

Luke McLean Evans, Ph.D.
Faculty Fellow, Institute for Behavioral Genetics
Assistant Professor, Department of Ecology and Evolutionary Biology, University of Colorado
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Profiles: [Google Scholar](#); [ResearchGate](#); [LinkedIn](#)

POSITIONS AND EDUCATION

2018-present Faculty Fellow, Institute for Behavioral Genetics
Assistant Professor, Ecology and Evolutionary Biology, University of Colorado, Boulder, CO.
2015-2018 Postdoctoral Fellow, Institute for Behavioral Genetics, University of Colorado
Boulder, CO. Supervisor Dr. Matthew C. Keller
2012-2015 Postdoctoral Fellow, Department of Biology, West Virginia University
Morgantown, WV. Supervisor Dr. Stephen P. DiFazio
2012 Ph.D. in Biology, with distinction
Northern Arizona University, Flagstaff, AZ. Major Advisors: Drs. Tom Whitham, Gery Allan
2007 M.S. in Biology
Northern Arizona University, Flagstaff, AZ. Major Advisors: Drs. Tom Whitham, Gery Allan
2005 B.A. in Environmental and Evolutionary Biology, *cum laude*
Dartmouth College, Hanover, NH

PUBLICATIONS

*Equal contribution, †Undergraduate student mentee, ‡Graduate student mentee, †Postdoctoral mentee

46. **Evans, LM**, CH Arehart[†], AD Grotzinger, TJ Mize[†], MS Brasher[†], JA Stitzel, MA Ehringer, CA Hoeffler. *In press*. Transcriptome-Wide Gene-Gene Interaction Association Study Elucidates Pathways and Functional Enrichment of Complex Traits. *PLoS Genetics*. Preprint on BioRxiv: <https://doi.org/10.1101/2022.08.16.504187>
45. Evans, LM, PN Romero Villela. 2023. News & Views: Contributions of rare variants to complex traits. *Nature*. 614:418-419. <https://doi.org/10.1038/d41586-023-00272-1>
44. Mize, TM[†], SA Funkhouser⁺, JM Buck, JA Stitzel, MA Ehringer, **LM Evans**. 2022. Testing association of previously implicated gene-sets and gene-networks in nicotine exposed mouse models with human smoking phenotypes. *Accepted at Nicotine & Tobacco Research*.
43. Mize, TM[†], **LM Evans**. 2022. Examination of a novel expression-based gene-SNP annotation strategy to identify tissue-specific contributions to heritability in multiple phenotypes. *Accepted at European Journal of Human Genetics*.
42. Booher, W, L Vanderlinden, L Hall, A Thomas, **LM Evans**, L Saba, MA Ehringer. *In press*. Hippocampal RNA Sequencing in Mice Selectively Bred for High and Low Activity. *Genes Brain and Behavior*. <http://doi.org/10.1111/gbb.12832>
41. Hatoum, AS, CL Morrison, EC Mitchell, M Lam, CE Benca-Bachman, AE Reineberg, RHC Palmer, **LM Evans**, MC Keller, NP Friedman. 2023. Genome-Wide Association Study Shows that Executive Functioning Is Influenced by GABAergic Processes and Is a Neurocognitive Genetic Correlate of Psychiatric Disorders. *Biological Psychiatry*. 93(1):59-70. <https://doi.org/10.1016/j.biopsych.2022.06.034>
40. Jang, S-K, **LM Evans**, and 61 others. 2022. Rare variant heritability of smoking from deep whole-genome sequencing of up to 26,000 individuals. *Nature Human Behavior*. 6:1577–1586. <https://doi.org/10.1038/s41562-022-01408-5>
39. Jami, ES. And 95 others (**LM Evans** co-author on consortium paper). 2022. Genome-wide association meta-analysis of childhood and adolescent internalizing symptoms. *Journal of the American Academy of Child & Adolescent Psychiatry*. 61(7):934-945. DOI: 10.1016/j.jaac.2021.11.035
38. Howe, LJ, and 102 others (**LM Evans** co-author on consortium paper). 2022. Within-sibship GWAS of 25 phenotypes improve estimates of direct genetic effects. *Nature Genetics*. 54(5):581+
37. **Evans, LM**, S Jang, MA Ehringer, DB Hancock, J Otto, SI Vrieze, MC Keller. 2021. Genetic architecture of four smoking behaviors using partitioned SNP heritability. *Addiction*. 116(9): 2498-2508. DOI:10.1111/add.15450. PMC8759147
36. Colbert, SMC[‡], S Funkhouser⁺, EC Johnson, CL Morrison, C Hoeffler, NP Friedman, MA Ehringer, **LM Evans**. 2021. Novel characterization of the multivariate genetic architecture of internalizing psychopathology and alcohol use. *American Journal of Medical Genetics Part B Neuropsychiatric Genetics*. 186(6):353-366. DOI:10.1002/ajmg.b.32874. PMC8556277
35. Ip, HF, and 142 others. (**Evans** co-author on consortium paper). 2021. Genetic association study of childhood aggression across raters, instruments, and age. *Translational Psychiatry*. 11:413. <https://doi.org/10.1038/s41398-021-01480-x>. PMC8324785.
34. Adjangba, A[‡], R Border, P Romero Villela, MA Ehringer, **LM Evans**. 2021. Limited evidence of modified genetic susceptibility to tobacco smoking at rs16969968 based on age of onset of regular smoking. *Nicotine & Tobacco Research*. 23(6):1055-1063. DOI:10.1093/ntr/ntaa229. PMC8150133

