1. Cover page

Hope College HHMI Faculty/Students Collaborative Research Grant Proposal

Title of the Proposal: Exploring the Association of Rapid Diversification of Maple Lineages and the Diversity of Protective Pigments

Principal Investigators

Jianhua Li (Biology Department, Hope College)
Kenneth Brown (Chemistry Department, Hope College)
Airat Bekmetjev (Mathematics Department, Hope College)

Current undergraduate research students: Kaleb Skinner and Parker Bussies (Jianhua Li, Airat Bekmetjev), Gerardo Ochoa and Tanweer Ismail (Kenneth Brown)

Dear HHMI Steering Committee,

We write to submit a faculty/students collaborative research proposal titled “Exploring the association of rapid diversification of maple lineages and the diversity of protective pigments.”

Maples are one of the most important trees in the Northern Hemisphere, and have been divided into 19 subgroups (sections) based on morphological traits. The RD (rapid diversification) hypothesis states that maple sections may have diversified rapidly within a short time span by the Mid-Eocene. Maples are famous for colorful foliage due to the presence of various pigments, which protect plants from damages of the sunlight and/or herbivores. Thus, we hypothesize that the pigment diversity underlines the rapid diversification of maple lineages. In the proposed research we will work together with students to explore the association between the pigment diversity and the rapid radiation of maple lineages using quantitative statistical analyses and a solid phylogenetic framework to be constructed with plastid genome sequence data.

We have worked out the detailed protocol of plastid genome sequencing technology and obtained plastid genome data from five maple species using the IonTorrent PGM Sequencing Machine. Biology Department has recently acquired via a NSF MRI (major research instrumentation) grant. We have also secured sources of plant samples for the project and designed a protocol for determining the diversity of the protective pigments. Therefore, we are confident that the proposed research will be implemented with great success. The results will be presented in professional meetings and published in peer-reviewed journals. We will also use the results in a collaborative research proposal to be submitted to NSF in collaboration with Michigan State University and Oregon State University.

With the HHMI grant support, we will establish an interdisciplinary research area with a focus on the quantitative analyses of interactions of plants, insects, and chemicals, train students to become research leaders in the STEM fields, and develop materials for a research-based, interdisciplinary course based on the results from the proposed research.

We are excited about the opportunity to work across different disciplines and sincerely hope you will grant the application serious consideration.

Sincerely yours,

Jianhua Li, Ken Brown, and Airat Bekmetjev
2. Abstract

Maples are an important tree group in the Northern Hemisphere with the center of diversity in China, and several unique species in Europe, the Middle East, Japan, and North America. Albeit with a long history of study, our understanding of the natural history of maples remains limited; many fundamental questions have not been answered with satisfaction. For example, where and when did maples originate? how did maples migrate throughout the Northern Hemisphere? what are the evolutionary relationships among major groups of maples? and what are the temporal patterns of and causes for the diversification of maple lineages? Studies of the fossil records have led to the RD (rapid diversification) hypothesis that maple lineages may have diversified rapidly within a short time span by the Mid-Eocene. Recent molecular analyses using less than 5,000 data points have not provided enough information to establish a well-supported phylogenetic framework. The lack of the framework hampers our ability to test the RD hypothesis. Therefore, the first objective of the proposed research is to establish the phylogenetic framework using plastid genome sequences with over 100,000 data points. Maples are well known for their beautiful foliage in the spring and fall due to the presence of colorful pigments (xanthophylls and anthocyanins). Because of their protective function against environmental factors (e.g., drought, excessive sunlight, and herbivores), the pigments provide adaptive advantages to plants, thus promoting lineage RD. Based on this, we propose the CP (colorful pigments) hypothesis that colorful pigments may have played an important role in the rapid radiation of maple lineages. In the proposed research, we will test the CP hypothesis based on chemical determination of the pigment diversity and quantitative analysis of the association between the diversity of colorful pigments and the lineage diversification. The solid phylogenetic framework will also provide answers to the other fundamental questions about the natural history of maples in the world. The interdisciplinary project will for the first time examine the potential association of pigment production and adaptive radiation of maples in the world. We will cross-train students in biology, chemistry, and mathematics. The successful implementation of the project will provide materials and protocols for developing a research-based, interdisciplinary course. In addition, we will present our results to the scientific communities via professional meetings and peer-reviewed publications as well as to the general public via talks and websites.
3. Project Description
3.1. Background Information and Significance of the Proposed Work

