Joel Sharbrough

Department of Biology, Colorado State University, Fort Collins, CO 80523-1878
✉ jsharbro@gmail.com 530.414.0312 Google Scholar Website GitHub

EDUCATION

2016 Ph.D. Biology
University of Iowa, Iowa City, IA 52241
Advisor: Dr. Maurine Neiman

2016 Bioinformatics Certificate
University of Iowa, Iowa City, IA 52241

2009 B.Sc. Biological Sciences
University of Notre Dame, Notre Dame, IN 46556
Advisor: Dr. Jeffrey L. Feder

2009 Secondary Education Teaching Certification
Saint Mary's College, Notre Dame, IN 46556
Advisor: Dr. Catherine Green

PROFESSIONAL EXPERIENCE

2016- Postdoctoral Fellow with Dr. Daniel B. Sloan
Department of Biology, Colorado State University, Fort Collins, CO

RESEARCH FUNDING

2019-2021 National Science Foundation. The Cytonuclear Dimension of Allopolyploidy PGRP – 1829176 ($1,829,880). Role: co-PI and co-author (with PI Daniel B. Sloan, co-PI Jonathan F. Wendel, and co-PI Corrine E. Grover). **[*This was a collaboration I helped forge between CSU and ISU. I was largely responsible for producing the first draft of the research plan for this proposal, which was then collaboratively developed into the now funded proposal, with a start date of January 1st, 2019. See link for CSU press release.*]**

2018-2020 National Science Foundation. Genomic and functional tests of mitochondrial-nuclear coevolution. DEB – 1753851 ($189,998). Role: Senior personnel and co-author (with PI Maurine Neiman and co-PI Kristi L. Montooth). [***I was responsible for drafting the molecular evolution aim of this proposal, which was awarded jointly to UI and UNL on July 1st, 2018.]***

2013-2015 National Science Foundation Doctoral Dissertation Improvement Grant. Evaluating phenotypic consequences of accelerated mutation accumulation in the absence of sex. DEB – 1310825 ($19,600). Role: Co-PI and lead author (with PI Maurine Neiman and co-PI Jennifer L. Cruise).

2013-2014 Iowa Academy of Sciences. Evaluating phenotypic consequences of accelerated mutation accumulation in the absence of sex. ISF #13-10 ($5,000). Role: Co-PI and lead author (with PI Maurine Neiman and co-PI Jennifer L. Cruise).

PUBLICATIONS

† – Corresponding author; * – Supervised Undergraduate Researcher; § – Supervised High School Intern

Peer-Reviewed Research Papers

1. Forsythe ES[1], **Sharbrough J[1],** Havird JC, Warren JW, Sloan DB. 2019. CyMIRA: the Cytonuclear Molecular Interactions Reference for *Arabidopsis*. *Genome Biology and Evolution*. 11: 2194-2202 DOI: https://doi.org/10.1093/gbe/evz144 **[[1] – Authors contributed equally to this work.]**
2. **Sharbrough J**†, Luse M*, Boore JL, Logsdon Jr JM, Neiman M. 2018. Radical amino acid mutations persist longer in the absence of sex. *Evolution*. 72: 808-824. DOI: https://doi.org/10.1111/evo.13465
3. Sloan DB, Wu Z, **Sharbrough J**. 2018. Correction of persistent errors in *Arabidopsis Col-0* reference mitochondrial genome sequence. *The Plant Cell.* 30: 525-527. DOI: https://doi.org/10.1105/tpc.18.00024
4. **Sharbrough J[1]**, Havird JC[1], Noe GR, Warren JW, Sloan DB. 2017. The mitonuclear dimension of Neanderthal and Denisovan ancestry in modern human genomes. *Genome Biology and Evolution*. 9: 1567-1581. DOI: https://doi.org/10.1093/gbe/evx114 **[[1] – Authors contributed equally to this work.]**
5. **Sharbrough J**†, Cruise JL, Beetch M, Enright NM*, Neiman M. 2017. Genetic variation for mitochondrial function in the New Zealand freshwater snail *Potamopyrgus antipodarum*. *Journal of Heredity*. 108: 759-768. DOI: https://doi.org/10.1093/jhered/esx041 **[** – Featured cover article.]**
6. McElroy KE, Denton RD, **Sharbrough J**, Bankers L, Neiman M, Gibbs HL. 2017. Genome expression balance in a triploid trihybrid vertebrate. *Genome Biology and Evolution.* 9: 968-980. DOI: https://doi.org/10.1093/gbe/evx059
7. Beck EA, Thompson AC, **Sharbrough J**, Brud E, Llopart A. 2015. Gene flow between *Drosophila yakuba* and *D. santomea* in subunit V of cytochrome c oxidase: A potential case of cytonuclear co-introgression. *Evolution*. 69: 1973-1986. DOI: https://doi.org/10.1111/evo.12718