33. Gouker, FE, CH Carlson, J Zou, **LM Evans**, CR Crowell, CD Smart, SP DiFazio, LB Smart. 2021. Sexual dimorphism in the dioecious willow, *Salix purpurea*. *American Journal of Botany*. 108(8):1374-1387. <http://doi.org/10.1002/ajb2.1704>
32. Thomas, AL*, **LM Evans***, MD Nelsen, EJ Chesler, MS Powers, WC Booher, C Lowry, JD DeFries, MA Ehringer. 2021. Whole genome sequencing of inbred mouse strains selected for high and low open-field activity. *Behavior Genetics*. 51:68-81. <https://doi.org/10.1007/s10519-020-10014-y>. PMC7854991
31. Bothwell, H, **LM Evans**, EI Hersch-Green, S Woolbright, G Allan, TG Whitham. 2020. Genetic data improves niche model discrimination and alters the direction and magnitude of climate change forecasts. *Ecological Applications*. 31(3):e02254. <https://doi.org/10.1002/eap.2254>
30. **Evans, LM**, EC Johnson, WE Melroy-Greif, JK Hewitt, CA Hoeffler, MC Keller, LM Saba, JA Stitzel, MA Ehringer. 2020. The role of *a priori*-identified addiction and smoking gene sets in smoking behaviors. *Nicotine & Tobacco Research*. 22:1310-1315. <https://doi.org/10.1093/ntr/ntaa006>. PMC7749195
29. Border R, EC Johnson, **LM Evans**, MC Keller. 2019. Measurement Error Cannot Account for Failed Replications of Historic Candidate Gene-by-Environment Hypotheses: Response to Vrshek-Schallhorn et al. *The American Journal of Psychiatry*. 176:668-669. <https://doi.org/10.1176/appi.ajp.2019.19040374r>
28. Border R, A Smolen, R Crowley, M Stallings, S Brown, RD Conger, J Derringer, MB Donnellan, BC Haberstick, J Hewitt, C Hopfer, K Krauter, MB McQueen, TL Wall, MC Keller, **LM Evans**. 2019. Imputation of behavioral candidate gene repeat variants in 486,565 publicly-available UK Biobank individuals. *European Journal of Human Genetics*. 27:963-969. DOI:10.1038/s41431-019-0349-x. PMC6777532
27. Border R, EC Johnson, **LM Evans**, A Smolen, N Berley, PF Sullivan, MC Keller. 2019. No support for candidate gene or candidate gene-by-interaction hypotheses for major depression across multiple large samples. *The American Journal of Psychiatry*. 176:376-387. DOI:10.1176/appi.ajp.2018.18070881. PMC6548317
26. Carlson, C, F Gouker, C Crowell, **L Evans**, S DiFazio, C Smart, L Smart. 2019. Joint linkage and association mapping of complex traits in shrub willow (*Salix purpurea* L.). *Annals of Botany*. 124:701-715. DOI:10.1093/aob/mcz047
25. Chhetri, HB, D Macaya-Sanz, D Kainer, **LM Evans**, K Ault, T Rosentiel, SH Strauss, D Jacobson, TJ Tschaplinski, GA Tuskan, SP DiFazio. 2019. Genome-wide association analysis of *Populus trichocarpa* identifies key polymorphisms controlling morphological and physiological traits. *New Phytologist*. 223:293-309. DOI:10.1111/nph.15777.
24. Zhou R, Macaya-Sanz D, Rodgers-Melnick E, Carlson CH, Gouker FE, **Evans LM**, Schmutz J, Jenkins JW, Yan J, Tuskan JA, Smart LB, DiFazio SP. 2018. Characterization of a large sexually dimorphic genome interval in *Salix purpurea* L. (Salicaceae). *Molecular Genetics and Genomics*. 293:1473-1452. DOI:10.1007/s00438-018-1473-y
