

**BIOGRAPHICAL SKETCH**

Provide the following information for the Senior/key personnel and other significant contributors.  
Follow this format for each person. DO NOT EXCEED FIVE PAGES.

NAME: Aramayo, Rodolfo

eRA COMMONS USER NAME (credential, e.g., agency login):

POSITION TITLE: Associate Professor

EDUCATION/TRAINING (*Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE (if applicable)	END DATE MM/YYYY	FIELD OF STUDY
University of Brasília, Brasilia, D.F.	BS	1983	Molecular Biology
University of Brasília, Brasilia, D.F.	MS	1986	Molecular Biology
University of Georgia, Athens, GA	PHD	1992	Genetics
University of Wisconsin, Madison, WI	Postdoctoral Fellow	1996	Genetics
Stanford University, Palo Alto, CA	Postdoctoral Fellow	1997	Genetics

**A. Personal Statement**

My laboratory is centered on understanding the function(s) of RNAs, especially non-coding RNAs in all aspects of Biology. The initial work was based on studying Meiotic Silencing, a very unusual genetic phenomenon we discovered in *Neurospora crassa*. From this work, it became clear that the RNA silencing mechanism invoked by Meiotic Silencing had been adapted from, and evolved to, fulfill key highly-related roles in all eukaryotic cells. The complexity of the problem demanded the use of sophisticated molecular tools and techniques, especially the extensive use of Next Generation DNA Sequencing, Single Cell Sequencing and the subsequent manipulation of the emerging information. In the process of mastering these computational tools and techniques, we branched into studying the Computational Genomics aspect of these problems. The expertise we generated can be applied to all organisms and/or other systems. In the process, we have established active collaborations with researchers studying the biology of RNAs in Neurobiology and Cell Cycle. Our computational expertise has also generated an active collaboration with Materials Sciences. The wet-lab aspect of this laboratory is still centered on understanding Meiotic Silencing, one of the most amazing and intriguing mechanisms observed in meiotic cells of eukaryotic organisms. In the *Neurospora* meiosis, if a DNA segment is absent or highly mutated on the opposite homologous chromosome, the resulting "unpaired" DNA segment is targeted for silencing. This situation can occur when a DNA element gets inserted at a particular chromosomal position (e.g., a situation akin to the "invasion" of a genome by transposable DNA elements). Alternatively, it can also occur when a normal region gets deleted. In both situations, the resulting "loop" of "unpaired" DNA seems to activate a genome-wide "alert" system that results in the silencing not only of the genes present in the "unpaired" DNA segment, but also of those same genes if present elsewhere in the genome, even if they are in a "paired" symmetrical condition. Although meiotic silencing was originally described in *Neurospora crassa*, it has since been observed in nematodes and mammals. In all these organisms, "unpaired or unsynapsed" regions (or chromosomes) are targeted for gene silencing. Our working hypothesis is that meiotic silencing is a two-step process. First meiotic *trans*-sensing compares the chromosomes from each parent and identifies significant differences as unpaired DNA. Second, if unpaired DNA is identified, a process called meiotic silencing silences expression of genes within the unpaired region and regions sharing sequence identity. We are using a combination of genetics, molecular biology and biochemistry aimed at identifying all the molecular players of the process and at understanding how they work together. The long term objective of our work is to understand Meiotic Silencing not only in *Neurospora*, but also, to map its connections with the meiotic silencing observed in other organisms

1. 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 Aug 14;18(1):611. PubMed PMID: [28806931](#); PubMed Central PMCID: [PMC5557070](#).
2. 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 Feb 15;36(4):487-502. PubMed PMID: [28057705](#); PubMed Central PMCID: [PMC5694946](#).
3. 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 Oct 8;5:14918. PubMed PMID: [26446566](#); PubMed Central PMCID: [PMC4597359](#).
4. 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 Sep;186(1):127-33. PubMed PMID: [20592262](#); PubMed Central PMCID: [PMC2940281](#).