*Acer* is the largest tree genus in the broad-leaved deciduous forests of the Northern Hemisphere (Wolfe and Tanai 1987) and includes well-known and horticulturally important species such as sugar maple (*A. saccharum*), red maple (*A. rubrum*), Japanese maple (*A. palmatum*), and Norway maple (*A. platanoides*). Many species are also important sources of commercial products, e.g., maple syrup from *Acer saccharum* and construction timber from *Acer saccharum*, *A. rubrum*, and *A. pseudoplatanus* (van Gelderen et al. 1994).

*Acer* is most closely related to *Dipteronia* (2 species) and *Aesculus* (13 species) in the family Sapindaceae (Judd et al. 1994; Gadek, Fernando et al. 1996). Within *Acer*, the most important early monograph by Pax (1885, 1886, 1902) divided then 114 species into 13 sections. Many authors have since adopted this system with some revisions (Rehder 1905; Koidzumi 1911; Nakai 1915; Pojarkova 1933; Hu and Cheng 1948; Momotani 1962; Fang 1966; Ogata 1967; de Jong 1976, 1994; Delendick 1981; Mai 1984; Huang et al. 2002). The most recent taxonomic system of *Acer* (de Jong 2004) recognized 19 sections. Sections of *Acer* have also been grouped in various ways based on different morphological characters. Although there have been several molecular phylogenetic studies of maples (Hasebe et al. 1998; Suh et al. 2000; Tian et al. 2002; Li et al. 2006), none have used a large amount of DNA sequence data from either the plastid or nuclear genomes, and as a result relationships among sections of *Acer* remain largely unresolved, which hampers our understanding of the natural history of maples in the world. In addition, for morphologically unique species such as *Acer carpinifolium* and *A. spicatum*, our ignorance of which species are their close relatives makes it difficult for directing the plant breeding and conservation efforts. It is therefore urgently needed to establish a well-resolved phylogeny for the genus. The recent development of sequencing the entire plastid genome holds great promises in resolving phylogenetic relationships among maple sections because it can potentially provide nearly 100,000 data points (Atherton et al. 2010). It is possible that the poor resolution of relationships among sections of *Acer* reflects a history of rapid diversification (RD), as observed in many other groups of organisms (Morrison et al. 2004; Soltis et al. 2005). The RD hypothesis seems to be consistent with the fossil history of *Acer*. Fossil species of *Acer* first appeared in late Cretaceous and diversified during the Eocene, and by the Mid-Eocene most lineages had evolved. Based on this, Wolfe and Tanai (1987) concluded that there was a rapid diversification of *Acer* lineages in the Mid-Eocene. The solid phylogenetic framework will help test the RD hypothesis.

If the RD hypothesis is true, what may have accounted for the successful rapid diversification of maple lineages? Maples are well known for their beautiful spring and fall foliage due to the presence of colorful pigments. The colorful pigments other than chlorophylls, which are the key pigment for photosynthesis, function as a sunscreen to protect against damage from excess solar energy (Field et al. 2001; Gould et al. 1995; Hoch et al. 2003) or as a warning to potential herbivores (Archetti et al. 2009). Therefore, it is reasonable to hypothesize that the colorful pigments (CP) may have played an important role in the successful diversification of maples. In the proposed research we will test the CP hypothesis by exploring the association between the pigment diversity and the rapid radiation of maple lineages with the reference to the close relatives of maples, which have low species diversity.

