three origins of eusociality (9, 10); and two different forms of eusocial lifestyle, “highly eusocial” and “primitively eusocial” (ref. 8; Fig. 1A). We combined the ESTs with genome sequence from the highly eusocial honey bee *Apis mellifera* (15), and created manually curated, 10-species, partial gene sequence alignments. We searched among the alignments for genes with accelerated rates of amino acid substitution in eusocial relative to non-eusocial lineages. Accelerated rates of protein evolution can reflect a molecular signature of positive natural selection (16), and shared patterns of acceleration among lineages can suggest an association between genetic changes and the evolution of shared traits.

Results

Characterization of Alignments. Our alignments corresponded to ~33% of the genes ($n = 3,647$, 3,638 after removal of alignments showing evidence of saturation) in the *A. mellifera* Official Gene Set (Dataset S1). To improve the utility of this genomic resource for evolutionary analysis, we used stringent criteria for assessing orthology to minimize misclassification of paralogous sequences within the alignments (SI Text). We also looked for functional biases in the set of genes represented by our alignments by performing Gene Ontology enrichment analyses. We identified biological processes that were over-represented and under-represented in our set of genes relative to all genes in the *A. mellifera* Official Gene Set (Dataset S1).

Phylogenetic Tree Inference from EST Data. We used Bayesian inference to estimate the phylogenetic relationships among bee species from our set of 3,638 alignments (SI Text). The phylogenetic tree inferred from third nucleotide positions was identical in structure to trees inferred in published studies that included

Author contributions: S.H.W., B.J.F., A.G.C., and G.E.R. designed research; S.H.W., B.J.F., A.V., M.E.H., K.V., and S.A.C. performed research; S.H.W., B.J.F., A.V., M.E.H., K.V., S.A.C., A.G.C., and G.E.R. analyzed data; and S.H.W., B.J.F., and G.E.R. wrote the paper. The authors declare no conflict of interest.

Data deposition: Transcriptome sequences reported in this paper are available at <http://ncbi.nlm.nih.gov/geo> and have been deposited in the NCBI Transcriptome Shotgun Assembly (TSA) database, <http://www.ncbi.nlm.nih.gov/tx/taxonomy/> (the accession nos. are in Table S1).

Freely available online through the PNAS open access option.

*S.H.W. and B.J.F. contributed equally to this work.

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This article contains supporting information online at www.pnas.org/lookup/suppl/doi:10.1073/pnas.1103672108.

What makes honey bees work together?

Lesson 4: What is the genetic basis for the evolution of eusocial behaviors?

July 2013

Genes involved in convergent evolution of eusociality in bees

S. Hollis Woodard¹, Brielle J. Fischman¹, Aarti Venkat², Matt E. Hudson³, Kranthi Varala³, Sydney A. Cameron¹, Andrew G. Clark⁴, and Gene E. Robinson^{1,5,6,7}

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Proceedings of the National Academy of Sciences (2011).

108: 7472–7477.

Abstract

Eusociality has evolved at least 11 different times in insects. There are many types of eusocial lifestyles, ranging from species living in small colonies with open conflict over reproduction (primitively eusocial), to species in which colonies contain hundreds of thousands of highly specialized sterile workers produced by one or a few queens (high or advanced eusociality). Although the evolution of eusociality has been intensively studied, the genetic changes involved in the evolution of eusociality are relatively unknown. We examined patterns of genetic changes across three independent origins of eusociality. We did this by sequencing mRNA of nine socially diverse bee species, and comparing the sequence from each species with each other, and with genome sequence from the honey bee *Apis mellifera*. We found a group of 212 genes with changes in amino acid sequence indicating accelerated evolution across all types of eusociality studied. We also found unique groups of 173 and 218 genes with accelerated evolution specific to either highly or primitively eusocial lineages, respectively. These results demonstrate that convergent evolution can involve a complicated pattern of genetic changes in both shared and lineage-specific groups of genes. Genes involved in signal transduction, gland development, and carbohydrate metabolism are among the most notable rapidly evolving genes in eusocial lineages. These findings provide a starting point for linking specific genetic changes to the evolution of eusociality.

