

# Daniel L. Vera

## Curriculum Vitae

### Contact

Daniel Vera  
Postdoctoral Fellow  
David Sinclair Lab  
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### Education

#### **Research Fellow**

Harvard Translational Research in Aging Training Program  
Harvard Medical School, 2020

#### **PhD in Cell and Molecular Biology**

Florida State University, 2014

#### **BS in Biology**

Florida State University, 2010

### Employment

#### **Postdoctoral Fellow**

Advisor: David Sinclair  
Harvard Medical School (2018 - present)

#### **Research Scientist**

Center for Genomics and Personalized Medicine  
Florida State University (2015 - 2018)

#### **Graduate Research Assistant**

Advisor: Hank Bass and Jonathan Dennis  
Florida State University (2010 - 2014)

#### **Undergraduate Research Assistant**

Florida State University (2009 - 2010)

## Grants and Awards

Development of a targeted DNA methylation sequencing assay for the assessment of metabolic disease progression

MMPC MICROMouse Program Award (2020)

Lead PI: **Daniel Vera**

Identification of novel peptides modulating insulin sensitivity for the treatment of Type 2 Diabetes.

American Diabetes Association Minority Postdoctoral Fellowship (2020, deferred due to epidemic)

Lead PI: **Daniel Vera**. Mentor: David Sinclair

Epigenomic drift as a driving mechanism of aging (2018 - 2020)

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

Lead PI: **Daniel Vera**. Mentor: David Sinclair. Co-mentors: Shalender Bhasin, Monty Montano.

Nuclease Profiling as an Integrative Resource for Maize Epigenomics (2015 - 2019)

NSF Plant Genome Research Program Grant (IOS #1444532)

Lead PI: HW Bass FSU. co-PIs: JH Dennis, J Zhang, **DL Vera**, OU Onokpise, V Tsoleva

## Publications

**Vera, D. L.**, Madzima, T. F., Labonne, J. D., Alam, M. P., Hoffman, G. G., Girmurugan, 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.

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.

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., ... & Bhakta, M. (2019). Erosion of the Epigenetic Landscape and Loss of Cellular Identity as a Cause of Aging in Mammals.

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.

Sasaki, T., Rivera-Mulia, J. C., **Vera, D. L.**, Zimmerman, J., Das, S., Padget, M., Nakamichi, N., Chang, B. H., Tyner, J., Druker, B. J., et al. (2017). Stability of patient-specific features of altered DNA replication timing in xenografts of primary human acute lymphoblastic leukemia. *Experimental Hematology*, 51:71--82.e3.

