

CURRICULUM VITAE

NAME:

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CITIZENSHIP:

USA

POSITION TITLE:

Associate Professor

EDUCATION/TRAINING:

INSTITUTION AND LOCATION	DEGREE/TITLE	END DATE	FIELD OF STUDY
University of Brasília, Brasília, D.F., Brazil	BS	1982	Molecular Biology
University of Brasília, Brasília, D.F., Brazil	MS	1986	Molecular Biology
University of Georgia, Athens, GA, USA	PHD	1992	Genetics
University of Wisconsin, Madison, WI, USA	Research Assistant	1993	Genetics
University of Wisconsin, Madison, WI, USA	Assistant Researcher	1996	Genetics
Stanford University, Palo Alto, CA, USA	Basic Life Science Research Associate	1997	Genetics

A. Personal Statement

I am a Molecular Geneticist and an expert Molecular Biologists that has formal training and extensive experience in molecular cloning, strain construction (both prokaryotic and eukaryotic), DNA, RNA, and protein purification and characterization. I have a deep understanding of the different processes associated with protein/metabolites production and strains engineering. I am a natural troubleshooter that knows how to find simple solutions to complex problems. I am a natural engineer that understands the intricacies associated with molecular techniques. As a consultant for Industry, I have acquired extensive experience designing industry-related experiments and evaluating results. As a principal investigator, I have been in charge of an active research group and maintained a complex interdisciplinary active laboratory for many years, oriented at both constructing strain and performing detailed molecular characterization at the DNA, RNA and protein levels. I am naturally meticulous and pay special attention to details. This has the benefit of being able to maintain consistency throughout different experimental protocols and to be able to detect subtle experimental behaviors.

This academic foundation seamlessly merged with my innate affinity for computers, shaping me into a unique hybrid: a Classical Geneticist and Molecular Biologist with a profound mastery of Computational Genomics and Data Sciences at large. My expertise also extends to developing intricate bioinformatic pipelines tailored for the human genome, characterized by meticulous attention to detail. As a natural engineer, my forte lies in crafting algorithms that adeptly convert intricate biological and genomics data into digital formats, facilitating their seamless integration with Machine Learning and Artificial Intelligence algorithms. I excel at deciphering complexity, translating innovative concepts into reproducible, practical algorithms, and scripting intricate tasks. My proficiency encompasses not only mastery of unix/linux operational systems and their interaction with other computers and Supercomputers, but also my ability to deploy and administer complex web-based computational tools. I am proficient at using version control systems, like Git, using interfaces like github, and gitlab. Moreover, my skill set also includes comprehensive expertise in diverse areas such as Next-Generation Sequencing data analysis, Genome Assembly, and Transcriptome Assembly and Quantification. I have a proven track record of overseeing the successful implementation of advanced Bioinformatics packages

and software, across a spectrum of computing platforms. Recently, I have completed an important Industry-related Bioinformatics project aimed at detecting how the expression of Ribosomal proteins affect Human protein production in large scale fermentation processes.

My commitment to information sharing has endowed me with substantial experience in elucidating complex concepts to individuals uninitiated in the fields of Genomics and/or Data Sciences, a skill honed over years of teaching and developing teaching tools and materials. My unwavering belief in the primacy of teamwork is the cornerstone of my professional ethos. Throughout my career, I have championed collaboration and nurtured environments conducive to growth. As a Principal Investigator, I have finely tuned my leadership acumen by guiding teams of both undergraduate and graduate students, empowering them to translate their research concepts into well designed experiments, functional code and rigorous testing and verification. I firmly acknowledge that the triumph of any venture hinges upon the collective strength of the team.

In summary, I am a highly imaginative professional with an extensive interdisciplinary background. My expertise spans Genetics, the art of molecular manipulation of organisms' genomes. In addition, I am also proficient in translating complex algorithms into code. My role as a Principal Investigator has empowered me with the capacity to adeptly oversee and mentor teams of budding academics, aiding them in translating their ideas into functional deliverables. Moreover, my immersion in the industry as a consultant has sharpened my aptitude for discerning priorities.

B. Research Statement

My current research primarily focuses on understanding the organization, distribution, and comparison of information in Biological Systems. Our work encompasses two key levels of investigation:

Molecular Genetics: We employ the filamentous fungus *Neurospora crassa* as a model organism to uncover and comprehend the intricate molecular components responsible for sequence-based comparisons between homologous chromosomes, leading to the initiation of Meiotic Silencing, a phenomenon driven by RNA-mediated processes. Currently, our primary focus centers on the exploration of whether genes recognized for their significance in Meiotic Transvection/Silencing also contribute to the occurrence of Repeat Induced Point Mutation (RIP) phenomena.

Computational Analysis: We are developing novel computational pipelines dedicated to detecting sequence variations within related genomes. We are particularly intrigued by the prospect of simplifying (i.e., digitizing) the information present in DNA, RNA, and Proteins so as to simplify its manipulation and analysis. We think that digitizing emerging genomic data will not only enable us to use this data effectively but also to integrate it into Artificial Intelligence, Data Clustering, and Image Recognition Algorithms, in ways not done before. We posit that this process of converting biological features into digital equivalents has the potential to simplify genomic information, making it easier to uncover previously unnoticed patterns through complex computational comparisons. This approach has already yielded promising results by revealing unexpected informational patterns across various organisms' chromosomes. We believe that it will streamline and enhance our ability to comprehend different cellular and organismal states. Moreover, it holds significant promise in revolutionizing our understanding of diseases, particularly Cancer and Metagenomics. This informational perspective also contributes to our comprehension of genome evolution, especially in the field of comparative genomics and microbial metagenomics.

C. Peer-Reviewed Publications

1. Bennett CJ, Aramayo R. A Re-Analysis of an Existing *Drosophila melanogaster* Dataset Reveals a New Set of Genes Involved in Post-Mating Response. bioRxiv. 2024:2024.04.10.588867. doi: 10.1101/2024.04.10.588867.
2. Aramayo R. Evaluating the impact of sequence duplications on the measurement of transcriptional profiling in the Human genome.2024;In Preparation.
3. Aramayo R, Nan B. De Novo Assembly and Annotation of the Complete Genome Sequence of *Myxococcus xanthus* DZ2. Microbiol Resour Announc. 2022;11(5):e0107421. Epub 20220406. doi: 10.1128/mra.01074-21. PubMed PMID: 35384715; PMCID: PMC9119067.

