

Vikram E. Chhatre

Wyoming INBRE Senior Research Scientist

May 22, 2019

Wyoming INBRE Bioinformatics Core
Department of Molecular Biology
University of Wyoming
Laramie, WY 82071

Email: vchhatre@uwyo.edu
Web: www.uwyo.edu/vchhatre
Phone: (307)766-3362
Twitterbot: @popgen_papers

Scholar Citation Index: goo.gl/YcWgC1

165 Citations | H: 7

Code: software.popgen.org | github.com/cryptic0

Education

- **PhD in Genetics** - 2013, Texas A&M University
- **MSc in Botany** - 1997, Amravati University, Maharashtra, INDIA
- **BSc in Biology & Chemistry** - 1995, Amravati University, Maharashtra, INDIA

Peer-Reviewed Publications

12. **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:** 3000].
11. **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>. **Published: 08/02/2018 | Github repo:** <https://cryptic0.github.io/HybridPoplar> [**4 Citations**]
 - **Also see:** News & Views Perspectives article in *Molecular Ecology* highlighting this paper: Cronk & Suarez-Gonzalez, 2019 <https://doi.org/10.1111/mec.14927>
10. 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) [**3 Citations | 710 Accesses | 228 PDF Downloads | Published: 11/08/2017**].
9. **Chhatre VE** and Emerson, KJ. StrAuto: Automation and Parallelization of STRUCTURE Analysis. *BMC Bioinformatics* (2017) 18:192. (10.1186/s12859-017-1593-0) [**39 Citations | 4516 Accesses | Published: 03/24/2017**].
8. 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) [**10 Citations | 1550 Accesses**].
7. 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. [**14 Citations | 2005 Accesses | 977 PDF downloads**]

6. **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) [**14 Citations** | **4329 Accesses** | **702 PDF downloads**]
5. **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) [**37 citations**]
4. 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**]
3. **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)
2. 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) [**11 citations**]
1. 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) [**20 citations**]

Manuscripts

2. **Chhatre VE** (2019) Some modest and practical advice for undergraduate researchers.
1. **Chhatre VE**, Fetter KC, Fitzpatrick MC, Keller SR (2017) Is standing genetic variation for local adaptation concentrated in rear edge populations? A test of range limit theory in *Populus balsamifera*. **Under review**

Awards & Grants

8. Wyoming Science Initiative Grant 2019 **\$77K** Genomic Analyses of Embryonic Diapause in the Musteloidea with an Eye Towards Improving Assisted Reproductive Technologies. PI: Merav Ben-David, Univ. Wyoming, Zoo/Phys
7. Wyoming INBRE Collaborative Bioinformatics Research Grant 2017–2019 **\$35,000**. Genetic Architecture of Stress Tolerance in Wyoming Grapevine Varieties. Co-PI with S. Dhekney, University of Wyoming in Sheridan.
6. Wyoming INBRE Small Sequencing Grant 2016–2017 **\$10,000**. RNAseq analysis of the role of adaptive introgression in the Maintenance of a Tri-Species Complex of *Populus* in the Rocky Mountains.
5. USDA Secretary’s Honor for Excellence in Research, 2011
Conifer Translational Genomics Network (<http://dendrome.ucdavis.edu/ctgn>)
4. Guest Research Scholarship - 2000–01, The Swedish Institute: <http://www.si.se>
3. Early Career Travel Award, 2013 & 2011, Southern Forest Tree Improvement Committee
2. Regents Graduate Fellowship - 2009–10, Texas A&M University
1. Junior Research Fellowship - 1998–00, Institute of Forest Genetics & Tree Breeding, India

Service

- **National Academy of Sciences Study Committee Member 2017–18:** “The Potential for Biotechnology to Address Forest Health”. See details at: <https://nas-sites.org/dels/studies/forest-biotech/>. Final report published. See list of publications for details.
- **Grant Reviewer:** Reviewed grant application for CESAB (Center for the Synthesis & Analysis of Biodiversity, France) August 2018
- **Peer Reviewer:** 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 2010–2019:** STRUCTURE software mailing list (<http://goo.gl/gKaB3C>).
- **Curator: @Popgen_Papers** – A Twitter Literature Bot [**1300 Followers, ~8000 Articles**].

Professional Appointments & Experience

9. **Senior Research Scientist, Wyoming INBRE Bioinformatics Core** – Since June 2016.
8. **Postdoctoral Research, University of Vermont** – August 2014 - May 2016.
Population genomics of adaptation and introgressive hybridization in *Populus*.
7. **Postdoctoral Research, Appalachian Laboratory, UMCES**, March to July, 2014
Range-wide climate adaptation of balsam poplar
6. **Postdoctoral Research, USDA Forest Service, Saucier, MS**, Summer 2012 – Spring 2014
Construction of an integrated reference linkage map in *Pinus taeda* L.
5. **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.
4. **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)
3. **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.
2. **Swedish University of Agricultural Sciences, Umeå**, Fall 2000 – Summer 2001
Island population establishment and genetic structure of *Picea abies* (L.) Karst. in northern Sweden
1. **Institute of Forest Genetics & Tree Breeding, India**, 1998 – 2000
Genetic diversity in Teak (*Tectona grandis* L.) from peninsular India

Computational

- Mac OSX, GNU Linux, Python, R, L^AT_EX₂ ϵ , HTML, CSS, Markdown, RMarkdown
- **StrAuto v1.0** - Automation and Parallelization of STRUCTURE analysis.
strauto.popgen.org. [39 Citations, ~1500 downloads in over 50 countries]
- **Distruct v2.3** - Modification of the original distruct.py plotting script by Anil Raj (github.com/rajanil/fastStructure) that allows users to assign arbitrary population order in the barplot.
<http://distruct2.popgen.org>. [80 downloads]

