Vikram E. Chhatre

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Education

- **PhD** in **Genetics** - 2013, Texas A&M University
- **MS** in **Botany** - 1997, Amravati University, India

Publications & Manuscripts

20. Fitzpatrick MC, **Chhatre VE**, Soolanayakanahally R, Keller SR (2021) Experimental support for genomic prediction of climate maladaptation using the machine learning approach Gradient Forests. **Molecular Ecology Resources:**21(8): 2749–2765 https://onlinelibrary.wiley.com/doi/abs/10.1111/1755-0998.13374 [**34 Citations**]

19. Fay S, Fay DS, **Chhatre VE** (2021) CRISPRcruncher: A Tool for Engineering Restriction Sites into Coding Regions. **MicroPublications Biology**. **doi:** https://doi.org/10.17912/micropub.biology.000343; **Software:** https://crisprcruncher.io. [**2 Citations**]

18. Yusifov A, **Chhatre VE**, Bruns DR *et al* (2021) Transcriptomic analysis of cardiac gene expression across the life course in male and female mice. Physiological Reports, 9, e14940. https://doi.org/10.14814/phy2.14940 [**4 Citations**]

17. Yusifov A, **Chhatre VE**, Bruns DR *et al* (2021) Cardiac response to adrenergic stress differs by sex and across the lifespan. GeroScience 43: 1799–1813. https://link.springer.com/article/10.1007/s11357-021-00345-x [**7 Citations**]

16. **Chhatre VE** (2020) Some Modest and Practical Advice for Undergraduate Researchers. **Bulletin of the Ecological Society of America**: Section on *Undergraduate Education*. https://doi.org/10.1002/bes2.1745. **Among top 10 most downloaded articles in this journal during 2019–2020.**

15. Gougherty AV, **Chhatre VE**, Fitzpatrick MC, Keller SR (2020). Contemporary Range Positions Predict the Range-Wide Pattern of Genetic Diversity in Balsam Poplar (*Populus balsamifera* L.). **Journal of Biogeography**; 00:1–12. **doi:** https://doi.org/10.1111/jbi.13811 [**11 Citations**].

14. **Chhatre VE**, Fetter KC, Gougherty AV, Fitzpatrick MC, Soolanayakanahally RY, Zelesny RS Jr., Keller SR (2021). Climatic Niche Predicts the Landscape Structure of Locally Adaptive Standing Genetic Variation. BiorXiv Preprint dated October 24, 2019; https://doi.org/10.1101/817411. [**11 citations**]; Under revision at Nature Communications Biology.

13. **Forest Health and Biotechnology: Possibilities and Considerations.** National Academy of Sciences Consensus Report; Published January 8, 2019. The National Academies Press **doi:** https://doi.org/10.17226/25221. [**Downloads:** ∼4400, **36 Citations**].

12. **Chhatre VE**, Evans LM, DiFazio S, Keller SR (2018) Adaptive Introgression and Maintenance of a Trispecies Hybrid Complex in Range-Edge Populations of *Populus*. Molecular Ecology 27(23):4820–4838 https://doi.org/10.1111/mec.14820. | [**52 Citations**]
    - **Also see:** News & Views Perspectives article in Molecular Ecology highlighting this paper: Cronk & Suarez-Gonzalez, 2019 https://doi.org/10.1111/mec.14927

11. Keller SR, **Chhatre VE**, Fitzpatrick MC (2017) Influence of Range Position on Locally Adaptive Gene-Environment Associations in *Populus* Flowering Time Genes. Journal of Heredity (10.1093/jhered/esx098) (Sp. Issue: Local Adaptation) [**20 Citations**].

10. **Chhatre VE** and Emerson, KJ. StrAuto: Automation and Parallelization of STRUCTURE Analysis. BMC Bioinformatics (2017) 18:192. (10.1186/s12859-017-1593-0) [**145 Citations**].

9. Kazyak DC, Hilderbrand RH, King TL, Keller SR & **Chhatre VE** (2016) Hiding in Plain Sight: A Case for Cryptic Metapopulations in Brook Trout (*Salvelinus fontinalis*). PLoS ONE 11(1): e0146295 (10.1371/journal.pone.0146295) [**21 Citations**].

8. Westbrook JW* & **Chhatre VE*** et al. (2015) A consensus genetic map of *Pinus taeda* and *Pinus elliottii* and the extent of linkage disequilibrium in two genotype-phenotype discovery populations of *Pinus taeda*. G3: Genes, Genomes and Genetics 5(8):1685-1694. (10.1534/g3.115.019588)
   * Joint first authors. [**36 Citations**]

7. **Chhatre VE** and Rajora OP (2014). Genetic divergence and signatures of natural selection in marginal populations of a keystone, long-lived conifer eastern white pine (*Pinus strobus* L.) from northern Ontario. PLoS ONE 9(5): e97291 (10.1371/journal.pone.0097291) [**35 Citations**]