23. **Evans, LM**, R Tahmasbi, SI Vrieze, G Abecasis, S Das, D Bjelland, T DeCandia, Haplotype Reference Consortium, ME Goddard, BM Neale, J Yang, PM Visscher, MC Keller. 2018 Comparison of methods that use whole genome data to estimate the heritability and genetic architecture of complex traits. *Nature Genetics*. 50:737-745. DOI:10.1038/s41588-018-0108-x. PMC5934350
22. **Evans, LM**, R Tahmasbi, SI Vrieze, G Abecasis, S Das, D Bjelland, T DeCandia, Haplotype Reference Consortium, ME Goddard, J Yang, PM Visscher, MC Keller. 2018. Narrow-sense heritability estimation of complex traits using identity-by-descent information. *Heredity*. 121:616-630. DOI:10.1038/s41437-018-0067-0. PMC6221881.
21. **Evans, LM**, MC Keller. 2018. Correspondence: Using partitioned heritability methods to explore genetic architecture. *Nature Reviews Genetics*. DOI:10.1038/nrg.2018.6
20. Johnson, EC, **LM Evans**, MC Keller. 2018 Relationship between estimated autozygosity and complex traits in the UK Biobank. *PLoS Genetics*. 14(7):e1007556. DOI:10.1371/journal.pgen.1007556.
19. Chhatre, VE, **LM Evans**, SP DiFazio, SR Keller. 2018. Adaptive introgression and maintenance of a trispecies hybrid complex in range-edge populations of *Populus*. *Molecular Ecology*. 27:4820-4838. DOI:10.1111/mec.14820
18. Xie, M, W Muchero, AC Bryan, K Yee, H-B Guo, J Zhang, TJ Tschaplinski, VR Singan, E Lindquist, RS Payyavula, J Barros-Rios, R Dixon, N Engle, RW Sykes, M Davis, SS Jawdy, LE Gunter, O Thompson, SP DiFazio, **LM Evans**, K Winkeler, C Collins, J Schmutz, H Guo, U Kalluri, M Rodriguez, K Feng, J-G Chen, GA Tuskan. 2018. A 5-Enolpyruvylshikimate 3-Phosphate Synthase Functions as a Transcriptional Repressor in *Populus*. *The Plant Cell*. 30:1645-1660. DOI:10.1105/tpc.18.00168
17. Wills, AG, **LM Evans**, C Hopfer. 2017. Phenotypic and genetic relationship between BMI and drinking in a sample of UK adults. *Behavior Genetics*. 47(3):290-297. DOI:10.1007/s10519-017-9838-2. PMC5546738.
16. Bothwell, HM, SA Cushman, SA Woolbright, EI Hersch-Green, **LM Evans**, TG Whitham, GJ Allan. 2017. Conserving threatened riparian ecosystems in the American West: Precipitation gradients and river networks drive genetic connectivity and diversity in a foundation riparian tree (*Populus angustifolia*). *Molecular Ecology*. 26:5114-5132.
15. **Evans, LM**, S Kaluthota, DW Pearce, GJ Allan, K Floate, SB Rood, TG Whitham. 2016. Bud phenology and growth are subject to divergent selection across a latitudinal gradient in *Populus angustifolia* and impact adaptation across the distributional range and associated arthropods. *Ecology and Evolution*. 6:2565-4582. DOI:10.1002/ece3.2222
14. **Evans LM**, GJ Allan, SP DiFazio, GT Slavov, JA Wilder, SB Rood, KD Floate, TG Whitham. 2015. Geographical barriers and climate influence demographic history in narrowleaf cottonwoods. *Heredity*. 114:387-396. DOI:10.1038/hdy.2014.115

