

Curriculum Vitae

Achal Neupane

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Education

- Master of Science (Bioinformatics), May 2013. South Dakota State University, Brookings, South Dakota, USA.
- Bachelor of Science (Biological Science), December 2009. University of the District of Columbia (UDC), Washington, DC, USA.

Experience

- **Research Assistant (PhD student)**
Department of Biology and Microbiology, South Dakota State University, USA (Aug 2017- present)
 - Studying the effects of hypovirulence-associated DNA virus 1 (SsHADV-1) and Sclerotinia sclerotiorum hypovirus 2 Lactuca (SsHV2L) on white mold fungus pathogen *Sclerotinia sclerotiorum* using small RNAseq and RNAseq data
 - Studying the evidence/effect of RNAi by induction of virus in *Sclerotinia sclerotiorum* using bioinformatics approaches.
 - Studying the roles of dicers and argonautes on *Sclerotinia sclerotiorum* Antiviral Small RNA Processing
 - Analyzing metatranscriptomic data to study novel mycoviruses infecting arbuscular mycorrhizal fungus *Rhizophagus* spp and other pathogenic fungi.
- **Research scholar**
Translational Research Institute, University of Queensland, Brisbane, Australia (Jan 2015- Jun 2016)
 - Analyzed a cohort of 150 clinically characterized acute myeloid leukemia (AML) sequenced with whole exome and whole genome sequencing to validate and compare genotyping algorithms and sequencing technologies.
 - Additionally, analyzed a cohort of 900 control exomes and 600 whole genomes to perform gene discovery for both somatic and germline risk variants using sophisticated statistical genetics algorithms that identify both protective and deleterious variants.
 - Used several variant calling methods to characterize germline, copy number and structural variants in AML and control samples in whole exome sequenced samples.
 - Compared pathology, cytogenetic and Sequenom genotyping data to refine and calibrate these algorithms.
 - Discovered AML related genes using SKAT and burden like statistical genetics tools.
 - Developed algorithms to identify sample contamination, identity and ethnicity for quality control of Next Generation Sequencing (NGS) data.

- **Research Assistant**

School of Biological Sciences, University of Nebraska-Lincoln, Nebraska, USA (Aug 2013- May 2014)

- Analyzed western corn rootworm (WCR) larval/egg transcriptome data and identified 54 gustatory receptor genes.
- Identified gamma-aminobutyric acid type A (GABAA) receptor and gustatory receptors from the WCR transcriptome.
- Performed bioinformatics analysis to study the conservation of gene structure and function of chemoreceptor protein family across insect genomes.

- **Teaching Assistant**

Department of Biology and Microbiology, South Dakota State University, USA (Aug 2011- May 2013)

- Taught undergraduate level biology/genetics laboratory courses
- Graded weekly assignments, quizzes and exams.

Courses taught:

- General Biology I (BIOL 151) lab, Fall 2011
- General Biology II (BIOL153) lab, Spring 2012
- General Biology I (BIOL 151) lab, Fall 2012
- General Biology I (BIOL 153) lab, Spring 2013

- **Research Assistant**

Department of Biology and Microbiology, South Dakota State University, USA (Aug 2011- Jul 2013)

- Identified all three families of mitogen-activated protein kinases (MAPKs), and characterized the legume specific MAPK genes involved in *Rhizobium*-legume interaction.
- Identified MAPK and MAPKK gene members in soybean, *Lotus*, *Medicago* and *Phaseolous* and studied their evolutionary relationships with respect to their counterparts in different non-legume species.
- Used approaches in bioinformatics and comparative genomics to study functional and evolutionary divergence of MAPK genes in legumes.
- Performed MAPK silencing and hairy root transformation using RNAi constructs in soybean.
- Performed time-course expression analysis of MAPKs in root nodulation of mock and *Rhizobium* inoculated soybean seedlings using RT-PCR and Microarray analysis.
- Mentored undergraduate researchers.

- **Research Fellow**

MERCK Pharmaceuticals-University of the District of Columbia Cancer Research, DC, USA Project (Apr 2009-Dec 2009)

- Studied molecular mechanisms involved in apoptosis (programmed cell death) induced by organotin drugs in various cancer cell lines.
- Provided research support in chemical and cellular studies designed to determine the carcinogenic effects on humans.
- Performed various biological techniques: cell culture, gel electrophoresis/SDS-PAGE, immunofluorescence, western blot and various biological assays.