The proposed research will for the first time establish a solid phylogenetic framework for maple sections in the world based on plastid genome data, which will in turn provide new
insights into the natural history of maples in the world. It will provide the first quantitative test for the RD hypothesis and for the newly proposed CP hypothesis. The positive association of RD and CP in maples may be tested in other plant groups to see whether it can be generalized. Students will be cross-trained in biology, chemistry, and mathematics. The successful implementation of the project will also provide materials and protocols for developing a research-based, interdisciplinary course.

3.2. Objectives of the Project
The main goals of the proposed project are dual: 1) to establish a robust phylogeny of all section and series of _Acer_ and test the RD hypothesis that maple lineages diversified rapidly in the Mid-Eocene, and 2) to determine the diversity of colorful pigments in maples and relatives and test the CP hypothesis that there is an association between the pigment diversity and the diversification of maple lineages.

3.3. Materials and Methods
3.3.1. Species to be included in the project
We will obtain plastid genome data from 26 species, 20 of which are maples representing all sections and series, and the other three species represent close relatives of _Acer_ (Table 1).

Table 1. Species to be included. **Boldface** indicates species that we have recently completed the PCR amplification of the plastid genome.

<table>
<thead>
<tr>
<th>Classification (de Jong 2004)</th>
<th>Species</th>
<th>Source</th>
<th>DNA number</th>
</tr>
</thead>
<tbody>
<tr>
<td>Section Parviflora</td>
<td><em>A. nipponicum</em></td>
<td>RBGE 19795193</td>
<td>Li 4045</td>
</tr>
<tr>
<td>Section Spicata</td>
<td><em>A. spicatum</em></td>
<td>Arnold Arb. 359-79*D</td>
<td>Li 6444</td>
</tr>
<tr>
<td>Section Palmata</td>
<td><em>A. palmatum</em></td>
<td>Arnold Arb. 585-88*C</td>
<td>Li 6451</td>
</tr>
<tr>
<td>Section Wardiana</td>
<td><em>A. wardii</em></td>
<td>Yunnan. Li 4890</td>
<td>Li 4890</td>
</tr>
<tr>
<td>Section Macrantha</td>
<td><em>A. pensylvanicum</em></td>
<td>Arnold Arb. 1331-79*B</td>
<td>Li 6446</td>
</tr>
<tr>
<td>Section Glabra</td>
<td><em>A. glabrum</em></td>
<td>Aaron Liston</td>
<td>Li 4275</td>
</tr>
<tr>
<td>Section Arguta</td>
<td><em>A. argutum</em></td>
<td>Arnold Arb. 640-77*B</td>
<td>Li 6445</td>
</tr>
<tr>
<td>Section Negundo</td>
<td><em>A. negundo</em></td>
<td>Holland, MI</td>
<td>Li 4041</td>
</tr>
<tr>
<td></td>
<td><em>A. henryi</em></td>
<td>Arnold Arb. 164-83*A</td>
<td>Li 6450</td>
</tr>
<tr>
<td>Section Indivisa</td>
<td><em>A. carpinifolium</em></td>
<td>Arnold Arb. 10959*B</td>
<td>Li 6443</td>
</tr>
<tr>
<td>Section Acer</td>
<td><em>A. saccharum</em></td>
<td>Holland, MI</td>
<td>Li 6439</td>
</tr>
<tr>
<td>Section Pentaphylla</td>
<td><em>A. pentaphyllum</em></td>
<td>Quarryhill Arb.2001.430B</td>
<td>Li 4262</td>
</tr>
<tr>
<td>Section Trifoliata</td>
<td><em>A. triflorum</em></td>
<td>Arnold Arb.</td>
<td>Li 6442</td>
</tr>
<tr>
<td>Section</td>
<td>Species</td>
<td>Location</td>
<td>Accession</td>
</tr>
<tr>
<td>---------------------</td>
<td>------------------</td>
<td>-------------------------------</td>
<td>-----------</td>
</tr>
<tr>
<td>Section Lithocarpa</td>
<td><em>A. diabolicum</em></td>
<td>Arnold Arb. 2625<em>A</em></td>
<td>Li 6447</td>
</tr>
<tr>
<td>Section Macrophylla</td>
<td><em>A. macrophyllum</em></td>
<td>Morton Arb. 31-86</td>
<td>Li 4240</td>
</tr>
<tr>
<td>Section Plantanoidea</td>
<td><em>A. platanoides</em></td>
<td>Holland, MI</td>
<td>Li 6440</td>
</tr>
<tr>
<td>Section Pubescentia</td>
<td><em>A. stenolobum</em></td>
<td>De Jong, P.</td>
<td>Li 5646</td>
</tr>
<tr>
<td>Section Ginnala</td>
<td><em>A. tataricum</em></td>
<td>Arnold Arb. 1302-80<em>A</em></td>
<td>Li 6449</td>
</tr>
<tr>
<td>Section Rubra</td>
<td><em>A. saccharinum</em></td>
<td>Holland, MI</td>
<td>Li 3521</td>
</tr>
<tr>
<td>Section Hyptiocarpa</td>
<td><em>A. laurinum</em></td>
<td>Tian 2079, XSBN Bot. Gard.</td>
<td>Li 3353</td>
</tr>
<tr>
<td>Aesculus</td>
<td><em>A. glabra</em></td>
<td>Arnold Arb. 1221-79<em>A</em></td>
<td>Li 6448</td>
</tr>
<tr>
<td>Aesculus</td>
<td><em>A. chinensis</em></td>
<td>Arnold Arb. 156-2001</td>
<td>-</td>
</tr>
<tr>
<td>Aesculus</td>
<td><em>A. hippocastanum</em></td>
<td>Arnold Arb. 12648</td>
<td>-</td>
</tr>
<tr>
<td>Aesculus</td>
<td><em>A. californica</em></td>
<td>UBC Bot. Gard.</td>
<td>-</td>
</tr>
<tr>
<td>Dipteronia</td>
<td><em>D. sinensis</em></td>
<td>Liu; NACPEC 08003</td>
<td>Li 6075</td>
</tr>
<tr>
<td>Dipteronia</td>
<td><em>D. dyeriana</em></td>
<td>Tian</td>
<td>Li 3363</td>
</tr>
</tbody>
</table>