Eusociality: A highly organized form of animal society. A species of animal is considered eusocial if its individuals live in groups that meet three criteria: 1. Reproductive division of labor: only a few members of society get to have offspring. 2. Cooperative care of offspring: members of the society help care for offspring that are not their own. 3. Multiple generations (for example, parents and offspring) live together.

Evolution: Change in inherited characteristics of populations over generations. Multiple factors, including natural selection, contribute to evolution.

Convergent, divergent: In convergent evolution, two species that are not closely related evolve to have similar traits; for example, both some birds and some butterflies use plant nectar for food. In divergent evolution, two species that are closely related evolve to be more different; for example, the shape of beaks in different species of finches in the Galapagos have become very different over time, as species adapt to different food sources. These terms can be used to describe molecular evolution, as well as evolution on the level of phenotypes. **Accelerated rate of evolution:** A quicker accumulation of evolutionary changes over time, often detected on the molecular level, in one species relative to another. Accelerated evolution can indicate an increase in the influence of natural selection on the evolution of a species.

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Adapted Primary Literature

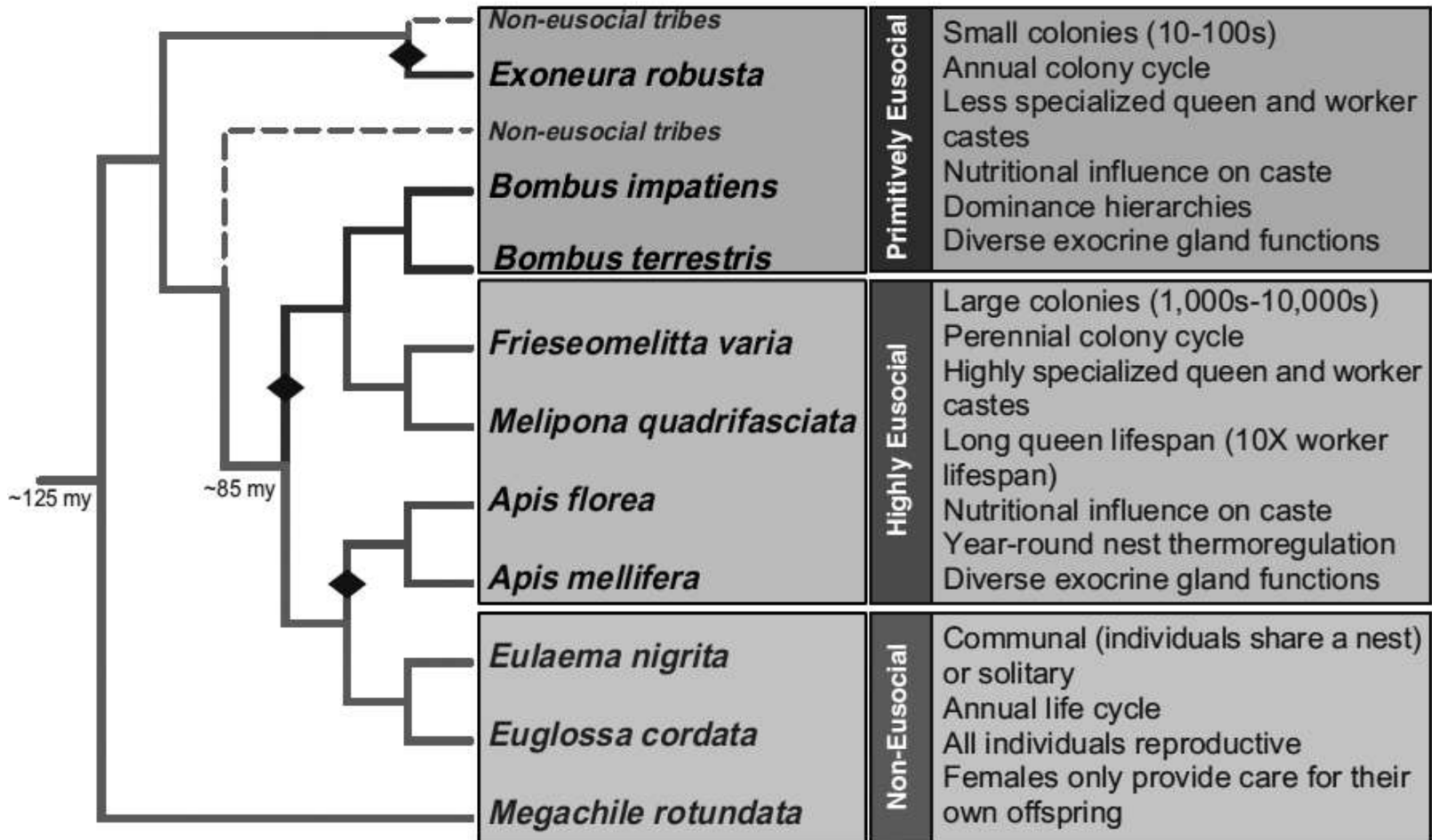


Figure 1

Adapted Primary Literature

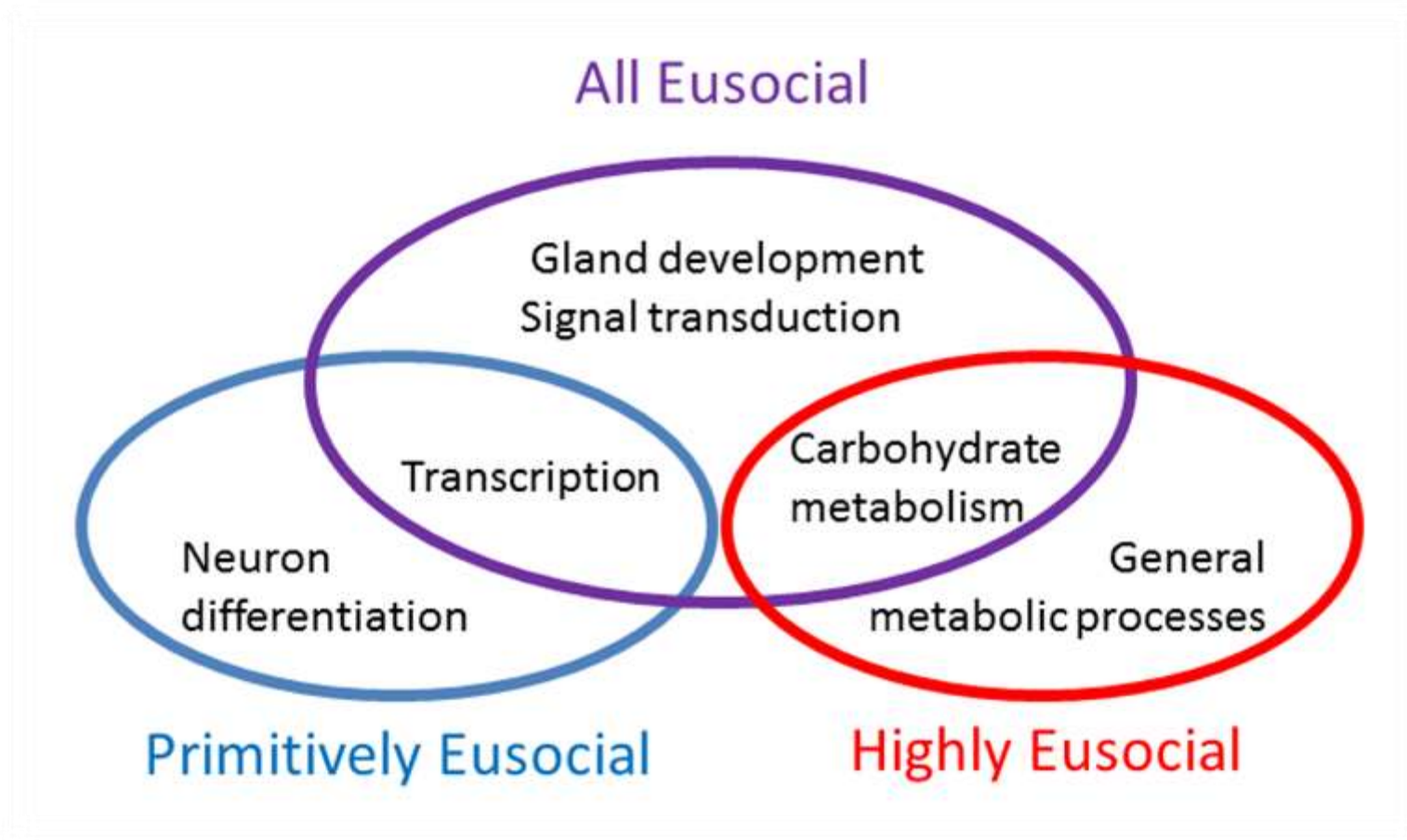
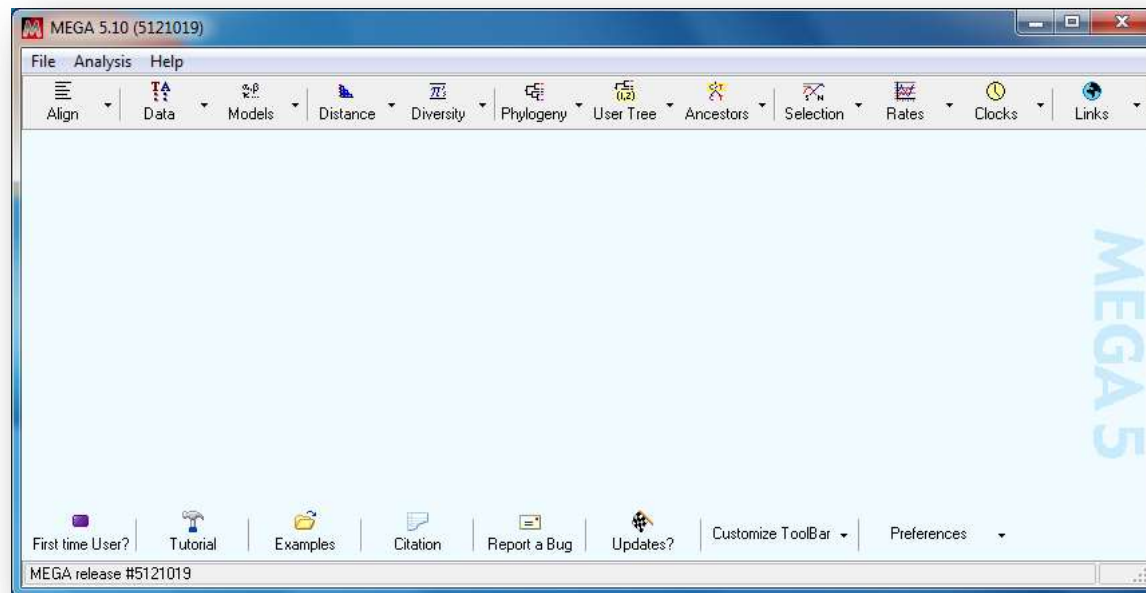


