

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: Zuberi, Aamir R.

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

POSITION TITLE: Technology & Resource Development Scientist

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 London, UK	B.Sc (hons.)	05/1982	Biochemistry & Microbiology
University of Sheffield, UK	Ph.D.	10/1985	Molecular Microbial Genetics
University of California, Davis	Postdoctoral	03/1988	Bacterial differentiation
University of Illinois, Champaign-Urbana	Postdoctoral	03/1991	Bacterial Chemotaxis
The Jackson Laboratory, ME	Postdoctoral	04/1994	Murine Molecular Immunology

A. Personal Statement

I have the expertise, leadership skills and training to carry out the proposed research project. My broad interest has always been in the genetic mechanisms that control differentiation, adaptation to environmental changes and how genetic disorders are expressed within complex mammalian systems. I have a broad background in bacterial and murine molecular biology, genetics and genomics with research expertise in bacterial differentiation, transcriptional and physiologic regulation of adaptation, and in murine immunology, metabolism and in the development and early stage characterization of mouse models of rare and orphan diseases. As a PI at the Pennington Biomedical Research Center, Louisiana State University, I was the recipient of two NIH grants; one as PI investigating the role of murine natural genetic variation in dietary induced Obesity, and as co-PI investigating the role of a natural human adenovirus on murine insulin resistance on normal and high fat diets. I also served as Core Director on a NIH funded program project managing a murine research team investigating the molecular and physiologic effects of botanical dietary supplements on mice fed a high fat diet. I administered projects (managing staffing, promotions, budget, training and publications), collaborated with other researchers and coordinated activities with other Program projects funded investigators leading to several peer-reviewed publications. In 2015, I accepted a position at the Jackson Laboratory, where I developed a new precision genetic modification platform for internal and external clients. Specifically, I established and manage a diverse multidisciplinary team focused on developing new mouse models as surrogates for clinical rare and orphan diseases using CRISPR/Cas9, transgenesis and conventional ES cell approaches. My team has developed over 200 new models with a diverse portfolio of academic, pharmaceutical, and foundations as clients. During this work, I established and support a separate Research team to genetically and biochemically validate these new models and to develop additional research tools (e.g antibodies, qRT-PCR and high throughput genotyping) as needed to complete these studies. This work requires me to develop and maintain multiple business relationships with different Core groups throughout the Jackson Laboratory.

B. Positions and Honors

Positions and Employment

1994 - 1998	Postdoctoral Associate, Molecular Immunogenetics, The Jackson Laboratory, Bar Harbor, ME
1999 - 2010	Assistant Professor, Functional Genomics Laboratory, Pennington Biomedical Research Center, Louisiana State University, Baton Rouge, LA
2005 - 2010	Animal Research Core Leader, Botanical Research Center, Pennington Biomedical Research Center, Baton Rouge, LA
2006 - 2010	Adjunct Assistant Professor, Department of Nutrition, Louisiana State University, Baton Rouge, LA.
2006 - 2010	Associate member, Louisiana State University Graduate College Faculty
2010 - 2015	Molecular Genetics and Genomics Research Consultant
2013 - 2015	Customer Service and Account Manager, Home Depot and Bank of America
2015 - 2017	Process Improvement Program Manager, Rare and Orphan Disease Program, The Jackson Laboratory, Bar Harbor, ME
2017 - current	Technology and Resource Development Scientist, Rare and Orphan Disease Program, The Jackson Laboratory, Bar Harbor, ME

Other Experience and Professional Memberships

1991 - 2010	International Mammalian Genome Society
1999 - 2010	American Diabetes Association
1991 - 2010	American Association for the Advancement of Science
1999 - 2010	The Obesity Society
1999 - 2010	Ad hoc Reviewer; American Journal of Physiology, Mammalian Genome, Genomics, Physiological Genomics, Biotechniques
2005 - 2020	Ad hoc reviewer; Obesity Research

Honors/Committee Memberships

1991 - 1994	NIH Postdoctoral Training Grant Recipient, The Jackson Laboratory, Bar Harbor, ME
1997 - 2001	Member, International Mammalian Genome Society Mouse Chromosome 2 Committee
1999 - 2001	Chair, International Mammalian Genome Society Mouse Chromosome 2 Committee
2002 - 2009	Member, International Mammalian Genome Society Nomenclature Committee
2005 - 2010	Member, Botanical Research Center Executive Steering Committee, PBRC, LA
2005 - 2008	Member, Institutional Animal Care and Use Committee, PBRC, LA
2010	Session Reviewer, American Diabetes Association, Annual Meeting, Orlando, FL
2010	Session Chair, American Diabetes Association Annual Meeting, Orlando, FL