## B. Positions and Honors

### Positions and Employment

- 1983 - 1986     Researcher II, Division of Genetic Engineering, National Center for Genetic Resources and Biotechnology (CENARGEN), EMBRAPA, Brasilia
- 1997 - 2004     Assistant Professor, Department of Biology, College of Science, Texas A&M University, College Station, TX
- 2004 -           Associate Professor, Department of Biology, College of Science, Texas A&M University, College Station, TX

### Other Experience and Professional Memberships

- 1982 - 1986     Consultant and System Analyst: Research and Development of Software for the analysis of nucleic acids and proteins, Department of Informatics. National Center for Genetic Resources and Biotechnology (CENARGEN-EMBRAPA). Brasilia, D. F., Brazil
- 1983 - 1986     Project Coordinator: Genetic Engineering applied to Plant Pathology, Department of Genetic Engineering National Center for Genetic Resources and Biotechnology (CENARGEN-EMBRAPA). Brasilia, D. F., Brazil
- 1983 - 1986     Interdisciplinary Consultant: Research and development of Artificial Intelligence (AI) applied to Biotechnology and Agriculture, Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN-EMBRAPA). Brasilia, D. F., Brazil
- 1983 - 1986     Interdisciplinary Consultant: Laboratory automation applied to Biotechnology, Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN-EMBRAPA). Brasilia, D. F., Brazil
- 1983 - 1986     System Analyst: Development of databases to catalog, store and retrieve information in the Brazilian Germoplasm DataBank, Department of Informatics National Center for Genetic Resources and Biotechnology (CENARGEN-EMBRAPA). Brasilia, D. F., Brazil
- 1996 - 1998     Consultant: Aspergillus Genetics, Scriptgen Pharmaceuticals. Waltham, Massachusetts, USA
- 1996 - 1999     Member, ad hoc Committee for the Sequencing of the *Neurospora crassa* Genome
- 1997 -           Member, Intercollegiate Program in Genetics. Texas A&M University
- 1997 -           Member, Program for the Biology of Filamentous Fungi (PBOFF). Department of Biology. Texas A&M University
- 1997 - 1997     Consultant: Antifungal Genomics Program, Schering-Plough Research Institute. Kenilworth, New Jersey, USA
- 1997 - 1999     Co-Principal Investigator for Texas A&M Proposal for the creation of a National Center for Fungal Genomics, Department of Biology Texas A&M University. College Station, Texas, USA

1997 - 1999 Member, Seminar Committee. Program for the Biology of Filamentous Fungi (PBOFF). Texas A&M University

1997 - 1999 Member, Steering Committee. National Science and Technology Center (NSTC). Texas A&M University

1997 - 2008 Member, Computer Committee. Department of Biology. Texas A&M University

1997 - 2008 ad hoc Reviewer, MCB—Microbial Genetics. National Science Foundation. 4201 Wilson Blvd. Arlington, VA 22230, USA

1998 - 2001 Member, Graduate Student Recruiting Committee. Intercollegiate Program in Genetics. Texas A&M University

1998 - 2002 Chair, Seminar Committee. Department of Biology. Texas A&M University

1999 - 1999 Member, Faculty Recruitment Committee: Genome Informatics, Non-Tenure Track Position The Texas Agricultural Experimental Station. Texas A&M University

1999 - 1999 Member, Faculty Recruitment Committee Microbial Genomics, Faculty Tenure Track Position Department of Biology. Texas A&M University

1999 - 1999 Chair, Symposium Committee Program for the Biology of Filamentous Fungi (PBOFF). Texas A&M University

1999 - 1999 Member, Faculty Recruitment Committee: Genome Informatics, Faculty Tenure Track Position Department of Biology. Texas A&M University

1999 - 1999 Member, Faculty Recruitment Committee: Faculty Tenure Track Position Department of Biology. Texas A&M University

1999 - 2000 Member of the Advisory Board, F2G, Ltd. Manchester, UK

1999 - 2001 Consultant: Fungal Genetics and Genomics, Genencor International, Inc. Palo Alto, California, USA

2000 - 2001 Member, Steering Committee for the Sequencing of the *Aspergillus fumigatus* Genome

2000 - 2005 Member, Program for Microbial Genetics and Genomics (PMGG). Department of Biology. Texas A&M University

2002 - 2007 Member, Seminar Committee. Department of Biology. Texas A&M University

2002 - 2008 Árbitro, Consejo Nacional de Ciencia y Tecnología (CONACYT) CONACYT-DAIC, Consulta de Proyectos. C.P.:11950, Mexico, D. F., Mexico

2002 - 2008 Member, Graduate Curriculum Committee. Intercollegiate Program in Genetics. Texas A&M University

2002 - 2012 Editorial Board, Fungal Genetics Newsletter. Fungal Genetics Stock Center. Department of Microbiology. University of Kansas Medical Center. Kansas City, Kansas 66160-7420 USA

2003 - 2008 ad hoc Reviewer , Biology and Fungal Biology. Israel Science Foundation. The Israel Academy of Sciences and Humanities

2004 - Member, Graduate Faculty of the Health Science Center. Graduate School of Biomedical Sciences. Health Science Center. Texas A&M University

