BIOGRAPHICAL SKETCH

Provide the following information for the Senior/key personnel and other significant contributors in the order listed on Form Page 2.
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NAME	POSITION TITLE
Mandal, Diptasri, M.	Professor
eRA COMMONS USER NAME (credential, e.g., agency login) dmanda	

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)*	MM/YY	FIELD OF STUDY
Calcutta University, Calcutta, India.	B.Sc.(Hons.)	1984	Zoology
Burdwan University, Burdwan, India.	M.Sc.(Hons.)	1986	Zoology with Entomology
Northeast Louisiana University, Monroe, LA	M.S.	1991	Biology
Louisiana State University Medical Center, New Orleans, LA	Ph.D.	1996	Human Genetics

Please refer to the application instructions in order to complete sections A, B, C, and D of the Biographical Sketch.

A. Positions and Honors

Positions and Employment

1990-1991	Instructor, Department of Biology, University of Louisiana at Monroe
1997	Visiting Instructor, Department of Biometry and Genetics, LSU Health Sciences Center, New Orleans
1997-2000	Instructor, Department of Medicine, Section of Genetics and Geriatrics, LSU Health Sciences Center, New Orleans
2000-2001	Instructor, Department of Genetics, LSU Health Sciences Center, New Orleans
2001-2008	Assistant Professor, Department of Genetics, LSU Health Sciences Center, New Orleans
2008-2015	Associate Professor, Department of Genetics, LSU Health Sciences Center
2015-present	Professor, Department of Genetics, LSU Health Sciences Center

Memberships in Professional Organizations

1995-present	The American Society of Human Genetics
1995-present	The International Genetic Epidemiology Society
2014	American Association for the Advancement of Science

Awards and Honors

1998-	Member, GELCC - Genetic Epidemiology of Lung Cancer Consortium
2001	Research Enhancement Funds from LSUHSC-NO
2002-	Ad hoc member NIH/NIGMS Study Section
2003-	International Genetic Epidemiology Society, ELSI Task Force
2006	Travel Grant for attendance at AACR annual meeting from AACR
2006	Chair, Scientific Session, International Genetic Epidemiology Society Meeting, Tampa Bay, FL
2007-	Ad hoc member NCI Small Grants Program Study Section
2009	NCI ARRA Study Section
2010	NCI SPORE Study Section
2011	Reviewer: Italian Ministry of Health General Directorate for Health and Technologies Research
2011	Ad hoc member NCI-G Study Section
2011-	Member, ICPCG – International Consortium of Prostate Cancer Genetics

2011-	Associate, Johns Hopkins Bloomberg School of Public Health
2012	Reviewer: Medical Research Council, United Kingdom
2012	Ad hoc member NIH/EPIC Study Section

