BIOGRAPHICAL SKETCH

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NAME: Quintana, Anita

eRA COMMONS USER NAME (agency login): amquintana

POSITION TITLE: Assistant Professor

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

INSTITUTION AND LOCATION	DEGREE (if applicable)	Completion Date MM/YYYY	FIELD OF STUDY
New Mexico State University, Las Cruces, New Mexico	BS	05/2005	Microbiology
University of New Mexico, Albuquerque, New Mexico	PHD	07/2010	Biomedical Sciences
St. Jude Children's Research Hospital, Memphis, Tennessee	Postdoctoral Fellow	07/2012	Functional Genetics, Oncogenes, Leukemia
University of Colorado School of Medicine, Aurora, Colorado	NIH training grant	07/2015	Functional Genetics associated with Multiple Congenital Anomalies

A. Personal Statement

A fundamental problem facing human medical genetics is the lack of functional evidence linking gene function to specific disease phenotypes. My research closes this gap by utilizing a multidisciplinary approach to understand the molecular and cellular mechanisms associated with disease. Over the last 10 years I have developed a highly translational research program aimed to understand the mechanisms associated with developmental disorders, particularly those affecting the developing brain. Early in my career, I received expert training in the field of cancer genetics at both the University of New Mexico and St. Jude Children's Research Hospital. More recently, I have focused on identifying novel genes associated with developmental abnormalities. In the last two decades, the cost of high throughput genetic sequencing has dropped, enabling geneticist to uncover over 200 single gene defects associated with developmental disease. However, translation of these findings into better treatment options has been difficult, primarily due to the lack of a cost-effective preclinical animal model. Thus, I developed a highly effective interdisciplinary approach, which is rooted in human medical genetics, but uses animal model genetics to identify the molecular mechanisms associated with disease. My work has the possibility to revolutionize how we view translational research and offers the potential to discover potential therapies for both rare and common genetic disorders.

1. Yu HC, Sloan JL, Scharer G, Brebner A, Quintana AM, Achilly NP, Manoli I, Coughlin CR 2nd, Geiger EA, Schneck U, Watkins D, Suormala T, Van Hove JL, Fowler B, Baumgartner MR, Rosenblatt DS, Venditti CP, Shaikh TH. An X-linked cobalamin disorder caused by mutations in transcriptional coregulator HCFC1. Am J Hum Genet. 2013 Sep 5;93(3):506-14. PubMed PMID: 24011988; PubMed Central PMCID: PMC3769968.
2. Quintana AM, Picchione F, Klein Geltink RI, Taylor MR, Grosveld GC. Zebrafish ETV7 regulates red blood cell development through the cholesterol synthesis pathway. Dis Model Mech. 2014 Feb;7(2):265-70. PubMed PMID: 24357328; PubMed Central PMCID: PMC3917247.
3. Quintana AM, Geiger EA, Achilly N, Rosenblatt DS, Maclean KN, Stabler SP, Artinger KB, Appel B, Shaikh TH. Hcfc1b, a zebrafish ortholog of HCFC1, regulates craniofacial development by modulating mmachc expression. Dev Biol. 2014 Dec 1;396(1):94-106. PubMed PMID: 25281006; PubMed Central PMCID: PMC4391465.
4. Van Laarhoven PM, Neitzel LR, Quintana AM, Geiger EA, Zackai EH, Clouthier DE, Artinger KB, Ming JE, Shaikh TH. Kabuki syndrome genes KMT2D and KDM6A: functional analyses demonstrate critical

roles in craniofacial, heart and brain development. Hum Mol Genet. 2015 Aug 1;24(15):4443-53. PubMed PMID: 25972376; PubMed Central PMCID: PMC4492403.

B. Positions and Honors

Positions and Employment

2010 - 2012	Post- Doctoral Fellow, St. Jude Children's Hospital, Memphis, TN
2012 - 2015	Post-Doctoral Fellow, University of Colorado School of Medicine, Aurora, CO
2015 -	Assistant Professor, University of Texas at El Paso, El Paso, TX

Other Experience and Professional Memberships

2007 - 2008	Member, Science Advisory Board
2007 - 2008	Member, American Society for Cancer Research
2007 - 2008	Member, Society for the Advancement of Chicanos and Native Americans in Science (SACNAS)
2010 - 2012	Member, AAAS
2012 - 2015	Member, Colorado Clinical and Translational Sciences Institute

Honors

2004	Minority Access to Research Careers Fellow, New Mexico State University
2007	Ruth kirschstein Pre-doctoral Fellowship, National Institutes of Health
2007	Initiative to Maximize Student Development Fellow, University of New Mexico
2011	Faculty of 1000 Peer Review, Faculty of 1000
2011	Highly Rated Poster, American Association of Cancer Research
2012	Developmental Psychobiology Research Group Fellow, University of Colorado

C. Contribution to Science

1. In my professional career, I have performed cutting edge research in two primary areas of interest; genetics and developmental biology. I was originally trained in the genetics of leukemia, where I studied the role of oncogenic transcription factors in the formation and progression of both T-cell and myeloid cell leukemia. I focused primarily on understanding the biochemical mechanisms that modulate transcription factor binding to DNA and how these factors are modulated during different phases of the cell cycle. I was the first to demonstrate the genome-wide downstream targets of the c-Myb transcription factor (Quintana et. al 2011 PMCID PMC3038977) by coupling chromatin immunoprecipitation with genome wide microarray analysis. My manuscript significantly contributed to the field of oncogene biology and was noted as "Highly Assessed" with over 2000 views/downloads in as little as 6 months. Concurrently, I determined that the c-Myb oncoprotein repositioned itself onto unique promoters in a cell cycle dependent manner. As part of my work, I developed a novel "fix and sort procedure" to study transcription factor binding in a cell cycle dependent manner. My novel "fix and sort" procedure was cited by the prestigious Faculty of 1000 publication, demonstrating the impact of discovery (Quintana et. al. 2011 PMCID:PMC3043100).

