Michael R. Garvin, Ph.D.

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RESEARCH SCIENTIST | MOLECULAR & EVOLUTIONARY GENETICS | MULTI-OMICS | MULTI-OMICS | AI-AUGMENTED COMPUTATIONAL BIOLOGY

I am a highly productive molecular geneticist with over 20 years of experience spanning academic, government, and biotechnology research environments. My work integrates structural variant discovery, multi-omic analysis, and evolutionary genomics to address complex problems in human disease, plant genetics, and environmental systems.

I develop and deploy advanced computational pipelines that combine next-generation and long-read sequencing with statistical genetics, machine learning, and AI-assisted research workflows. I routinely leverage large language models (e.g., ChatGPT, Claude) to accelerate code development, optimize analytical pipelines, enhance reproducibility, and support high-efficiency scientific writing and grant preparation.

My research emphasizes methodological innovation, including novel approaches to structural variant detection, haplotype architecture analysis, and integrative genomic interpretation across populations and families.

AREAS OF EXPERTISE

Structural Variant Discovery | Statistical Genetics | AI-Assisted Research Workflows | R & Python Programming | Bioinformatics Pipeline Development | Plant Genetics | Neuropsychiatric Disease | Environmental DNA | Evolutionary Genomics | Computational Biology | Machine Learning for Genomics | Next-Generation Sequencing | Long-Read Sequencing | Salmon Genetics | Ancient DNA | Multi-Omics Integration |

EDUCATION

Certificate in Personalized & Genomic Medicine, University of Colorado Denver, 2022
Ph. D., University of Alaska Fairbanks, 2012
Master of Science, University of Alaska Fairbanks, 2009
Bachelor of Science, University of Washington, 1991

PROFESSIONAL EXPERIENCE

Williwaw Biosciences, LLC Clarkston, MI — January 2018 – Present
Owner, Chief Scientific Officer

Our mission is to identify the genetic basis of disease and other human traits to contribute products to the field of Personalized Medicine.

University of New Mexico, Albuquerque, NM — June 2025 – Present
Research Professor

Expanding work on long-read genome assemblies and identifying genomic structural variants linked to human diseases and disorders.

Developing new methods for identifying causative genomic changes in rare diseases.

Assisting in the development of a Rare Disease Center at the University of New Mexico.

Continuing work using ancient DNA to assess historical salmon abundances in Alaska

Oak Ridge National Laboratory, Oak Ridge, TN January 2019 – March 2025
Staff Scientist

Developed novel approaches to identify the role of epistasis and genomic structural variation in biomedical phenotypes including neuropsychiatric disorders, addiction, cardiovascular disease, and longevity.

Identification of copy number variation and genomic structural variants in *Populus trichocarpa* for bioenergy production.

Developing new approaches to leverage PacBio generated long read assemblies to identify the genetic basis of traits important for biofuel crops such as *Populus trichocarpa*

Leading several projects that use environmental DNA as a management tool including identification of community assemblages from marine, freshwater, and sediment core samples to manage fisheries in response to hydropower infrastructure and climate change.

Working with large multi-disciplinary teams to identify genetic and environmental associations with substance abuse, neuropsychiatric disorders, cancer, cardiovascular disease and suicidal behavior as part of the Million Veterans Program.

Implemented an internal program to track variants of concern during the COVID-19 pandemic.

Oregon State University, Corvallis OR February 2016 - January 2019
Postdoctoral Fellow

Use of multi-omic approaches in conjunction with family-based ecological and behavioral experiments to determine the molecular processes that underlie the domestication of salmonids to hatcheries.

University of Haifa, Haifa Israel September 2014 - February 2016
Postdoctoral Fellow

Use of novel statistical approaches to identify biological networks to understand the genetic basis of the adaptation of fire salamanders (Salamandra infraimmaculata) to xeric environments with an emphasis on bioenergetics.

University of Alaska Fairbanks, Fairbanks AK December 2012 - September 2014
Postdoctoral Fellow

Led a collaborative project between University of Alaska Fairbanks, Alaska Department of Fish and Game, the National Marine Fisheries Service, and Alaskan native tribal entities to identify genetic markers that show divergence and local adaptation among chum salmon populations for management of multi-billion dollar commercial fisheries.