Peer-Reviewed Review Articles and Perspectives

8. Sloan DB, Broz AK, **Sharbrough J**, Wu Z. 2018. Detecting rare mutations and DNA damage with sequencing-based methods. *Trends in Biotechnology.* 36: 729-740. DOI: https://doi.org/10.1016/j.tibtech.2018.02.009
9. **Sharbrough J**†, Conover JL, Tate JA, Wendel JF, Sloan DB. 2017. Cytonuclear responses to genome doubling. *American Journal of Botany.* 104: 1277-1280. DOI: https://doi.org/10.3732/ajb.1700293
10. Sloan DB, Havird JC, **Sharbrough J**. 2017. The on-again, off-again relationship between mitochondrial genomes and species boundaries. *Molecular Ecology*. 26: 2212-2236. DOI: https://doi.org/10.1111/mec.13959

Preprints Submitted to Peer-Reviewed Journals

11. Greimann ES*, Fahrner S, Woodell JD*, Hennessey SK*, Kline MR*, Moreno JA*, Peters MR*, Cruise JL, Neiman M, **Sharbrough J**†. 2018. Variation in physiological function across source populations of a New Zealand freshwater snail. In revision for *Integrative and Comparative Biology*. bioRχiv DOI: https://doi.org/10.1101/230979

INVITED SEMINARS AND CONFERENCE PRESENTATIONS

* – Supervised Undergraduate Researcher; § – Supervised High School Intern

Invited

1. **Sharbrough J**, Conover JL, Grover CE, Gyorfy M*, Wendel JF, Sloan SB. Genetics Society of America Early Career Seminar Series. *Cytonuclear coevolution in allopolyploid wheat.* September 20th, 2018.
2. **Sharbrough J**, Conover JL, Grover CE, Wendel JF, Sloan DB. Biology Department, Colorado State University. *Cytonuclear coevolution in allopolyploid wheat.* April 4th, 2018.
3. **Sharbrough J**, Conover JL, Grover CE, Wendel JF, Sloan DB. Plant Super Group, Colorado State University. *Cytonuclear coordination and coevolution in polyploid wheat.* February 23rd, 2018.
4. **Sharbrough J**, Neiman M. 3rd Annual Bioinformatics Retreat, University of Iowa. *Comparing radical and conservative amino acid substitutions in mitochondrial genomes of sexual and asexual lineages of* Potamopyrgus antipodarum*.* August 2013.

Contributed

1. **Sharbrough J**, Conover JL, Grover CE, Wendel JF, Sloan SB. Population, Evolutionary, and Quantitative Genetics Conference. Genetics Society of America*. Cytonuclear coordination and evolution in allotetraploid wheat.* May 2018.
2. **Sharbrough J**, Sloan DB, Montooth KL, Neiman M, Bankers LA, Boore JL, Fields PD, Jalinsky J, Logsdon Jr. JM, McElroy KE, Wilton PR. Evolution Conference. Society for the Study of Evolution. *Mitonuclear coevolution in the absence of sex.* June 2017.
3. **Sharbrough J**, Luse M*, Cherukurri P§, Greimann E*, Lin M*, Zhang M§, Boore JL, Logsdon, Jr. JM, Neiman M. Evolution Conference. Society for the Study of Evolution. *Effects of mutation-drift-equilibrium, purifying selection, and sex on mitochondrial mutation accumulation.* June 2016.
4. **Sharbrough J**, Luse M*, Boore JL, Logsdon Jr. JM, Neiman M. Evolution Conference. Society for the Study of Evolution. *Patterns of amino acid sequence evolution across various time scales in mtDNA of sexual and asexual lineages.* June 2014.
5. **Sharbrough J**. Midwest Ecology and Evolution Conference. *Patterns of molecular evolution across mating systems and ploidy classes*. March 2012.