B. Peer-reviewed Publications (in chronological order)

1. E. W. Pugh, **D. M. Mandal** and A. F. Wilson. A graphical approach for presenting linkage results from a genomic screen. *Genetic Epidemiology.* 1995. 12:807-812.
2. **D. M. Mandal,** A. J. M. Sorant, E W. Pugh, S. E. Marcus, A. P. Klein, R. A. Mathias, J. O'Neill, L. F. Temiyakarn, A. F. Wilson, J.E. Bailey-Wilson. Environmental covariates: effects on the power of sib-pair linkage methods. *Genetic Epidemiology.* 1999. 17:S643-S648.
3. **D.M. Mandal,** A.F.Wilson, R.C. Elston, K. Weissbecker, B. J. Keats, J. E. Bailey-Wilson. Effect of misspecification of allele frequencies on the Type I error of model-free linkage analysis. *Human Heredity.* 2000. 50:126-132.
4. J. E. Bailey-Wilson, A. J. M. Sorant, J. D. Malley, S. Presciuttini, R. A. Redner, T. A. Severini, J. A. Badner, S. Pajevic , R. Jufer, A. Baffoe-Bonnie, L. Kao, B.Q. Doan, J.L. Goldstein, T. N. Holmes, D. Behnemann, **D. M. Mandal,** T. N. Turley, K. A. Weissbecker, J. O'Neil and E. W. Pugh. Comparison of novel and existing methods for detection of linkage disequilibrium using parent-child trios in the GAW12 genetic isolate simulated data. *Genetic Epidemiology.* 2001. 21(1):S378-S383.
5. **D. M. Mandal,** A. F. Wilson and J. E. Bailey-Wilson. Effects of Misspecification of Allele Frequencies on the Power of Haseman-Elston Sib-pair Linkage Method for Quantitative Traits. *American Journal of Medical Genetics.* 2001.103:308-313.
6. A. P. Klein, I. Kovac, A. J. M. Sorant, A. Baffoe-Bonnie, B. Q. Doan, G. Ibay, E. Lockwood, **D. M. Mandal,** L. Santhosh, K. Weissbecker, J. Woo, A. Zambelli-Weiner, J. Zhang, D. Q. Naiman, J. Malley, J. E. Bailey-Wilson. Importance Sampling Method of Correction for Multiple Testing in Affected Sib-pair Linkage Analysis. *BMC Genet (Suppl)* 2003; 4:73.
7. J. E. Bailey-Wilson, C. I. Amos, S. Pinney, G. M. Petersen, M. de Andrade, J. S. Wiest, P. Fain, A. G. Schwartz, M. You, W. Franklin, C. Klein, A. Gazdar, H. Rothschild, **D. M. Mandal,** T. Coons, J. Slusser, J. Lee, C. Gaba, E. Kupert, A. Perez, X. Zhou, D. Zeng, Q. Liu, D. Seminara, J. Minna, M. Anderson. A major lung cancer susceptibility locus maps to chromosome 6q23-25. *American Journal of Human Genetics.* 2004. 75:460-484.
8. A. Y. Kinney, L. Bloor, **D. M. Mandal,** S. E. Simonsen, B. J. Baty, R. Holubkov, K. Seggar, S. Neuhausen, and K. Smith. Impact of Receiving Genetic Test Results on General and Cancer-Specific Psychological Distress Among Members of an African-American Kindred with a BRCA1 Mutation. *Cancer.* 2005. 104:2508-2516.
9. A. Y. Kinney, S. E. Simonsen, B. J. Baty, **D. M. Mandal,** S. Neuhausen, K. Seggar, R. Holubkov, and K. Smith. Acceptance of Genetic Testing for Hereditary Breast Ovarian Cancer among Study Enrollees from an African American Kindred. *American Journal of Medical Genetics.* 2006. 140:813-826.
10. A. Y. Kinney, S. E. Simonsen, B. J. Baty, **D. M. Mandal,** S. E. Neuhausen, K. Seggar, R. Holubkov, L. Bloor, K. Smith. Risk reduction behaviors and provider communication following genetic counseling and *BRCA1* mutation testing in an African-American kindred. *Journal of Genetic Counseling.* 2006. 15:293-305.
11. **D. M. Mandal,** A.J.M. Sorant, L.D. Atwood, A.F. Wilson, J.E. Bailey-Wilson. Allele Frequency Misspecification: Effect on Power and Type I Error of Model-dependent Linkage Analysis of Quantitative Traits under Random Ascertainment. *BMC Genetics.* 2006. 7:21.
12. M. Wang, H. Vikis, Y. Wang, D. Jia, D. Wang, L. J. Bierut, J. E. Bailey-Wilson, C. I. Amos, S. M. Pinney, G. P. Peterson, M. de Andrade, P. Yang, J. S. Wiest, P. R. Fain, A. G. Schwartz, A. Gazdar, J. Minna, C. Gaba, H. Rothschild, **D. M. Mandal,** E. Kupert, D. Seminara, Y. Liu, J. Clark, M. Watson, A. Viswanathan, R. Govindan, M. W. Anderson, M. You. Identification of a novel tumor suppressor gene *p34* on human chromosome 6q25.1. *Cancer Research.* 2007. 67:93-99.
13. H. Vikis, M. Sato, M. James, D. Wang, Y. Wang, M. Wang, D. Jia, Y. Liu, J. E. Bailey-Wilson, C. I. Amos, S. M. Pinney, G. P. Peterson, M. de Andrade, P. Yang, J. S. Wiest, P. R. Fain, A. G. Schwartz, A. Gazdar, C. Gaba, H. Rothschild, **D. M. Mandal,** E. Kupert, D. Seminara, A. Viswanathan, R.