4. Gerth M, Martinez-Montoya H, Ramirez P, Masson F, Griffin JS, Aramayo R, Siozios S, Lemaitre B, Mateos M, Hurst GDD. Rapid molecular evolution of *Spiroplasma* symbionts of *Drosophila*. *Microb Genom*. 2021;7(2). doi: 10.1099/mgen.0.000503. PubMed PMID: 33591248; PMCID: PMC8208695.
5. Maitra N, He C, Blank HM, Tsuchiya M, Schilling B, Kaeberlein M, Aramayo R, Kennedy BK, Polymenis M. Translational control of methionine and serine metabolic pathways underpin the paralog-specific phenotypes of Rpl22 ribosomal protein mutants in cell division and replicative longevity. *bioRxiv*. 2020.
6. Maitra N, He C, Blank HM, Tsuchiya M, Schilling B, Kaeberlein M, Aramayo R, Kennedy BK, Polymenis M. Translational control of one-carbon metabolism underpins ribosomal protein phenotypes in cell division and longevity. *Elife*. 2020;9:e53127. Epub 20200520. doi: 10.7554/eLife.53127. PubMed PMID: 32432546; PMCID: PMC7263821.
7. Mateos M, Silva NO, Ramirez P, Higareda-Alvear VM, Aramayo R, Erickson JW. Effect of heritable symbionts on maternally-derived embryo transcripts. *Sci Rep*. 2019;9(1):8847. Epub 20190620. doi: 10.1038/s41598-019-45371-0. PubMed PMID: 31222094; PMCID: PMC6586653.
8. Stavrianakou M, Perez R, Wu C, Sachs MS, Aramayo R, Harlow M. Draft de novo transcriptome assembly and proteome characterization of the electric lobe of *Tetronarce californica*: a molecular tool for the study of cholinergic neurotransmission in the electric organ. *BMC Genomics*. 2017;18(1):611. Epub 20170814. doi: 10.1186/s12864-017-3890-4. PubMed PMID: 28806931; PMCID: PMC5557070.
9. Li H, Wu C, Aramayo R, Sachs MS, Harlow ML. Synaptic vesicles isolated from the electric organ of *Torpedo californica* and from the central nervous system of *Mus musculus* contain small ribonucleic acids (sRNAs). *Genom Data*. 2017;12:52-3. Epub 20170308. doi: 10.1016/j.gdata.2017.02.015. PubMed PMID: 28367405; PMCID: PMC5361766.
10. Clanton RM, Wu G, Akabani G, Aramayo R. Control of seizures by ketogenic diet-induced modulation of metabolic pathways. *Amino Acids*. 2017;49(1):1-20. Epub 20160928. doi: 10.1007/s00726-016-2336-7. PubMed PMID: 27683025.
11. Blank HM, Perez R, He C, Maitra N, Metz R, Hill J, Lin Y, Johnson CD, Bankaitis VA, Kennedy BK, Aramayo R, Polymenis M. Translational control of lipogenic enzymes in the cell cycle of synchronous, growing yeast cells. *EMBO J*. 2017;36(4):487-502. Epub 20170105. doi: 10.15252/embj.201695050. PubMed PMID: 28057705; PMCID: PMC5694946.
12. Aramayo R, Polymenis M. Ribosome profiling the cell cycle: lessons and challenges. *Curr Genet*. 2017;63(6):959-64. Epub 20170427. doi: 10.1007/s00294-017-0698-3. PubMed PMID: 28451847; PMCID: PMC5790165.
13. Saucedo DJ AR, Youssef S, Dima A, Chaudhary N, Karaman I, Perez R, Aramayo R., editor. Data and Tools for Materials Discovery and Design. Data and Tools for Materials Discovery and Design Materials Science & Technology 2015; 2015 October 4; Columbus, OH, USA Columbus, OH: Conference Tools for Materials Science & Technology 2015; c2015; 2015.
14. Polymenis M, Aramayo R. Translate to divide: small es, Cyrillic control of the cell cycle by protein synthesis. *Microb Cell*. 2015;2(4):94-104. Epub 20150320. doi: 10.15698/mic2015.04.198. PubMed PMID: 28357283; PMCID: PMC5348972.
15. Li H, Wu C, Aramayo R, Sachs MS, Harlow ML. Synaptic vesicles contain small ribonucleic acids (sRNAs) including transfer RNA fragments (trfRNA) and microRNAs (miRNA). *Sci Rep*. 2015;5(1):14918. Epub 20151008. doi: 10.1038/srep14918. PubMed PMID: 26446566; PMCID: PMC4597359.
16. Ilori MO, Picardal FW, Aramayo R, Adebuseye SA, Obayori OS, Benedik MJ. Catabolic plasmid specifying polychlorinated biphenyl degradation in *Cupriavidus* sp. strain SK-4: mobilization and expression in a pseudomonad. *J Basic Microbiol*. 2015;55(3):338-45. Epub 20130621. doi: 10.1002/jobm.201200807. PubMed PMID: 23787897.
17. Aramayo R, Selker EU. *Neurospora crassa*, a model system for epigenetics research. *Cold Spring Harb Perspect Biol*. 2013;5(10):a017921. Epub 20131001. doi: 10.1101/cshperspect.a017921. PubMed PMID: 24086046; PMCID: PMC3783048.
18. Wajid B AR, Serpedin E., editor. Exploring Minimum Description Length and Probabilistic Distributions of the Reference Sequences for Comparative Assembly of Genomes. In: Cristea P, editor Proceedings of the International Conference International Conference on Genomic Signal Processing; 2011.
19. Lee DW, Millimaki R, Aramayo R. QIP, a component of the vegetative RNA silencing pathway, is essential for meiosis and suppresses meiotic silencing in *Neurospora crassa*. *Genetics*. 2010;186(1):127-33.

20. Borkovich K, Ebbole DJ. Cellular and molecular biology of filamentous fungi. American Society for Microbiology Press; 2010.
21. Aramayo R, Pratt RJ. Meiotic trans□Sensing and Silencing in *Neurospora*. Cellular and Molecular Biology of Filamentous Fungi. 2010:132-44.
22. Lee DW, Freitag M, Selker EU, Aramayo R. A cytosine methyltransferase homologue is essential for sexual development in *Aspergillus nidulans*. PLoS one. 2008;3(6):e2531.
23. Hu JC, Aramayo R, Bolser D, Conway T, Elsik CG, Gribskov M, Kelder T, Kihara D, Knight TF, Jr., Pico AR, Siegele DA, Wanner BL, Welch RD. The emerging world of wikis. Science. 2008;320(5881):1289-90. doi: 10.1126/science.320.5881.1289b. PubMed PMID: 18535227.
24. Ng DW, Wang T, Chandrasekharan MB, Aramayo R, Kertbundit S, Hall TC. Plant SET domain-containing proteins: structure, function and regulation. Biochim Biophys Acta. 2007;1769(5-6):316-29. Epub 20070412. doi: 10.1016/j.bbaexp.2007.04.003. PubMed PMID: 17512990; PMCID: PMC2794661.
25. Kelly WG, Aramayo R. Meiotic silencing and the epigenetics of sex. Chromosome Res. 2007;15(5):633-51. doi: 10.1007/s10577-007-1143-0. PubMed PMID: 17674151; PMCID: PMC4090689.
26. Pratt RJ, Lee DW, Aramayo R. DNA methylation affects meiotic trans-sensing, not meiotic silencing, in *Neurospora*. Genetics. 2004;168(4):1925-35.
27. Lee DW, Seong KY, Pratt RJ, Baker K, Aramayo R. Properties of unpaired DNA required for efficient silencing in *Neurospora crassa*. Genetics. 2004;167(1):131-50. doi: 10.1534/genetics.167.1.131. PubMed PMID: 15166142; PMCID: PMC1470857.
28. Freitag M, Lee DW, Kothe GO, Pratt RJ, Aramayo R, Selker EU. DNA methylation is independent of RNA interference in *Neurospora*. Science. 2004;304(5679):1939-.
29. Borkovich KA, Alex LA, Yarden O, Freitag M, Turner GE, Read ND, Seiler S, Bell-Pedersen D, Paietta J, Plesofsky N, Plamann M, Goodrich-Tanrikulu M, Schulte U, Mannhaupt G, Nargang FE, Radford A, Selitrennikoff C, Galagan JE, Dunlap JC, Loros JJ, Catcheside D, Inoue H, Aramayo R, Polymenis M, Selker EU, Sachs MS, Marzluf GA, Paulsen I, Davis R, Ebbole DJ, Zelter A, Kalkman ER, O'Rourke R, Bowring F, Yeadon J, Ishii C, Suzuki K, Sakai W, Pratt R. Lessons from the genome sequence of *Neurospora crassa*: tracing the path from genomic blueprint to multicellular organism. Microbiol Mol Biol Rev. 2004;68(1):1-108. doi: 10.1128/MMBR.68.1.1-108.2004. PubMed PMID: 15007097; PMCID: PMC362109.
30. Bogomolnaya LM, Pathak R, Guo J, Cham R, Aramayo R, Polymenis M. Hym1p affects cell cycle progression in *Saccharomyces cerevisiae*. Curr Genet. 2004;46(4):183-92. Epub 20040910. doi: 10.1007/s00294-004-0527-3. PubMed PMID: 15365764.
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34. JR H, R A. Construction of a *his-3* integration vector capable of performing GATEWAY™ recombinational cloning for high-throughput analysis of *Neurospora crassa*. Fungal Genetics Newsletter. 2003;50:6-8.
35. Han BK, Aramayo R, Polymenis M. The G1 cyclin *Cln3p* controls vacuolar biogenesis in *Saccharomyces cerevisiae*. Genetics. 2003;165(2):467-76. doi: 10.1093/genetics/165.2.467. PubMed PMID: 14573462; PMCID: PMC1462773.
36. Haag JR, Lee DW, Aramayo R. A GATEWAY™ Destination Vector For High-Throughput Construction of *Neurospora crassa* histidine-3 Gene Replacement Plasmids. Fungal Genetics Newsletter. 2003:6-8.
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- Seiler S, Dunlap J, Radford A, Aramayo R, Natvig DO, Alex LA, Mannhaupt G, Ebbole DJ, Freitag M, Paulsen I, Sachs MS, Lander ES, Nusbaum C, Birren B. The genome sequence of the filamentous fungus *Neurospora crassa*. *Nature*. 2003;422(6934):859-68. doi: 10.1038/nature01554. PubMed PMID: 12712197.
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39. DiDomenico B, Aramayo R. Pathogenesis In Fungi. *Encyclopedia of Molecular Biology*. 2002.
40. DiDomenico B, Aramayo R. Circadian Rhythms and Clocks in Fungi. *Encyclopedia of Molecular Biology*. 2002.
41. DiDomenico B, Aramayo R. Mating In Fungi. *Encyclopedia of Molecular Biology*. 2002.
42. DiDomenico B, Aramayo R. Filamentous Fungi. *Encyclopedia of Molecular Biology*. 2002(10.1002/047120918X.emb0564).
43. Chang P YJ, Bhatnagar D, Cotty P, Keller N, Aramayo R, Roe B, Kupfer D, Cleveland T. *Aspergillus* EST Databases Provide Insights into Aflatoxin Biosynthesis Research. *Mycopathologia*. 2002;155(1-2).
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45. Peleg Y, Aramayo R, Kang S, Hall JG, Metzenberg RL. NUC-2, a component of the phosphate-regulated signal transduction pathway in *Neurospora crassa*, is an ankyrin repeat protein. *Molecular and General Genetics MGG*. 1996;252(6):709-16.
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48. Bruno KS, Aramayo R, Minke PF, Metzenberg RL, Plamann M. Loss of growth polarity and mislocalization of septa in a *Neurospora* mutant altered in the regulatory subunit of cAMP-dependent protein kinase. *EMBO J*. 1996;15(21):5772-82. PubMed PMID: 8918454; PMCID: PMC452324.
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D. Electronic Publications