6. **Chhatre VE**, Byram TD, Neale DB, Wegrzyn JL and Krutovsky KV (2013). Genetic structure and association mapping of adaptive and selective traits in East Texas loblolly pine (*Pinus taeda* L.) breeding populations. Tree Genetics & Genomes (10.1007/s11295-013-0624-x) [**50 citations**]

5. Grogan, K, **Chhatre VE** and Abbot P (2010). The cost of conflict in aphid societies. Journal of Evolutionary Biology 23(1): 185–193. (10.1111/j.1420-9101.2009.01892.x) [**7 citations**]

4. **Chhatre VE**, Morales MA and Abbot P (2009). Isolation and characterization of nine microsatellite loci in an ant-tended treehopper *Publilia concava*. Molecular Ecology Resources 9: 1185–1188. (10.1111/j.1755-0998.2009.02598.x)

3. Abbot P and **Chhatre VE** (2007). Kin structure provides no explanation for intruders in social aphids. Molecular Ecology 16(17): 3659–3670. (10.1111/j.1365-294X.2007.03404.x) [**14 citations**]

2. Wang X-R, **Chhatre VE**, Nilsson M-C, Song W, Zackrisson O and Szmidt AE (2003). Island population structure of Norway spruce (*Picea abies* L.) Karst. in northern Sweden. International Journal of Plant Sciences 164(5): 711–717. (10.1086/376811) [**21 citations**]

Computational Expertise

- **Scientific:** R, Python, population genomics tools and nextgen sequencing tools
- **Reproducibility & Publishing:** Git & GitHub, RMarkdown, LaTeX
- **Authorship – StrAuto v1.0** - Automation and Parallelization of STRUCTURE analysis. https://strauto.popgen.org. [**145 Citations**].
- **Authorship – Distruct v2.3** - Modified Admixture Plotting Script (2018). Available from http://distruct2.popgen.org.

Teaching & Mentoring

Guest Instructor: University of Wyoming (Spring 2021–23)

MOLB-5700: Professional skills for Biomedical Researchers
Teaching 3 modules in using the `R` environment for data analysis, publication quality figures and reproducibility. **https://wyoibc.github.io/r4grads**

Primary Co-Instructor: University of Wyoming (Fall 2016–19)

MOLB-4485/5485 - Computers in Biology **http://molb4485.uwyo.online**

Undergrad Resarch Mentor

- **Samuel Fay, Sophomore – U Michigan, Major: Computer Sci:** Development of analytical tools in population genomics and molecular biology. Summer & Fall 2020.
- **Benjamin Romanjenko, Junior UG:** Bioinformatics tools for analysis of next generation sequencing data. (Wyoming Research Scholar 2019–20, Wyoming INBRE Summer Fellow 2019)
- **Cailin Deiter, B.S.:** Search for transcriptomic signatures of novel pathogens (**Currently:** Professional Research Assistant at Barbara-Davis Pediatrics Center, University of Colorado, Denver.)
- **Jelard Aquino, B.S.:** Analysis of RNAseq data (McNair Scholar, Fellowship with Smithsonian Tropical Research Institute, Panama; **Currently:** Bioinformatics PhD Student with Mira Han group at UNLV)
- **Asia Williams, B.S.:** Using R to analyze national immunization data (**Currently:** Dentistry Program at University of Iowa.

Primary Instructor: University of Vermont

PBIO104 - Plant Physiology – Spring 2016

Service

- **Advisory Board Member**: Advance Research Computing Center, Univ. Wyoming: 2022–
- **National Academy of Sciences Study Committee Member 2017–18:** "The Potential for Biotechnology to Address Forest Health". https://nas-sites.org/dels/studies/forest-biotech/.
- **Graduate Advisory Committees**
  1. Jelard Aquino, Bioinformatics PhD Program, University of Nevada
  2. Aykhan Yusifov, Molecular Biology PhD Program, University of Wyoming
- **Grant Reviewer:** Reviewed grant application for CESAB (Center for the Synthesis & Analysis of Biodiversity, France) August 2018
- **Peer Reviewer:** Annals of Botany, Molecular Ecology, Evolutionary Applications, Nature Communications Biology, Heredity, New Phytologist, American Journal of Botany, Biological Invasions, BMC Genetics, BMC Genomics, BMC EVOB, PLoS ONE, Tree Genetics & Genomes, Frontiers of Plant Science, Frontiers of Genetics.
- **Moderator since 2010:** STRUCTURE software mailing list (http://goo.gl/gKaB3C).

Professional Appointments & Experience

9. **Research Geneticist, United States Forest Service** – Beginning Feb 2023.
8. **Senior Research Scientist, Wyoming INBRE Data Science Core** – June 2016 to Jan 2023.

   Increase awareness of bioinformatics tools and high performance computing. Provide research and teaching support to statewide community.

7. **Postdoctoral Research, University of Vermont** – August 2014 - May 2016.

   Population genomics of adaptation and introgressive hybridization in *Populus*.

6. **Postdoctoral Research, Appalachian Laboratory, UMCES**, March to July, 2014

   Range-wide climate adaptation of balsam poplar

5. **Postdoctoral Research, USDA Forest Service, Saucier, MS**, Summer 2012 – Spring 2014

   Construction of an integrated reference linkage map in *Pinus taeda* L.

