

## NEPAL LAB RESEARCH PROJECTS

Our research interests are in understanding relationships and evolution of biological entities ranging from molecules to various levels of biological hierarchy using approaches in comparative genomics, molecular phylogenetics and population genetics. We believe that as researchers, we should not confine ourselves into our labs, but rather communicate/educate of what we find in our labs to stakeholders. We envision for a larger interdisciplinary collaboration of plant researchers at regional, national and international level to enhance integration of research and citizen-education. The main research goals are to provide our undergraduate and graduate students with a cutting-edge research experience that they can apply to their daily lives and to protect our environments. Our team is currently focusing on the following projects on population genetics and genomics of plant species.

### ***1. Identification and Characterization of Legume-specific Mitogen Activated Protein Kinase (MAPK) Genes in Soybean (Glycine max) (Researcher graduate student: Achal Neupane)***

Mitogen Activated Protein Kinases (MAPKs) are serine/threonine specific protein kinases that are highly conserved gene families in eukaryotes and play important roles in cellular and biochemical signal transductions. With the recent completion of the soybean genome sequencing, identification and characterization of its important genes including MAPKs have become imperative to enhance soybean research. The main objectives of Achal's project are to conduct *in silico* analyses (and rigorous phylogentic analyses) to identify soybean MAPKs and to characterize the MAPKs involved in root nodulation process.



**Achal Neupane is busy in *in-silico* analyses of MAPK gene families in plants.**

### ***2. Evolutionary Divergence of Mitogen Activated Protein Kinase Kinase (MAP2K) Gene Family in Legumes (Researcher: Undergraduate student Kenton MacArthur)***

Plant Mitogen Activated Protein Kinases (MAPKs) play important role in plant signaling pathways associated with biotic and abiotic stresses. The MAPK gene members belong to three functionally linked families: MAPKs, MAP2Ks, and MAP3Ks, all of which are involved in various stress-associated signal transduction pathways. Increasing availability of complete genome sequences



**Kenton MacArthur is Orville and Enolia Bentley Undergraduate Research Award winner.**

of legume species allows us to identify the genes of interest and study their evolutionary history. Kenton is interested to study genealogical relationships and evolutionary divergence of MAP2K genes across plant species. The outcomes of the project are expected to yield insights into the evolutionary history of the MAP2K genes.

### ***3. Diversity and Evolutionary History of NBS-LRR-Genes in Legumes (Researcher: Graduate student, Benjamin Benson)***



**Ben Benson is reconstructing genealogy of R-genes using the program PAUP.**

Disease-resistant genes (R-genes) in plants encode proteins that regulate signaling associated with specific biotic stresses. Out of five families of the R-genes, Nucleotide Binding Site Lucien Rich Region (NBS-LRR) is the largest family and these genes vary greatly in number across plant species. Recent availability of genome sequences of several legume species allows us to conduct phylogenomic analyses of the NBS-LRR genes among not only the members within the gene family, but also their divergence across the legume species. The main objectives of this project are to identify the NBS-LRR gene in legumes, and elucidate the evolutionary divergence of these genes across plant species.

Graduate student Benjamin is undertaking this project and analyzing all publicly available genomic, transcriptomic and proteomic sequences of these genes.

### ***4. Introduction History and Population Genetics of *Falcaria vulgaris* (Sickleweed) in the United States (Researcher: Graduate student, Sarbottam Piya)***



**Graduate student Sarbottam Piya is locating the polyloid Sickleweed plant (Boyd Co. NE).**

*Falcaria vulgaris* Bernh. (Family Apiaceae), commonly known as Sickleweed, is native to Europe and Asia and occurs disjunctly in the Midwest and East Coast of the United States. Sickleweed was first reported in the United States from Franklin County, Pennsylvania in 1922 and it is reported to occur in 35 counties across 16 states. The plant is described as annual, biennial or perennial and can produce large number of seeds (ca. 5000 seed per square meter per year) with a characteristic seed dispersal mechanism: when the plant senescences, the stems break in the node and drift in the air to disperse the seed. In addition, it can also reproduce asexually through its root stock. The plasticity in life history traits (habit, seed dispersal mechanism, and clonal reproduction) is perhaps attributed to

its emergence as an aggressive weed in the Midwest. A recent study on this plant indicated that this plant is outcompeting the native grasses by reducing their biomass production and is also decreasing species richness. Documenting the information about where and when the first introduction occurred and assessing genetic diversity and population structure of the introduced species are important steps towards understanding the potential invasiveness of the introduced plant and designing the proper management strategies especially biological control. Researcher Sarbottam Piya is using data from natural history museum to explore the introduction history of the Sickleweed populations in the United States, and using molecular markers (nuclear microsatellite and chloroplast DNA regions) to study genetic structure of Sickleweed populations in the United States.

### **5. Population Genetics of Endangered Populations of Native Red Mulberry at its Northwestern Boundary (Researcher: Undergraduate student Spencer Schreier)**

*Morus* L. (Family Moraceae), commonly known as mulberry, is a genus of 13 species distributed throughout Asia, Africa, Europe, and North, Central, and South America. Species within the genus are known for their economic importance in the silk industry because their leaves are the primary source of food for silkworm. The species of interest in this study is *Morus rubra*, which is native to North America and occurs in the eastern half of the United States and some extension into the Midwest. *M. rubra* distribution pattern in North America suggests that the period of historical glaciation that occurred in North America may have instigated founder effect through leading edge expansion, affecting present-day populations. Founder effect is the change in allele frequencies

that occurs as small samples of a larger population colonize an open niche. Undergraduate student Spencer Scleier is engaged in thei project. The main objective of this project is to use nuclear and chloroplast DNA markers to compare the genetic variation between northern and southern populations of *M. rubra* and determine if founder effect occurred because of glaciation. Genetic diversity is especially important to *M. rubra* because it is endangered or threatened in many areas of the United States. Low genetic diversity makes populations more susceptible to endangerment or extinction through disease, genetic swamping, and other factors.



**Spencer Schreier, an Honors College Undergraduate Research Award winner, is explaining his research poster.**