1. Aramayo R. Fasta_GFF3_Equalizer_Bash. In: <https://doi.org/10.5281/zenodo.11396812>, editor. Zenodo. v1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
2. Aramayo R. Assessing the Influence of Sequence Duplications and Genome Annotations on Transcriptional Profiling Measurements. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
3. Aramayo R. Busco_Plot. In: <https://doi.org/10.5281/zenodo.10945685>, editor. Zenodo. v1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
4. Aramayo R. Fasta_Seq_Prepare_Bash. In: <https://zenodo.org/doi/10.5281/zenodo.10905863>, editor. Zenodo. v1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
5. Aramayo R. Fasta_Seq_Plot_Bash. In: <https://zenodo.org/doi/10.5281/zenodo.10892498>, editor. Zenodo. v1.0.2 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
6. Aramayo R. PepStats_Tables_Python. In: <https://zenodo.org/doi/10.5281/zenodo.10889791>, editor. Zenodo. v1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
7. Aramayo R. PepStats_Tables_Bash. In: <https://zenodo.org/doi/10.5281/zenodo.10888521>, editor. Zenodo. v1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2024.
8. Gallucci JL, Aramayo R. Do Public Databases Need Higher Standards for Next-Generation Data Submissions? In: <https://zenodo.org/doi/10.5281/zenodo.7943044>, editor. Zenodo. DOI: 10.5281/zenodo.7943045 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2023.
9. Aramayo R. Computational_Genomics. In: <https://zenodo.org/doi/10.5281/zenodo.6625427>, editor. Zenodo. v2023-1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2023.
10. Aramayo R. Compara_lists. In: <https://zenodo.org/doi/10.5281/zenodo.6582472>, editor. Zenodo. v1.0.1 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.
11. Aramayo R. Bioinformatics_Fall_2021. In: <https://zenodo.org/doi/10.5281/zenodo.6618284>, editor. Zenodo. v2021-1.0.2 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.
12. Aramayo R. Computational_Genomics. In: <https://doi.org/10.5281/zenodo.6628964>, editor. Zenodo. v2023-1.0.2 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.
13. Aramayo R. Teaching Computational Genomics: A Tale of Tables and Tests. In: <https://zenodo.org/doi/10.5281/zenodo.6634706>, editor. Zenodo. v1 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.
14. Aramayo R. A Re-Analysis of an Existing Drosophila melanogaster Dataset Reveals a New Set of Genes Involved in Post-Mating Response. In: <https://zenodo.org/doi/10.5281/zenodo.6685976>, editor. Zenodo. v2022-09-06 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.
15. Aramayo R. Digital_Biology. In: <https://zenodo.org/doi/10.5281/zenodo.6626235>, editor. Zenodo. v2022-1.0.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.
16. Aramayo R. Myxococcus xanthus DZ2 Genome Assembly. In: <https://zenodo.org/doi/10.5281/zenodo.6359693>, editor. Zenodo. v1.0 ed. Zenodo (CERN Data Centre & Invenio): CERN Data Centre & InvenioRDM; 2022.

E. Funding

1. Aramayo R, Thakar H. Type I – An Exploration on the Authenticity of the Ancient Triactyl Peruvian Mummies Using Radiocarbon Dating and Potential Genetic Characterization. Texas A&M University: Seed Grant Program for Promoting Research Collaborations (College of Liberal Arts, College of Science, and College of Geosciences); 2022.
2. Aramayo R. Digital Biology - BIO210035. Texas A&M University: Advanced Cyberinfrastructure Coordination Ecosystem: Services & Support (ACCESS) - National Science Foundation (NSF); 2022.
3. Aramayo R. Digital Biology – BIO210035. Texas A&M University: The Extreme Science and Engineering Discovery Environment (XSEDE) - National Science Foundation (NSF); 2021.
4. Aramayo R, Smith L. Drug Use and Abuse: Defining How Cocaine Affects the Addition of Wild-Type and Fragile X Mental Retardation-1 Mutants Texas A&M University: Texas A&M University. College of Sciences (COS) FY19 - Strategic Transformative Research Program 2019.

5. Posada JR, Aramayo R, Medina R. Characterizing The RNAs And DNAs Populations In Eggs As Tools To Assess Honey Bee Queen Fertility. Texas A&M University: T3 – Texas A&M Triads for Transformation; 2018.
6. Polymenis M, Aramayo R, Kennedy B. Coupling of Protein Synthesis with Cell Division. Texas A&M University: R01 GM123139-01, National Institutes of Health; 2017.
7. Aramayo R. Computational Detection of Novel Structural Variants in Cancer Genomes. Texas A&M University: dbGaP: 18340, National Institutes of Health – NCBI; 2017.
8. Aramayo R. Molecular Structure of the Monoamine Oxidase A (MAOA) Gene In Patients Diagnosed with Antisocial Personality Disorder. Texas A&M University: dbGaP: 18414, National Institutes of Health - NCBI; 2017.
9. Aramayo R. Computational Detection of Structural Variants Present in Standard Somatic Reference and Cancer Genomes. Texas A&M University: dbGap: 19769, National Institutes of Health - NCBI; 2017.
10. Aramayo R, Arroyave R, Gutierrez-Osuna R. Development of “Big Data” Scientific Workflow Management Tools for the Materials Genome Initiative: Materials Galaxy. Texas A&M University: Interdisciplinary Seed Grants in Big Data program of the Texas A&M Engineering Experiment Station and the Dwight Look College of Engineering in partnership with Texas A&M University Division of Research; 2014.
11. Aramayo R, Arroyave R. Materials Science Galaxy: A Web-based Materials Scientific Workflow Management System. Texas A&M University: Department of Materials Sciences. Texas A&M University; 2014.
12. Aramayo R. Advancing Big Data in Science. Texas A&M University: Texas A&M University: 230082, VPR Seed Grant; 2014.
13. Aramayo R. The Aggie Undergraduate Genomics Corps (AUGC): A catalytic concept for advancing undergraduate biological education at Texas A&M. Texas A&M University: Texas A&M University: 246049, Tier One Program (TOP) 2012.
14. Aramayo R. Genetic and Molecular Study of Meiotic Trans-sensing and Meiotic Silencing. Texas A&M University: RGM058770, National Institutes of Health; 1999.