August 2004 – December 2012 – see Education

Tularik, Inc. (now Amgen), South San Francisco CA May 2001- May 2004

Research Associate

Development and evaluation of gene expression technologies to develop drugs to treat metabolic disorders and cancer including RNA*i*, qPCR, and cDNA microarrays.

CV Therapeutics, Inc. (now Gilead Biosciences) May 1998 - April 2001
Research Associate

Development of cDNA microarrays with Incyte Genomics to measure expression of genes associated with cardiovascular disease.

Roche Molecular Systems, Alameda CA May 1997 - April 1998
Research Associate

Development of quantitative PCR (qPCR) to identify viruses in human plasma based on their DNA content. This is the laboratory in which PCR was invented by Kary Mullis (who won the Nobel Prize for it in 1993).

University of Ottawa Heart Institute, Ontario Canada March 1994 - April 1997
Research Associate

Assess the expression of genes in human tissues affected by cardiovascular disease using in situ hybridization and several emerging molecular biology techniques.

University of Washington, Seattle WA December 1991- March 1994
Research Associate

Development of animal models to uncover the mechanism of restenosis after balloon angioplasty. This work was followed up with work with stents, which is currently the therapy of choice for many patients with coronary artery disease.

Manuscripts under review or in prep (4)

Kainer D, Martin S, Hopp D, Mosher S, Tschaplinkski T, Hyatt PD, Martin MZ, LeBoldus JM, Sondreli KL, Furches A, Zhao N, Jacobson DA, Chen JG, Pavicic M, Priya R, Muchero W, Tuskan GA, **Garvin MR**. Telomere-to-telomere assemblies reveal complex adaptive variation of 3-ketoacyl-CoA-synthases in Populus trichocarpa likely driven by Helitrons *in review*

Garvin MR, Rosenblum D, Kainer D, Bergen A, Climer S, Goedert JJ, Attia PJ, Sullivan KA, Gaddis NC, Johnson EO, Jacobson DA, Weiss SH. Genetic loci associated with cocaine use identified using a novel approach to detect epistasis *in review*

Garvin MR, Kainer D Explaining the missing heritability of hereditary hemochromatosis *in prep*

Garvin MR, Kainer D, Muchero W, Chen J, Climer S, Hyatt D, Martin S, Jacobson DA Missing heritability: Epistatic eQTL networks in *Populus trichocarpa* associated with blight *in prep*

Publications (37)

Garvin MR & Kainer D (2025) Dysregulation of heterochromatin caused by genomic structural variants may be central to autism spectrum disorder. *Frontiers in Molecular Neuroscience doi: 10.3389/fnmol.2025.1553575*

Li H, Liang X, Peng Y, Liu Z, Wang P, Zhang L, Jin M, **Garvin MR**, Wilson K, Xiao Y (2024) Novel mito-nuclear combinations facilitate the global invasion of a major agricultural crop pest *Advanced Science* 11(34)

Sullivan KA, Kainer D, Lane M, Cashman M, Miller JI, **Garvin MR**, Townsend A, Quach BC, Willis C, Kruse P, Gaddis NC, Mathur R, Corradin O, Maher BS, Scacheri PC, Sanchez-Roige S, Palmer AA, Troiani V, Chesler EJ, Kember RL, Kranzler HR, Justice AC, Xu K, Aouizerat BE, Hancock DB, Johnson EO, Jacobson DA, VA Million Veteran Program (2024) Multiomic Network Analysis Identifies Dysregulated Neurobiological Pathways in Opioid Addiction *Biological Psychiatry*

Sullivan KA, Lane M, Cashman M, Miller JI, Pavicic M, Walker AM, Cliff A, Romero J, Qin X, Mullins N, Docherty A, Coon H, Ruderfer DM, International Suicide Genetics Consortium, VA Million Veteran Program, MVP Suicide Exemplar Workgroup, **Garvin MR**, Pestian JP, Ashley-Koch AE, Beckham JC, McMahon B, Oslin DW, Kimbrel NA, Jacobson DA, Kainer D (2024) Analyses of GWAS signal using GRIN identify additional genes contributing to suicidal behavior *Communications Biology* 7(1)

Pavicic M, Walker AM, Sullivan K, Lagergren J, Cliff A, Romero J, Streich J, **Garvin MR**, Pestian J, McMahon B, Beckham JC, Kimbrel NA, Jacobson DA (2023) Using iterative random forest to find geospatial environmental and Sociodemographic predictors of suicide attempts *Frontiers in Psychiatry* 14