### 3.3.2. Plastid genome amplification using Phusion PCR and primer walking method

The circular plastid genome of plants has four major regions: the large single copy region (LSC), small single region (SSC), and two inverted repeats (IRa and IRb) situated between LSC and SSC. We have used 73 pairs of primers to amplify the three regions (IRa and IRb are identical to each other) from 13 species (12 maples and 1 *Aesculus*). We will use the same method to amplify the plastid genome of the remaining species (see Table 1).

### 3.3.3. DNA library construction and sequencing

We will use Life Technologies’s Ion Xpress Plus gDNA fragment library preparation kits to construct library for each of the amplified plastid genomes. The template will be prepared using Ion OneTouch 200 Ion Sphere particles, which will then be enriched using an Ion OneTouch ES station. The enriched ISPs will be sequenced with an IonTorrent PGM sequencing machine. The DNA sequences of ca. 200 bp will be assembled *de novo* using the IonTorrent Assembler. And the contiguous sequences will be aligned against known plastid genomes in a SEQUENCHER program.

### 3.3.4. Phylogenetic analysis and testing the RD hypothesis

Plastid sequences of all species will be aligned using MUSCLE program and a maximum likelihood method will be used to reconstruct the phylogenetic tree using MEGA program (Tamura et al., 2011). Reliable fossils of maples and relatives with known ages will be used to estimate the times of divergence of different lineages (sections) of maples under the Bayesian theorem as implemented in the BEAST program (Drummond et al., 2012). Statistical analysis will be conducted to test the RD hypothesis based on the reconstructed phylogenetic framework.
3.3.5. Determination of pigment diversity and its association with species diversity

Tools from analytical chemistry (e.g., HPLC) will be used to determine the diversity of xanthophylls and anthocyanins in the leaves of the selected species (Table 1). The association of species diversity and the diversity of the pigments will be analyzed using independent contrasts method by comparing maples and their relatives (Dipteronia and Aesculus) as well as the pairs of sections in the phylogeny with differential diversity of pigments and number of species (Garland 1992).