   As a post-doctoral fellow at St. Jude Children's Research Hospital, I continued my work studying the effects of somatic mutations on the function of oncogenic transcription factors. However, my hypotheses evolved suggesting that developmental pathways became "reactivated" in cancer cells promoting migration and proliferation. Given my new interest in developmental pathways, I developed a project aimed at understanding the function of oncogenes during normal development. To accomplish my goals, I initiated an interdisciplinary training team that offered not only genetics training, but also training in the utility of zebrafish as a cancer model. I used transient loss/gain of function analysis to connect the ETV7 transcription factor to the cholesterol synthesis pathway. I was the first to show that ETV7 regulates red blood cell development by modulating the downstream expression of *LSS*, a gene that is essential for cholesterol production and has been implicated in the self-renewal of progenitor cell populations. My work in the developing zebrafish demonstrated a putative mechanism whereby, somatic alteration of ETV7 affects the self- renewal of blood cells, and potentially contributes to cancer progression.

My work demonstrating the parallels between human cancer and development, prompted me to transition my career to the University of Colorado, where I combined human medical genetics and *in vivo* functional analyses to understand gene function. To do so, I enlisted the expertise of an interdisciplinary team consisting of an expert geneticist, an expert neurobiologist, and an expert in craniofacial development. With their guidance, I developed a unique and insightful project aimed at understanding how the HCFC1 transcription factor causes multiple congenital anomalies. My project was rooted in medical genetics because I was part of an international effort that identified novel mutations in the HCFC1 transcription factor as the cause of *cblX* disorder, a multiple congenital anomaly syndrome. As a major contributor of the project, I provided key functional analysis demonstrating that mutations in HCFC1 resulted in disease via modulation of *MMACHC* expression (Yu et. al. 2013). Together with my colleagues, we demonstrated a novel mechanism associated with inborn errors of metabolism and our work has now initiated genetic studies world-wide that have uncovered additional mutations in *HCFC1* gene. After our initial discovery of *HCFC1*, I developed an independent project analyzing the role of HCFC1 in craniofacial development. I discovered that loss of this gene caused craniofacial defects and was the first to demonstrate that the facial abnormalities in *cblX* patients were the result of aberrant *MMACHC* expression. Thus, I was able to link two independent phenotypes of *cblX* to one common molecular mechanism (Quintana et. al. 2014). These data were recently published in Developmental Biology and are a testament to my expertise in both human genetics and developmental biology.

I am currently a new assistant professor at the University of Texas El Paso (UTEP). As a new faculty, I am continuing my human genetic research through collaboration with the University of Colorado. Together, my team will continue to use high throughput exome sequencing to identify novel mutations associated with disease. However, in addition, I have developed a functional genetics work-flow for my new laboratory, where we use animal model genetics to understand the molecular underpinnings associated with disease. Currently, my research focuses on understanding the molecular and cellular mechanisms associated with the neurological phenotypes present in *cblX* disorder. I have gained expertise in endogenous genome editing, animal model genetics, and live imaging techniques, which will help to unravel the molecular basis of disease. However, my work will be heavily based in neuroscience, therefore, I have enlisted the mentorship of a team of faculty at UTEP, led by Dr. Michael Kenney, an expert neurobiologist, to effectively accomplish my future research goals.

Complete List of Published Work in My Bibliography:
http://www.ncbi.nlm.nih.gov/myncbi/anita.quintana.1/bibliography/48643387/public/?sort=date&direction=ascending

D. Research Support

Ongoing Research Support

T32 MH015442-36
ROSS, Randal G (PI)
07/01/78-06/30/16
Developmental Psychopathology, Psychobiology & Behavior
Role: TA

Completed Research Support

M-14-166, Colorado Clinical and Translational Sciences Institute Mentored Award
Quintana, Anita (PI)
01/01/15-07/31/15
Hcfc1 regulates neural precursor specification, differentiation, and proliferation by modulating the expression of Phactr4.
Determine if loss of hcfc1 in zebrafish affects the number and function of neural precursors and whether the cellular phenotypes associated with loss of hcfc1 are modulated by the expression of phactr4.
Role: PI

20279, Developmental Psychobiology Endowment Fund
Anita Quintana (PI)
03/01/12-02/28/13
Characterization of the cellular and molecular mechanisms associated with mutation of HCFC1.
Develop loss of function assays and analyses to study the role of HCFC1 in the developing neural crest.
Role: PI

F31 HL090024-04
Quintana, Anita M (PI)
08/06/07-07/31/11
Post-translational modifications affect c-Myb specificity.
Role: PI