2004 - Editorial Board, The International Journal of Biological Sciences. Editorial. P.O. Box 19617, 55 Bloor St. W., Toronto M4W 3T9 Canada

2004 - 2006 Faculty Advisor, Beta Beta Beta Division of Student Affairs. Department of Student Activities. Texas A&M University

2004 - 2006 Member of the Advisory Committee: Fungal Genomics, Rede Nordeste de Biotecnologia (RENORBIO). Brazilian Biotechnology Society. Brasília, D. F., Brazil

2004 - 2007 Member, Graduate Recruitment and Admissions Committee (GRAC). Department of Biology. Texas A&M University

2006 - 2011 Editorial Board, PLoS ONE Public Library of Science. 185 Berry Street, Suite 3100. San Francisco, CA 94107 USA

2007 - 2012 Editorial Board, The Open Mycology Journal. Bentham Open

2008 - 2016 Director, Laboratory for Genome Bioinformatics. Department of Biology. Texas A&M University

- 2009 - 2011 Member, Export Control Task Force. Texas A&M University
- 2009 - 2011 Member, Information Technology Committee. College of Science, Texas A&M University
- 2012 - 2016 Member, University Disciplinary Appeals Panel. Texas A&M University
- 2013 - 2015 Member, Dean Search Advisory Committee. Texas A&M University
- 2013 - 2016 Member, Whole Systems Genomics. Computational Advisory Group Texas A&M University
- 2016 - Member, Diversity Fellowship Committee. The Office of Graduate and Professional Studies (OGAPS). Texas A&M University
- 2016 - Member, Computer Committee. Department of Biology. Texas A&M University
- 2016 - Member, Graduate Recruitment and Admissions Committee (GRAC). Department of Biology. Texas A&M University
- 2016 - Member, Task Force on IT Security. College of Sciences (COS). Texas A&M University

## **Honors**

- 1982 - 1983 Pre-doctoral Traineeship, EMBRAPA. Brasília, D. F., Brazil
- 1983 - 1984 Master Research Fellowship, EMBRAPA. Brasília, D. F., Brazil
- 1987 - 1988 Doctoral Fellowship, EMBRAPA. Brasília, D. F., Brazil
- 1989 - 1990 Doctoral Fellowship, CNPq. Brasília, D. F., Brazil
- 1991 - 1992 Research Assistantship, University of Georgia. Athens, Georgia, USA
- 2004 - 2005 Fellow: Beckman Frontiers of Science Symposium, The National Academies. Irvine, California, USA
- 2009 - 2012 Section Editor: Genetics and Genomics, Public Library of Science One (PLoS ONE)

## **C. Contribution 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 PMID: [2471671](https://pubmed.ncbi.nlm.nih.gov/2471671/); PubMed Central PMCID: [PMC1203693](https://pubmed.ncbi.nlm.nih.gov/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*, *abacusA* 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 PMID: [8491194](https://pubmed.ncbi.nlm.nih.gov/8491194/); PubMed Central PMCID: [PMC413426](https://pubmed.ncbi.nlm.nih.gov/PMC413426/).
  - b. Aramayo R. Construction of a 24-h developmental cDNA library from *Aspergillus nidulans*. *Fungal*

Genetics Newsletter. 1993; 40:103.

- 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 PMID: [2192364](#); PubMed Central PMCID: [PMC330968](#).

3. I discovered **Meiotic 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 PMID: [15611165](#); 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 PMID: [15166142](#); 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 PMID: [12807800](#); PubMed Central PMCID: [PMC1462569](#).
- d. Aramayo R, Metzberg RL. Meiotic transvection in fungi. *Cell.* 1996 Jul 12;86(1):103-13. PubMed PMID: [8689677](#).

## **D. Additional Information: Research Support and/or Scholastic Performance**

### **Ongoing Research Support**

R01 GM123139-01, National Institutes of Health      Aramayo, Rodolfo (PI)      05/26/17-03/31/21  
Coupling of Protein Synthesis with Cell Division  
Role: CPI

### **Completed Research Support**

230044, 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

Aramayo, Rodolfo (PI)      01/02/16-01/02/17  
Development of "Big Data" Scientific Workflow Management Tools for the Materials Genome Initiative: Materials Galaxy  
Role: PI

RGM058770, National Institutes of Health      Aramayo, Rodolfo (PI)      01/01/99-12/31/12  
Genetic and Molecular Study of Meiotic Trans-sensing and Meiotic Silencing  
Role: PI