F. Contributions to Science

1. I was the first to report that a large cluster of genes (~40 kbp) present in *Aspergillus nidulans* was completely irrelevant for growth and development. At the time this observation was very surprising, because the *SpoC1* cluster was thought to encode nearly 10% of the asexual spores transcripts. The fact that the gene cluster was irrelevant for the organisms, under the conditions tested, call in question the use of the *SpoC1* cluster as a model for studying gene regulation. In addition, this work reported the targeted deletion of a ~40 kbp chromosomal region, which at the time was the largest deletion obtained in an eukaryotic organism
 - a. Aramayo R, Adams TH, Timberlake WE. A large cluster of highly expressed genes is dispensable for growth and development in *Aspergillus nidulans*. *Genetics*. 1989 May;122(1):65-71. PubMed Central PMCID: PMC1203693.
2. I was the first one to describe a target gene for the long predicted "Master" regulators of conidiophore development in *Aspergillus nidulans*. The work of John Clutterbuck described classic developmental mutants of conidiophore formation in *Aspergillus nidulans*: *bristleA*, *abacusaA* and *wetA*. A major goal in the field at that time was to demonstrate how these genes regulated development. It was hypothesized that their gene products were transcription factors required to sequentially activate genes involved on different stages of conidiophore development. I took the opposite approach. I selected a gene, *yellowA* (*yA*), known to be involved in spore color production and predicted to be direct target for developmental transcriptional activators and characterized it. By sequencing its coding region, I demonstrated that *yA* encodes a laccase enzyme and reported for the first time the Copper-binding sites of a fungal enzyme. By dissecting *yA* promoter I demonstrated that the gene was target for *abaA*'s gene product (ABAA), thus establishing for the first time a direct connection between a classical "Master" regulator and a target gene
 - a. Aramayo R, Timberlake WE. The *Aspergillus nidulans* *yA* gene is regulated by *abaA*. *EMBO J*. 1993 May;12(5):2039-48. PubMed Central PMCID: PMC413426.

- b. Aramayo R, Timberlake WE. Construction of a 24-h developmental cDNA library from *Aspergillus nidulans*. *Fungal Genetics Newsletter*. 1990; 40(11):103.
 - c. Aramayo R, Timberlake WE. Sequence and molecular structure of the *Aspergillus nidulans* yA (laccase I) gene. *Nucleic Acids Res*. 1990 Jun 11;18(11):3415. PubMed Central PMCID: PMC330968.
3. I discovered **Meiotic Transvection/Silencing**. A phenomenon that went undetected and undiscovered and for nearly 50 years of *Neurospora* genetics and I did this because I had the courage to follow what the data was telling me without allowing myself to be influenced by existing and persistent dogma and/or by what my Postdoctoral advisor thought of what I was doing at the moment. The discovery of both Meiotic Silencing and trans-sensing opened a new field of investigation not only in *Neurospora*, but also in all organisms. Meiotic trans-sensing and meiotic silencing are two highly interrelated but different mechanisms that, together, scan and control the integrity of the genomes that participate in meiosis. My lab since then has identified a total of ~20 genes involved in this pathway and, in the process, developed key technology to facilitate our studies
- a. Pratt RJ, Lee DW, Aramayo R. DNA methylation affects meiotic trans-sensing, not meiotic silencing, in *Neurospora*. *Genetics*. 2004 Dec;168(4):1925-35. PubMed Central PMCID: PMC1448707.
 - b. Lee DW, Seong KY, Pratt RJ, Baker K, Aramayo R. Properties of unpaired DNA required for efficient silencing in *Neurospora crassa*. *Genetics*. 2004 May;167(1):131-50. PubMed Central PMCID: PMC1470857.
 - c. Lee DW, Pratt RJ, McLaughlin M, Aramayo R. An argonaute-like protein is required for meiotic silencing. *Genetics*. 2003 Jun;164(2):821-8. PubMed Central PMCID: PMC1462569.
 - d. Aramayo R, Metzenberg RL. Meiotic transvection in fungi. *Cell*. 1996 Jul 12;86(1):103-13. PubMed PMID: 8689677.

G. Teaching

G.1 Courses Developed

G.1.1 Computational Genomics (Undergraduate Level) and Genomics (Graduate Level)

Both, *Computational Genomics* and *Genomics*, are courses designed to prepare students for the *Genomics* Revolution. They both provide a broad, basic understanding of the different approaches used in the acquisition and study of genome data. Students learn how to obtain, organize, manipulate, and process biological data, using local-, super- and cloud-computers. For this, we use web-interface-based computational tools like Galaxy and CyVerse, to study genome data. Both courses aim at preparing students to understand and to perform basic genome analysis, which will in turn prepare them to follow and understand the most up-to-date work performed in biology. *Computational Genomics* and *Genomics* make extensive use of [XSEDE](#) and [Jetstream](#) cloud computational resources. *Genomics* and *Computational Genomics* are both mature courses that have been offered since the years 2000 and 2010, respectively.

G.1.2. Digital Biology (Graduate Level)

Digital Biology is a command-line-driven introductory course, designed to prepare students for the paradigm shift in our understanding of biology that has been generated by the quick development of the fields of *Genomics* and *Computational Genomics*. This course aims at developing terminal-based skills to obtain, organize, manipulate, and process biological data, with a focus on mapping and assembly of transcriptome data. Students learn the fundamentals of version control, scripting, text manipulation, and emerging computational tools available on local computers, super computers, and in the cloud. Learning the fundamentals of Version Control (GIT), scripting (BASH), text manipulation (SED/AWK), as well as other essential Genomics tools including, but not restricted to SAM, BED and Picard, allows students to ask and answer important biologically relevant questions. This helps them design, perform and analyze experiments using Mapping and Assembling software available at Cyverse and the TAMU Supercomputer Grace. *Digital Biology* makes extensive use of [XSEDE](#) and [Jetstream](#) cloud computational resources. *Digital Biology* is a mature course that has been offered since 2012.

G.1.3. Advanced Eukaryotic Genetics and Epigenetics (Graduate Level)

This is an advanced graduate level course developed to provide a comprehensive understanding of both genetics and epigenetics topics related to RNA silencing. The course is based on the study of the use of

genetic approaches to understand basic biological processes and genetic processes in both small (e.g., fungi) and large (e.g., mouse) eukaryotic organisms. In addition, we study classical examples where a non-mendelian genetic segregation is observed. In particular, we explore the exploding literature in the RNA silencing field, paying particular attention to the biology of the newly discovered non-coding RNAs. Students are exposed to the most up-to-date molecular and genetic literature in these fields. At the end of the course, students are expected to have an advanced understanding of the genetic and epigenetics of the most important eukaryotic model organisms and of the most relevant epigenetic problems.

G.1.4. Information In Biology (Undergraduate and Graduate Level)

This course was an attempt to tackle a heavily interdisciplinary subject. It focused on identifying and understanding the laws that govern and the processes that control information transfer in Biology. Our working hypothesis is that the same laws that control information transfer in other systems (e.g., large corporations) are present in unicellular organisms like *Escherichia coli* and vice-versa. Our dream is to translate these concepts in the production of software or hardware with "evolvability" properties.

G.2. Courses Taught As Professor

G.2.1. Graduate Level

NAME	NUMBER	YEAR(s)	CREDIT(S)
Advanced Eukaryotic Genetics and Epigenetics	BIOL689	2003 – 2005	04 Credits

G.2.2. Undergraduate Level

NAME	NUMBER	YEAR(s)	CREDIT(S)
Cellular and Molecular Biology	BIOL213	2023	03 Credits
Fundamentals of Microbiology	MICR351	2004 – 2005	04 Credits
Bacterial Genetics	MICR406	1997 – 2000	03 Credits

G.3. Courses Taught As Teaching Assistant

G.3.2. Graduate Level

NAME	NUMBER	YEAR(s)	CREDIT(S)
Laboratory Course in Molecular Biology	Molecular Biology	1985	02 Credits

G.3.1. Undergraduate Level

NAME	NUMBER	YEAR(s)	CREDIT(S)
Genetics	GENE301	1989	03 Credits
Advanced Molecular Biology	Molecular Biology II	1984	03 Credits
Biology 101	BIOL101	1978	03 Credits

H. Post-Doctoral Mentoring

NAME	DEPARTMENT AND INSTITUTION	YEAR(s)
Kye-Yong Seong	Department of Biology. Texas A&M University	1997 – 2002
Dong Whan Lee	Department of Biology. Texas A&M University	1999 – 2010