Levin MG, Huffman JE, Verma A, Sullivan KA, Rodriguez AA, Kainer D, **Garvin MR**, Lane M, Won H, Li B, Luo Y, Jarvik GP, Hakonarson H, Jasper EA, Bick AG, Ritchie MD, Jacobon DA, Madduri RK, Damrauer SM, Million Veterans Program (2023) Multi-ancestry Genome-wide Association Study of Varicose Veins Reveals Polygenic Architecture, Genetic Overlap with Arterial and Venous Disease, and Novel Therapeutic Opportunities Nature Cardiovascular Research 2

Wang L, Western D, Timsina J, Repaci C, Song W, Norton J, Kohlfeld P, Budde J, Climer S, Butt OH, Jacobson D, **Garvin MR**, Templeton AR, Campagna S, O'Halloran J, Presti R, Goss CW, Mudd PA, Ances BM, Zhang B, Sung YU, Cruchaga C. (2023) Plasma proteomics of SARS-CoV-2 infection and severity reveals impact on Alzheimer's and coronary disease pathways. *iScience* 26(4):106408

Kainer D, Templeton A, Prates ET, Allan E, Climer D, Jacobson DA, **Garvin MR** (2023) Structural variants identified using non-Mendelian inheritance patterns advance the mechanistic understanding of autism spectrum disorder *Human Genetics and Genomic Advances 4, 100150*

Hameedi MA, Prates ET, **Garvin MR**, Mathews II, Amos BK, Demerdash O, Bechthold M, Iyer M, Rahighi S, Kneller DW, Kovalevsky A, Irle S, Vuong VQ, Mitchell JC, Labbe A, Galanie S, Wakatsuki S, Jacobson D (2022) *Nature Communications 13 (5285)* Structural and functional characterization of NEMO cleavage by SARS-CoV-2 3CLpro

Ko KI, Merlet JJ, DerGarabedian BP, Zhen H, Horiuchi Y, Hu E, Nguuyen AT, Prouty S, Alawi F, Walsch MC, Choi Y, Millar SE, Cliff A, Romero J, **Garvin MR**, Seykora JT, Jacobson D, Graves DT (2022) NF-kB Perturbation Reveals Unique Immunomodulatory Functions in Prx1+ Fibroblasts that Promote Atopic Dermatitis (2022) *Science Translational Medicine 14(630)*

Garcia BJ, Simha R, **Garvin MR**, Furches A, Jones P, Gazolla JGFM, Hyatt PD, Schadt CW, Pelletier D, Jacobson D (2021) A k-mer based approach for classifying viruses without taxonomy identifies viral associations in human autism and plant microbiomes. *Computational and Structural Biotechnology Journal 19: 5911-5919*

Mast, AE; Wolberg, AS; Gailani, D; **Garvin, MR**; Alvarez, C; Miller, JI; Aronow, B; Jacobson, DA (2021) SARS-CoV-2 suppresses anticoagulant and fibrinolytic gene expression in the lung. *eLife 10:e64330*

Garvin MR*, Prates ET*, Pavicic M, Jones P, Amos BK, Geiger A, Shah MB, Streich J, Gazolla JGFM, Kainer D, Cliff A, Romero J, Keith N, Brown JB, Jacobson DA (2020) Potentially adaptive SARS-CoV-2 mutations discovered with novel spatiotemporal and explainable AI models. *Genome Biology 21:304*
*contributed equally

Prates ET*, **Garvin MR*,** Pavicic MP, Jones P, Shah MB, Demerdash O, Amos BK, Geiger A, Jacobson DA (2020) Potential Pathogenicity Determinants Identified from Structural Proteomics of SARS-CoV and SARS-CoV-2. *Molecular Biology and Evolution msaa231*
*contributed equally

Garvin MR, Alvarez C, Miller JI, Prates ET, Walker AM, Amos BK, Mast AE, Justice A, Aronow B, Jacobson D (2020) A mechanistic model and therapeutic interventions for COVID-19 involving a RAS-mediated bradykinin storm. *eLife 2020;9:e59177*

Streich J, Romero J, Gazolla JGFM, Kainer D, Cliff A, Prates ET, Brown JB, Khoury S, Tuskan GA, **Garvin MR**, Jacobson DA (2020) Can exascale plant biology and explainable artificial intelligence deliver on the sustainable development goals? *Current Opinion in Biotechnology 61: 217-225*.

