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| CURRICULUM VITAE**HARI BAHADUR CHHETRI**Computational and Predictive Biology, Oak Ridge National Laboratory1 Bethel Valley Road, Oak Ridge, TN 37830, USAPhone: (681) 212-9725 (cell)E-mails: harichhetri@gmail.com  chhetrihb@ornl.gov |
| RESEARCH INTERESTSQuantitative and Statistical Genetics, Evolutionary Biology, Population Genomics and Bioinformatics, Systems Biology |
| EDUCATION |
| 2010 – 2019 |  PhD Forest Genetics/Computational Biology, Department of Biology, West Virginia University, Morgantown, West Virginia, USA*Dissertation Title*: Association genetics and local adaptation of *Populus trichocarpa* Torr. & Gray |
| 2006 – 2009 | MS Molecular Systematics and Evolution, Department of Botany, Claremont Graduate University and Rancho Santa Ana Botanic Garden, Claremont, California, USA |
| 1999 – 2001 | M.Sc. Botany, Tribhuvan University, Kathmandu, Nepal |
| 1996 – 1999 | B.Sc. Biology, Tribhuvan University, Kathmandu, Nepal |
| **EXPERIENCE** |
| August 2023 – Present | *Computational Systems Biologist,* Computational and Predictive Biology, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA |
| July 2020 – July 2023 | *Postdoctoral Research Associate,* Computational and Predictive Biology, Oak Ridge National Laboratory, Oak Ridge, Tennessee, USA |
| **Projects** : Working on multiple projects related to statistical, quantitative genomics and systems biology in switchgrass (*Panicum virgatum*), black cottonwood (*Populus trichocarpa*), pennycress (*Thlapsi arvense*), and bacteria (*Bacillus* sp.)**Role** : Build quantitative genetic analysis pipeline and perform statistical genetics and bioinformatics and systems biology network analysis using climate, phenotypic, and omics data using High-Performance Computing, interpret results, and write manuscripts.**Accomplishments**: * Built quantitative genetics and systems biology analysis pipeline and performed Genome-wide association study (GWAS), statistical and bioinformatics analysis, and systems biology analysis using climate, phenotypic, and genome sequencing and other omics data across the plant and microbial systems.
* Co-authored multiple research papers (published, under review, and in preparation)
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| December 2019 – June 2020 | *Postdoctoral Research Fellow - Quantitative Genetics,* Department of Biology West Virginia University, Morgantown, West Virginia, USA |
| July 2019 – November 2019  | *Research Assistant,* Department of Biology, West Virginia University, Morgantown, West Virginia, USA |
| **Project** : Genome-wide association study (GWAS), local adaptation and genomic prediction in *Populus trichocarpa* **Role** : Apply statistical genetics methods for identifying genomic variants associated with the phenotypic traits using re-sequencing data from more than 1500 trees (more than 20 million SNPs), identify loci conferring local adaptation using multivariate statistics and genotype-environment association (GEA) analysis methods; develop and use genomic prediction models to estimate breeding values; analyze tree growth ring metrics and integrate with climate and genomic data to find a link between genotype, phenotype and environment; write R and Bash scripts as necessary; use centralized High Performance Computing (HPC) university cluster for big data analysis; write progress reports and papers. **Accomplishments**: * Performed all Quantitative genetic analysis, published a paper on genome-wide association study of wood anatomical and morphological traits in *Populus trichocpa* in Frontiers in Plant Science Journal, wrote a draft of the paper for local adaption in *Populus* project for submission to Molecular ecology journal.
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| January 2010 – June 2019 | *Dissertation Research,* PhD student, Forest Genetics,Department of Biology, West Virginia University, Morgantown, West Virginia, USA.*Advisor: Dr. Stephen DiFazio*[*http://www.as.wvu.edu/~sdifazio/*](http://www.as.wvu.edu/~sdifazio/) |
| **Project 1**: Genome-wide association study (GWAS) of morphological and physiological traits in *Populus trichocarpa***Role** : Collect phenotypic data in the field, perform bioinformatic and statistical analysis using whole genome re-sequencing data from more than one thousand trees (more than 20 million SNPs) and write the paper**Accomplishments**: * Analyzed whole genome re-sequencing and phenotypic data from more than one thousand trees using Bash, R and Python scripts to find the critical link between genotype and the phenotype.