3.4. Expected Outcomes

Li has confirmed the sources of all the plant materials for this project with botanical gardens and arboreta and has successfully obtained the plastid genome data from five maple species and one species of Aesculus. Brown has worked out the detailed protocol of determining the diversity of pigments. Bekmetjev has compared different statistical methods for testing the RD and CP hypotheses within a phylogenetic framework. Therefore, we expect to implement the proposed research successfully within the timetable without serious difficulties. The results will be presented in local, national, and international conferences and published in peer-reviewed journals. Three students will be cross-trained in chemistry, biology, and mathematics through the project. The project will provide materials and protocols for developing a research-based, interdisciplinary course or case study. Dr. Li was one of the PIs on a preliminary collaborative research proposal submitted via Michigan State University to the NSF on January 23, 2013 with a focus on the species diversity of maples in Europe, North America, and Asia. The results from the HHMI project will be used as preliminary data for the full proposal if the preliminary proposal passes the NSF panel review.

3.5. How the Project will Connect to Other HHMI 2012 Programs

The proposed project will strengthen the other HHMI 2012 programs. First, students trained via the project will gain a deeper understanding of the interdisciplinary nature of scientific research and become well-trained research leaders in any STEM fields. Second, successful implementation of the project will lay a foundation for designing a research-based interdisciplinary course involving biology, chemistry, and mathematics. Third, students in the project will be actively engaged with students involved in other HHMI-supported projects (such as course-based research experience program).

3.6. Plans for External Funding to Continue Work

We will seek external funding from NSF to expand our species sampling in each of the sections and series within Acer to gain more comprehensive insights into the association of species diversification and the diversity of protective pigments in plant species.

3.7. Timeline

The project will be conducted from June 1, 2013 through May 31, 2014. Plant materials will be collected in June 2013 from various arboreta and botanical gardens (see Table 1), and DNA and chemical extraction will be completed in the summer of 2013. We will focus on gathering DNA sequence and colorful pigment data and testing various statistical methods in the first 9 months of the project. In the last three months of the project we will concentrate on data analyses and writing manuscripts based on the results.
4. Literature cited


5. **Budget and justification**
A total budget of $15,000 is requested for the proposed research covering two major areas:

1) **Plastid genomic sequencing ($11,310)**
   The fund is for plant material acquisition ($500) and molecular kits ($10,810) for DNA extraction, PCR amplification of plastid genome, PCR product cleanup, library construction, enrichment, and genomic sequencing of 26 species of maples and close relatives (see Table 2 for details).

2) **Chemical determination of pigments ($3,690)**
   The fund is for supplies for testing types and concentrations of various pigments in maple species.

Table 2. Budget items for each of the steps needed to obtain the plastid genome data for 26 samples. The fund will be spent on PCR and sequencing reagents and supplies. There are generally two or three students working in our labs during the semester for research credits.