I. Graduate Advising

I.1. Chair

NAME	DEGREE	PROGRAM AND INSTITUTION	YEAR(s)
Deepthi Sri Kanigiri	MBT	BIOT. Texas A&M University	Fall 2023 – Ongoing
Eswar Sai Abhishek	MBT	BIOT. Texas A&M University	Summer 2022 – Ongoing
Brian White	PhD	BIOL. Texas A&M University	Fall 2015 – Ongoing
Julio Rincones Gamboa	PhD	BIOL. Texas A&M University	Fall 2018 – Ongoing
Chloe Bennett	PhD	BIOL. Texas A&M University	Fall 2014 – Fall 2022

NAME	DEGREE	PROGRAM AND INSTITUTION	YEAR(s)
Monisha S. S. Subramaniam	MBT	BIOT. Texas A&M University	Fall 2018 – Spring 2020
Brian White	MS	GENE. Texas A&M University	Summer 2017 – Summer 2019
Pranesh Rao	MBT	BIOT. Texas A&M University	Fall 2016 – Spring 2018
Ana Suescún Torres	PhD	MBIO. Texas A&M University	Fall 2006 – Summer 2014
Michelle Yeoman	MS	BIOL. Texas A&M University	Fall 2009 – Spring 2012
David Michael Stovall	MS	BIOT. Texas A&M University	Fall 2006 – Spring 2008
Harikishore Kandula	MS	BIOT. Texas A&M University	Fall 2006 – Spring 2008
Malcolm McLaughlin	MS	BIOL. Texas A&M University	Fall 2002 – Spring 2007
Robert L. Pratt II	PhD	BIOL. Texas A&M University	Fall 2001 – Spring 2008

I.2. Co-Chair

NAME	DEGREE	PROGRAM AND INSTITUTION	YEAR(s)
Ryan Clanton	PhD	NUEN. Texas A&M University	Spring 2014 – Fall 2017
Juan Anzola	PhD	BIOL. Texas A&M University	Fall 2006 – Spring 2008

I.3. Committee Member

NAME	DEGREE	PROGRAM AND INSTITUTION	YEAR(s)
Pinal Kamleshbhai	MBT	BIOT. Texas A&M University	Fall 2022 – Ongoing
Revanth Anishetti	MBT	BIOT. Texas A&M University	Fall 2022 – Ongoing
Samuel Joseph Kandikatla	MBT	BIOT. Texas A&M University	Fall 2022 – Ongoing
Kevin Wann	PhD	ANTH. Texas A&M University	Fall 2020 – Ongoing
Sabin Khanal	PhD	PLPA. Texas A&M University	Summer 2020 – Ongoing
Eddie Hernandez	MED	BESL. Texas A&M University	Spring 2019 – Ongoing
Taryn Johnson	PhD	ANTH. Texas A&M University	Fall 2016 – Fall 2023
Elyssa Garza	PhD	GENE. Texas A&M University	Fall 2013 – Fall 2023
Sathvik Patchametla	MBT	BIOT. Texas A&M University	Fall 2021 – Spring 2023
Kevin Wann	MS	ANTH. Texas A&M University	Fall 2020 – Spring 2023
Taryn Johnson	MS	ANTH. Texas A&M University	Fall 2016 – Fall 2022
Taryn Johnson	MA	ANTH. Texas A&M University	Summer 2020 – Summer 2021
Lucas Watson Mendelson	MBT	BIOT. Texas A&M University	Fall 2018 – Spring 2020
Kelsey McWilliams	MS	PLPA. Texas A&M University	Fall 2018 – Spring 2020
I-Fan Wu	PhD	BICH. Texas A&M University	Summer 2016 – Summer 2021
Xiaotian Tang	PhD	ENTO. Texas A&M University	Fall 2016 – Spring 2020
Lauren Davis	MS	BIMS. Texas A&M University	Fall 2016 – Spring 2018
Yi-Tsang Lee	MBT	BIOT. Texas A&M University	Fall 2015 – Fall 2017
Chloe Hawkings	PhD	ENTO. Texas A&M University	Spring 2014 – Fall 2018
Fahad Alshanbari	PhD	BIMS. Texas A&M University	Fall 2013 – Fall 2019
Adam Salazar	PhD	GENE. Texas A&M University	Summer 2013 – Spring 2019
Daniel Browne	PhD	BICH. Texas A&M University	Summer 2012 – Fall 2018
Karan Kohli	MBT	BIOT. Texas A&M University	Fall 2009 – Fall 2010
Humberto Martinez Montoya	PhD	WFSC. Texas A&M University	Fall 2009 – Spring 2017
Jinbai Guo	PhD	GENE. Texas A&M University	2007
Pinnaduwege Silva	PhD	Zool. Texas A&M University	Fall 2006 – Fall 2013
Brian Wayne Gardunia	PhD	PB. Texas A&M University	2006
Wang Kit Ng	PhD	BIOL. Texas A&M University	2005
Lida Silvana Paredes, Martinez	PhD	BIOL. Texas A&M University	Fall 2004 – Spring 2011
Leonardo Marino-Ramirez	PhD	BICH. Texas A&M University	2002
Lakshminarayan M. Iyer	PhD	BIOL. Texas A&M University	1999
Julie Kay Hicks	PhD	PPT. Texas A&M University	1999

J. Undergraduate Advising

NAME	DEGREE	PROGRAM	YEAR(s)
Abby Marie Ramos	BS	BIOLOGY/BIOINFORMATICS	Spring 2024 – Ongoing
Daniel Paul Nguyen	BS	BIOLOGY	Spring 2023 – Ongoing
Mariana Fauteux Decastro	BS	GENETICS	Spring 2022 – Ongoing
Andrea Emma Barrantes Travi	USCC	BIOINFORMATICS	Spring 2023 – Fall 2023
Kara Z. Leyendecker	USCC	BIOINFORMATICS	Spring 2023 – Fall 2023
Luke Gallucci	BS	GENETICS	Spring 2022 – Fall 2023
Katherine Rose Weaver	BS	BIOLOGY	2022
William Cameron Walker	BS	BIOLOGY	2022
Ryan Alexander LeGresley	CS	COMPUTER SCIENCES	2022
Yonvikai Tanachote	BS	BIOLOGY	2020 – 2021
Lisset Salinas	BS	BIOLOGY	2020 – 2022
Barbara Alexandra Moreno Diaz	BS	BIOLOGY	2020 – 2021
Jin Seung Lee	BS	BIOLOGY	2020 – 2021
Annaliese Claire Fowler	BS	BIOLOGY	2020 – 2021
Austin Daigle	BS	GENETICS	2020 – 2022
Beatrice Burton	BS	BIOLOGY	2020 – 2021
Ammarah Sattar	BS	BIOLOGY	2018
Janine Olivia Klar	BS	BIOLOGY	2018
Emily Morgan Drzymalla	BS	GENETICS	2017 – 2019
Janine Olivia Klar	BS	BIOLOGY	2018
Vishrut K Rao	BS	BIOLOGY	2018
Irving Eliu Palma Castro	BS	BIOLOGY	2015
Daniel Saucedo	BS	ENGINEERING	2015 – 2019
Hannah Renee Bolton	BS	BIOLOGY	2014 – 2016
Victoria Suzanne Blackert	BS	BIOLOGY	2014 – 2017
Lauren Alyssa Davis	BS	BIOLOGY	2014 – 2017
Anjali Teresa Gomes	BS	BIOLOGY	2015 – 2017
Jennifer Bernadette Cuaderes	BS	BIOLOGY	2014 – 2017
Jesus Fernando Lechuga	BS	BIOLOGY	2014 – 2016
Ricardo Perez	BS	GENETICS	2012 – 2015
Ben Jefferson Greenwell	BS	GENETICS	2012 – 2015
Charles Zheng	BS	BIOLOGY	2010 – 2011
Megan MacSwain	BS	BIOLOGY	2010 – 2011
Alvaro Rodriguez	BS	BIOLOGY	2010 – 2011
Sameer Gajjar	BS	BIOLOGY	2009 – 2012
Roy Weckiewicz	BS	BIOLOGY	2009 – 2010
Daniel Garzon	BS	BIOLOGY	2007 – 2010
Alicia Israel	BS	BIOLOGY	2009 – 2010
Michael Jules Schrago	BS	BIOLOGY	2008 – 2009
Jonathan Vollmert	BS	BIOLOGY	2008 – 2010, 2018 – 2019
Amanda Corder	BS	BIOLOGY	2008 – 2011
Kristen Cole	BS	BIOLOGY	2007 – 2008
Amanda Williams	BS	BIOLOGY	2007
Alexis Marie Bennet	BS	BIOLOGY	2006 – 2009
Jessica Tracy	BS	BIOLOGY	2005 – 2006
Paras Patel	BS	BIOLOGY	2005 – 2006