* Identified key genes controlling 14 morphological and physiological traits using single-trait and multi-trait GWAS methods using GEMMA.
* Network analysis (in collaboration with Oak Ridge National Lab, ORNL) to understand the possible biological functions of the candidate genes: examined the position of the genes in networks constructed based on coexpression, comethylation and metabolite data for the same *P. trichocarpa* population.
* Wrote the paper – published in New Phytologist.<https://doi.org/10.1111/nph.15777>.
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| **Project 2** : Genomics of local adaptation in *Populus trichocarpa***Role** : Collect phenotypic and environmental data, perform bioinformatic and statistical analysis using whole genome re-sequencing data from more than one thousand trees (more than 20 million SNPs) and write the paper**Accomplishments**: * Analyzed whole genome re-sequencing, environmental and phenotypic data from more than one thousand trees using Bash, R and Python scripts to find the loci under selection.
* Identified several genes conferring local adaptation in *P. trichocarpa* from genotype environment association (GEA) analysis using GEMMA.
* Estimated the relative contribution of climate and geography on population structure using multivariate statistical methods (Redundancy Analysis, RDA).
* Performed correlation of phenotypic data with the climate of the source locations of the genotypes and compared the Quantitative genetic differentiation (*QST*) with the neutral molecular differentiation (*FST*). The results showed the evidence for local adaptation.
* Prepared a draft of the paper for submission to Molecular Ecology.
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| **Project 3**: Genotype × Environment (G×E) interaction and genome-wide association study (GWAS) of anatomical, morphological and physiological traits in *Populus trichocarpa***Role** : Collect phenotypic data from three common gardens, perform quantitative genetic, bioinformatic and statistical analysis using whole genome re-sequencing and phenotypic data and write the paper**Accomplishments**: * Quantitative genetic and statistical analysis of carbon isotope composition and wood anatomy traits using Analysis of Variance (ANOVA) and Genotype x Environment Interaction (GEI) models in R showed variable genotypic and genotype x environment effects.
* Analyzed whole genome re-sequencing and phenotypic data from more than one thousand trees using Bash, R and Python scripts to find the critical link between genotype and the phenotype.
* Identified key genes controlling 25 anatomical and morphological traits using single-trait and multi-trait GWAS methods using GEMMA.
* Network analysis (in collaboration with Oak Ridge National Lab, ORNL) to understand the possible biological functions of the candidate genes: examined the position of the genes in networks constructed based on coexpression, comethylation and metabolite data for the same *P. trichocarpa* population.
* Wrote the paper and published in Frontiers in Plant Science. <https://doi.org/10.3389/fpls.2020.545748>
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| January 2010 – May 2019 | *Graduate Teaching Assistant*BIOL 115, Principles of Biology, Fall 2010, 2016, 2017, 2018BIOL 117, Introductory Physiology, Spring 2010, 2011, 2012, 2013, 2014BIOL 219, The Living Cell, Fall 2011, 2012, 2013 BIOL 298D (BIOL 115 honors), Fall 2013, 2014BIOL 321, The Total Science Experience: Genomics, Spring 2015BIOL 464/GEN 535, Population Genetics, Fall 2014*Graduate Research Assistant*, Spring 2016, 2017 |
| October 2009 – December 2009 | *Research Technician*Department of Biology, West Virginia University*Advisor: Dr. Stephen DiFazio**Project Title:* Association genetics of bud phenology in *Populus angustifolia**Major responsibilities:* PCR amplification, purification of PCR product, prepare sequencing plates, analyze sequence data. |