C. Contribution to Science

1. In 1982, almost nothing was known about the molecular basis of how dormant bacterial spores responded to chemical triggers in the environment to initiate germination leading to a viable bacterium. Recent bioterrorism threats and incidents using bacterial sporeformers such as anthrax make this a very relevant area of study today because bacterial spores are resistant to bactericides whereas germinated bacteria are susceptible. Using *Bacillus subtilis* as a model system, I was part of a team that characterized a set of genes that were specifically needed for the ability of bacterial spores to germinate in response to L-alanine. I defined the relative location of the three genes in the *gerA* operon and specifically sequenced one of these using Sanger sequencing (at the time a novel approach for bench top research). Using transcriptional *lacZ* fusions, I simultaneously generated new bacterial mutants and determined the expression profile of the operon during sporulation.
 - a. Zuberi, A.R., Feavers, I.M., and Moir, A. Identification of three complementation groups in the *gerA* spore germination locus of *Bacillus subtilis*. *J. Bacteriol* 162:756-762, 1985.
 - b. Zuberi, A.R., Moir, A., and Feavers, I.M. The nucleotide sequence and gene organization of the *gerA* spore germination operon of *Bacillus subtilis*. *Gene* 51:1-11, 1987.

- c. Moir, A., Feavers, I.M., and Zuberi, A.R. A spore germination operon in *Bacillus subtilis* 168. In: *Bacillus Molecular Genetics and Biotechnology Applications*, Ganesan A.T., Hoch J.A. (eds), Academic Press, pp. 183-94, 1985.
 - d. Moir, A., Feavers, I.M., Zuberi, A.R., Sammons, R.L., Roberts, R.S., Yon, J.R., Wolff, E.A., and Smith, D.A. 1985. Progress in the molecular genetics of spore germination in *Bacillus subtilis* 168. In: *The Molecular Biology of Microbial Differentiation*, Setlow P., Hoch J.A. (eds), Proceedings of the IX Spores Conference, The American Society of Microbiology, pp. 35-46, 1985.
2. Bacterial sporulation is an energy intensive process with an uncertain outcome with respect to the timeline to bioavailability of new nutrients. Hence, *Bacillus subtilis* initiates new flagellar and motor biosynthesis to promote directed bacterial movement to seek out fresh nutrient as an alternative to sporulation initiation. Working as a senior postdoctoral researcher in a laboratory that contained no established molecular expertise, I, working with the PI of the laboratory, directed the work of a team of graduate students, one tech and another postdoctoral scientist to coordinate the complete sequencing and functional characterization of a larger Chemotaxis operon.
 - a. Zuberi, A.R., Ying, C.Y., Parker, H.M., and Ordal, G.W. Transposon Tn917lacZ mutagenesis of *Bacillus subtilis*: identification of two new loci required for motility and chemotaxis. *J. Bacteriol.* 172:6841-6848, 1990.
 - b. Zuberi, A.R., Ying, C.Y., Weinreich, M., and Ordal, G.W. Transcriptional organization of a cloned chemotaxis locus of *Bacillus subtilis*. *J. Bacteriol.* 172:1870-1876, 1990.
 - c. Zuberi, A.R., Ying, C.Y., Bischoff, D.S., and Ordal, G.W. Gene-protein relationships in the flagellar basal body of *Bacillus subtilis*: sequences of *flgB*, *flgC*, *fliE* and *fliF* genes. *Gene* 101:23-31, 1991.
 - d. Kirsch, M.L., Zuberi, A.R., Henner, D., Peters, P.D., Yazdi, M., and Ordal, G.W. Chemotactic methyltransferase promotes adaptation of repellents in *Bacillus subtilis*. *J Biol Chem* 268:25350-25356, 1993.
 3. High resolution genetic mapping and positional cloning of a murine minor histocompatibility antigen gene. Although it was well established that specific regions of the mouse genome were sufficient in promoting transplantation rejection between otherwise genetically identical congenic strains of mice, the molecular nature of the genes responsible for this effects were unknown. Using an array of cellular immunological and molecular genetic studies including high resolution genetic mapping, I developed a new molecular biology laboratory and determine the genetic location of two genes within the historically relevant H3a locus of the mouse. One of these genes was positionally cloned using YACs, BACs and P1's leading to the discovery of a novel 9.5kb transcript gene that contained a polymorphism between mouse strains and that this polymorphism was contained with a region that was expressed on H2-D^b class I MHC molecules.
 - a. Zuberi, A.R., Nguyen, H.Q., Auman, H.J., Taylor, B.A., and Roopenian, D.C. A genetic linkage map of mouse Chromosome 2 extending from thrombospondin to paired box gene 1, including the H3 minor histocompatibility complex. *Genomics* 33:75-84, 1996.
 - b. Zuberi, A.R., Christianson, G.J., Dave, S., Bradley, J.A., and Roopenian, D.C. Expression screening of a yeast artificial chromosome contig refines the location of the mouse H3a minor histocompatibility antigen gene. *J Immunol* 161:821-828, 1998.
 - c. Zuberi, A.R., Christianson, G.J., Mendoza, L., Shastri, N., and Roopenian, D.C. Positional cloning and molecular characterization of an immunodominant cytotoxic determinant of the mouse H3 minor histocompatibility complex. *Immunity* 9: 687-698, 1998.
 4. As an NIH funded Assistant Professor of Functional Genomics and Director of the Preclinical research Core of the Botanical Research Center at Pennington Biomedical Research Center, LSU, LA, I operated two parallel laboratories using tactical, strategic and operational objectives to achieve multiple overlapping time and mission-sensitive project goals. As a key member of the Botanical Research Center cross-functional team, I significantly contributed to the project proposal, successful funding and operational management of the 1st National Institutes of Health Center Grant awarded to the Pennington Biomedical Research Center (\$5.8 million in total direct costs). My group discovered novel anthocyanin-diet and Russian tarragon-genotype interactions in the regulation of obesity and insulin