13. Kaluthota, S, DW Pearce, **LM Evans**, MG Letts, TG Whitham, SB Rood. 2015. Higher photosynthetic capacity from higher latitude: foliar characteristics and gas exchange of southern, central and northern populations of *Populus angustifolia*. *Tree Physiology*. 35:936-948. DOI: 10.1093/treephys/tpv069
12. **Evans LM**, GT Slavov, E Rodgers-Melnick, J Martin, P Ranjan, W Muchero, AM Brunner, W Schackwitz, L Gunter, J-G Chen, GA Tuskan, SP DiFazio. 2014. Population genomics of *Populus trichocarpa* identifies signatures of selection and adaptive trait associations. *Nature Genetics*. 46:1089-1096. DOI:10.1038/ng.3075 **Press release at: <http://jgi.doe.gov/signatures-selection-inscribed-poplar-genomes/>
11. Muchero W, J Guo, SP DiFazio, J-G Chen, PRanjan, GT Slavov, LE Gunter, S Jawdy, AC Bryan, R Sykes, A Ziebell, I Porth, O Skyba, F Unda, YA El-Kassaby, CJ Douglas, SD Mansfield, J Martin, W Schackwitz, **LM Evans**, O Czarnecki, GA Tuskan. 2014. Multi-environment Identification and Molecular Validation of Allelic Variants Associated With Cell Wall Chemistry in *Populus*. *BMC Genomics*. 16:24.
10. Brunner AM, **LM Evans**, C-Y Hsu, S Xiaoyan. 2014. Vernalization and the chilling requirement to exit bud dormancy: shared or separate regulation? *Frontiers in Plant Science*. 5:732. DOI: 10.3389/fpls.2014.00732
9. Cushman, SA, T Max, N Meneses, **LM Evans**, SM Ferrier, B Honchak, TG Whitham, GJ Allan. 2014. Landscape genetic connectivity in a riparian foundation tree is jointly driven by climatic gradients and river networks. *Ecological Applications*. 24:1000-1014.
8. Bangert RK, SM Ferrier, **LM Evans**, K Kennedy, KC Grady, GJ Allan, TG Whitham. 2013. The proportion of three foundation plant species and their genotypes influence an arthropod community: restoration implications for the endangered southwestern willow flycatcher. *Restoration Ecology* 21:447-456.
7. **Evans LM**, GJ Allan, N Meneses, TL Max, TG Whitham. 2013. Herbivore host-associated genetic differentiation depends on the scale of plant genetic variation examined. *Evolutionary Ecology* 27:65-81.
6. **Evans LM**, GJ Allan, and TG Whitham. 2012. *Populus* hybrid hosts drive divergence in the herbivorous mite, *Aceria parapopuli*: Implications for conservation of plant hybrid zones as essential habitat. *Conservation Genetics* 13:1601-1609.
5. **Evans, LM**, JS Clark, AV Whipple, TG Whitham. 2012. The relative influences of host plant genotype and yearly abiotic variability in determining herbivore abundance. *Oecologia*. 168:483-489.
4. Whitham, TG, CA Gehring, LJ Lamit, T Wojtowicz, **LM Evans**, AR Keith, DS Smith. 2012. Community specificity: life and afterlife effects of genes. *Trends in Plant Science* 17:271-281.
3. **Evans, LM**, RW Hofstetter, MP Ayres, KD Klepzig. 2011. Temperature alters the relative abundance and population growth rates of species within the *Dendroctonus frontalis* (Coleoptera: Curculionidae) community. *Environmental Entomology* 40:824-834.
2. Whitham TG, CA Gehring, **LM Evans**, CJ LeRoy, RK Bangert, JA Schweitzer, GJ Allan, RC Barbour, DG Fischer, BM Potts, JK Bailey. 2010. A community and ecosystem genetics approach to conservation biology and management. Pp. 50-73. In *Molecular Approaches in Natural Resource Conservation* (J.A DeWoody, J.W. Bickham, C. Michler, K. Nichols, O.E. Rhodes, and K. Woeste, eds.). Cambridge University Press.
1. **Evans, LM**, GJ Allan, S Woolbright, S Shuster, TG Whitham. 2008. Hybridization and genotypic variation in a foundation tree drive cryptic speciation of a specialist herbivore. *Evolution* 62:3027-3040.