| August 2006 – July 2009 | *Graduate Research Assistant*Department of Botany, Claremont Graduate University and Rancho Santa Ana Botanic Garden*Advisor: Dr. J. Travis Columbus*(<https://www.cgu.edu/people/travis-columbus/>; <https://www.rsabg.org/research/research-staff>)*Project 1:* Ontogeny of inflorescence development in chloridoid grasses.*Major responsibilities:* Grow plants in growth chamber, dissect inflorescences at different developmental stages, sample preparation via alcohol dehydration series, critical point drying, mounting on stubs, sputter gold coating and taking pictures using Scanning Electron Microscope (SEM).*Project 2:* Leaf blade anatomy of *Bouteloua* (Poaceae).*Major responsibilities:* Prepare permanent slides - perform alcohol dehydration and xylene infiltration processes, embed tissue in paraffin wax, section tissue using rotary microtome and prepare slides.*Project 3:* Molecular phylogenetics of chloridoid grasses based on chloroplast and nuclear gene sequences.*Major Responsibilities:* DNA extraction and quantification, PCR amplification, purification of PCR product using PEG, sephadex column cleaning, setting up the sequencing plate and running the sequencher (454 Genetic Analyzer). |
| January 2002 – August 2006 | *Plant Ecologist*Nepal Forest Resources and Institutions (NFRI)International Forestry Resources and Institutions (IFRI), Collaborating Research Center (CRC), Nepal.*Major Responsibilities:* Conducting vegetation and household surveys in various community forests in the central and eastern parts of Nepal, data compilation and report preparation. |
| August 2005 – October 2005 | *Ecologist/Environmentalist (part time)*Geotech Engineers Pvt. Ltd. (GEOCE), Kathmandu, Nepal. *Major Responsibilities:* Baseline survey of flora and fauna in the project affected area, identify likely environmental hazards during and after implementation of the project, propose mitigation measures and, report preparation. |
| July 2003 – October 2003 | *Non-timber Forest Product (NTFP) Research Consultant* *(subcontract)*Nepal Trust for Nature Conservation (NTNC)/Annapurna Conservation Area Project (ACAP), Pokhara, Nepal.*Project Title:* Survey of NTFPs (Non-timber Forest Products) in upper Mustang, Western Nepal. *Major Responsibilities:* Identify NTFP species, their status & distribution, recommend strategies specific to upper Mustang for sustainability and NTFP commercialization and, report preparation. |
| February 2006 – July 2006 | *Biology Instructor (part time)* New Summit College, Old Baneshwor, Kathmandu, Nepal. |
| December 1996 – January 1999 | *Science Instructor (part time)* Little Stars English Boarding School, Chitwan, Nepal.Taught science for junior high students. |
| **COMPUTATIONAL AND BIOINFORMATICS SKILLS***Whole Genome Re-sequencing data Analysis** Genome-wide association study (GWAS) using big data (more than 20 million SNPs) in *Populus trichocarpa* (black cottonwood).
* Experienced in using UNIX/LINUX based high performance computing cluster for NGS data analysis tasks.
* Software used for analyses: GEMMA and EMMAX, PLINK: a Toolset for Whole-Genome Association and Population-based Linkage Analysis, VCFtools, EIGENSOFT
* Sequence alignments

*Computer programming** Proficient in working with Linux environment.
* Shell scripting in Bash, batch processing on high performance computing cluster.
* Experienced with PBS/Torque job schedulers.
* Basic programming Matlab and Python.
* R scripting for statistics and graphing with ggplot2
* Python Jupyter for statistics
* Image analysis in Matlab – use Matlab scripts to perform operations such as area measurement and particle counts of complex structures and objects.

*Software** DNA sequence editing and assembly software Sequencher v4.8
* ImageJ - use imageJ macros to perform operations such as area measurement and particle counts of complex structures.