Aw WC, **Garvin MR**, Ballard JWO (2019) Exogenous factors may differentially influence the selective costs of mtDNA mutations. *In: Cellular and Molecular Basis of Mitochondrial Inheritance* - Mitochondrial Disease and Fitness

Aw WC, Towarnicki SG, Melvin RG, Youngson NA, **Garvin MR**, Nielsen S, Thomas T, Pikcford R, Bustamante S, Vila-Sanjurjo A, Smyth GK, Ballard JWO (2018) Genotype to phenotype: diet-by-mitochondrial DNA haplotype interactions drive metabolic flexibility and organismal fitness. *PLoS Genetics 14(11): e1007735*.

Aw WC, **Garvin MR**, Melvin RG, Ballard JWO (2017) Sex-specific influences of mtDNA mitotype and diet on mitochondrial functions and physiological traits in Drosophila melanogaster. *PLoS ONE 12(11): e0187554*.

Garvin MR, Templin WD, Gharrett AJ, DeCovich N, Kondzela CM, Guyon JR, and McPhee MV (2017) Potentially Adaptive Mitochondrial Haplotypes as a Tool to Identify Divergent Nuclear Loci. *Methods in Ecology and Evolution, 8(7): 821-834*

Garvin MR, Thorgaard GH, Narum SR (2015) Differential Expression of Genes that Control Respiration Contribute to Thermal Adaptation in Redband Trout. (*Oncorhynchus mykiss gairdneri*). *Genome Biology and Evolution, 7, 1404–1414.*

Garvin MR, Bielawski JP, Sazanov L, and Gharrett AJ (2015) Review and Meta-analysis of Natural Selection in Mitochondrial Complex I in Metazoans. *Journal of Zoological Systematics and Evolutionary Research: 53(1): Editor's Choice.*

Garvin MR & Gharrett AJ (2014) Evolution: Are the Monkeys' Typewriters Rigged? *Royal Society Open Science 1: 140172.*

Garvin MR, Masuda MM, Pella JJ et al. (2014) NOAA Technical Memorandum NMFS-AFSC-283 A Bayesian Cross-Validation Approach to Evaluate Genetic Baselines and Forecast the Necessary Number of Informative Single Nucleotide Polymorphisms.

Garvin MR, Kondzela CM, Martin PC, Finney B, Guyon J, Templin WD, DeCovich N, Gilk-Baumer S, & Gharrett AJ (2013) Recent Physical Connections May Explain Weak Genetic Structure in Western Alaskan Chum Salmon (*Oncorhynchus keta)* Populations. *Ecology and Evolution 3(7): 2362-2377.*

Garvin MR, Marcotte RW, Palof KJ, Riley RJ, Kamin LM, & Gharrett AJ (2011) Diagnostic Single Nucleotide Polymorphisms Identify Pacific Ocean Perch and Delineate Blackspotted and Rougheye Rockfish. *Transactions of the American Fisheries Society 140(4):984-988.*

Garvin MR, Bielwaski JP, & Gharrett AJ (2011) Positive Darwinian Selection in the Piston that Powers Proton Pumps in Complex I of the Mitochondria of Pacific Salmon. *PLoS One 6(9):e24127.*

Garvin MR, Saitoh K, & Gharrett AJ (2010) Application of Single Nucleotide Polymorphisms to Non-model Species: A Technical Review. *Molecular Ecology Resources 10(6):91-108*.

Garvin MR, Saitoh K, Brykov V, Churikov D, & Gharrett AJ (2010) Single Nucleotide Polymorphisms in Chum Salmon (*Oncorhynchus keta*) Mitochondrial DNA Derived from Restriction Site Haplotype Information. *Genome 53:501-507.*

Garvin MR & Gharrett AJ (2010) Application of SNP Markers to Chum Salmon (*Oncorhynchus keta*): Discovery, Genotyping, and Linkage Phase Resolution. Journal of Fish Biology 77(9):2137-2162.