Preprints, In Review, and In Preparation:

- Evans, LM**, AD Grotzinger. How SNP-heritability informs biological understanding of psychiatric disorders. *Invited Review at Translational Psychiatry*. In revision.
- Brasher, M[‡], TM Mize[†], AL Thomas, CA Hoeffler, MA Ehringer, **LM Evans**. Testing human anxiety associations of genes previously implicated by mouse anxiety models. *Revision in review at Genes, Brain & Behavior*. Preprint on BioRxiv: <https://doi.org/10.1101/2022.07.08.499186>
- Arehart, CH[†], JD Sterrett, R Garris, RQ Pilco, CR Gignoux, **LM Evans***, MA Stanislawski*. Poly-omic risk scores predict inflammatory bowel disease diagnosis. *Submitted to mSystems*. <https://doi.org/10.1101/2022.09.14.508056>
- Romero Viella, PN, **LM Evans**, T Palviainen, R Border, J Kaprio, RHC Palmer, MC Keller, MA Ehringer. Loci on Chromosome 20 Interact with rs16969968 to Influence Cigarettes per Day in European Ancestry Individuals. *In revision*. Preprint on ResearchSquare: <https://doi.org/10.21203/rs.3.rs-1981574/v1>

Other publications, not peer-reviewed:

- Funkhouser, SA⁺, JD Boardman, JK Hewitt, MC Stallings, CJ Hopfer, SA Brown, TA Wall, CA Reynolds, MC Keller, **LM Evans**. Investigating heterogeneous genetic effects contributing to smoking behaviors. *MedRxiv*: <https://www.medrxiv.org/content/10.1101/2021.08.08.21261764v1>
- Tahmasbi, R, **LM Evans**, E Turkheimer, MC Keller. Testing the moderation of quantitative gene by environment interactions in unrelated individuals. *BioRxiv*: <https://doi.org/10.1101/191080>

GRANTS AND FELLOWSHIPS

- NIH/NIA 1 R01 AG046938-06 (PI: Reynolds) "Colorado Adoption/Twin Study of Lifespan Behavioral Development & Cognitive Aging (CATSLife2)." Project duration 06/01/15-05/31/25, total award \$9,254,749 (Co-Investigator)
- NIH/NIDA 1 R01 DA044283-01, (PI: Vrieze) "Deep sequencing, phenotyping, and imputation in large-scale biobanks: A novel and cost-effective framework to identify rare mutations associated with addiction." Project duration 05/01/19-02/28/24, total award \$1,236,721 (Co-Investigator)
- NIH/NIMH 5 R01 MH100141-06 (PI: Keller) "Estimating the genetic and environmental architecture of psychiatric disorders" project duration: 7/1/18-6/30/23, total award: \$3,192,862 (Co-Investigator)
- NIH/NIA 1 R01 AG046938-05 (MPI: Reynolds/Wadsworth), "Colorado Adoption/Twin Study of Lifespan Behavioral Development & Cognitive Aging (CATSLife) Subcontract to Institute for Behavioral Genetics" (Wadsworth), project duration 06/01/15-02/28/20, total award \$5,831,433 (Co-Investigator)
- 2015 NSF DEB 1542509. (P.I. Matt Olson) NSF Dimensions US-China: Collaborative Research: Sex chromosomes and dioecy in plants as drivers of multi-level biodiversity. \$1,945,825. (Co-Investigator, disbursed after I left WVU.)
- 2014 Faculty Senate Travel Award, WVU. \$400
- 2010-2012 NSF Dissertation Improvement Grant, "Climate change and candidate gene variation in *Populus*: Impacts on dependent communities and biotic interactions." \$15,000 NSF DEB 1011554
- 2007-2012 Science Foundation Arizona Graduate Fellowship
- 2007-2012 NSF IGERT Traineeship
- 2004 Paul K. Richter and Evalyn E. Cook Richter Memorial Fund, Dartmouth College