Figure 2

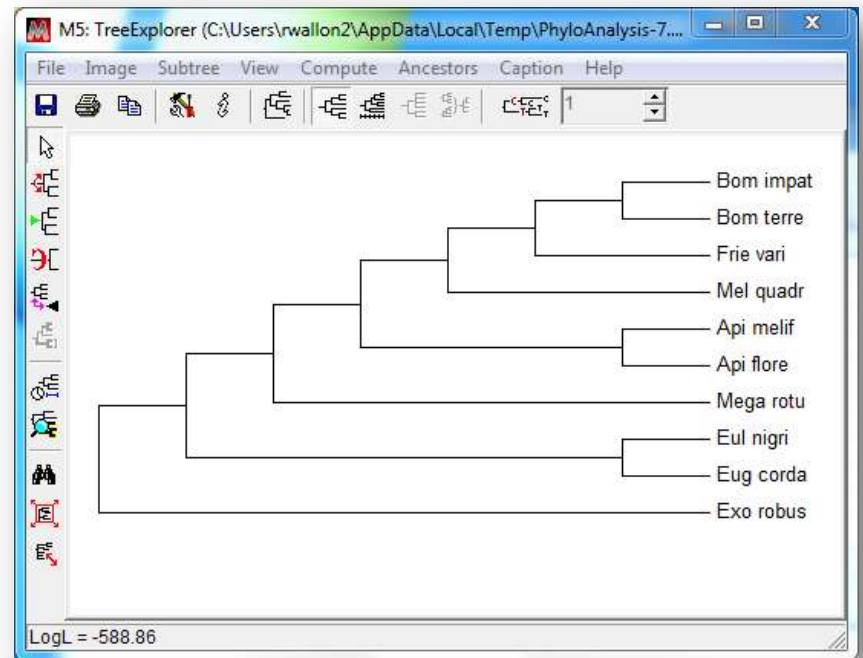
Construct a Phylogenetic Tree

- Pick a gene to study from the gene database and provide a rationale
- Create a phylogenetic tree with MEGA (<http://www.megasoftware.net>)