*Phylogenetic and population genetics analysis software** Phylogenetic analyses based on maximum parsimony, maximum likelihood, and bayesian methods – PAUP, Phylip, Mr Bayes, Mesquite and MEGA
* Population genetics software and programs including STRUCTURE, GENEIOUS, GENEPOP, TASSEL, Arlequin and GenAlEx

**STATISTICAL SKILLS*** Multiple linear regression analysis
* Logistic regression analysis
* Cluster analysis
* Design of experiments
* ANOVA/MANOVA/ANCOVA/MANCOVA
* Mixed model analysis
* Multivariate statistics including Principal Component Analysis, ordination methods (redundancy analysis [RDA] in particular)

**MOLECULAR BIOLOGY SKILLS*** Gene cloning and transformation
* DNA sequencing and fragment analysis on ABI 3700XL sequencing system, multi-plex SNaPshot sequencing
* DNA extraction using Qiagen and FastPrep kits and CTAB protocol
* PCR based techniques – qPCR, RT-PCR
* Agarose gel electrophoresis
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| **WORKSHOPS AND TRAINING** |
| **June 2010**  | West Virginia University Summer Institute for Scientific Teaching, June 2010. Department of Biology, West Virginia University, Morgantown, WV 26506.  |
| **July 2010** | Summer Institute on Statistical Genetics, 2010, conducted by School of Public Health, University of Washington, Seattle. Modules: QTL mapping, and plant and animal association mapping. |
| **March 2008** | Botanical Survey Reports for Botanists, Planners and Citizens, March 2008. Rancho Santa Ana Botanic Garden, Claremont, California 91711-3157. Instructor: Scott White, Biological Consultant. |
| **March 2007** | Grass Identification Workshop (2 days), March 2007. Rancho Santa Ana Botanic Garden, Claremont, California 91711-3157. Instructor: Dr. J. Travis Columbus, Research Scientist, Rancho Santa Ana Botanic Garden. |
| JOURNALS REVIEWED (number of papers reviewed in parentheses) |
| 1. New phytologist (1)
2. PeerJ (2)
3. Frontiers in Plant Science (1)
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| PUBLICATIONS |
| *Journals* |
| 1. **Chhetri HB,** Gancho T. Slavov, Nesatalu Hiese, David Macaya-Sanz,Gerald A. Tuskan, and Stephen P. DiFazio.Local adaptation in *Populus trichocarpa (in prep for submission to Molecular Ecology).*
2. Sandra J. Simon, Anna Furches, **Hari B. Chhetri**, Luke Evans, Piet Jones, Gina Wimp, Daniel Jacobson, Timothy J. Tschaplinski, Gerald A. Tuskan, S. P. DiFazio. Genetic underpinnings of arthropod community distributions in *Populus trichocarpa (under review, New Phytologist)*.
3. Lagergren, J., Pavicic, M., **Chhetri, H. B**., York, L. M., Hyatt, P. D., Kainer, D., Rutter, E. M., Flores, K., Bailey-Bale, J., Klein, M., Taylor, G., Jacobson, D., & Streich, J. (2023). Few-Shot Learning Enables Population-Scale Analysis of Leaf Traits in Populus trichocarpa. *ArXiv*. <https://arxiv.org/abs/2301.10351v2>
4. Lagergren, J., Cashman, M., Melesse Vergara, V., Eller, P., Gazolla, J. G. F. M., **Chhetri, H**. **B.**, Streich, J., Climer, S., Thornton, P., Joubert, W., & Jacobson, D. (2022). Climatic clustering and longitudinal analysis with impacts on food, bioenergy, and pandemics. In *Phytobiomes Journal*. <https://doi.org/10.1094/pbiomes-02-22-0007-r>
5. Shrestha, V., **Chhetri, H. B**., Kainer, D., Xu, Y., Hamilton, L., Piasecki, C., Wolfe, B., Wang, X., Saha, M., Jacobson, D., Millwood, R. J., Mazarei, M., & Stewart, C. N. (2022). The Genetic Architecture of Nitrogen Use Efficiency in Switchgrass (Panicum virgatum L.). *Frontiers in Plant Science*, *13*(May), 1–12. <https://doi.org/10.3389/fpls.2022.893610>
6. Vasileva, D. P., Streich, J. C., Burdick, L. H., Klingeman, D. M., **Chhetri, H. B.,** Brelsford, C. M., Ellis, J. C., Close, D. M., Jacobson, D. A., & Michener, J. K. (2022). Protoplast fusion in Bacillus species produces frequent, unbiased, genome-wide homologous recombination . *Nucleic Acids Research*, 1–13. <https://doi.org/10.1093/nar/gkac025>
7. **Chhetri HB**, A. Furches, D. Macaya-Sanz, AR Walker, D Kainer, P Jones, AE Harman-Ware, TJ Tschaplinski, D Jacobson, GA Tuskan, SP DiFazio 2020. Genome-Wide Association Study of Wood Anatomical and Morphological Traits in *Populus trichocarpa*. *Frontiers in Plant Science* 11:1–20. DOI: <https://doi.org/10.3389/fpls.2020.545748>.