FELLOWSHIPS AND SCHOLARSHIPS

2015	Evelyn Hart Watson Summer Fellowship, University of Iowa ($2,448)
2014	Graduate College Summer Fellowship, University of Iowa ($3,000)
2013-2014	NIH Bioinformatics T32 Training Grant, University of Iowa ($32,000)
2008	National Science Foundation Global Linkages of Biology, Environment, and Society Research Experience for Undergraduates Fellowship University of Notre Dame ($4,500)

HONORS AND AWARDS

2015	Outstanding Teaching Assistant Award, Department of Biology, University of Iowa
2013	W.D. Hamilton Award Finalist, Society for the Study of Evolution, Evolution Conference

PROFESSIONAL DEVELOPMENT

2019	Next Generation Sequencing Platforms and Libraries Course. CSU – Fort Collins, CO.
2019	Illumina Sequencing Symposium. CSU – Fort Collins, CO
2017-2018	Genetics Society of America Peer Reviewing Training Program

2017 Plant Genome Editing Conference, Colorado State University, Fort Collins, CO

PROFESSIONAL SOCIETIES

2019- Global Invertebrate Genomics Alliance
2019- Society for Integrative and Comparative Biology
2017- Genetics Society of America
2014- Society for the Study of Evolution
2013- Society for Molecular Biology and Evolution

PROGRAMMING LANGUAGES

1. Python
2. R
3. Bash
4. Perl

TEACHING AND MENTORING EXPERIENCE

Guest Lecturer

2019 Molecular and General Genetics – *Sex-Linked Inheritance*
2015-2016 Genetic Analysis of Biological Systems – *Potamopyrgus antipodarum*
2015 Evolution – *Endosymbiotic origin of mitochondria*

Teaching Assistant

2012-2016 Evolution
2014-2015 Foundations of Biology I
2011 Principles of Biology I

High School Science Teacher

2010 Biology, Earth Sciences, Mishawaka High School, Mishawaka, IN 46544
2009-2010 Biology, Biology II, Mishawaka High School, Mishawaka, IN 46544

Supervised Undergraduate Researchers

2017-2019 Matheus Gyorfy
2016-2018 Marissa Roseman
2015-2016 Emma Greimann
2014-2015 James D. Woodell
2013-2015 Nicole Enright
2013-2014 Michelle Sullivan
2013 Nikhil Puttagunta
2011-2014 Meagan Luse

Supervised High School Interns

2014 Michelle Zhang
2013 Praakruti Cherukuri

ACADEMIC SERVICE

Review Editor for –

2019- *Frontiers in Genetics*

Journal Reviewer for –

2019 *Evolution; Genes; Genetics; Molecular Biology and Evolution; Open Biology*

2018 *Canadian Journal of Zoology; Genetics* (3)*; Heredity; Plant Biology; The Plant Journal; Proceedings of the Royal Society of London B*

2017 *BioEssays; Canadian Journal of Zoology; Current Biology; Proceedings of the Royal Society of London B*

2016 *Molecular Biology and Evolution* (2)

2014 *Journal of Experimental Zoology*; *Molecular Biology and Evolution*

2013 *Biological Journal of the Linnean Society*

Committees –

2019 *GSA Peer Review Training Program Committee*

COMMUNITY OUTREACH

2017- Co-organizer. Presentations for first-year "Key Communities" undergraduates at Colorado State University on career opportunities and educational resources in bioinformatics