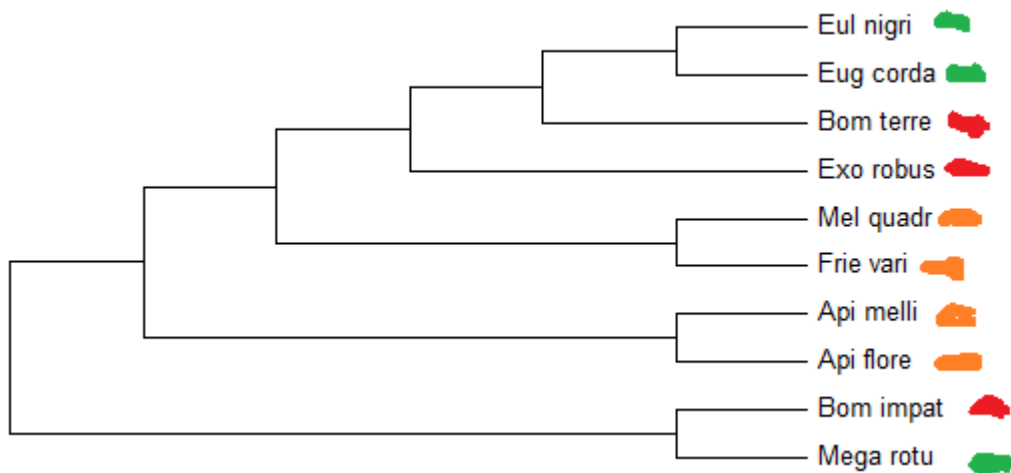
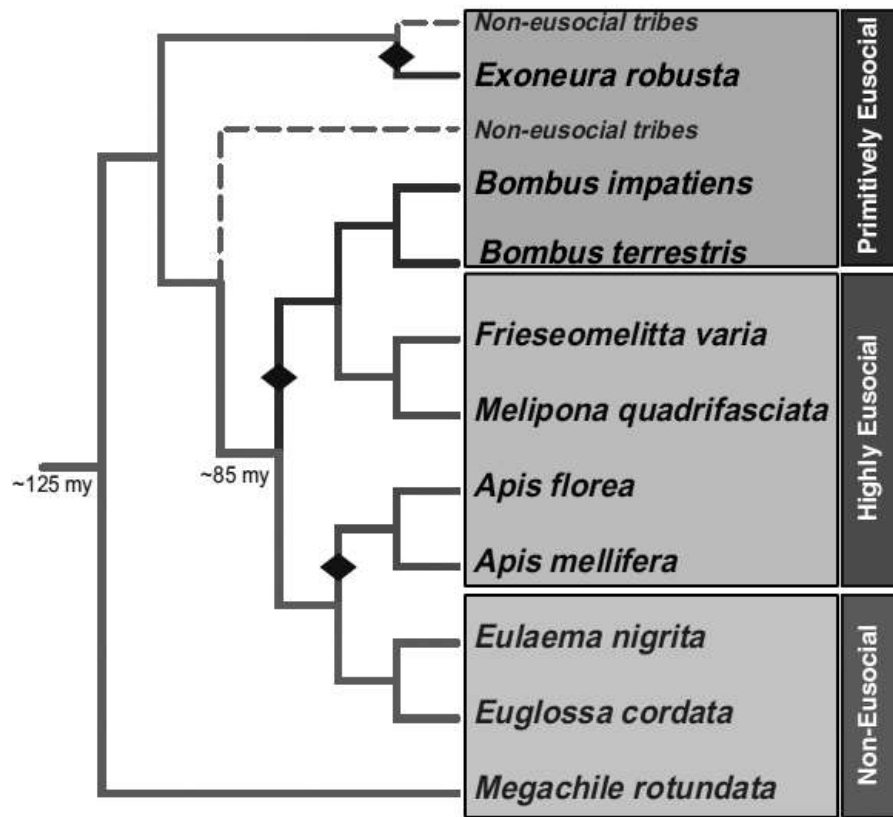
Compare Phylogenetic Trees