- **Undergraduate Teaching Assistant**

Department of Biology, University of the District of Columbia, DC, USA (Aug 2007 – Apr 2009)

- Assisted professors and students in performing experiments, prepared biological samples and chemical reagents for general biology classes.
- Performed laboratory inventory, ordered and maintained laboratory chemicals and supplies.
- Handled biological specimens and worked under GLP guidelines.

Publications

Peer- reviewed journal articles

- **Neupane, A.**, Feng, C., Mochama, PK., Saleem H., and Lee Marzano SY. (2019). Roles of Argonautes and Dicers on *Sclerotinia sclerotiorum* Antiviral RNA Silencing. *Frontiers in Plant Science*; 10:976.
- SY., Marzano, **Neupane, A.**, Domier, L. (2018). Transcriptional and Small RNA Responses of the White Mold Fungus *Sclerotinia sclerotiorum* to Infection by a Virulence-Attenuating Hypovirus. *Viruses*; 10 (12), 713.
- **Neupane, A.**, Feng, C., Feng, J., Kafle, A., Bücking, H., and Marzano, SY. (2018) Metatranscriptomic Analysis and In Silico Approach Identified Mycoviruses in the Arbuscular Mycorrhizal Fungus *Rhizophagus* spp. *Viruses* 10 (12), 707.
- Neupane, S., Schweitzer, SE., **Neupane, A.**, Andersen, EJ., Fennell, A., Zhou and Nepal, MP. (2019). Identification and Characterization of Mitogen-Activated Protein Kinase (MAPK) Genes in Sunflower (*Helianthus annuus* L.). *Plants (Basel)* 8.
- Neupane, S., Andersen, E., **Neupane, A.**, and Nepal, M. (2018) Genome-Wide Identification of NBS-Encoding Resistance Genes in Sunflower (*Helianthus annuus* L.). *Genes* 9 (8), 384.
- Mochama, P., Jadhav, P., **Neupane, A.**, Marzano, SY. (2018) Mycoviruses as Triggers and Targets of RNA Silencing in White Mold Fungus *Sclerotinia sclerotiorum*. *Viruses* 10 (4).
- S. Piya, **Neupane, A.**, Butler, J., Larson, GE., and Nepal, MP. (2014) Genetic Diversity and Population Structure of Sickleweed (*Falcaria vulgaris* L.) in the Upper Midwest USA Midwest USA. *Biological Invasions* 2014:1-11.
- **Neupane, A.**, Nepal, MP., Benson, BV., MacArthur, KJ., and Piya, S. (2013). Mitogen-Activated Protein Kinase Genes and their Evolutionary History in *Lotus*, *Medicago* and *Phaseolus*. *Plant Signaling & Behavior*; 8:e27189.
- **Neupane, A.**, Piya, S., Subramanian, S., Rohila, JS., Reese, N., and Nepal, MP. (2013). Identification, Nomenclature, and Evolutionary Relationships of Mitogen-Activated Protein Kinase (MAPK) Genes in Soybean. *Evolutionary Bioinformatics*; 9:363-86.
- Piya, S., **Neupane, A.**, Butler, J., Larson, GE., and Nepal, MP. (2012). Inferring the introduction history of sickleweed (*Falcaria vulgaris* L.) in the United States. *Proceedings of the South Dakota Academy of Science*; 91:113-129.

Presentations

- **Neupane, A.**, and Marzano, S. Profiling the Classes of the RNA Editing in Virus-derived small RNAs in White Mold *Sclerotinia sclerotiorum*. *American Society for Virology*, 2019, 20-24 July, Minneapolis, USA (Oral).