ACADEMIC AWARDS

- 2012 Best Dissertation Award, NAU Biology Department
- 2009 Best Graduate Student Paper, NAU Biology Department
- 2006 1st Place Student Presentation Competition, Natural Areas Conf., Flagstaff, AZ
- 2005 Christopher B. Reed Biologist Award, Dartmouth College
- 2004 Academic Citation, *Introd. to Problems of Philosophy*, Dartmouth College

PROFESSIONAL TALKS AND PRESENTATIONS

- * Equal contribution, ‡ Undergraduate student mentee, † Graduate student or postdoctoral mentee
- Reynolds, CA, A Smolen, CD Link, D Evans, R Bruellman, **LM Evans**, SJ Wadsworth. *Poster*. Neurofilament Light Chain (NfL) and General Cognitive Ability in Adults Approaching Midlife. Gerontological Society of America. October, 2022.
- Arehart C, M Lin, **LM Evans**, CR Gignoux. *Poster*. Improving the selection of variants included in polygenic risk scoring models. American Society of Human Genetics Annual Meeting, October, 2022, Los Angeles, CA.
- Evans, LM**. *Invited seminar*. Genome-wide gene-gene interaction associations in complex traits. Division of Biomedical Informatics & Personalized Medicine seminar series, School of Medicine, Anschutz Medical Campus. February 16, 2022.
- Evans LM**, S Jang, DB Hancock, MA Ehringer, JM Otto, SI Vrieze, MC Keller. *Poster*. Genetic architecture of four smoking behaviors using partitioned SNP heritability. NIDA Genetics Consortium Virtual Genetics and Epigenetics Cross-Cutting Research Team Meeting. March 8, 2021.
- Mize, TM†, SA Funkhouser†, JM Buck, JA Stitzel, MA Ehringer, **LM Evans**. *Poster*. Testing Association of Previously Implicated Gene-Sets in Nicotine Exposed Mouse Models with Human Smoking Phenotypes. Behavior Genetics Association Annual Meeting (virtual). June 29, 2021.
- Carlton Colbert S‡, Funkhouser S†, Johnson E, Ehringer MA, **Evans LM**. *Poster*. Differential shared genetic influences on anxiety with problematic alcohol use compared to alcohol consumption. World Congress of Psychiatric Genetics annual meeting. (Virtual) October 19th, 2020
- Funkhouser SA†, **Evans LM**. *Poster*. Investigating heterogenous genetic effects contributing to smoking behavior using the UK Biobank. World Congress of Psychiatric Genetics annual meeting. (Virtual) October 19th, 2020
- Carlton Colbert S‡, Funkhouser S, Johnson E, Ehringer MA, **Evans LM**. *Talk*. Differential shared genetic influences on anxiety with problematic alcohol use compared to alcohol consumption. Presentation at the Behavior Genetics Association annual meeting. (Virtual) June 25th, 2020
- Funkhouser SA†, **Evans LM**. *Talk*. Investigating heterogenous genetic effects contributing to smoking behavior using the UK Biobank. Presentation at the Behavior Genetics Association annual meeting. (Virtual) June 25th, 2020