4. **Doctoral Research, Texas A&M University**, Fall 2009 – Spring 2013

   Population structure and association genetics of *Pinus taeda* L. from East Texas
   Landscape genomics: Correlation of environmental variables with SNP variation in *Pinus taeda* L.

3. **Vanderbilt University**, Summer 2004 – Summer 2009

   Ecology and evolution of gall-forming social aphids, Abbot Lab (4 years)
   Zebrafish developmental genetics, Solnica-Krezel Lab (1 year)

2. **Dalhousie University**, Fall 2001 – Spring 2004

   Central-marginal hypothesis testing with microsatellite genetic variation, Signatures of natural selection and genetic divergence in marginal populations of *Pinus strobus* L.

1. **Swedish University of Agricultural Sciences, Umeå**, Fall 2000 – Summer 2001

   Island population establishment and genetic structure of *Picea abies* (L.) Karst. in northern Sweden

0. **Institute of Forest Genetics & Tree Breeding, India**, 1998 – 2000

   Genetic diversity in Teak (*Tectona grandis* L.) from peninsular India

Selected Talks, Posters & Workshops

17. **Chhatre VE** (2022). Reproducible Data Science for Biologists - A Workshop at University of Wyoming. May-August, 2022. https://ibc.uwyo.online/rds.

16. **Chhatre VE** & Harrington, S. (2022) R Programming Language for Data Analysis and Publishing. 3 Modules in Graduate Course on Development of Skills for Biomedical Researchers. University of Wyoming, Spring 2022.

15. **Chhatre VE** & Harrington, S. (2021) Population Genomics Workshop, University of Wyoming. Fall 2021.

14. **Chhatre VE** 2020 & 2021. Wyoming INBRE Summer of Code – A Virtual Annual Summer Workshop Focussing on Learning Tools for Reproducible Data Analysis and Publishing. May through August. Latest website: https://wyoibc.github.io/soc2021

13. **Chhatre VE** 2020. Climate Change and the Health of North American Forests. Invited Sheridan Science Museum Lecture, Sheridan, Wyoming. December 9, 2020.

12. **Chhatre VE** 2020. Introduction to R Environment & Data Wrangling: Workshop for community college faculty and students in Wyoming, University of Wyoming, Casper. January 31 & February 1. https://github.com/cryptic0/introR.

11. **Chhatre VE**, Blouin NA 2019. Reproducible Methods in Research and Teaching: A Hands-On workshop delivered at the IDeA Western Regional Meeting, Las Vegas Nevada, USA on October 7, 2019.

10. **Chhatre VE**, Fetter KC & Keller SR *et al* 2018. Is standing genetic variation for local adaptation concentrated in rear edge populations? A test of range limit theory in *Populus balsamifera*. Selected talk at the Joint Evolution Societies Meeting, Montpellier France August 2018.

9. **Chhatre VE** & Blouin NA 2017. Data Visualization in R. A Workshop at IDEA/NIH Western Regional Meeting, Jackson Wyoming October 18, 2017.

8. **Chhatre VE** & Blouin N. 2017. Bioinformatics Data Analysis Workshop, July 17-18, University of Wyoming at Casper

7. **Chhatre VE** 2017 The Genomics Revolution. **Invited Public Lecture**, Science Museum, Sheridan College, Wyoming. April 5, 2017.

6. **Chhatre VE** & Blouin N 2017 Data analysis and visualization in R: Phenological onset of spring. Workshop on bioinformatics, Sheridan College, Wyoming. April 4, 2017.

5. **Chhatre VE & Blouin N** 2016 A workshop on introduction to linux and phylogenetic data analysis for undergraduates. University of Wyoming. June 14, 2016.

4. **Chhatre VE**: A bioinformatics workshop on introduction to Unix and NGS data analysis. January 12, 2016. University of Wyoming, Laramie, WY.

3. **Chhatre VE**, Fetter KC, Fitzpatrick MC, Keller SR (2015) Are rear edge populations a concern for climate mitigation? Harnessing genome scans for understanding climate adaptation in range-wide populations of a widely-distributed boreal tree *Populus balsamifera* **Invited Talk**: Ecological Society of America, Baltimore MD. August 12, SYMP10: Genetics and Climate Change.

2. **Chhatre VE**, Fitzpatrick M, Keller SR (2015). Understanding Climate Adaptation through Genome-Wide Patterns of Differentiation and Local Selection in *Populus balsamifera*. How Important Are Peripheral Populations? **Invited Talk**: Plant & Animal Genome XXIII, January 10, 2015.

1. **Chhatre VE**, Resende, M.F. Jr., Muñoz, P., Peter, G.F., Davis, J.M., Kirst, M., Echt, C.S., Krutovsky, K.V. and Nelson, CD (2013). An integrated linkage map of loblolly pine and its application in QTL mapping in a multi-parent, pedigree-structured population. Forest Tree Workshop, Plant & Animal Genome Conference XXI, Jan. 12–16, 2013, San Diego, CA. **Invited Talk**