2017 Colorado Science Education Foundation State Science Fair Judge

2014-2016 Organized and implemented evolutionary biology lab module at Taylor Elementary School, Cedar Rapids, IA

2010-2016 Designer and executer of Iowa City Darwin Day High School outreach program

2010-2015 Organizing Committee for Iowa City's Darwin Day Celebration

2011-2012 Organized and implemented evolutionary biology lab module at Solon High School, Solon, IA

2011-2016 Solon High School Science Fair Judge

2012 St. Matthias Transfiguration School Science Fair Judge

RESEARCH STATEMENT – Joel Sharbrough

Cellular energy – a billion years of separate inheritance

The enzymes that carry out cellular respiration and photosynthesis are distributed across three entirely distinct and separately inherited genomes, yet eukaryotic health and fitness is critically dependent upon their successful interaction. Moreover, maternally inherited cytoplasmic genomes rarely undergo sexual recombination and exist in dozens to thousands of copies per cell, while corresponding nuclear genomes are bi-parentally inherited, one or more copies from each parent, via sexual reproduction. My research investigates how, in the face of these fundamentally different genetic systems, mitochondria and chloroplasts are able to successfully maintain the molecular machinery responsible for nearly the entire supply of cellular energy.

Mitonuclear coevolution in the absence of sex

Sexual reproduction is expected to increase the efficacy of natural selection by breaking down linkage disequilibria (LD) and allowing mutations to be selected independently from their genetic background. Because cytoplasmic genomes are uniparentally inherited, sexual reproduction also breaks down LD between nuclear and cytoplasmic genomes (i.e., cytonuclear LD). As a result, mutations in cytoplasmic genomes can be selected independently from nuclear variants, increasing the efficacy of selection in these "asexual" genomes. Accordingly, breakdown of cytonuclear LD should reduce the rate of deleterious mutation accumulation in cytoplasmic genomes; however, reduced cytonuclear LD will also decrease heritability of epistatic combinations of nuclear and cytoplasmic genotypes (Fig. 1).

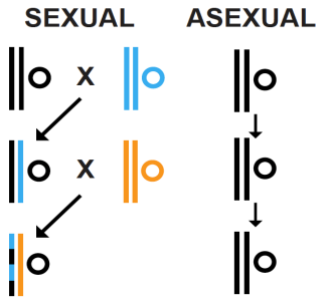

Figure 1. Mitochondrial genomes are swapped across diverse nuclear backgrounds in sexual lineages, but are co-inherited with nuclear genomes in asexual lineages.

Potamopyrgus antipodarum is a New Zealand freshwater snail species that features coexisting and competing sexual and asexual lineages, and asexual *P. antipodarum* are the product of multiple separate transitions from sexual ancestors, meaning that they represent independent "natural experiments" into the evolutionary consequences of sex. In collaboration with Dr. Maurine Neiman at the University of Iowa and Dr. Jennifer Cruise at the University of St. Thomas, I have shown that deleterious mutations persist as polymorphisms longer in mitochondrial genomes of asexual lineages than those of sexual lineages of *P. antipodarum* (Sharbrough et al., 2018 *Evolution*), and that asexual *P. antipodarum* exhibit heritable variation for mitochondrial function at the organellar and organismal levels (Sharbrough et al. 2017, *Journal of Heredity* **Featured Cover Article). Variation for mitochondrial function appears to be structured by lake of origin, such that snails from different lakes consume different amounts of oxygen when exposed to high temperatures (Greimann et al., In revision for *Integrative and Comparative Biology*). What has yet to be evaluated is whether the pattern of deleterious mutation accumulation I observed in mitochondrial genomes of asexual *P. antipodarum* 1) extends to the nuclear-encoded genes that function in the mitochondria and 2) contributes to variation in mitochondrial function, especially compared to sympatric sexual lineages.