Teaching & Mentoring

Undergrad Research Mentor at UWyoming

- Bioinformatics tools for analysis of next generation sequencing data – **Benjamin Romanjenko**, Sophomore & Wyoming INBRE Summer Fellow
- Search for novel pathogens – **Cailin Deiter**, Senior Undergraduate
- Analysis of RNAseq data – **Jelard Aquino**, McNair Scholar and currently a bioinformatics research intern at Smithsonian Tropical Research Institute, Panama.
- Using R to analyze national immunization data – **Asia Williams**

Instructor: University of Wyoming

MOLB-4485/5485 - Computers in Biology – Fall 2016–18
<http://molb4485.uwyo.online>

Co-Instructor: University of Vermont

PBIO381 - Ecological Genomics (Graduate Level) – Fall 2015
Taught a module on Gene-Environment association with BAYENV2.
Wrote Unix and population genomic analysis tutorials.

Graduate Teaching Assistant: Texas A&M University

Genetics 612 - Population Genetics (Graduate Level) – Fall 2011
Genetics 302 - UG Lab Course – Fall 2009 & Spring 2010

Selected Talks, Posters & Workshops

22. **Chhatre VE** 2018. Leveraging computational tools to increase productivity in education and research. Wyoming INBRE Seminar, November 30, 2018.
21. **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.
20. **Chhatre VE** & Blouin NA 2017. Data Visualization in R. A Workshop at IDEA/NIH Western Regional Meeting, Jackson Wyoming October 18, 2017.
19. **Chhatre VE** & Blouin N. 2017. Bioinformatics Data Analysis Workshop, July 17-18, University of Wyoming at Casper
18. **Chhatre VE** 2017. Phylogenetic Reconstruction - A Webinar Presented to Wyoming Dept. of Public Health, Cheyenne, WY. May 18, 2017.
17. **Chhatre VE** 2017 The Genomics Revolution. **Invited Public Lecture**, Science Museum, Sheridan College, Wyoming. April 5, 2017.

16. **Chhatre VE** & Blouin N 2017 Data analysis and visualization in R: Phenological onset of spring. Workshop on bioinformatics, Sheridan College, Wyoming. April 4, 2017.
15. **Chhatre VE** & Keller SR & Fitzpatrick M 2017 Importance of range context in understanding local adaptation – Insights from a boreal tree *Populus balsamifera*. Invited Seminar: Dept. of Botany, University of Wyoming. March 30, 2017.
14. **Chhatre VE** & **Blouin N** 2016 A workshop on introduction to linux and phylogenetic data analysis for undergraduates. University of Wyoming. June 14, 2016.
13. **Chhatre VE** (2016) Genome-Wide Patterns of Local Adaptation and Introgressive Hybridization in *Populus*. Marvin Seminar, Dept. of Plant Biology, University of Vermont. March 24, 2016.
12. **Chhatre VE**: A bioinformatics workshop on introduction to Unix and NGS data analysis. January 12, 2016. University of Wyoming, Laramie, WY.
11. **Chhatre VE**, Fetter KC, Fitzpatrick MC, Keller SR (2015) Rear-edge populations and climate change mitigation. Understanding local adaptation in widely-distributed boreal tree *Populus balsamifera*. **Invited Talk**: Concordia University, Montreal, Canada. December 11, 2015.
10. **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.
9. **Chhatre VE**, Fitzpatrick MC & Keller SR (2015) Detecting selection in spatially heterogenous environments: Clues from simulations and empirical data from a widely distributed boreal tree *Populus balsamifera*. 35th New Phytologist Symposium: The genomes of forest trees: new frontiers of forest biology - Harvard Arboretum June 16-17, 2015 **Poster**.
8. **Chhatre VE**, Schmidting RC & Nelson CD (2015) Salt tolerance of barrier island slash pine. Southern Forest Tree Improvement Committee Meeting, June 8-11, Hot Springs, AR **Poster**.
7. **Chhatre VE**, Fitzpatrick MC & Keller SR (Feb 5, 2015) Local adaptation in forest tree populations. Insights from empirical and simulation data. Marvin Seminar, Dept. of Plant Biology, University of Vermont.
6. **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.
5. **Chhatre VE** (2013). STRAUTO: A Python program to automate structure analysis for Linux and Mac platforms. North American Quantitative Genetics Meeting, Southern Forest Tree Improvement Conference, June 10, 2013, Clemson University, Clemson, SC **Talk**.
4. **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**
3. **Chhatre VE**, Byram TD, Krutovsky KV (2012) Population and evolutionary genetics of the lost pines: Lessons from history. Contact meeting, Western Gulf Forest Tree Improvement Program, Bastrop State Park, Texas, May 22–23, 2012. **Talk**
2. **Chhatre VE**, Byram TD, Neale DB, Wegrzyn JL and Krutovsky KV (2011). **Talk**: Association mapping of adaptive traits in East Texas loblolly pine (*Pinus taeda* L.) breeding

populations using high-density SNP genotyping.

Southern Forest Tree Improvement Conference, June 13–16, 2011, Biloxi, MS.

1. **Chhatre VE**, Byram TD, Neale DB, Wegrzyn JL and Krutovsky KV (2011).

Invited Talk: High density SNP genotyping of east Texas loblolly pine (*Pinus taeda* L.).

Forest Tree Workshop, Plant & Animal Genome Conference XIX, Jan. 15–19, 2011, San Diego, CA.