8. **Chhetri, H.B**., D. Macaya-Sanz, D. Kainer, A.K. Biswal, Luke M. Evans et al. 2019. Multitrait genome-wide association analysis of *Populus trichocarpa* identifies key polymorphisms controlling morphological and physiological traits. *New Phytologist* 223: 293-309. DOI:

 <https://doi.org/10.1111/nph.15777>.1. Kunwar, R.M., B.K. Nepal, **H.B. Chhetri**, S.K. Rai and R.W. Bussmann 2006. Ethnomedicine in the Himalayas: A case study from Dolpa, Humla, Jumla and Mustang districts of Nepal. *Journal of Ethnoecology and Ethnomedicine* 2: 27.
2. **Chhetri, H.B.** and V.N.P. Gupta 2007. A Survey of Non-timber Forest Products (NTFPS) in Upper Mustang. *Scientific World* 5 (5): 89-94.
3. **Chhetri, H.B.** and V.N.P. Gupta 2006. NTFP Potential of Upper Mustang–A trans–Himalayan Region in Western Nepal. *Scientific World* 4 (4): 38-43.
4. **Chhetri, H.B.** and S. Shrestha 2004. Floristic Study of Chock Chisapani Area, Tanahun, Central Nepal. *In*: Bajracharya et al. (Eds.), *Proceedings of the Forth National Conference on Science and Technology March 2004* (pp. 114-120). Nepal Academy of Science and Technology, Kathmandu, Nepal.
 |
| *Technical Reports* |
| 1. **Chhetri, H.B.** and V.N.P. Gupta 2005. *Environmental Impact Assessment (EIA) of Solu River Small Hydro-power Project, Salleri, Solukhumbu*. Report prepared for the Ministry of Forest and Soil Conservation (MoFC), Kathmandu, Nepal.
2. **Chhetri, H.B.** 2003. *Survey of Non-timber Forest Products (NTFPs) in Upper Mustang, Central Nepal.* Report prepared for Annapurna Conservation Area Project (ACAP)/Trust for Nature Conservation (KMTNC), Kathmandu, Nepal.
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| SCHOLARSHIPS/GRANTS |
| * 15th Annual Summer Institute in Statistical Genetics (SISG 2010), University of Washington, Seattle, Washington, USA, 2010, $300.
* University Club of Claremont Scholarship, 2008, $750.
* Annapurna Conservation Area Project (ACAP) Noni-timber Forest Product (NTFP) Research. 07/03-10/03, $1,000. Survey of Non-timber Forest Products in Upper Mustang with the focus on Potentiality of Commercialization.
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| PRESENTATIONS  |
| *Oral*  |
| * 1. **Hari B. Chhetri**, Mirko Pavicic, John Lagergren, Jared Streich, Manesh Shah, Kyle Sullivan, Gail Taylor, Dan Jacobson. A Systems Biology Study of Leaf Morphology and Vein Architecture in *Populus trichocarpa. CBI Annual Science Meeting, June 5 – 9, 2023 – Ashville, NC.*
	2. **Hari B. Chhetri**, Jared Streich, John Lagergren, Daniel Jacobson, Delyana P. Vasileva, Josh K. Michener. QTL Mapping in *Bacillus subtilis* Identifies Genes Controlling Swarming Motility and Spore Germination Traits.*BER Plant Genomic Science,**Plant and Animal Genome XXX Conference, January 13 – 18, 2023 – San Diego, California, USA.*
	3. **Hari B. Chhetri**, David Macaya-Sanz, Anna K. Furches, Alejandro RiverosWalker, David Kainer,Daniel Jacobson, Gerald A. Tuskan, and Stephen P. DiFazio.Genome-wide association study of wood anatomical and morphological traits in *Populus trichocarpa.**Forest Tree Workshop,**Plant and Animal Genome XXVIII Conference, January 11 – 15, 2020 – San Diego, California, USA.*