While the genes encoded by the mitochondrial genome play a critical role in mitochondrial function, the overwhelming majority of proteins (>1000) that function in the mitochondria are encoded by the nuclear genome and are directly affected by sexual reproduction. Using a tremendous genomic dataset, I am currently comparing deleterious mutation accumulation in nuclear-encoded mitochondrial genes relative to genome-wide patterns in sexual vs. asexual lineages in collaboration with Dr. Kristi Montooth at University of

Nebraska-Lincoln. Genomic data is only one side of the story though: the extent of mitonuclear coevolution in sexual *vs*. asexual lineages must ultimately be evaluated in terms of mitochondrial function. Toward this end, Dr. Neiman, Dr. Montooth, and I have recently received a $189,998 award from the National Science Foundation to compare mitonuclear coevolution and oxygen consumption in extracted, living mitochondria from sexual vs. asexual lineages (role: co-author, Senior Personnel).

My dedicated investigation over the past five years into genotype-phenotype connections in *P. antipodarum* has already uncovered astounding biology. For example, in 2016 I helped discover that *P. antipodarum* underwent a relatively recent whole genome duplication, which has tremendous potential to affect cellular biology, including mitochondrial function (see below). Even more recently, I discovered that *P. antipodarum* and its close relative *P. estuarinus* exhibit signs of intra- and inter-molecular mitochondrial recombination, a process thought to be rare or absent from bilaterian mitochondrial genomes. Mitochondrial recombination in *Potamopyrgus* appears to be associated with a genome architecture that is remarkably reminiscent to that of chloroplast genomes, and my experience with plant organelle genomes as a postdoctoral researcher in Dr. Daniel B. Sloan's lab at Colorado State University opened my eyes to this astounding possibility. Though often neglected in animal mitochondrial research, mitochondrial recombination has tremendous potential to influence the evolution of mitochondrial genomes and mitochondrial function. In particular, I suspect this recombination activity is playing a role in DNA damage repair, but over evolutionary time, it may also aid in the maintenance of separate inheritance of cytoplasmic genomes by facilitating the removal of deleterious mutations.

Cytonuclear incompatibility and stoichiometry in allopolyploids

Hybridization and whole-genome duplication events (WGDs) have played a central role in the evolutionary history of eukaryotes in general and angiosperms in particular, and the extensive diversity of flowering plants is closely tied to a "wash-rinse-repeat" pattern of ploidy elevations and subsequent returns to diploidy. The maternal progenitor of a newly formed allopolyploid donates two critical pieces of genetic information: the mitochondrial and the plastid genomes, which encode some – but not all – of the machinery necessary to carry out cellular respiration and photosynthesis, respectively. Hybrids face a unique biological challenge in that the nuclear and cytoplasmic genes must successfully interact with one another, despite being inherited from different species (Sharbrough et al., 2017, *American Journal of Botany*). Maternal copies (i.e., homoeologs) of nuclear genes that encode proteins targeted to the mitochondria and plastids are thus expected to be more closely "matched" to cytoplasmic genomes than paternal homoeologs in hybrids. Consequently, the sorting out and stabilization of these cytonuclear interactions likely represent central determinants of the success of hybrid lineages (Fig. 2).

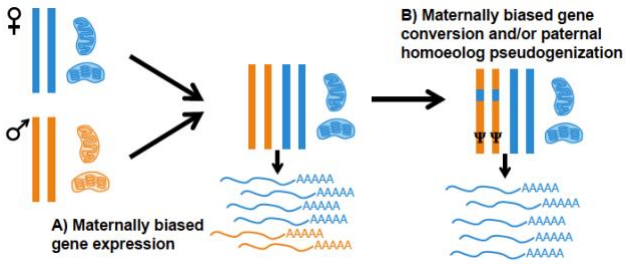

Figure 2. Resolution of cytonuclear incompatibilities in allopolyploids. Image from Sharbrough et al. 2017, Am J Bot.

