Daniel Vera, PhD

Computational biologist with 11 years of extensive dry and wet research experience in genomics and molecular biology. Intense passion for genomics of human disease. Expert in integrative analysis of multi-omic (genomics, epigenomics, transcriptomics, and proteomics) data to understand processes driving aging, disease and phenotypic variation. Resourceful and creative problem solver. Highly collaborative scientific leader with exceptional communication skills.

contact

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📍 Melrose, Massachusetts

🎌 US citizen

education

Fellow, Harvard Translational Research in Aging Training Program, 2020

PhD, Cell and Molecular Biology, Florida State University, 2014

BS in Biology
Florida State University
2010

experience

HARVARD MEDICAL SCHOOL
Research Fellow (2018 - present)

CRISPR screens for pro-rejuvenation genes
DNA methylation (epigenetic) clocks
Epigenetic reprogramming mechanisms
Epigenetic mechanisms of aging
OSK-based retinal rejuvenation
Proteomics data analysis
Hybrid (2nd/3rd gen) genome assembly
Sequencing assay development
3D chromatin organization
Integrative data analysis (RNA/ATAC/ChIP-seq, Hi-C)
Supervised 3 full time students (MS and PhD level)

SILICO LLC
Owner (2018 - present)

Led/managed numerous multi-omic projects
Novel microprotein discovery (proteomics)
Hybrid (2nd/3rd gen, Hi-C) genome assembly
Novel genome annotation/characterization
Personalized genomic/proteomic analysis
High-throughput genomic assay development
Metagenomic profiling and characterization
Extremophile genomics/proteomics
Presented findings in board meetings
Clients/collaborators:
    NASA, Jet Propulsion Laboratory
    Life Biosciences LLC
    Liberty Biosecurity LLC

skills

DATA TYPES

- RNA-seq
- ATAC-seq
- MNase-seq
- DNase-seq
- ChIP-seq
- WGS (variation)
- RRBS
- De novo assembly/annotation
- WGBS
- Shotgun metagenomics
- 16/18s amplicon sequencing
- Hi-C, 4C
- Repli-seq
- CRISPR screens
- Pacbio/nanopore sequencing
- Microarray analysis

COMPUTATIONAL

- R & Bioconductor
- Linux & Bash
- Docker
- Git & Github
- AWS/Cloud Computing
- Nextflow
- MySQL
- Parallel/Cluster Computing
- Python & Perl
- Adobe Photoshop & Illustrator

LABORATORY

- Molecular biology
- Assay development
- Illumina sequencing
- Nanopore sequencing
- FISH, immunofluorescence
- Fluorescence Microscopy
- Sequence Capture
- Microarray hybridization
- Cloning, plasmid design

experience (cont.)

CENTER OF GENOMICS
FLORIDA STATE UNIVERSITY
Director (2015 - 2018)

- Directed and helped start a genomics center
- Led numerous genomics projects from start to finish
- Genomic data generation and analysis
- Organized and ran genomics workshops
- Consulted on all aspects of genomic experiments
- Project-specific pipeline/algorithm development
- Generated/analyzed many chromatin structure data
- Mapped genetic mutations to phenotypic variation
- Allele-specific RNA-seq, Hi-C, chromatin structure
- CRISPR/mutational screening sequencing analysis
- Genome browser software development
- (see skills/publications for list of data types/papers)

FLORIDA STATE UNIVERSITY
Graduate Research Assistant (2010 - 2014)

- Nucleosome position assay dev, data analysis
- MNase/RNA/Repli-seq, Hi-C data integration
- Chromatin structure dynamics in cancer/stress
- Nucleosome position prediction/machine learning
- Telomere length biology

awards

MMPC MICROMouse Program Award (2020)

American Diabetes Association Minority Postdoctoral Fellowship (2020)

Harvard Translational Research in Aging Training Program (T32) Postdoctoral Award (2018)

NSF Plant Genome Research Program Grant, co-PI (2015)

training

Fundamentals of Clinical and Translational Research (FACTOR), Harvard Catalyst, 2020

Human iPSC Derivation and Culture Course, Harvard University, 2019

iCARB: Immersion in Comparative Aging and Regenerative Biology, MDIBL, 2019

Advanced Aging Research Training Seminar Series (AARTSS), Harvard Medical School, 2019-2020

Genome Engineering Workshop, Broad Institute, 2018 and 2019

Hi-C Data Analysis Bootcamp, Harvard University, 2018

selected publications

Vera, D. L., Madzima, T. F., Labonne, J. D., Alam, M. P., Hoffman, G. G., Girimurugan, S., Zhang, J., McGinnis, K. M., Dennis, J. H., and Bass, H. W. (2014). Differential nuclease sensitivity profiling of chromatin reveals biochemical footprints coupled to gene expression and functional DNA elements in maize. The Plant Cell, 26(10):3883--3893.

Lu, Y., Krishnan, A., Brommer, B., Tian, X., Meer, M., Vera, D. L., ... & Yang, J. H. (2019). Reversal of ageing-and injury-induced vision loss by Tet-dependent epigenetic reprogramming. BioRxiv, 710210.

Yang, J. H., Griffin, P. T., Vera, D. L., Apostolides, J. K., Hayano, M., Meer, M. V., ... (2019). Erosion of the Epigenetic Landscape and Loss of Cellular Identity as a Cause of Aging in Mammals. BioRxiv.

Hayano, M., Yang, J. H., Bonkowski, M. S., Amorim, J. A., Ross, J. M., Coppotelli, G., ... & Vera, D. L, ... (2019). DNA Break-Induced Epigenetic Drift as a Cause of Mammalian Aging. BioRxiv.

Rodgers-Melnick, E., Vera, D. L., Bass, H. W., and Buckler, E. S. (2016). Open chromatin reveals the functional maize genome. Proceedings of the National Academy of Sciences, 113(22):E3177--E3184.

Dileep, V., Ay, F., Sima, J., Vera, D. L., Noble, W. S., and Gilbert, D. M. (2015). Topologically-associating domains and their long-range contacts are established during early G1 coincident with the establishment of the replication timing program. Genome Research, 24:974--88.

Rivera-Mulia, J. C., Dimond, A., Vera, D., Trevilla-Garcia, C., Sasaki, T., Zimmerman, J., ... & Gilbert, D. M. (2018). Allele-specific control of replication timing and genome organization during development. Genome research, 28(6), 800-811.

complete list of publications available at: https://pubs.danielvera.org