	4. **Hari B. Chhetri**, Gancho T. Slavov, Nesatalu Hiese, David Macaya-Sanz,Gerald A. Tuskan, and Stephen P. DiFazio.Local adaptation in *Populus trichocarpa****.*** *Population and Conservation Genomics Workshop,**Plant and Animal Genome XXVIII Conference, January 11 – 15, 2020 – San Diego, California, USA.*
	5. **\*\*Hari B. Chhetri,** David Macaya-Sanz, Stephen P. DiFazo.2019.Genome-wide association study and genomics of local adaptation in forest tree, *Populus trichocarpa* (black cottonwood) - implications for identifying causal variants associated with complex traits. *IUFRO, Tree Biotechnology conference, July 23 – 28, 2019 – Raleigh, North Carolina, USA.*
	6. **\*Hari B. Chhetri.** 2019.Multitrait genome-wide association analysis of *Populus trichocarpa* identifies key polymorphisms controlling morphological and physiological traits. *Pfizer Inc., May 12, 2019 – Boston, Massachusetts, USA.*
	7. **Hari B. Chhetri**, David Macaya-Sanz, Luke Evans, Jonathan R. Cumming, Lee Gunter, Wellington Muchero, Jay Chen, Anthony Bryan, Steven H. Strauss, Emily Helliwell, Kori K. Ault, Anna C. Magnuson, Eli Rodgers-Melnick, Alejandro Riveros Walker, Todd N. Rosenstiel, Gerald A. Tuskan, and Stephen P. DiFazio. 2008. Association genetics of carbon isotope discrimination in *Populus trichocarpa* Torr. & Gray, *Department of Biology Retreat West Virginia University, October 21, 2016 – Morgantown, West Virginia, USA.*
	8. **Hari B. Chhetri** and J Travis Columbus. 2008. Systematics of the tribe Zoysieae (Poaceae, Chloridoideae) based on chloroplast and nuclear sequences: a preliminary report, *Botany Conference, July 26 – 30, 2008 – Vancouver, Canada.*
	9. **Hari B. Chhetri** and J Travis Columbus. 2007. Systematics of the *Sporobolus* clade (Poaceae, Chloridoideae). *Bi-annual meetings of the California Botanical Society (CBS), February 2007 – San Luis Obispo, California, USA*.
	10. **Hari B. Chhetri**. 2004. Non-timber forest products survey in upper Mustang, Central Himalaya, *National Seminar on Natural Resource Management organized by Ecological Society (ECOS), February 14, 2004 – Biratnagar, Nepal.*
	11. **Hari B. Chhetri** and Sangita Shrestha. 2004. Floristic study of Chock Chisapani area, Tanahun, Central Nepal, *Fourth National Conference on Science and Technology, March 2004 – Kathmandu, Nepal.*

Note: \* invited seminar, \*\* early-career keynote, presenting author in bold letters |
| *Poster*  |
| 1. **Hari B. Chhetri,** Mirko Pavicic, Matthew Lane, John Lagergren, William Perry, Tad Wesley, Winthrop Phippen, Daniel Jacobson. Systems Biology of *Thlaspi arvense* L. : Phenotype to Functional Genetic Mechanisms. *Integrated Pennycress Resilience Project (IPReP) Annual Meeting, July 31, 2023 – Minneapolis, MN*
2. **Hari B. Chhetri,**David Kainer, Jared Streich, Mirko Pavicic, Daniel Jacobson. Time-resolved genetic architectures for environmental adaptations in *Populus trichocarpa* Torr. & Gray. *The Center for Bioenergy Innovation (CBI), Annual Science Meeting,* June 6 – 9, 2023 – Ashville, NC.
3. Shiva Makaju, **Hari Chhetri**, Hari Poudel, Jazib Ali Irfan, Anita Giabardo, Thomas Pendergast, Vivek Shrestha, Reggie Millwood, Mitra Mazarei, Katrien Devos, Charls Neal Stewart, Jr., Daniel Jacobson, Ali Missaoui. GGE Biplot Analysis on Yield Performance and Stability of 25 Switchgrass Accessions in Two Locations**.**  *The Center for Bioenergy Innovation (CBI), Annual Science Meeting,* June 6 – 9, 2023 – Ashville, NC.