Allopolyploids must also face the critically important task of maintaining coordinated gene expression of interacting genes in the face of a suddenly doubled (or more!) nuclear genome. Stoichiometric imbalance may be especially relevant to cytonuclear interactions, because although cytoplasmic genomes are commonly described as "effectively haploid" due to

their uniparental inheritance, each of these genomes actually exists in dozens to thousands of copies per cell. Thus, even in diploid species there are complex stoichiometric relationships between nuclear and cytoplasmic genomes. While the number of mitochondrial and plastid genomes within a cell varies tremendously across tissue types and development, these numbers are likely to be perturbed by WGD, as cytoplasmic genomes exist in a cellular environment in which all nuclear genes have been instantly doubled. Selection is therefore expected to favor compensatory mechanisms (see Fig. 3) that maintain coordinated expression between cytoplasmic and nuclear genes immediately following polyploidization (e.g., down-regulated expression of mitochondrial- and plastid-targeted genes in the nucleus, up-regulated cytoplasmic genome copy number, elevated levels of organelle biogenesis) as well as over longer timescales (e.g., subfunctionalization, pseudogenization).

In collaboration with Dr. Jonathan Wendel's lab at Iowa State University, Dr. Sloan and myself have recently been awarded $1,829,880 from the Plant Genome Research Program at the National Science Foundation to investigate cytonuclear incompatibility and stoichiometry in allopolyploid plants (role: co-author, Co-PI). This ambitious proposal will utilize a diverse panel of plant allopolyploids, including bread and pasta wheat, cotton, coffee, quinoa, peanuts, tobacco, *Brachypodium*, and *Arabidopsis* to compare patterns of selection, pseudogenization, and gene conversion in maternal *vs*. paternal homoeologs of organelle-targeted genes. I am also using this panel of polyploid species to evaluate the extent to which polyploids employ compensatory mechanisms to maintain cytonuclear stoichiometry at genomic, transcriptomic, and cellular levels compared to diploid relatives. Broadly, these analyses will reveal the "rules" of cytonuclear incompatibility and stoichiometry in allopolyploids, providing a nuanced understanding of how evolutionary phenomena affecting the nuclear genome can have profound consequences for cytonuclear genetics and organismal energy production.

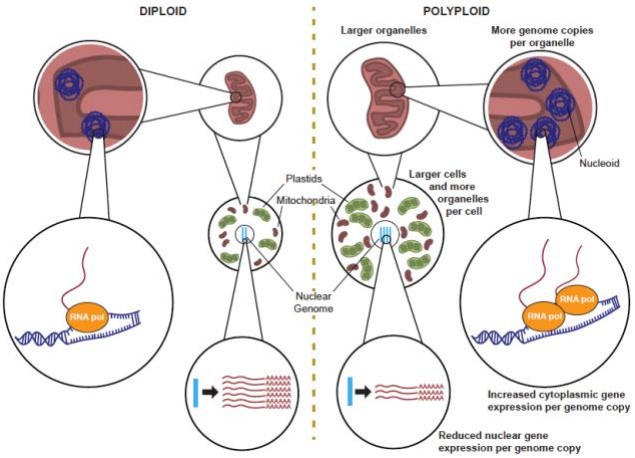

Figure 3. Mechanisms to restore cytonuclear stoichiometry in the wake of genome doubling. Image from Sharbrough et al. 2017, Am J Bot.

A broad look forward

With a primary eye turned towards graduate and undergraduate training in the biological sciences, my research program will take interdisciplinary, collaborative, and orthogonal approaches to investigate the evolution and function of eukaryotic energy production. Along the way, I will incorporate a wide diversity of organisms spanning the eukaryotic tree of life, whose whose unique reproductive systems, evolutionary histories, and ecologies can setup powerful natural experiments to tease apart how the co-dependency and separate inheritance of nuclear and cytoplasmic genomes affect cytonuclear co-evolution.