- (student sheet p. 11)
- Data analysis
- Scientific explanation
- Opportunity for engaging in argument



Connect to Your Classroom

- How would you use the activities in your classroom?



Acknowledgements

- NIH, SEPA
- University of Illinois

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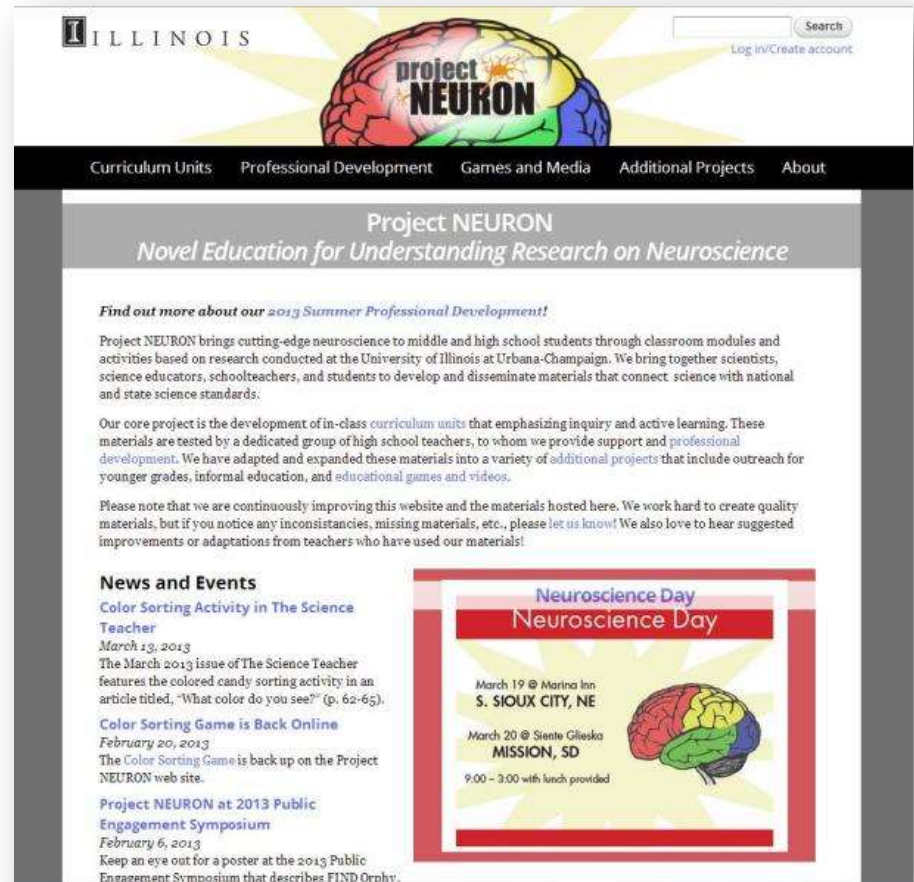
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The screenshot shows the Project NEURON website homepage. At the top, there is a navigation bar with the University of Illinois logo and the Project NEURON logo, which features a colorful brain. Below the navigation bar, the main content area is titled "Project NEURON" and "Novel Education for Understanding Research on Neuroscience". The page includes a search bar, a "Log in/Create account" link, and a navigation menu with items like "Curriculum Units", "Professional Development", "Games and Media", "Additional Projects", and "About". The main content area features a section for "Find out more about our 2013 Summer Professional Development!" followed by a paragraph of text. Below this, there is a "News and Events" section with several entries, including "Color Sorting Activity in The Science Teacher" and "Color Sorting Game is Back Online". On the right side, there is a "Neuroscience Day" event poster for March 19 and 20, 2013, in Sioux City, NE and Mission, SD.