Amanda Bost	BS	BIOLOGY	2004 – 2005
John B. Carroll	BS	BIOLOGY	2004 – 20005
Thomas B. Lentz	BS	BIOLOGY	2003 – 2004
Barrie L. Glasberg	BS	BIOLOGY	2003
Devin L. Allison	BS	BIOLOGY	2003 – 2004
Jeremy R. Haag	BS	BIOLOGY	2002
Joana Dado	BS	BIOLOGY	2001 – 2002
Malcolm McLaughlin	BS	BIOLOGY	2001 – 2002
Brian Harris	BS	BIOLOGY	2000 – 2004
Stephen Bruce Boulware	BS	BIOLOGY	2000
Cheryl Lynn Newman	BS	BIOLOGY	2000
Shanna Marie Hyde	BS	BIOLOGY	2000
Robert L. Pratt II	BS	BIOLOGY	1999 – 2000
Leonardo da Silva	BS	BIOLOGY	1985 – 1986
Monica Coqueiro	BS	BIOLOGY	1984 – 1985

K. Non-Credit Instruction (Other Teaching & Instruction)

Aramayo, Rodolfo. "The Future of Genomics: Comparative Genomics." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2019.

Aramayo, Rodolfo. "Why We Need Diversity in Genomics." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2018.

Aramayo, Rodolfo. "Why We Need Diversity in Genomics." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2017.

Aramayo, Rodolfo. "Genomics: Where We Were, Where We Are and Where We Are Going." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2016.

Aramayo, Rodolfo. "Genomics: Where We Were, Where We Are and Where We Are Going." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2015.

Aramayo, Rodolfo. "Genomics: Where We Were, Where We Are and Where We Are Going." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2014.

Aramayo, Rodolfo. "Genomics: Where We Were, Where We Are and Where We Are Going." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2013.

Aramayo, Rodolfo. "UCSC Genome Browser – Basic and New Features. Texas a&M University. Summer 2015. Bioinformatics/Biostatistics Workshops."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), July 15 2015. https://sites.google.com/a/tamu.edu/training/2015_s03_ws04.

Aramayo, Rodolfo. "Getting More of out the UCSC Genome Browser. Texas a&M University. Summer 2015. Bioinformatics/Biostatistics Workshops."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), July 16 2015. https://sites.google.com/a/tamu.edu/training/2015_s03_ws05.

Aramayo, Rodolfo. "Introduction to R/R-Studio. Texas a&M University, Summer 2015. Bioinformatics/Biostatistics Workshops."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), June 17 2015. https://sites.google.com/a/tamu.edu/training/2015_s03_ws01.

Aramayo, Rodolfo. "Accessing Genomes, Assemblies and Annotation Products. Texas a&M University. Summer 2015. Bioinformatics/Biostatistics Workshops."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), July 13 2015. https://sites.google.com/a/tamu.edu/training/2015_s03_ws02.

Aramayo, Rodolfo. "Accessing NCBI Human Variation and Medical Genetics Resources. Texas a&M University. Summer 2015. Bioinformatics/Biostatistics Workshops."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), July 14 2015. https://sites.google.com/a/tamu.edu/training/2015_s03_ws03.

Aramayo, Rodolfo. "Summer Bioinformatics Workshop IV."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), August 14

2014.

Aramayo, Rodolfo. "Summer Bioinformatics Workshop III."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), August 12 2014.

Aramayo, Rodolfo. "Summer Bioinformatics Workshop II."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), August 08 2014.

Aramayo, Rodolfo. "Summer Bioinformatics Workshop I."

College Station, Texas USA: The Texas A&M Institute for Genome Sciences and Society (TIGSS), August 06 2014.

Aramayo, Rodolfo. "5th Workshop: Genome Annotation (Maker)."

College Station, Texas USA: Workshops in Computational Biology, 2010.

Aramayo, Rodolfo. "4th Workshop: Emboss and Bioperl."

College Station, Texas USA: Workshops in Computational Biology, 2010.

Aramayo, Rodolfo. "3th Workshop: Galaxy."

College Station, Texas USA: Workshops in Computational Biology, 2010.

Aramayo, Rodolfo. "2nd Workshop: Ncbi, Ucsd, Ensemble, Biomart, and Pfam."

College Station, Texas USA: Workshops in Computational Biology, 2010.

Aramayo, Rodolfo. "1st Workshop: Blast."

College Station, Texas USA: Workshops in Computational Biology, 2010.

L. Conferences

YEAR	DATES	NAME
2011	March, 15 to 20	Session Co-Chair (with Yi Liu) Twenty-sixth Fungal Genetics Conference. Genome Defense Mechanisms, Epigenetics and RNAi Section. Asilomar Conference Center. Pacific Grove, CA, USA
2008	March, 27 to 30	Invited Speaker Neurospora 2008. Gene Silencing, Sex, Repair and Recombination. Asilomar Conference Center. Pacific Grove, CA, USA
2008	January, 5 to 8	Invited Speaker MOHB--2nd Genetic Analysis: Model Organisms to Human Biology. Chromatin Session. Town and Country Resort & Conference Center, San Diego, CA, USA
2006	August, 21 to 25	Session Co-Chair (with Carlo Cogoni) 8th International Mycological Congress. Importance of Small Non-coding RNAs in Fungi. Cairns Convention Centre, Queensland, Australia
2005	November, 2 to 4	Invited Participant and Chair (by the NAS, USA) Eight Annual Chinese-American Frontiers of Science Symposium. RNAi and genome Defense Session. Xiamen University, Xiamen, China
2004	October, 22 to 24	Invited Participant (by the NAS, USA) Seventh Annual Chinese-American Frontiers of Science Symposium. Arnold and Mabel Beckman Center Irvine, CA, USA
2003	August, 10 to 15	Invited Speaker Fifth Epigenetics Gordon Research Conference. Holderness School, Plymouth, NH, USA
2003	April, 24 to 25	Invited Speaker 11th Annual Program for the Biology of Filamentous Fungi (PBOFF) Symposium. Fungal Evolution: Genes and Genomes.

2003	March, 18 to 23	Texas A&M University, TX, USA Invited Speaker 22nd Fungal Genetics Conference. Epigenetics, Transposable Elements and Prions Session. Asilomar Conference Center. Pacific Grove, CA, USA
2002	June, 13 to 16	Invited Speaker Neurospora Sequence Analysis Workshop. Whitehead Institute, MIT, Boston, MA
2002	March, 14 to 17	Invited Speaker Neurospora 2002. Asilomar Conference Center. Pacific Grove, CA, USA
2001	August, 12 to 17	Invited Speaker Fourth Epigenetics Gordon Research Conference. Holderness School, Plymouth, NH, USA
2000	October, 15 to 19	Session Co-Chair (with Dr. Joan Bennett) Genetics and Molecular Biology of Industrial Microorganisms. New Developments in Fungal Molecular Biology. Indiana University. Bloomington, IN USA
2000	July, 27 to 18	Invited Speaker IBC's Third International Symposium on Fungal Genomics. Georgia Center. University of Georgia, Athens, GA, USA
1998	July, 19 to 24	Invited Speaker Gordon Research Conference. Cellular and Molecular Mycology. Holderness School, Plymouth, NH, USA
1995	March, 21 to 26	Invited Speaker Eighteenth Fungal Genetics Conference. Cell Biology and Morphogenesis Section. Asilomar Conference Center. Pacific Grove, CA, USA
1995	March, 21 to 26	Speaker Eighteenth Fungal Genetics Conference. Neurospora workshop. Asilomar Conference Center. Pacific Grove, CA, USA
1986	--	Invited Speaker 19th Brazilian Congress of Phytopathology. Centro de Convenções de Brasília. Brasília, D. F., Brazil.