Building upon those who came before me and on my own discoveries, my first grant proposal will catalogue the extent to which mitochondrial genome architecture and recombination influence the evolution of mitochondrial genes and phenotypes across metazoans. My recent discovery of intra- and inter-molecular mitochondrial recombination in bilaterians

suggests that our understanding of mitochondrial genomics is terribly incomplete. Therefore, I will seek funding to (1) sequence the mitochondrial genomes of a taxonomically diverse set of animals using single-molecule sequencing technologies (e.g., PacBio, Oxford Nanopore) and (2) evaluate the dynamics of heteroplasmy and mitochondrial recombination in a series of intra-specific crosses of *P. antipodarum* lineages. This project will re-evaluate mitochondrial genome biology across metazoans and seek to connect those rules to phenotypic evolution. Together, these analyses represent critical avenues of investigation into the effects of sexual reproduction, mitochondrial recombination, polyploidy, and biogeography on cytonuclear coevolution and energy production.

Rubisco, the enzyme at the heart of carbon fixation within the chloroplast, is comprised of just two subunits, large (plastid encoded) and small (nuclear encoded). The nuclear-encoded *rbcS* gene is typically a multi-copy gene family that tends to experience high levels of inter-copy gene conversion. Intriguingly, this gene conversion appears to be maternally biased in allopolyploids (Gong et al., 2012 MBE, Gong et. Al 2014 MBE), suggesting that cytoplasmic incompatibilities may contribute to photosynthetic inefficiency, and may therefore reduce yield in allopolyploid crops. In collaboration with Zhi-qiang Wu (Agricultural Genomics Institute, Chinese Academy of Agricultural Sciences), I will leverage the resources developed in the course of our current PGRP grant (i.e., cytonuclear interacting gene identification, Iso-Seq transcriptome profiling, ribo-depleted RNA-seq, etc.) to (1) characterize the phylogenetic history, gene conversion status, and expression of *rbcS* gene copies in allopolyploid crops, (2) edit allopolyploid crop genomes to knock out and/or replace paternally derived copies of *rbcS* with maternally derived copies, and (3) compare photosynthetic efficiency and yield in edited plants compared to their unedited counterparts. Together, these analyses will characterize the extent to which allopolyploids experience selection to "fix" their paternally derived *rbcS* copies and will test a primary candidate for crop improvement using the plant's own genome as the editing template.

TEACHING PHILOSOPHY– Joel Sharbrough

In this era of cheap and highly accessible information, it takes very little effort to access much of the body of human knowledge within seconds. Given the availability of information, from what then should educators draw their purpose? What need have we of instructors and mentors if knowledge is so easily won?

The answer, of course, is that technological paradigm shifts do not alter the purpose of education. The province of educators still resides in guiding others to synthesize information into understanding, to use practical wisdom to evaluate choices amid complex variables, and to develop creative solutions for difficult problems. While information is now literally at our fingertips, understanding, wisdom, and creativity remain as essential as ever. As an award-winning teaching assistant, my teaching philosophy bridges the gap between my students and the biological sciences by guiding students to understanding through connection, wisdom through experience, and creativity through questioning.

One of the primary challenges that students face is in compiling the diverse array of facts at their disposal into a coherent understanding. Biology is a massive and complex field, and students are easily overwhelmed in their attempts to compile and integrate information. To help students overcome this challenge, I use broad ideas to build connections between disparate facts. Intuitively, this mental "scaffolding" is well suited to the natural sciences (see e.g., Bliss et al. 1996), in which biological mechanisms form the bridges connecting biological entities. Major concepts and mechanisms allow many facts to be gathered together into a consistent worldview, and as connectivity between ideas increases, so too does one's understanding. In my classroom, the mechanisms of organismal physiology (e.g., cellular respiration, photosynthesis) are first understood through the lenses of their origin and evolution. In this way, students can come to understand disparate concepts, including mechanisms of inheritance, the Central Dogma of Molecular Biology, epistasis, and the endosymbiotic origin of mitochondria and chloroplasts to name a few. While Evolution represents only one facet of a 21st century education in the biological sciences, it is one in which many different ideas can be clearly connected into a unified whole.