4. Bikash Ghimire Mitra Mazarei, Morgan Willis, Thomas Pendergast IV, **Hari B. Chhetri,** Mirko Pavicic, John Lagergren, Manesh Shah, Kyle Sullivan, David Kainer, Samikshya Rijal, Vivek Shrestha, Yaping Xu, Reggie Millwood, Daniel Jacobson, C. Neal Stewart, Jr., Ali Missaoui ,Katrien Devos, James W. Buck, and Bochra A. Bahri. Genome-wide association studies reveal novel genomic regions associated with rust and false smut resistance in switchgrass.*The Center for Bioenergy Innovation (CBI), Annual Science Meeting,* June 6 – 9, 2023 – Ashville, NC.
5. \***Hari B. Chhetri**, David Kainer, Jared Streich and Daniel Jacobson. Time-resolved genetic architectures for environmental adaptations in *Populus trichocarpa. The Center for Bioenergy Innovation (CBI), Annual Science Meeting, June 28 – 30, 2021 (Virtual Meeting)*.
6. \*Vivek Shrestha, **Hari B. Chhetri**, Yaping Xu, Lance Hamilton Cristiano Piasecki, Ben Wolfe, Xueyan Wang, Malay Saha, Daniel Jacobson, Reginald J. Millwood, Mitra Mazarei and C. Neal Stewart Jr. Uncovering the Genetic Architecture of Nitrogen (N) Related Sustainability Traits and the Relationship of Nitrogen with other Feedstock Traits in Switchgrass.*The Center for Bioenergy Innovation (CBI), Annual Science Meeting, June 28 – 30, 2021 (Virtual Meeting)*.
7. \*Shiva Makaju, Ali Missaoui, Hari Poudel, **Hari B. Chhetri**, Thomas Pendergast, Kishan Mahmud and Jonathan Markham. Genomic Prediction for Switchgrass Yield and Associated Morphological Traits.*The Center for Bioenergy Innovation (CBI), Annual Science Meeting, June 28 – 30, 2021 (Virtual Meeting)*.
8. \*Delyana Vasileva, Leah H. Burdick, Jared C. Streich, Dawn M. Klingeman, **Hari B. Chhetri**, Stephanie S. Galanie, Dan M. Close, J. Christopher Ellis, Daniel A. Jacobson and Joshua K. Michener. Quantitative trait-loci (QTL) mapping – a novel method for gene discovery in bacteria. *The Center for Bioenergy Innovation (CBI), Annual Science Meeting, June 28 – 30, 2021 (Virtual Meeting)*.
9. **\*Hari B. Chhetri**, Gancho T. Slavov, Nesatalu Hiese, David Macaya-Sanz,Gerald A. Tuskan, and Stephen P. DiFazio. **Local adaptation in *Populus trichocarpa.*** *Plant and Animal Genome XXVIII Conference, January 11 – 15, 2020 – San Diego, California, USA.*
10. \***Hari B. Chhetri**, David Macaya-Sanz, Luke Evans, Jonathan R. Cumming, Lee Gunter, Wellington Muchero, Jay Chen, Anthony Bryan, Steven H. Strauss, Emily Helliwell, Kori K. Ault, Anna C. Magnuson, Eli Rodgers-Melnick, Alejandro Riveros Walker, Todd N. Rosenstiel, Gerald A. Tuskan, and Stephen P. DiFazio. 2017. Association genetics of morphological and physiological traits in *Populus trichocarpa* Torr. & Gray. *Bioenergy Science Center Annual Retreat, July 11- 13, 2017 – Chattanooga, Tennessee, USA.*
11. \*Kori K. Ault, Steven H. Strauss, Anna C. Magnuson, Scott Kiel, H. Rose McClung, Upendra K Devisetty, Luke Evans, **Hari B. Chhetri**, Gerald A. Tuskan, Wellington Muchero, Alejandro R. Walker, Eli Rodgers-Melnick, Stephen DiFazio, Todd Rosenstiel. 2016. Genetic variation and genomic associations of leaf physiological traits in an association population of *Populus trichocarpa* Torr. & Gray. *Plant & Animal Genome Conference XXIV. January 8 – 13, 2016 – San Diego, California, USA.*
12. \***Hari B. Chhetri**, D Macaya-Sanz, L Evans, AR Walker, A Bryan, W Muchero, J Chen, 3, GA Tuskan, and SP DiFazio. 2016. Association genetics of wood carbon isotope discrimination in *Populus trichocarpa* Torr. & Gray. *Bioenergy Science Center Annual Retreat, June 13- 15, 2016 – Chattanooga, Tennessee, USA.*
13. \***Hari B. Chhetri**, L Evans, AR Walker, LE Gunter, W Muchero, J Labbe, SS Jawdy, GA Tuskan, and SP DiFazio. 2015. Association genetics of wood anatomy and leaf morphology in *Populus trichocarpa* Torr. & Gray. *Bioenergy Science Center Annual Retreat, June 15- 17, 2015 – Chattanooga, Tennessee, USA.*
14. \***Hari B. Chhetri**, L Evans, and SP DiFazio, LE Gunter, W. Muchero, and GA Tuskan, Association genetics of anatomical and morphological traits in *Populus trichocarpa* Torr. & Gray. *Bioenergy Science Center Annual Retreat, June 9- 11, 2014 – Chattanooga, Tennessee, USA.*
15. \*J. Travis Columbus, Nancy F. Refulio-Rodriguez and**Hari B. Chhetri**. 2009. Molecular phylogenetics of *Aegopogon* (Poaceae, Chloridoideae).
