Marcos MORGAN - CV

PERSONAL INFORMATION

***Place and Date of Birth**:* Buenos Aires, Argentina | 7 May 1982

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EDUCATION

2008-2011 Ph.D. in Life and Biomolecular Sciences, The Open University, UK, for studies conducted at the International Centre for Genetic Engineering and Biotechnology, Trieste, Italy.

2000-2005 Degree in Biology, Department of Natural and Exact Sciences, University of Buenos Aires, Argentina.

EMPLOYMENT AND TRAINING

2019-Current Principal Investigator, National Institute of Environmental Health Sciences, National Institutes of Health, North Carolina.

2016-2019 Postdoctoral fellow, MRC Centre for Regenerative Medicine, University of Edinburgh, UK, laboratory of Prof. Donal O'Carroll.

2014-2016 Postdoctoral fellow, European Molecular Biology Laboratory, Italy, laboratory of Prof. Donal O'Carroll.

2011-2014 Postdoctoral fellow, European Molecular Biology Laboratory, Italy, laboratory of Prof. Donal O'Carroll and European Bioinformatics Institute, UK, research group of Dr. Anton J. Enright.

2007-2011 Graduate student, International Centre for Genetic Engineering and Biotechnology, Italy, laboratory of Dr. Andres F. Muro.

2006-2007 Graduate student, Center of Advanced Microscopies, University of Buenos Aires, Argentina, laboratory of Dr. Lia Pietrasanta.

SELECTED FELLOWSHIPS AND AWARDS

2019 Stadtman Tenure-Track Investigator appointment at the National Institutes of Health.

2011-2013 EIPOD Postdoctoral fellowship from the European Molecular Biology Laboratory.

2007-2011 Ph.D. fellowship from the International Centre for Genetic Engineering and Biotechnology.

LANGUAGES

First language: **Spanish**. I completed my undergraduate studies in Spanish.

Second language: **English**. I completed my Ph.D. in English.

Foreign language: **Italian**. I lived and worked in Italy for over eight years and used Italian daily.

SELECTED ORAL COMMUNICATIONS

o Invited speaker, 2019 Symposium on RNA Biology: Tool and Target, Duke University, North Carolina, 2019.

o Invited speaker, Society for the Study of Reproduction annual meeting, San Jose, California, 2019.

o Invited seminar, Department of Natural and Exact Sciences, University of Buenos Aires, Argentina, 2019.

o Invited seminar, Department of Biochemistry, Cambridge University, UK, 2017.

o Selected oral presentation at the Epitranscriptome, EMBL conference, Heidelberg, Germany, 2016. Role of Tut4/7-mediated 3' uridylation *in vivo*.

o Invited seminar, Sir William Dunn School of Pathology, Oxford University, UK, 2012.

PUBLICATIONS

Paris, J.*, **Morgan, M.***, Campos, J.*, Spencer, G. J., Shmakova, A., Ivanova, I., … Kranc, K. R. (2019). Targeting the RNA m6A Reader YTHDF2 Selectively Compromises Cancer Stem Cells in Acute Myeloid Leukemia. Cell Stem Cell.
https://doi.org/10.1016/j.stem.2019.03.021

*Equal contribution.

Morgan, M., Kabayama, Y., Much, C., Ivanova, I., Di Giacomo, M., Auchynnikava, T., … O'Carroll, D. (2019). A programmed wave of uridylation-primed mRNA degradation is essential for meiotic progression and mammalian spermatogenesis. Cell Research, 29(3), 221–232.
https://doi.org/10.1038/s41422-018-0128-1

Le Pen, J., Jiang, H., Di Domenico, T., Kneuss, E., Kosałka, J., Leung, C., … Miska, E. A. (2018). Terminal uridylyltransferases target RNA viruses as part of the innate immune system. Nature Structural & Molecular Biology, 25(9), 778–786.
https://doi.org/10.1038/s41594-018-0106-9

In this paper, we show that the uridylation of viral RNAs by conserved terminal uridylyltransferases triggers a novel mechanism of innate immunity in C. elegans and mammalian cells.

Carrieri, C., Comazzetto, S., Grover, A., **Morgan, M.**, Buness, A., Nerlov, C., & O'Carroll, D. (2017). A transit-amplifying population underpins the efficient regenerative capacity of the testis. Journal of Experimental Medicine, 214(6).
https://doi.org/10.1084/jem.20161371

Morgan, M.*, Much, C.*, DiGiacomo, M., Azzi, C., Ivanova, I., Vitsios, D. M., … O'Carroll, D. (2017). mRNA 3' uridylation and poly(A) tail length sculpt the mammalian maternal transcriptome. Nature, 548(7667), 347–351.
https://doi.org/10.1038/nature23318

In this paper, we show that oligo-uridylation is absolutely required to sculpt a functional maternal transcriptome. We generated Tut4 and Tut7 conditional mutants in the mouse female germline. These enzymes are required to oligo-uridylate transcripts targeted for degradation. Without the oligo-uridylation signal, these transcripts cannot be cleared, compromising meiotic progression.