- Evans, LM.** *Invited seminar.* Genetic influences on smoking behaviors. Presented at the Statistical Genomics Working Group, Biostatistics and Informatics Department, Colorado School of Public Health, Anschutz Medical Campus. November 7, 2019.
- Evans, LM.** *Invited talk.* Exploring the genetic architecture of nicotine use. Presented at the Integrative and Quantitative Biology Symposium, April 16, 2019, Biofrontiers Institute, University of Colorado Boulder, CO.
- Evans, LM.** *Invited seminar.* Exploring the genetic architecture of nicotine use and identifying novel associations. Presented at the PAGE SC Meeting, January 10, 2019, Colorado Center for Personalized Medicine - CU Anschutz Medical Center, Aurora, CO.
- Evans, LM.** *Talk.* Exploring the genetic architecture of psychiatric disorders using partitioned heritability approaches. Presented at the World Congress of Psychiatric Genetics, October 13, 2018, Glasgow, Scotland.
- Evans, LM.** *Invited talk.* Exploring the genetic architecture of psychiatric disorders using partitioned heritability approaches. Presented at the Colorado Center for Personalized Medicine and Biobank Retreat, September 14, 2018, Vail, CO.
- Ehringer, MA, MS Powers, **LM Evans**, JC DeFries (2018) *Talk.* Whole genome sequencing of replicate inbred strains of mice selected for high and low open-field activity. 20th Annual Meeting of the International Behavioural and Neural Genetics Society.
- Evans, LM,** R Tahmasbi, SI Vrieze, G Abecasis, S Das, D Bjelland, T DeCandia, M Goddard, B Neale, J Yang, P Visscher, MC Keller, Haplotype Reference Consortium. Methods to estimate heritability of complex traits under a variety of complex genetic architectures. Poster 2881. Presented at the 67th Annual Meeting of The American Society of Human Genetics, October 18, 2017, Orlando, Florida.
- Evans, LM,** R Tahmasbi, P Visscher, J Yang, M Goddard, SI Vrieze, G Abecasis, S Das, D Bjelland, T DeCandia, B Neale, Haplotype Reference Consortium, MC Keller. Utility and biases of multiple whole genome methods to estimate heritability and examine genetic architecture of complex traits. Poster 509. Presented at the 66th Annual Meeting of The American Society of Human Genetics, October 19, 2016, Vancouver Canada.
- Evans LM,** W Muchero, G Tuskan, and SP DiFazio. *Talk.* Quaternary demography of *Populus trichocarpa* throughout its range. International Poplar Symposium VI. July 20-24, 2014. Vancouver, BC.
- Evans LM,** GT Slavov, E Rodgers-Melnick, J Martin, P Ranjan, W Muchero, A Brunner, W Schackwitz, J-G Chen, L Gunter, G Howe, G Tuskan, and SP DiFazio. Genome resequencing in an ecologically and economically important forest tree, *Populus trichocarpa*: selection and association genetics. *Talk.* International Plant & Animal Genome XXII. January 11-15, 2014. San Diego, CA.
- Evans LM.** *Invited seminar.* Genome resequencing in an ecologically and economically important forest tree, *Populus trichocarpa*: selection and demographic history. Virginia Tech Department of Forest Resources and Environmental Conservation. September 23, 2013. Blacksburg, VA.
- Evans LM,** SP DiFazio, GT Slavov, J Martin, W Muchero, W Shackwitz, E Rodgers-Melnick, G Howe, G Tuskan. *Talk.* Adaptive trait quantitative genetics and population genomics of *Populus trichocarpa* across its latitudinal range. IUFRO Tree Biotechnology, May 26-June 1, 2013. Asheville, NC.
- Evans LM,** GT Slavov, G Allan, T Whitham, G Tuskan, W Muchero, J Martin, W Schackwitz, SP DiFazio. *Talk.* Comparative genetics of *Populus angustifolia* and *P. trichocarpa* across their similar latitudinal ranges. International Plant & Animal Genome XXI. January 12-16, 2013. San Diego, CA.
- Evans LM,** GT Slavov, SP DiFazio, W Muchero, J Chen, LE Gunter, S Kolpak, GT Howe, and GA Tuskan. *Poster.* Climate-driven productivity in *Populus trichocarpa*. Bioenergy Science Center Science Retreat. Chattanooga, TN. July 15-19, 2012.
- Evans LM,** Whitham TG, Pearce D, Rood S, Allan GJ, DiFazio SP, Slavov G, Floate K, and Max T. Molecular and phenotypic evidence of climate-driven selection in a dominant riparian tree, *Populus angustifolia*. Poster, AZ Board of Regents Meeting, Tempe, AZ. Aug. 4, 2011.
- Evans LM,** GJ Allan, and TG Whitham. *Invited talk.* Herbivore differentiation along a scale of host plant genetic variation. Entomological Society of America Annual Meeting, San Diego, CA. December, 2010.
- Evans, LM,** GJ Allan, and TG Whitham. *Invited talk.* Natural forest hybrid zones drive cryptic speciation in arthropods. Western Forest Insect Work Conference. Flagstaff, AZ. April 6-8, 2010.
- Evans, LM,** GJ Allan, N Meneses, and TG Whitham. *Poster.* Comparative population structure of a common herbivore and its host. Gordon Research Conference Plant-Herbivore Interaction. Galveston, TX. February 21-26, 2010.
- Evans, LM,** GJ Allan, S Woolbright, SM Shuster, and TG Whitham. Hybridization and genotypic variation in a foundation tree drive cryptic speciation of a specialist herbivore. Evolution Conference. Christchurch, New Zealand. June 2007.
- Evans, LM,** GJ Allan, S Woolbright, S Shuster, and TG Whitham. *Talk.* Morphologically cryptic host race formation in the poplar bud gall mite, *Aceria parapopuli*. Natural Areas Conference. Flagstaff, AZ September 2006.