16. \***Hari B. Chhetri**, Gilberto Ocampo and Elizabeth Kempton. 2007. Notes on reproductive biology of *Isomeris arborea* (Capparaceae), *Botany Conference, July 7 – 11, 2007 – Chicago, Illinois, USA.*

Note: \* indicates presenting author. |
| STUDENTS (UNDERGRADUATES, UNLESS SPECIFIED) TRAINED/SUPERVISED  |
| 1. Troy Silber, 2019; Jenna Ezarik, 2020, provided trainings for processing carbon isotope samples for the *Populus trichocarpa* genome wide association studies (GWAS) project.
2. \*Sunita Mahat, Summer 2016, 2017, provided trainings for processing wood anatomy images using matlab scripts for the *Populus trichocarpa* genome wide association study (GWAS) project.
3. Jacob Miller, 2016 and 2017, provided trainings for processing wood anatomy images using matlab scripts for the *Populus trichocarpa* genome wide association study (GWAS) project.
4. Patrick Whitehouse, Fall 2016, provided trainings for processing wood anatomy images using imageJ software for the *Populus trichocarpa* genome wide association studies (GWAS) project.
5. Luke Stover, 2015, provided trainings for processing wood anatomy and carbon isotope samples for the *Populus trichocarpa* genome wide association studies (GWAS) project.
6. Hoff Lindberg, Summer 2015, provided trainings for photographing wood cross sections for the *Populus trichocarpa* genome wide association studies (GWAS) and genotype × environment interaction project.
7. Savanna Plombon, Fall 2015, provided trainings for photographing wood cross sections for the *Populus trichocarpa* genome wide association studies (GWAS) project.
8. Niel Sprenkle, 2013, Honors research, Molecular control of wood anatomy in *Populus,* served as a graduate student mentor.
9. Amanda Emahizer, Summer 2011, NSF REU Program, Wood Anatomy of *Populus,* served as a graduate student mentor.
10. \*Zach Marnoy, Spring 2008, provided training for sectioning grass leaf blades using rotary microtome for the *Bouteloua* (Poaceae) leaf anatomy project.

\*Graduate student \*\*High school student |
| **FIELD EXPERIENCE** |
| * Nepal: Several places from tropical regions to high Himalayas.
* India: Calcutta.
* Mexico: Baja California.
* United States: Several states including Arizona, California, Colorado, Florida, Georgia, Illinois, Nebraska, New Jersey, New Mexico, Nevada, North Carolina, Ohio, Oklahoma, Oregon, South Carolina, Pennsylvania, Texas, Virginia, Wyoming and Utah.
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| **RESEARCH HIGHLIGHT (MAGAZINE)** |
| Flame 2009, Claremont Graduate University: Better living through classification ….. (page 30)[www.cgu.edu/wp-content/uploads/2017/01/flame-spring-2009.pdf](http://www.cgu.edu/wp-content/uploads/2017/01/flame-spring-2009.pdf) |
| **GOOGLE SCHOLAR PROFILE** |
|  |
| **LANGUAGES** |
| * + Fluent in (read, write and speak): Nepali (mother tongue), Hindi and English.
	+ Read and write only: Sanskrit
 |
| **REFERENCES** |
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