CHARACTERIZATION OF THE MDM2 BINDING REGIONS OF RIBOSOMAL PROTEIN L5

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Submitted to the faculty of the University Graduate School in partial fulfillment of the requirements for the degree Master of Science in the Department of Biochemistry & Molecular Biology, Indiana University

May 2010

Accepted by the Faculty of Indiana University, in partial fulfillment of the requirements for the degree of Master of Science.

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Dedication

This dissertation is dedicated to Ashlynne Nicole. You will always remain in my thoughts and within my heart.

Acknowledgments

To begin, I want to express by sincerest thanks and love to my wife, Angela, for her loving care and support not only during the drafting of this dissertation, but throughout our time together. She has always been a source of inspiration to me when I needed her. I can only say how grateful I am that she chose me as not only her husband, but also her best friend.

I would also like to express my sincerest thanks and deepest appreciation to my mentor, Dr. Hua Lu, for believing in me and giving me the opportunity to learn under his guidance. He has always made himself available not only to me, but to the rest of the laboratory and his knowledge and wisdom in this area of research has been an invaluable resource for me. I have gained the utmost respect for him over the last two years as a person to whom I could turn for sound advice regarding my research and the writing of this dissertation. Very seldom have I found someone possessing the unique ability to teach, write, and listen with such understanding as to know how to motivate me to seek out and find more from myself than I thought possible.

I would like to give my sincerest thanks to the members of my Thesis Advisory Committee, Dr. Thomas Hurley and Dr. Mark Goebl, for generously sharing their time, ideas, knowledge, and experience throughout my research project and the writing of this dissertation. In addition, a special thanks goes to Dr. Goebl for providing his advise on classes to take to cover the requirements for the MS degree.

Dr. Shelya Zeng deserves my deepest thanks for providing me with assistance in troubleshooting my experiments. I would like her to know that the time and knowledge she shared with me was greatly appreciated and was vital in the completion of my project.

A heart-felt thanks goes out to Dr. Millie Georgiadis, without whose support and recommendation I would not have had the opportunity to return to my passion in life. Also, for allowing me the privilege of performing my first rotation in her laboratory and in doing so providing me the occasion of entering a research lab for the first time in over a decade. Her patience and

understanding were extremely important for me during those first few months of learning to walk again.

I feel Dr. Ron Wek deserves my special thanks for mentoring me throughout my second rotation. Ron's door was always open and he was always available to everyone seeking his assistance, as I did quite often. I would also like to thank Dr. Skalnik and Dr. Bosron for their letters of support and time spent with me both inside and outside of the classroom.

This section would not even be close to complete without thanking all the graduate students, postdoctoral fellows, research associates, and professors that have so generously given their time and expertise, without which I would not have reached this point. Although to name all of them would be to numerous to mention here, there are a few I feel obliged to name specifically including:

Mushui Dai, Yetao Jin, Lawrence Quilliam, Qi Zhang, Yan Xiong, Yu Zhang, Adrianna Henson, Debra Barker, Kristie Goodwin, Junho Lee, Neilia Gracias, Lindsey Mayo, Simon Rhodes, Guifen He, Jun-Ming Liao, Arif Khan, Dorothy Lo, Anna DePaoli-Roach, Peter Roach, Hoa Nguyen, Justin Babcock, Sergio Chai, Souvik Dey, Jenna Jewell, Lakshmi Reddy Palam, Bill Ranahan, Sowmya Jairam, Sandra McLain, Sheila Reynolds, Monica Henry, Amber Pratcher, and Jack W. Arthur Jr.

Abstract

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The MDM2-p53 feedback loop is a well-characterized pathway. p53 is a transcription factor and regulates the transcriptional expression of genes that encode proteins responsible for cellular senescence, cell cycle arrest, apoptosis, and DNA repair. Various cellular stresses can result in p53 activation, including hypoxia, DNA damage by agents such as UV or IR, oncogenic signaling, nucleotide depletion and nucleolar stress from perturbation of ribosomal biogenesis. Under normal conditions, MDM2's role in the pathway is to inhibit p53 function by directly binding to this protein and facilitating its ubiquitylation and 26S proteasome-mediated degradation. Under stressful cellular conditions, certain proteins interact with and rescue MDM2's inhibition of p53. For example, upon exposure to small amounts of Actinomycin D, rRNA transcript synthesis is stalled resulting in the release of various ribosomal proteins including RPL5, RPL11 and RPL23; each of which has been shown to bind MDM2 within its central acidic domain and inhibit its ability to destabilize p53. Although the RPL5 binding region of MDM2 have been mapped in prior investigations, the MDM2-binding region(s) of RPL5 have yet to be characterized.

By employing RPL5 deletion mutagenesis and *in vitro* GST-fusion protein-protein association assays with purified proteins, this dissertation attempts to elucidate those regions of RPL5 that may interact with MDM2. Normalizing RPL5-WT to 1.00, our study reveals that the basic N and C-terminals of RPL5 appear to bind with MDM2 while RPL5's central region displays negligible binding to the central acidic domain of MDM2. Also, the possible meanings of these RPL5 MDM2 binding domains are discussed along with their utilization in potential future applications.

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