- Sotolongo-Lopez, M., Alvarez-Delfin, K., Saade, C. J., **Vera, D. L.**, and Fadool, J. M. (2016). Genetic dissection of dual roles for the transcription factor six7 in photoreceptor development and patterning in zebrafish. *PLoS genetics*, 12(4):e1005968.
- 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.
- Marchal, C., Sasaki, T., **Vera, D.**, Wilson, K., Sima, J., Rivera-Mulia, J. C., ... & Gilbert, D. M. (2018). Genome-wide analysis of replication timing by next-generation sequencing with E/L Repli-seq. *Nature protocols*, 13(5), 819.
- Rivera-Mulia, J. C., Dimond, A., **Vera, D.**, Trevilla-Garcia, C., Sasaki, T., Zimmerman, J., and Gilbert, D. M. (2017). Allele-specific control of replication timing and genome organization during development. *bioRxiv*, 221762.
- Brown, A. N., Lauter, N., **Vera, D. L.**, McLaughlin-Large, K. A., Steele, T. M., Fredette, N. C., and Bass, H. W. (2011). QTL Mapping and Candidate Gene Analysis of Telomere Length Control Factors in Maize (*Zea mays* L.). *G3: Genes, Genomes, Genetics*, 1(6):437--450.
- Fincher, J. A., **Vera, D. L.**, Hughes, D. D., McGinnis, K. M., Dennis, J. H., and Bass, H. W. (2013). Genome-wide prediction of nucleosome occupancy in maize reveals plant chromatin structural features at genes and other elements at multiple scales. *Plant Physiology*, 162(2):1127--1141.
- Druliner, B., Fincher, J., Sexton, B., **Vera, D.**, Roche, M., Lyle, S., and Dennis, J. (2013). Chromatin patterns associated with lung adenocarcinoma progression. *Cell Cycle*, 12(10):1536--1543.
- Pope, B. D., Ryba, T., Dileep, V., Yue, F., Wu, W., Denas, O., **Vera, D. L.**, Wang, Y., Hansen, R. S., Canfield, T. K., et al. (2014). Topologically-associating domains are stable units of replication-timing regulation. *Nature*, 515(7527):402.
- Sexton, B. S., Avey, D., Druliner, B. R., Fincher, J. A., **Vera, D. L.**, Grau, D. J., Borowsky, M. L., Gupta, S., Girimurugan, S. B., Chicken, E., et al. (2014). The spring-loaded genome: nucleosome redistributions are widespread, transient, and dna-directed. *Genome Research*, 24(2):251--259.
- Ren, Y., **Vera, D. L.**, Hughes, K. A., and Dennis, J. H. (2015). Stimulation of the *Drosophila* immune system alters genome-wide nucleosome occupancy. *Genomics Data*, 3:146--147.
- Druliner, B. R., **Vera, D.L.**, Johnson, R., Ruan, X., Apone, L. M., Dimalanta, E. T., Stewart, F. J., Boardman, L., and Dennis, J. H. (2016). Comprehensive nucleosome mapping of the human genome in cancer progression. *Oncotarget*, 7(12):13429.
- Sexton, B. S., Druliner, B. R., **Vera, D. L.**, Avey, D., Zhu, F., and Dennis, J. H. (2016). Hierarchical regulation of the genome: global changes in nucleosome organization potentiate genome response. *Oncotarget*, 7(6):6460.
- Lo, P.-K., Huang, Y.-C., Poulton, J. S., Leake, N., Palmer, W. H., **Vera, D. L.**, Xie, G., Klusza, S., and Deng, W.-M. (2016). RNA helicase Belle/DDX3 regulates transgene expression in *Drosophila*. *Developmental Biology*, 412(1):57--70.
- Lang, J., **Vera, D. L.**, Cheng, Y., and Tang, H. (2016). Modeling Dengue Virus-Hepatic Cell Interactions Using Human Pluripotent Stem Cell-Derived Hepatocyte-like Cells. *Stem Cell Reports*, 7(3):341--354.

- Wesolowski, S., **Vera, D. L.**, and Wu, W. (2017). SRSF shape analysis for sequencing data reveal new differentiating patterns. *Computational Biology and Chemistry*, 70:56--64.
- Girimurugan, S. B., Liu, Y., Lung, P.-Y., **Vera, D. L.**, Dennis, J., Bass, H., and Zhang, J. (2017). iSeg: an efficient algorithm for segmentation of genomic and epigenomic data. *bioRxiv*, page 184515.
- D'Alessandro, M., Beesley, S., Kim, J. K., Jones, Z., Chen, R., Kyle K. E., **Vera, D.L.**, Cheng W., Yi, P., Pagano, M., Nowakowski R., Lee, C. (2017) Disruption of PERIOD degradation causes instability of circadian rhythms. *Current Biology*, In Press.
- Nathan M. Springer, Sarah N. Anderson, Carson M. Andorf, Kevin R. Ahern, Fang Bai, Omer Barad, W. Brad Barbazuk, Hank W. Bass, Kobi Baruch, Gil Ben-Zvi, Edward S. Buckler, Robert Bukowski, Michael S. Campbell, Ethalinda K.S. Cannon, Paul Chomet, R. Kelly Dawe, Ruth Davenport, Hugo K. Dooner, Limei He Du, Chunguang Du, Katherine A. Easterling, Christine Gault, Jiahn-Chou Guan, Charles T. Hunter, Georg Jander, Yinping Jiao, Karen E. Koch, Guy Kol, Tobias Kollner, Toru Kudo, Qing Li, Fei Lu, Dustin Mayfield-Jones, Wenbin Mei, Donald R. McCarty, Jaclyn Noshay, John L. Portwood II, Gil Ronen, A. Mark Settles, Doron Shem-Tov, Jinghua Shi, Ilya Soifer, Joshua C. Stein, Masaharu Suzuki, **Daniel L. Vera**, Erik Vollbrecht, Julia T. Vrebalov, Doreen Ware , Sharon Wei, Kokulapalan Wimalanathan, Margaret R. Woodhouse, Wenwei Xiong, Thomas P. Brutnell. (2017). The W22 genome: a foundation for maize functional genomics and transposon biology. In revision.