sensitivity, respectively. My team also identified several novel obesity and diabetes genes and developed unique gene expression profiling tools to monitor all alternatively spliced variants. Verified candidacy of obesity genes by stable and transient transfection into cell lines to determine effect on differentiation and expression of adipogenic and myogenic biomarkers. In collaboration with clinical researchers at the Center, I also co-authored the human Obesity Gene map to specifically include a more detailed review of murine obesity and diabetes mutants.

- a. Wang ZQ, Zuberi AR, Zhang XH, Macgowan J, Qin J, Ye X, Son L, Wu Q, Lian K, Cefalu WT. Effect of dietary fibers on weight gain, carbohydrate metabolism, and gastric ghrelin gene expression in mice fed a high fat diet. *Metabolism* 56:1635-1642, 2007.
 - b. Cefalu, W.T., Ye, J., Zuberi, A., Ribnicky, D., Raskin, I., Liu, Z., Wang, Z.Q., Brantley, P., Howard, L. and Lefevre, M. Botanicals and the metabolic syndrome. *Am. J. of Clin. Nutr.* 87: 481S-487S, 2008.
 - c. Zuberi, A.R. Strategies for assessment of Botanical action on Metabolic Syndrome in the mouse and evidence for a Genotype-specific effect of Russian Tarragon in the regulation of insulin sensitivity. *Metabolism* 57:10-15, 2008.
 - d. Wang ZQ, Ribnicky D, Zhang XH, Zuberi A, Raskin I, Yu Y, Cefalu WT. An extract of *Artemisia dracuncululus* L. enhances insulin receptor signaling and modulates gene expression in skeletal muscle in KK-A^y mice. *J. Nutr. Biochem.* 22:71-78, 2011.
5. I have developed and maintain the operational continuity of a platform for using CRISPR/Cas9 generate mouse mutants carrying specific clinical KI mutations associated with Rare and Orphan Diseases. I also manage the development of more classically generated mouse mutants including cDNA BAC and cDNA transgenic lines, conditional KO mouse mutants and ES cell generated mouse mutants. A workflow spans several independent Jackson Laboratory Core services groups. My team currently develops more than 60 mouse mutants per year and supports the work of multiple foundations and research laboratories. Novel mouse mutants are distributed directly to collaborators or directly deposited into the Jackson Laboratory Repository of Mutants Mouse Strains or the Mouse Mutant Resource Repository Center (MMRRC) for public distribution.
- a. Zuberi, A., and Lutz, C. Mouse models for drug discovery. Can new tools and technology improve translational power. *ILAR J.* 57:178-185, 2016.
 - b. Burstein, S.R., Valsecchi, F., Kawamata, H., Bourens, M., Zeng, R., Zuberi, A., Milner T.A., Cloonan, S.M., Lutz, C., Barrientos, A., and Manfredi, G. In vitro and in vivo studies of the ALS-FTLD protein CHCHD10 reveal novel mitochondrial topology and protein interactions. *Hum. Mol. Genet.* 1:160-177, 2018.
 - c. Anderson, C.J., Bredvik, K., Burstein, S.R., Davis, C., Meadows, S.M., Dash, J., Case, L., Milner, T.A., Kawamata, H., Zuberi, A., Piersigilli, A., Lutz, C., and Manfredi, G. ALS/FTD mutant CHCHD10 mutant mice reveal a toxic gain of function and mitochondrial stress response. *Acta Neuropathol.* 138:103-121, 2019.

Complete List of Published Work in My Bibliography:

<https://www.ncbi.nlm.nih.gov/sites/myncbi/1LY1aoH20dTAK/bibliography/47694886/public/?sort=date&direction=ascending>

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

Ongoing Research Support

None within the last three years