TEACHING EXPERIENCE AND OUTREACH

- 2022 Spring EBIO4800/5800 Quantitative Genetics, 3 credits, University of Colorado Boulder.
- 2022 Spring EBIO3080 Evolutionary Biology, 4 credits, University of Colorado Boulder

- 2020 Fall EBIO3080 Evolutionary Biology, 4 credits, University of Colorado Boulder (2 sections)
- 2020 Fall EBIO5800/IPHY6010 Seminar in Behavioral Genetics, 3 credits, University of Colorado, Boulder
Co-taught with other faculty. Led three weeks of population genetics and GWAS methods and approaches and organized course with M.A. Ehringer (IPHY).
- 2020 Spring EBIO4800/5800 Quantitative Genetics, 3 credits, University of Colorado Boulder. *New course at CU, which I developed* as a cross-listed undergraduate & graduate course.
- 2019 Spring& Fall EBIO3080 Evolutionary Biology, 4 credits, University of Colorado Boulder
- 2019 Fall EBIO6100 Seminar in Environmental Biology, Evolution Reading Group, 1 credit, University of Colorado, Boulder
- 2019 Fall PSYC7102/IPHY6010 Seminar in Behavioral Genetics, 3 credits, University of Colorado, Boulder
Co-taught with other faculty. Led three weeks of population genetics and GWAS methods and approaches.
- 2019 Statistical Genetic Methods for Human Complex Traits Workshop. Junior Faculty. “Data Simulation.” Boulder, CO.
- 2017 Statistical Genetic Methods for Human Complex Traits Workshop. Junior Faculty. “Marker heritability: Biases, confounding factors, current methods, and best practices.” Boulder, CO.
- 2014 “Sensing the Seasons” public talk and walk at West Virginia Botanic Gardens
- 2011 Population and Quantitative Genetics, Northern Arizona University
Two lectures on signatures of natural selection. Professor: Dr. Phil Service
- 2009 Public Outreach Intern, Arboretum at Flagstaff, AZ
Designed exhibits and curricula on biodiversity, led visitor tours of the arboretum, and taught visiting school groups. Supervisor: Rachel Edelstein
- 2007 Laboratory Assistant, Molecular Techniques, Northern Arizona University
Helped setup, lead, and cleanup laboratory course of molecular techniques including DNA extraction, PCR, sequencing, gel visualization. Supervisor: Dr. Gery Allan
- 2005, 2006 Teaching Assistant, Northern Arizona University, Flagstaff, AZ
Human Anatomy and Physiology. Supervisor: Lara Dickson
- 2005 Undergraduate Teaching Assistant, Dartmouth College, Hanover, NH
Physiological Ecology. Supervisor: Dr. Matthew P. Ayres
- 2003 Assistant to the Laboratory Coordinator, Biology Department, Dartmouth College
Assisted in experiment organization and set-up. Supervisor: Craig Layne

REVIEWER in Last Year

Addiction, AJMG Part B Neuropsych., HGG Advances, Psychological Medicine, Genes Brain and Behavior

PROFESSIONAL MEMBERSHIPS

American Society of Human Genetics
International Society of Psychiatric Genetics
Behavior Genetics Association

PROGRAMMING PROFICIENCY

linux/unix, R, perl, and many standard bioinformatics tools, including bcftools, samtools, vcftools, EIGENSOFT, PLINK2, GCTA, EMMAX, GEMMA, etc.