<table>
<thead>
<tr>
<th>Reagent or kit</th>
<th>Vendor &amp; Catalog#</th>
<th>Unit price</th>
<th>Cost</th>
</tr>
</thead>
<tbody>
<tr>
<td>Phusion PCR master mix kit</td>
<td>NEBL M0531L</td>
<td>$435</td>
<td>2 x $435 = $870</td>
</tr>
<tr>
<td>Qiaquick PCR purification kit</td>
<td>Qiagen 28104</td>
<td>$105</td>
<td>$105</td>
</tr>
<tr>
<td>Pippin Prep Kit 2010</td>
<td>Invitrogen 4472170</td>
<td>$450</td>
<td>3 x $450 = $1,350</td>
</tr>
<tr>
<td>Ion Xpress™ Plus Fragment Library Kit</td>
<td>Invitrogen 4471269</td>
<td>$750</td>
<td>2 x $750 = $1,500</td>
</tr>
<tr>
<td>Ion PGMTM 200 Xpress Template Kit (replaces PN 4471253)</td>
<td>Invitrogen 4474280</td>
<td>$1250</td>
<td>2 x $1250 = $2,500</td>
</tr>
<tr>
<td>Ion Sphere™ Quality Control Kit</td>
<td>Invitrogen 4468656</td>
<td>$350</td>
<td>2 x $350 = $700</td>
</tr>
<tr>
<td>Ion PGMTM 200 Sequencing Kit (replaces PN 4471258)</td>
<td>Invitrogen 4474004</td>
<td>$1000</td>
<td>3 x $1,000 = $3,000</td>
</tr>
<tr>
<td>Ion 314 Chip Kit</td>
<td>Invitrogen 4462923</td>
<td>$792</td>
<td>2 x $792 = $1,584</td>
</tr>
<tr>
<td>Total:</td>
<td></td>
<td></td>
<td>$10,810</td>
</tr>
</tbody>
</table>
6. Biographical sketches
6.1. Jianhua Li

PROFESSIONAL PREPARATION

Postdoc, Plant Molecular Systematics, 1998, Harvard University  
Ph.D., Plant Biology, 1997, University of New Hampshire  
M.S., Botany, 1987, Huazhong Normal University  
B.S., Biology, 1984, Henan Normal University

APPOINTMENTS

2009-present: Associate Professor of Biology, Hope College, MI.  
2005-present: Adjunct Professor, Zhejiang University, Hangzhou, China  
1999-2004: Botanical/Horticultural Taxonomist, Arnold Arboretum  
1999: Putnam Postdoctoral Fellow, Harvard University Herbaria  
1993-1997: Graduate Assistant, University of New Hampshire  
1992: Visiting Researcher, Institute of Botany, Academia Sinica, Beijing  
1989-1991: Assistant Professor, Department of Biology, Henan Normal University  
1987-1988: Assistant Professor, Department of Geography, Henan University

RECENT SYNERGISTIC ACTIVITIES

Selected Awards and Honors
Adjunct Professor (Henan Agricultural University (2001-)); Member of the Editorial Committee of Arnoldia (2003-2009), and Associate Editor of the Journal of Systematics and Evolution (2007-present); Adjunct Professor (Zhejiang University, Henan Agricultural University, Nanyang Teachers College).

Selected Invited Seminars:
Harvard University, University of New Hampshire, Zhejiang University, Zhongshan University, South China Agricultural University, Northwest University, Beijing Institute Botany, Henan Agricultural University, Guizhou University, New England Botanical Club, Michigan Botanical Club.

Manuscript Reviews:

SELECTED PUBLICATIONS (* denotes an undergraduate student)


Li, J., J. Corajod*, H. Vander Stel*, and A. Homkes*. 2011. The mycorrhizal system of


6.2. Kenneth Brown

A. Professional Preparation
Oral Roberts University Chemistry B.S., 1993
Oklahoma State University Chemistry Ph.D., 1999

B. Appointments
Associate Professor of Chemistry, Hope College, 2006-Present.
Assistant Professor of Chemistry, Hope College, 2002-2006.
Assistant Professor of Chemistry (Term Position), Hope College, 1999-2002.
Teaching Assistant, Department of Chemistry, Oklahoma State University, 1995-1999.