- Neupane, A., Mochama, P., Saleem, H., Marzano, S. Roles of Dicers and Argonautes on *Sclerotinia sclerotiorum* Antiviral Small RNA Processing. *Plant and Animal Genome Conference XXVII*, 2019, 12-16 January, San Diego, CA, USA (Poster).
- Smith, A., **Neupane, A.**, Ellis, J., Afrin, S., Burow, R., Stinson, C., Leo, P., Cristino, A., Moore, A. MEK inhibitor resistance in acute myeloid leukaemia. *New Direction in Leukaemia Research*, 2016, 16-19 March, Peppers Noosa, Australia (Poster)
- Leo, P., **Neupane, A.**, Bassal, M., Maung, Z., Newell, F., Ellis, M., Boxall, G., Smith, A., Marlton, P., D'Andrea, R., Gonda, T., Brown, M., Saal, R., Moore, A. Gene Discovery in Acute Myeloid Leukaemia: somatic and germline mutations. *International Congress of Immunology*, 2016, 21-26 August, Melbourne, Australia (Oral).
- Moore, A., Leo, P., **Neupane, A.**, Bassal, M., Newell, F., Ellis, M., Boxall, G., Smith, A., Marlton, P., D'Andrea, R., Gonda, T., Brown, M., Saal, R., Anderson, L. Sensitivity of Whole Exome Sequencing for the Detection of FLT3-ITD and NPM1 Mutations in Acute Myeloid Leukaemia. *European School of Hematology (ESH)*. 2015, 10-12 September, Budapest, Hungary (Oral).
- **Neupane, A.**, Eyun, S., Wang, H., Siegfried, BD., and Moriyama, EN. Transcriptome analysis of western corn rootworm larvae and eggs. *IWGO & International Conference of Diabrotica Genetics*. 2014, 14-17 April. Chicago, IL, USA (Poster).
- **Neupane, A.**, Piya, S., Reese, N., Rohila, JS., Subramanian, S., and Nepal, MP. Identification of Mitogen Activated Protein Kinase Family members in Soybean. *Botanical Society of America Conference* 2012, 7-11 July. Columbus, OH, USA (Poster).
- Piya, S., **Neupane, A.**, Butler, J., Larson, GE., and Nepal, MP. Population Genetics of *Falcaria vulgaris* (Sickleweed) in North America. *Botanical Society of America Conference* 2012, 7 -11 July. Columbus, OH, USA (Poster).
- Piya, S., **Neupane, A.**, Butler, J., Larson, GE., and Nepal, MP. Introduction history and spread of *Falcaria vulgaris* Bernh. (Apiaceae) in the United States based on herbarium records. *South Dakota Academy of Science* 2012, 13-14 April. Vermillion, SD, USA (Oral).
- **Neupane, A.**, Piya, S., Subramanian, S., Rohila, JS., Reese, N., and Nepal, MP. A Nomenclatural Conundrum: Applying Existing Nomenclature to the Identification of Soybean (*Glycine max*) MAP Kinase Genes. *ASPB Midwestern Sectional Society* 2012, 24-25 March. Lincoln, NE, USA (Poster).
- **Neupane, A.**, Anjorin, C., Song, X., and Kumar, D. Anticancer Activity of Novel Ionic Triorganotin Derivatives against MDA-MB 231 Breast Cancer Cells. *HBCU-UP National Research Conference* 2009, October 29-November 1. Washington, DC, USA (Poster).

Research Grants

- University of Nebraska-Lincoln travel grants (\$1500, FY 2014)
- Center for Excellence in Drought Tolerance Research (CEDTR)-USDA/NIFA (#SA1100029): Identification and characterization of mitogen-activated protein kinases (MAPKs) involved in root nodulation in *Glycine max*. (\$4000, FY 2012/2013).
- MERCK/ AAAS: Anticancer activity of novel ionic triorganotin derivatives against MDA-MB 231 breast cancer cells. (\$5000, FY2009).

Computer Skills

- Programming languages: R, Python, JavaScript, Perl, PHP, ASP.NET, MySQL
- Operating systems: Linux/Unix, Linux based high performance computing (HPC) cluster
- Genome analysis tools: GATK, Picard, Samtools, bcftools
- Microbiome analysis: Qiime2, Vegan, Phyloseq
- *De novo* alignment/assembly tools (Trinity, MIRA2, Velvet, Bowtie, etc.)
- Sequence search tools (BLAST, HHblits, HMMER and various standalone programs)
- Phylogenetics software (RAxML, Mega, PhyML, Phylip, MrBayes, PAUP and Network)
- DNA assembly and analysis software (Sequencher and Geneious)
- GitHub/Bitbucket: achalneupane

Membership in Professional Organizations

- Associate member, Sigma XI
- Member, American Association for the Advancement of Science (AAAS)

Awards and Achievements

- Sigma Xi Masters Research Paper, South Dakota State University, (2012)
- Dean's List Honoree, University of the District of Columbia, (2006-2009)
- United Nations Mission in Nepal (UNMIN) Scholarship (2002)

References

Available upon request