My graduate school mentor, Dr. Maurine Neiman often remarks, "nature is inherently messy". This belief is exemplified in the countless experiments demonstrating that empirical evaluation supersedes even the most elegant of hypotheses. The reliance of Biology upon both ideas and data means that students that lack practical experience in their discipline necessarily have a shallow foundation upon which their understanding is built. John Dewey, in *Experience and Education*, wrote, "[T]here is an intimate and necessary relation between the processes of actual experience and education" (p. 20). Merging the conceptual with the empirical as Dewey described is ideally suited to the scientific classroom. Indeed, allowing students the opportunity to collect their own data and describe their own findings represents an essential first foray into the scientific community. In this way, students learn which strategies yield the best (and, perhaps more importantly, the worst!) results for generating new knowledge. I am a dedicated advocate of research in the classroom: students can learn most when they are challenged to generate new knowledge. Given a practical foundation from which to start, students can use their wisdom and understanding in concert to delve into mysteries of the natural world for themselves.

Our uniquely human ability to develop creative solutions to difficult problems represents one of the most important missions that educators must undertake. Immediate availability of information can undermine this goal: it is easier to Google than to think. Accordingly, I make creative development a core tenet of my classroom in culture and in practice by demanding that students ask and answer their own questions. One method by which I establish this culture

explicitly is through a process known as "wait time" (see e.g., Tobin 1980). For each question posed, I employ two distinct methods: the first is accomplished by waiting a period of time between when a question is asked and when I accept responses, and the second by waiting to give feedback for several moments following a student's answer. During these two periods, the creative motors underlying learning have time to churn away freely as the first wait period allows students a chance to create solutions and the second to critique them. Over the course of a semester, students unconsciously become adept at creating and critiquing methods of inquiry based on merits rather than on an instructor's authority.

At NMT, I would be particularly excited to design a course around the Biology of Energy, in which students learn how organisms obtain, assimilate, produce, and consume energy in Nature. The course would primarily delve into two aspects of biological energetics with approximately equal weight: (1) evolution, ecology, and genetics, and (2) biochemistry, physiology, and biotechnology. Together these topics will provide students with a broad exposure to topics of interest within the biological sciences. Individual lessons will be a combination of direct instruction, small group discussions, and literature-guided large group discussion centered around the day's topic. Students will have two primary projects during the semester, the first of which will be to team up to write a scientific review of biological energetics, with each student taking responsibility for a topic of their own interest. As a class, we will combine the individual reviews, edit the product as a group, and submit the combined, edited review to a peer-reviewed journal at the end of the semester. The second major project will require students to perform novel analyses of data available on public data repositories (e.g., FigShare, GenBank, etc.) under my supervision to evaluate hypotheses generated in the course of our collective reviewing. At the conclusion of the course, students will understand how organisms produce and consume energy, and how those energy systems originated, diversified, and are transmitted to future generations. During the course, students will learn how to read scientific papers, practice scientific writing, be introduced to the scientific publication process, provide and receive constructive critiques to and from their peers, and directly engage in original scientific research.

In conclusion, I am a life-long learner committed to learning and to helping others learn. I pledge to continue my pedagogical education at NMT by attending regional and national workshops on teaching in the sciences, and by enrolling in courses in the Psychology and Education Department. By instilling understanding through scaffolding, wisdom through experience, and creativity through questioning, my students will be leaders of the next generation of young biologists.

Courses at NMT that I am prepared to teach:
BIOL 111-112; BIOL 311; BIOL 411; BIOL 435; BIOL 444; BIOL 455

In addition to the Biology of Energy course described above, I would be excited to design the following courses at NMT:
Mitochondrial Biology & Evolution; Genomics; Genome Biology and Evolution; Evolutionary Agriculture; Major Transitions in Evolution

Literature Cited

TEACHING PHILOSOPHY– Joel Sharbrough

1. Bliss J, Askew M, Macrae S. 1996. Effective teaching and learning: Scaffolding revisited. *Oxford Review of Education*, 22:37-61.
2. Dewey, J. (1938). Experience and education. Kappa Delta Pi. Pg 20.
3. Tobin KG. 1980. The effect of an extended teacher wait-time on science achievement. *Journal of Research in Science Teaching*, 17:469-475.