C. Recent Significant Publications (* indicates undergraduate authors)

D. Synergistic Activities
(i) Talks

E. Collaborators and other Affiliations
Professor Tom Higgins (Harold Washington College, Chicago, IL)
Professor Tom Neils (Grand Rapids Community College)
Dr. Marc Wirtz (PPG Industries, Electrochemical Group, Pittsburgh, PA)
Professor Phillip Buhlman (University of Minnesota)
Professor Graham Peaslee (Hope College)
Professor Thomas Bultman (Hope College)
Dr. Jeffrey Hendricks (Biotectix, LLC)
Dr. Sarah Richardson-Burns (Biotectix, LLC)
Dr. Elizabeth M. Sanford (Hope College)

F. Graduate Advisor
Horacio A. Mottola (Oklahoma State University-Retired)

G. Undergraduate Students Supervised: 45
6.3. Airat Bekmetjev

PROFESSIONAL PREPARATION:

<table>
<thead>
<tr>
<th>Institution</th>
<th>Major</th>
<th>Degree &amp; Year</th>
</tr>
</thead>
<tbody>
<tr>
<td>Moscow State University, Moscow, Russia</td>
<td>Applied Mathematics</td>
<td>B.S. 1991</td>
</tr>
<tr>
<td>Arizona State University, Tempe, AZ</td>
<td>Mathematics</td>
<td>Ph.D. 2002</td>
</tr>
</tbody>
</table>

APPOINTMENTS:
- Associate Professor of Mathematics, Hope College, 2009 – present
- Assistant Professor of Mathematics, Hope College, 2003 - 2009.
- Assistant Professor, Gettysburg College, 2002 - 2003.
- Teaching Assistant/Graduate Student, Arizona State University, 1996-2002
- Scientist/Researcher, Center for Computing and Applied Mathematics, Moscow, Russia, 1991-1995

SELECTED PUBLICATIONS:

OTHER PUBLICATIONS
* undergraduate students

SYNERGISTIC ACTIVITIES:
- Undergraduate research advisor. Every summer I participated as an undergraduate research advisor in projects funded by NSF REU and NIH AREA15 programs
- Actuarial career. Participated in the development of a pre-professional program in actuarial science through the Crossroads Project at Hope College
- **REACH (Research Experience Across Cultures at Hope College).** Participated in Hope College’s REACH program by being an advisor of a summer research team of high school students. The goal of the program for high school students and teachers is to create opportunities for students and teachers to engage in research projects with Hope's science and math faculty.

- **Conferences and workshops.** Participated in organization of several students research conferences such as Spring Undergraduate Conference at Gettysburg College, Undergraduate Research Session at Pennsylvania MAA meeting, Undergraduate Research Conference at Moravian College. Participated as an invited speaker at Pew New Faculty Workshop at Hope College.

- **Publications Review.** Reviewer of publications for journals Ars Combinatoria and College Mathematics Journal.

**COLLABORATORS & OTHER AFFILIATIONS:**

- **Collaborators:**
  - Graham Brightwell (London School of Economics)
  - Charles Cusack (Hope College)
  - Andrzej Czygrinow (Arizona State University)
  - Glenn Hurlbert (Arizona State University)
  - Tim Pennings (Hope College)
  - Todd Swanson (Hope College)
  - Nathan Tintle (Hope College)

- **Graduate and Post Doctoral Advisors:**
  - Glenn Hurlbert (Arizona State University)

**7. Current and pending support**

- **7.1. Jianhua Li.** Pending from MSGC grant. $5000. Unraveling the differential speciation rates of eastern Asian and eastern North American disjunct plant genera based on plastid genome data. Match fund: $9569 from Hope College DNA and Biology Department.

- **7.2. Airat Bekmetjev.** Pending. Course-based research experiences HHMI grant. $12,000. Integrating Research and Statistical Investigation in a First Year Seminar.

- **7.3 Kenneth Brown**

  Kenneth Brown, Graham Peaslee, and Elizabeth Sanford. REU Site: Professional Excellence and Development Through Undergraduate Research, NSF-REU CHEM, $185,000, Status: Current


  Kenneth Brown and Elizabeth Sanford. GOALI: Probing Interfaces—A Collaboration Between Academics and Industry, NSF-Polymers, $446,816, Status: Pending