## **Presentations**

- DL Vera, AN Brown, and HW Bass. (TALK) Analysis of the Genetic Control of Telomere Length in Maize (*Zea mays*, L.). Beta Beta Beta Biological Honor Society, 2010 Biennial National Convention; Durango, Colorado, USA; May 19-22, 2010
- PM Alam, DL Vera, JA Fincher, KM McGinnis, HW Bass, and JH Dennis. (POSTER) Nucleosome distribution and promoter architecture at 400 genes in the maize genome. 53rd Annual Maize Genetics Conference; St. Charles, IL; March 17-20, 2011.
- DL Vera, KM McGinnis, JH Dennis, and HW Bass. (POSTER) Analysis of Chromatin Accessibility in the Maize Interphase Nucleus. 53rd Annual Maize Genetics Conference; St. Charles, IL; March 17-20, 2011.
- JA Fincher, DL Vera, HW Bass, JH Dennis. (POSTER) Overlapping but distinct DNA sequence features drive nucleosome organization in maize and humans. Dynamic DNA Packaging Across Kingdoms: Chromatin and Beyond; Biophysical Society; Asilomar, CA; July 5-5, 2011.
- Bass HW, JH Dennis, KM McGinnis, OU Onokpise, JA Fincher, DL Vera, JD Labonne, MP Alam, TF Madzima, and GG Hoffman (POSTER) Nucleosome Mapping and Chromatin Structure in Maize, a Novel Platform for Genome Response Assays. NSF Plant Genome Program (PGRP) Awardee meeting; Arlington VA; September 8-9, 2011.
- DL Vera, HW Bass, JH Dennis. (POSTER) Chromatin accessibility is largely unaltered by the transition to mitotic chromosomes. Keystone Symposia: Epigenomics; Keystone, CO; January 17-22, 2012.
- TF Madzima, JA Fincher, DL Vera, J Dorweiler, HW Bass, JH Dennis, & KM McGinnis. (TALK) Genome-wide effect of the *mop1-1* mutation on chromatin structure in maize. 54th Annual Maize Genetics Conference; Portland, OR; March 15-18, 2012.
- JDJ Labonne, DL Vera, PM Alam, TF Madzima, GG Hoffman, JH Dennis, KM McGinnis, & HW Bass. (POSTER) Development of a robust method for microscopic and molecular assays of nuclear architecture and chromatin structure in maize. 54th Annual Maize Genetics Conference; Portland, OR; March 15-18, 2012.
- DL Vera, DD Hughes, JH Dennis, & HW Bass. (POSTER) Defining the chromatin domain organization of the maize genome. 54th Annual Maize Genetics Conference; Portland, OR; March 15-18, 2012.
- Bass HW, DL Vera, DD Hughes, JA Fincher, PM Alam, JDJ Labonne, TF Madzima, Z Wiggins, OU Onokpise, SP Moose, KM McGinnis, & JH Dennis. (POSTER) Tissue specific nucleosome occupancy in the promoter/TSS region of 400 classical maize genes. 54th Annual Maize Genetics Conference; Portland, OR; March 15-18, 2012.