*Equal contribution.

Ivanova, I., Much, C., Di Giacomo, M., Azzi, C., **Morgan, M.**, Moreira, P. N., … O'Carroll, D. (2017). The RNA m 6 A Reader YTHDF2 Is Essential for the Post-transcriptional Regulation of the Maternal Transcriptome and Oocyte Competence. Molecular Cell, 67(6), 1059–1067.e4.
https://doi.org/10.1016/j.molcel.2017.08.003

m6A is the most abundant type of eukaryotic mRNA methylation and is known to critically affect transcript stability. Here we showed for the first time in mammals the physiological relevance of an m6A reader protein by generating YTHDF2 deficient animals.

Guitart, A. V., Panagopoulou, T. I., Villacreces, A., Vukovic, M., Sepulveda, C., Allen, L., … Kranc, K. R. (2017). Fumarate hydratase is a critical metabolic regulator of hematopoietic stem cell functions. The Journal of Experimental Medicine, 214(3), jem.20161087.
https://doi.org/10.1084/jem.20161087

Kozlowski, E., Wasserman, G. A., **Morgan, M.**, O'Carroll, D., Ramirez, N. G. P., Gummuluru, S., … Jones, M. R. (2017). The RNA uridyltransferaseZcchc6 is expressed in macrophages and impacts innate immune responses. PLoS ONE, 12(6), 1–16.
https://doi.org/10.1371/journal.pone.0179797

In this paper, I generated the first animal model for the uridyltransferaseZcchc6 (TUT7). This is the first study to show the physiological relevance of TUT7-mediated uridylation.

Comazzetto, S., Di Giacomo, M., Rasmussen, K. D., Much, C., Azzi, C., **Morgan, M.**, & O'Carroll, D. (2014). Oligoasthenoteratozoospermia and Infertility in Mice Deficient for miR-34b/c and miR-449 Loci. PLoS Genetics, 10(10), e1004597.
https://doi.org/10.1371/journal.pgen.1004597

In this paper, I contributed to the analysis of the molecular signature generated by removing a miRNA gene family in the mouse germline. By isolating purified populations of germ cells, we demonstrated that the dysregulated transcripts in the miRNA depleted germline were direct targets of the miRNA.

DiGiacomo, M., Comazzetto, S., Saini, H., DeFazio, S., Carrieri, C., **Morgan, M.**, … O'Carroll, D. (2013). Multiple Epigenetic Mechanisms and the piRNA Pathway Enforce LINE1 Silencing during Adult Spermatogenesis. Molecular Cell, 50(4).
https://doi.org/10.1016/j.molcel.2013.04.026

In this paper, I contributed to the dissection of the different transcriptional and posttranscriptional pathways regulating transposon silencing in adult spermatogenesis. I showed that the regulation of LINE1 transposons was not mediated by changes in the methylation status of their promoter sequence.

Morgan, M., Iaconcig, A., & Muro, A. F. (2012). Identification of 3' gene ends using transcriptional and genomic conservation across vertebrates. BMC Genomics, 13(1), 708.
https://doi.org/10.1186/1471-2164-13-708

In this work, we developed methods to annotate evolutionarily conserved 3'UTRs. I found a few hundred highly conserved mis-annotated 3'UTRs in mice and humans and several thousand in other vertebrates. We also found that many annotated, highly conserved non-coding RNAs were actually mis-annotated long 3'UTR extensions.

Morgan, M., Iaconcig, A., & Muro, A. F. (2010). CPEB2, CPEB3 and CPEB4 are coordinately regulated by miRNAs recognizing conserved binding sites in paralog positions of their 3'-UTRs. Nucleic Acids Research, 38(21), 7698–7710. https://doi.org/https://doi.org/10.1093/nar/gkq635

In this paper, We showed that the CPEB family of transcripts share a conserved miRNA regulatory signature in their 3'UTRs. We also showed that the microRNA signature preceded the formation of highly conserved elements in these 3'UTRs.

Roberti, M. J., **Morgan, M.**, Menéndez, G., Pietrasanta, L. I., Jovin, T. M., & Jares-Erijman, E. A. (2009). Quantum dots as ultrasensitive nanoactuators and sensors of amyloid aggregation in live cells. Journal of the American Chemical Society, 131(23), 8102–8107. https://doi.org/10.1021/ja900225w

Morgan, M. (2008). Models for the recent evolution of protocadherin gene clusters. Biocell, 32(1), 9–26.

The protocadherin gene clusters are of great interest because they provide an identity to neurons. In this paper, I show the mechanism by which these clusters evolve in mice and humans.