M. Seminars (Invited Speaker)

YEAR	PLACE
2019	Dovetail Genomics. Santa Cruz, California, USA
2012	Monsanto Company. St. Louis, Missouri, USA
2011	19th Annual Program for the Biology of Filamentous Fungi (PBOFF) Symposium. Texas A&M University, TX, USA.
2011	Genencor International, LLC. Palo Alto CA, USA
2010	Department of Embryology. Carnegie Institution. Baltimore, MD, USA
2008	Cell and Molecular Biology Program, The University of Texas at Austin. Austin, TX, USA
2005	Department of Biology, Emory University, Atlanta, GA, USA
2005	Seeds and Genomics, Monsanto Company, St. Louis, MO, USA
2004	Department of Biology. University of Kentucky, Lexington, KY, USA
2004	Division of Basic Sciences. Fred Hutchinson Cancer Research Center (FHCRC), Seattle, WA, USA
2004	Molecular Epigenetics Seminar Series. University of Florida, College of Medicine, Gainesville, FL, USA

2003 Department of Biology. Texas A&M University, TX, USA
 2002 Department of Veterinary Pathobiology. Texas A&M University, TX, USA
 2001 Genencor International, LLC. Palo Alto CA, USA.
 2000 Intercollegiate Program in Genetics. Texas A&M University, TX, USA
 2000 Genencor International, LLC. Palo Alto CA, USA
 2000 Intercollegiate Program in Genetics. Texas A&M University, TX, USA
 2000 *Aspergillus fumigatus* Genome Sequencing Group. Wellcome Trust Genome Campus, Hinxton, UK
 1998 SCRIPTGEN Pharmaceuticals, Inc. Waltham, MA, USA
 1998 6th Annual Program for the Biology of Filamentous Fungi (PBOFF) Symposium. Texas A&M University, TX, USA.
 1997 Schering-Plough Research Institute. Kenilworth, NJ, USA
 1997 Department of Genetics. University of Georgia, Athens, GA, USA
 1997 Department of Microbiology & Immunology. Medical College of Ohio, Toledo, Ohio, USA
 1997 Department of Plant and Microbial Biology. University of California, Berkeley, CA, USA
 1997 Department of Zoology and Genetics. Iowa State University, Ames, IA, USA
 1997 Department of Biology. Texas A&M University, College Station, TX, USA
 1996 SCRIPTGEN Pharmaceuticals, Inc. Medford, MA, USA
 1996 SCRIPTGEN Pharmaceuticals, Inc. Medford, MA, USA
 1995 Myco-Pharmaceuticals, Inc. Cambridge, MA, USA
 1990 Department of Genetics. University of Georgia, Athens, GA, USA
 1985 Department of Cellular Biology. University of Brasília, Brasília, D. F., Brazil

N. Positions, Scientific Appointments, Work Experience. Honors and Certificates

N.1. Positions and Scientific Appointments

2018 – Ongoing Editor
 PeerJ, The Journal of Life & Environmental Sciences
 San Diego, CA, USA
 2009 – 2012 Section Editor – Genetics and Genomics
 PLoS ONE, Public Library of Science One
 San Francisco, CA, USA
 2016 – 2022 Editor
 The International Journal of Biological Sciences. BiolSci Editorial. P.O. Box 19617, 55
 Bloor St. W.
 Toronto M4W 3T9 Canada
 2000 – 2016 Editor
 Fungal Genetics Newsletter. Fungal Genetics Stock Center. Department of Microbiology.
 University of Kansas Medical Center.
 Kansas City, Kansas 66160-7420 USA
 2000 – 2016 Editor
 The Open Mycology Journal. Bentham Open
 2004 – Ongoing Associate Professor
 Department of Biology, College of Arts and Sciences, Texas A&M University
 College Station, TX, USA
 1997 – 2004 Assistant Professor
 Department of Biology, College of Science, Texas A&M University
 College Station, TX, USA
 1996 – 1997 Basic Life Science Research Associate
 Department of Life Sciences, Stanford University
 Palo Alto, CA, USA
 1993 – 1996 Assistant Researcher
 Department of Biomolecular Chemistry

1992 – 1993	University of Wisconsin, Madison, WI, USA Research Assistant Department of Biomolecular Chemistry University of Wisconsin, Madison, WI, USA
1983 – 1986	Researcher II Division of Genetic Engineering National Center for Genetic Resources and Biotechnology (CENARGEN), EMBRAPA Brasilia, D.F., Brazil

N.2. Work Experience

1999 – 2000	Member of the Advisory Board F2G, Ltd., Manchester, UK
1991 – 1992	Work Type: Industry Research Assistantship Department of Genetics University of Georgia. Athens, Georgia, USA
1983 – 1986	Work Type: Academia Project Coordinator Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN) EMBRAPA Brasília, D. F., Brazil
1983 – 1986	Work Type: Government Project: Genetic Engineering applied to Plant Pathology System Analyst Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN), EMBRAPA Brasília, D. F., Brazil
	Work Type: Government Project: Development of databases to catalog, store and retrieve information in the Brazilian Germoplasm DataBank

N.3. Honors

2004 – 2005	Fellow: Beckman Frontiers of Science Symposium, The National Academies. Irvine, California, USA
1991 – 1992	Research Assistantship, University of Georgia. Athens, Georgia, USA
1989 – 1990	Doctoral Fellowship, CNPq. Brasília, D. F., Brazil
1987 – 1988	Doctoral Fellowship, EMBRAPA. Brasília, D. F., Brazil
1983 – 1984	Master Research Fellowship, EMBRAPA. Brasília, D. F., Brazil
1982 – 1983	Pre-doctoral Traineeship, EMBRAPA. Brasília, D. F., Brazil

N.4. Certificates of Appreciation

Aramayo, Rodolfo. "Certificate of Appreciation." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2019.

Aramayo, Rodolfo. "Certificate of Appreciation." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2017.

Aramayo, Rodolfo. "Certificate of Appreciation." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2016.

Aramayo, Rodolfo. "Certificate of Appreciation." Prairie View, Texas USA: Department of Biology. Prairie View A&M University, 2015.

O. Consulting

2018	Advisor (non-paid) Base10. A Pharmacogenomics and Nutrigenomics Company
2004 – 2006	Work Type: Industry Member of the Advisory Committee Rede Nordeste de Biotecnologia (RENORBIO). Brazilian Biotechnology Society. Brasília, D. F., Brazil
1999 – 2001	Work Type: Government Consultant Genencor, Palo Alto, CA, USA
1997 – 1997	Work Type: Industry Consultant Schering-Plough Research Institute, Kenilworth, NJ, USA
1996 – 1998	Work Type: Industry Consultant Scriptgen Pharmaceuticals, Waltham, MA, USA
1983 – 1986	Work Type: Industry Interdisciplinary Consultant Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN). EMBRAPA. Brasília, D. F., Brazil
1983 – 1986	Work Type: Government Project: Development of Optimization Algorithms applied to Biotechnology and Agriculture Interdisciplinary Consultant Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN). EMBRAPA Brasília, D. F., Brazil
1982 – 1986	Work Type: Government Project: Development of laboratory automation applied to Biotechnology Consultant and System Analyst Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN), EMBRAPA Brasília, D. F., Brazil
	Work Type: Government Project: Development of Software for the analysis of nucleic acids and proteins

P. Service

P.1. Editor

1. Abdueva D, Wing MR, Schaub B, Triche TJ. Experimental comparison and evaluation of the Affymetrix exon and U133Plus2 GeneChip arrays. PLoS One. 2007;2(9):e913. Epub 20070919. doi: 10.1371/journal.pone.0000913. PubMed PMID: 17878948; PMCID: PMC1976394.
2. Coulibaly MB, Lobo NF, Fitzpatrick MC, Kern M, Grushko O, Thaner DV, Traore SF, Collins FH, Besansky NJ. Segmental duplication implicated in the genesis of inversion 2Rj of Anopheles gambiae. PLoS One. 2007;2(9):e849. Epub 20070905. doi: 10.1371/journal.pone.0000849. PubMed PMID: 17786220;

PMCID: PMC1952172.