Garvin MR & Gharrett AJ (2007) DEco-TILLING: An Inexpensive Method for SNP Discovery that Reduces Ascertainment Bias. *Molecular Ecology Notes 7:735-746.*

Oram JF, Lawn RM, **Garvin MR**, & Wade DP (2000) ABCA1 is the cAMP-Inducible Apolipoprotein Receptor that Mediates Cholesterol Secretion from Macrophages. *Journal of Biological Chemistry 275(44):34508-34511*.

O'Brien ER, Urieli-Shoval S, **Garvin MR**, Stewart DK, Hinohara T, Simpson JB, Benditt EP, & Schwartz SM (2000) Replication in Restenotic Atherectomy Tissue. *Atherosclerosis 152(1):117-126.*

Lawn RM, Wade DP, **Garvin MR**, Wang X, Schwartz K, Porter GJ, Seilhamer JJ, Vaughan AM, & Oram JM (1999) The Tangier Disease Gene Product ABC1 Controls the Cellular Apolipoprotein-Mediated Lipid Removal Pathway. *Journal of Clinical Investigation 104:R25-R31.*

Garvin MR, Labinaz M, Pels K, Walley VM, Mizgala HF, & O'Brien ER (1997) Graft Vascular Disease: Potential Involvement of the Plasminogen Activator System. *Cardiovascular Research 35(2):241-249.*

O'Brien ER, Bennet KL, **Garvin MR**, Zederic TW, Hinohara T, Simpson JB, Kimura T, Nobuyoshi M, Mizgala HF, Purchio A, & Schwartz SM (1996) Big-H3, a Transforming Growth Factor-beta-inducible Gene, is Overexpressed in Atherosclerotic and Restenotic Human Vascular Lesions *Arteriosclerosis, Thrombosis and Vascular Biology 16:576-584.*

O'Brien ER, **Garvin MR**, Dev R, Stewart DK, Hinohara T, Simpson JB, & Schwartz SM (1994) Angiogenesis in Human Coronary Atherosclerotic Plaques. *American Journal of Pathology 145(4):883-894.*

Professional Addendum

June 2023 Guest editor Frontiers in Genetics for Research Topic: Energy-producing organelles and the nucleus: a phenomenal genomic friendship

February 2021 Personal thank you from the Director of the Office of Science, Department of Energy for efforts directed at the COVID-19 pandemic

August 2020 Our paper, *A mechanistic model and therapeutic interventions for COVID-19 involving a RAS-mediated bradykinin storm*, becomes the 2nd most viewed article in the history of the journal eLife (currently over 154,000 with 252 citations).

January 2000 Our discovery of mutations in the gene ABCA1 as causative of Tangier's Disease listed by American Heart Association as one of the top 10 discoveries of 1999.

Funding

Title: Integrative Omics Center for Accelerating Neurobiological Understanding of Opioid Addiction
Funder: National Institutes of Health
Project Number: P50DA054071
Dates: 7/01/2022 – 06/30/2027
Award: $1,687,650.00
Role: Co-Principal-Investigator

Title: Gene Network Identification and Integration (GNetii) Approach to Understanding the Biology Underlying HIV and Drug Abuse
Funder: National Institutes of Health
Project Number: NFE-20-08026 / RFA-DA-20-008

Dates: 07/01/2020 – 06/30/2025
Award: $1,334,860.00
Role: Co-Investigator

Title: Integrating Multiple Omics to Illuminate Gene Networks Underlying Cigarette Smoking and Opioids

Funder: National Institutes of Health
Project Number: RFA-DA-20-006
Dates: 10/1/2020 – 09/30/2025
Award: $2,029,372.00
Role: Co-Investigator

Title: Identification of Genetic Markers for Substance Abuse
Funder: Department of Energy Lab Director's Fund
Project Number: LOIS11652
Dates: 10/01/2023 – 09/30/2024
Award: $240,000.00
Role: Principal-Investigator

Title: Identification of Genomic Structural Variants that Underlie Traits in Feedstocks for Bioenergy Production
Funder: Center for Bioenergy and Innovation
Project Number: Project 5.3
Dates: 10/01/2022 – 09/30/2024
Award: $245,000.00
Role: Principal-Investigator

Title: Novel Approaches to Rapidly Advance Precision Medicine
Funder: Department of Energy Lab Director's Fund
Project Number: LOIS11264
Dates: 10/01/2022 – 09/30/2023
Award: $190,000.00
Role: Principal-Investigator