- JA Fincher, DL Vera, JH Dennis, HW Bass. (POSTER) Using empirical maize chromatin data to train a support vector machine to predict nucleosome occupancy likelihood (NOL). 54th Annual Maize Genetics Conference; Portland, OR; March 15-18, 2012.
- HW Bass HW, DL Vera, DD Hughes, JA Fincher, MP Alam, JDJ Labonne, TF Madzima, ZJ Wiggins, OU Onokpise, GH Hoffman, KM McGinnis, & JH Dennis. (POSTER) Chromatin Structure and Genome Response in Maize. NSF Plant Genome Research Program Awardee Meeting; Arlington, VA; September 6-7, 2012.
- HW Bass HW, DL Vera , TF Madzima, JD Labonne, P Alam, GG Hoffman, JH Dennis, KM McGinnis. (TALK) MNase Profiling of Chromatin Landscapes in Maize. Society for Experimental Biology Meeting, SEB 2013, Valencia, SPAIN; July 2 – 6, 2013.
- Bass HW, DL Vera, TF Madzima, JD Labonne, MP Alam, GG Hoffman, SB Girimurugan, J Zhang, JH Dennis, and KM McGinnis. (TALK) W282: MNase Profiling of the Chromatin Landscapes in the Maize Genome. Plant and Animal Genome XXII Conference; San Diego, CA; January 11-15, 2014.
- DL Vera, HW Bass, JH Dennis. (POSTER) Targeted-enrichment of MNase-seq libraries reveals hypersensitive and hyper-resistant nucleosomes at important regulatory regions in the human genome. Cold Spring Harbor Laboratory Meetings: Epigenetics and Chromatin; Cold Spring Harbor, NY; September 9-13, 2014.
- Bass HW, DL Vera, ZD Wiggins, J Zhang, KM McGinnis, JH Dennis, OU Onokpise, E Rodgers-Melnick, and ES Buckler. (TALK) Linking Chromatin Structure to Genomic Function through Differential Nuclease Sensitivity (DNS-seq) and Nucleosome Occupancy Mapping. 57th Annual Maize Genetics Conference; St. Charles, IL; March 12-15, 2015.
- EB Rodgers-Melnick, PJ Bradbury, DL Vera, HW Bass, and ES Buckler. (POSTER) Open Chromatin Reveals the Functional Portion of the Maize Genome. 57th Annual Maize Genetics Conference; St. Charles, IL; March 12-15, 2015.
- Bass HW, DL Vera, and JH Dennis. (POSTER) Nuclease Profiling as an Epigenomic Resource for Five Reference Tissues of Maize. NSF Plant Genome Research Program Awardee Meeting; Arlington, VA; September 10-11, 2015.
- Bass HW, DL Vera, E Rodgers-Melnick, and ES Buckler. (TALK) Functional Genomics in Maize using Differential Nuclease Sensitivity (DNS-seq) Chromatin Profiling. Invited Speaker, Workshop #3288; New England Biolabs - Recent advances in NGS sample prep. Plant and Animal Genome XXIV Conference; San Diego, CA, USA; January 9-13, 2016.
- Bass HW, DL Vera, E Rodgers-Melnick, and ES Buckler. (TALK) Investigating Chromatin Structure at Multiple Scales in Maize. Invited Speaker, Workshop #3086; EPIC: the Plant Epigenome Project. Plant and Animal Genome XXIV Conference; San Diego, CA, USA; January 9-13, 2016.