3. Hanson EK, Ballantyne J. An ultra-high discrimination Y chromosome short tandem repeat multiplex DNA typing system. *PLoS One*. 2007;2(8):e688. Epub 20070801. doi: 10.1371/journal.pone.0000688. PubMed PMID: 17668066; PMCID: PMC1925149.
4. Hawkins RD, Bashiardes S, Powder KE, Sajjan SA, Bhonagiri V, Alvarado DM, Speck J, Warchol ME, Lovett M. Large scale gene expression profiles of regenerating inner ear sensory epithelia. *PLoS One*. 2007;2(6):e525. Epub 20070613. doi: 10.1371/journal.pone.0000525. PubMed PMID: 17565378; PMCID: PMC1888727.
5. Houshdaran S, Cortessis VK, Siegmund K, Yang A, Laird PW, Sokol RZ. Widespread epigenetic abnormalities suggest a broad DNA methylation erasure defect in abnormal human sperm. *PLoS One*. 2007;2(12):e1289. Epub 20071212. doi: 10.1371/journal.pone.0001289. PubMed PMID: 18074014; PMCID: PMC2100168.
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7. Shaham S. Counting mutagenized genomes and optimizing genetic screens in *Caenorhabditis elegans*. *PLoS One*. 2007;2(11):e1117. Epub 20071107. doi: 10.1371/journal.pone.0001117. PubMed PMID: 17989770; PMCID: PMC2065842.
8. Coluccio AE, Rodriguez RK, Kernan MJ, Neiman AM. The yeast spore wall enables spores to survive passage through the digestive tract of *Drosophila*. *PLoS One*. 2008;3(8):e2873. Epub 20080806. doi: 10.1371/journal.pone.0002873. PubMed PMID: 18682732; PMCID: PMC2478712.
9. Mourier T, Willerslev E. Does selection against transcriptional interference shape retroelement-free regions in mammalian genomes? *PLoS One*. 2008;3(11):e3760. Epub 20081119. doi: 10.1371/journal.pone.0003760. PubMed PMID: 19018283; PMCID: PMC2582637.
10. Mudge J, Miller NA, Khrebtukova I, Lindquist IE, May GD, Huntley JJ, Luo S, Zhang L, van Velkinburgh JC, Farmer AD, Lewis S, Beavis WD, Schilkey FD, Virk SM, Black CF, Myers MK, Mader LC, Langley RJ, Utsey JP, Kim RW, Roberts RC, Khalsa SK, Garcia M, Ambriz-Griffith V, Harlan R, Czika W, Martin S, Wolfinger RD, Perrone-Bizzozero NI, Schroth GP, Kingsmore SF. Genomic convergence analysis of schizophrenia: mRNA sequencing reveals altered synaptic vesicular transport in post-mortem cerebellum. *PLoS One*. 2008;3(11):e3625. Epub 20081105. doi: 10.1371/journal.pone.0003625. PubMed PMID: 18985160; PMCID: PMC2576459.
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48. Zhao JS, Deng Y, Manno D, Hawari J. *Shewanella* spp. genomic evolution for a cold marine lifestyle and in-situ explosive biodegradation. PLoS One. 2010;5(2):e9109. Epub 20100208. doi: 10.1371/journal.pone.0009109. PubMed PMID: 20174598; PMCID: PMC2824531.
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P.1. Peer Reviewer

Aramayo, Rodolfo. "Reviewer: The Third International Hackathon for Applying Insights into Large-Scale Genomic Composition to Use Cases in a Wide Range of Organisms." [In English]. *F1000Research* (June 22 2022). <https://doi.org/10.5256/f1000research.121770.r139299>.

<https://f1000research.com/articles/11-530/v1#referee-response-139299>.

Reviewer: ELife

Reviewer: PLoS Genetics

Reviewer: Genetics

Reviewer: National Science Foundation (NSF)

Reviewer: National Institutes of Health (NIH)

Q. Institutional Committees

Q.1. Texas A&M University, Department of Biology Committees

2022 – Ongoing	Member: Academic Vision Committee
2022 – Ongoing	Member: Genomics/Bioinformatics Courses Committee
2021 – 2022	Member: New Building Core Facilities Committee
2015 – 2022	Member: Graduate Recruitment and Admissions Committee (GRAC)
2015 – 2022	Member: Computer Committee

Q.2. Texas A&M University

2022 – Ongoing	Member: Bioinformatics Major Committee
2018 – Ongoing	TAMU Genetics mentor. Interdisciplinary Graduate Program in Genetics
2015 – Ongoing	Faculty Mentor. Bridge to the Doctorate (BTD) Fellowship Program
2000 – Ongoing	Member: TAMU Master of Biotechnology (MBIOT) Program
2000 – Ongoing	Member: Graduate Faculty of the Health Science Center. Graduate School of Biomedical Sciences. Health Science Center. TAMU
1999 – Ongoing	Member: Intercollegiate Program in Genetics. TAMU
2015	Member: Dean Search Advisory Committee
2015 – 2019	Member: Diversity Fellowship Committee. The Office of Graduate and Professional Studies (OGAPS)
2014 – 2022	Member: Aggie Research Scholars
2014 – 2022	Member: Faculty Honors Program
2014 – 2019	Member: Task Force on IT Security. College of Sciences (COS)
2014 – 2019	Member: Whole Systems Genomics Computational Advisory Group
2014 – 2019	Member: University Disciplinary Appeals Panel
2010 – 2014	Member: Chromosome Biology Super Group Once a month Super Lab Meeting of the members of the laboratories from: Dr. Dorothy Shippen (Biochemistry and Biophysics), Dr. Geoffrey Kapler (Molecular and Cellular medicine), Dr. Kathryn Ryan (Biology), Dr. Keith Maggert (Biology), Dr. Mary Bryk (Biochemistry and Biophysics), Dr. Michael Polymenis (Biochemistry and Biophysics), Dr. Rodolfo Aramayo (Biology)
2013 – 2014	Member: TAMU Undergraduate MiniPharma
2010 – 2015	Director. Laboratory for Computational Genomics. TAMU
1998 – 2017	Member: Program for the Biology of Filamentous Fungi (PBOFF). TAMU

R. International Activities

2022 – Ongoing	Initiated and negotiated the terms for a potential collaboration between the Department of Biology and the Department of Anthropology at Texas A&M University (TAMU), USA and the University of Ica (UNICA), Peru.
2006 – 2008	Initiated and negotiated the terms to the creation of a Letter of Intent by and between Texas A&M University and the Universidade de São Paulo – Brazil. The Letter of Intent was finally signed between Dr. Robert Gates (President of Texas A&M University) and Professors Doctora Suely Vilela (Reitora da Universidade de São Paulo).
2004 – 2006	Member of the Advisory Committee Rede Nordeste de Biotecnologia (RENORBIO). Brazilian Biotechnology Society. Brasília, D. F., Brazil
2003 – 2006	Work Type: Government <i>Ad hoc</i> Reviewer Biology and Fungal Biology Israel Science Foundation.

2002 – 2008	The Israel Academy of Sciences and Humanities Árbitro Consejo Nacional de Ciencia y Tecnología (CONACYT) CONACYT-DAIC, Consulta de Proyectos. C.P.:11950, Mexico, D. F., Mexico
2002 – 2008	Reviewer Conselho Nacional Desenvolvimento Científico e Tecnológico (CNPQ) Brasília, DF Brasil
2002	Reviewer French Funding Agency for Research (Agence Nationale de la Recherche – ANR) Paris, France

S. Activities Supporting Multidisciplinary Collaboration

Aramayo R, Arroyave R, Gutierrez-Osuna R. Development of “Big Data” Scientific Workflow Management Tools for the Materials Genome Initiative: Materials Galaxy. Texas A&M University: Interdisciplinary Seed Grants in Big Data program of the Texas A&M Engineering Experiment Station and the Dwight Look College of Engineering in partnership with Texas A&M University Division of Research; 2014.

Aramayo R, Arroyave R. Materials Science Galaxy: A Web-based Materials Scientific Workflow Management System. Texas A&M University: Department of Materials Sciences. Texas A&M University; 2014.

Aramayo R. Advancing Big Data in Science. Texas A&M University: Texas A&M University: 230082, VPR Seed Grant; 2014.

T. Professional Development/Continuing Education

2012	CS101. Introduction to Computing Principles Stanford University
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U. Online Professional Profiles

[NCBI: My Bibliography](#)

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V. Professional Memberships

Member: Genomics Education Alliance

Member: Genome in a Bottle Consortium

Member: Free Software Foundation

Member: Electronic Frontier Foundation

Member: AAAs