- E Rodgers-Melnick, DL Vera, R Bradbury HW Bass, and ES Buckler. (TALK) The Stability and Consequences of Recombination in Maize. Workshop #3158; Recombination - mechanisms. Plant and Animal Genome XXIV Conference; San Diego, CA, USA; January 9-13, 2016.
- Bass, HW, DL Vera, ZD Wiggins, K Yu, JH Dennis, J Zhang, and OU Onokpise. (POSTER) DNS - NUPRIME: Differential Nuclease Sensitivity for Nuclease Profiling as an Integrative Resource for Maize Epigenomics. 58th Annual Maize Genetics Conference, Maize Genetics, Jacksonville, FL, USA, March 17-20, 2016.
- Easterling KA, HW Bass, DL Vera, and T. Brutnell (and the W22 Consortium). (POSTER). W22 Chromosomes and Chromatin: A Pachytene FISH Karyotype and Genome-wide Differential Nuclease Sensitivity Profile. 58th Annual Maize Genetics Conference, Maize Genetics, Jacksonville, FL, USA, March 17-20, 2016.
- Kyle KE, Vera DL, and Hughes KA. (POSTER) Developing a genome browser for a non-model vertebrate, *P. reticulata*. Undergraduate Research Symposium, Florida State University, Tallahassee, FL, USA, March 29, 2016.
- Kyle KE, Vera DL, and Hughes KA. (POSTER) Developing a genome browser for a non-model vertebrate, *P. reticulata*. WIMSE Research Symposium, Florida State University, Tallahassee, FL, USA, April 5, 2016.
- Kyle KE, Bass HW, and Vera DL. (POSTER) gTracks--A framework for creating and maintaining UCSC track databases using google spreadsheets. Biological Data Science, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, USA, October 26-29, 2016.
- Kyle KE, Bass HW, and Vera DL. (POSTER) gTracks--A framework for creating and maintaining UCSC track databases using google spreadsheets. Plant and Animal Genome XXV, San Diego, CA, USA, January 13-18, 2017.
- Parvathaneni RK, Shamimuzzaman, Md, Kovar LL, Vera, DL, Bass HW, and A Eveland. (POSTER) Defining gene regulatory networks controlling early inflorescence development in maize. 59th Annual Maize Genetics Conference, Maize Genetics, St. Louis, MO, USA, March 9-12, 2017.
- Vera DL, Kyle K, and H Bass (POSTER) Genomaize, a UCSC genome browser for maize genomes. 59th Annual Maize Genetics Conference, Maize Genetics, St. Louis, MO, USA, March 9-12, 2017.
- Turpin ZM, Vera DL, and HW Bass. (POSTER) Chromatin structure profile (MNase DNS-seq) for 15-DAP endosperm, a B73 core reference tissue. 59th Annual Maize Genetics Conference, Maize Genetics, St. Louis, MO, USA, March 9-12, 2017.
- Martinez J, Wesolowski S, Vera DL, Wu W. (POSTER) Functional Data Analysis for Next Generation Sequencing Experiments. SIAM-SEAS, Tallahassee, FL, USA, March 18-19, 2017.

Wesolowski S, Martinez J, Vera DL, Wu W. (POSTER) How changes in shape of nucleosomal DNA near TSS influence changes of gene expression. Workshop on Applications-Driven Geometric Functional Data Analysis, Florida State University, Tallahassee, FL, USA, October 8-11, 2017.

## Software projects

- travis** (<http://github.com/dvera/travis>) - An R package for genomic data processing and analysis. This package contains a large number of scripts that were/are used during my graduate studies and directorship of the FSU genomics center for many common data analysis workflows.
- genomaize** (<http://genomaize.org>) - A UCSC genome browser for maize genomes. This web-based genome browser is solely setup and maintained by me.
- cruise** (<http://github.com/dvera/cruise>) - A docker-based framework for installing and maintaining UCSC genome browsers using simple google spreadsheets. Intended as a simple way for end-users to setup their own web-based genome browsers.
- gtracks** (<http://github.com/dvera/gtracks2>) - A series of scripts that allow end users to easily maintain UCSC genome browser track hubs with simple google spreadsheets.
- harp** (<http://github.com/dvera/harp>) - An R package for allele-specific alignment of Illumina sequencing reads. This software was created for the analysis of allele-specific Repli-seq data, but can be applied to many genomic data types, including RNA-seq, Hi-C, and ChIP-seq.
- shart** (<http://github.com/dvera/shart>) - An automated pipeline for processing Repli-seq data.
- SRSFseq** (<http://github.com/FSUgenomics/SRSFseq>) - Square Root Slope Functions shape analysis for sequencing data.

## Workshops

- RNA-seq Workshop**, 2-day workshop outreach as part of NSF IOS 1354775, Department of Biological Science, FSU, May 24-25, 2015.
- ChIP-seq Workshop** as part of College of Medicine “Tools of the Trade” course, Department of Biological Science, FSU, June 26, 2015. Role: Workshop Lead.
- Plant Chromatin Workshop**, 2-week workshop as part of NSF PGRP 1444532, Department of Biological Science, FSU, July 11-21, 2015. Role: Workshop Organizer and Lead.
- Introduction to the UCSC Genome Browser Workshop**, College of Medicine, FSU, March 14, 2016. Role: Workshop Organizer and Lead.
- Plant Chromatin Workshop**, 2-week workshop as part of NSF PGRP 1444532, Department of Biological Science, FSU, August 8-21, 2016. Role: Workshop Organizer and Lead.
- NEB RNA-seq Library Prep Workshop**, 2-day workshop run by Daniela Mufano, Christine Rozzi, Chris Cook, and David Gdula. Role: Workshop Organizer.