Govindan, J. Minna, M. W. Anderson, M. You. *EGFR-T790M* is a rare lung cancer susceptibility allele with enhanced kinase activity. *Cancer Research.* 2007. 67:4665-70.

14. **D. M. Mandal,** O. Sartor, S.L. Halton, D.E. Mercante, J.E. Bailey-Wilson, W. Rayford. Identification of Prostate Cancer Cases in Louisiana and a Comparison of Prostate Cancer Specific Clinical Data on African-American and Caucasian Males with and without Family History. *Prostate Cancer and Prostatic Diseases.* 2008. 11:274-279.
15. P. Liu, H.G. Vikis, D. Wang, Y. Lu, Y. Wang, A.G. Schwartz, S.M. Pinney, P. Yang, M. de Andrade, G.M. Petersen, J.S. Wiest, P.R. Fain, A. Gazdar, C. Gaba, H. Rothschild, **D.M. Mandal**, T. Coons, J. Lee, E. Kupert, D. Seminara, J. Minna, J.E. Bailey-Wilson, X. Wu, M.R. Spitz, T. Eisen, R.S. Houlston, C.I. Amos, M.W. Anderson, M. You. Familial aggregation of common sequence variants on 15q24-25.1 in lung cancer. J Natl Cancer Inst. 2008. 100:1326-30.
16. M. You, D. Wang, P. Liu, H. Vikis, M. James, Y. Lu, Y. Wang, M. Wang, D. Jia, Y. Liu, L.J. Bierut, P. Yang, Z. Sun, Y. Wu, W. Zheng, X. Shu, J. Long, Y. Gao, Y. Xiang, W. Chow, N. Rothman, S.M. Pinney, G.M. Petersen, M. de Andrade, J.S. Wiest, P.R. Fain, A.G. Schwartz, A. Gazdar, C. Gaba, H. Rothschild, **D. M. Mandal**, J. Lee, E. Kupert, D. Seminara, J. Minna, J.E. Bailey-Wilson, C. I. Amos, and M.W. Anderson. Fine mapping of chromosome 6q23-25 region in familial lung cancer families reveals RGS17 is a likely candidate gene. *Clinical Cancer Research.* 2009. Clinical Cancer Research. 2009. 15:2666-74.
17. Y. Liu, P. Liu, W. Wen, M. A. James, Y. Wang, J. E. Bailey-Wilson, C. I. Amos, S. M. Pinney, P. Yang, M. de Andrade, G. M. Petersen, J. S. Wiest, P. R. Fain, A. G. Schwartz, A. Gazdar, C. Gaba, H. Rothschild, **D. M. Mandal**, E. Kupert, J. Lee, D. Seminara, J. Minna, M. W. Anderson, and M. You. Haplotype and Cell Proliferation Analyses of Candidate Lung Cancer Susceptibility Genes on Chromosome 15q24-25.1. Cancer Research. 2009. 69:7844-50.
18. J.C. Wang, C. Cruchaga, N.L. Saccone, S. Bertelsen, P. Liu, J.P. Budde, W. Duan, L. Fox, R.A. Grucza, J. Kern, K. Mayo, O. Reyes, J. Rice, S.F. Saccone, N. Spiegel, J.H. Steinbach, J.A. Stitzel, M.W. Anderson, M. You, V.L. Stevens, L.J. Bierut, A.M. Goate; COGEND collaborators and GELCC collaborators. Risk for nicotine dependence and lung cancer is conferred by mRNA expression levels and amino acid change in CHRNA5. Hum Mol Genet. 2009.18:3125-35.
19. P. Liu, H.G. Vikis, D. Wang, Y. Lu, A.G. Schwartz, S.M. Pinney, P. Yang, M. de Andrade, A. Gazdar, C. Gaba, **D.M. Mandal**, J. Lee, E. Kupert, D. Seminara, J. Minna, J.E. Bailey-Wilson, C.I. Amos, M.W. Anderson, M. You. Cumulative Effect of Multiple Loci on Genetic Susceptibility to Familial Lung Cancer. Cancer Epidemiology, Biomarkers, & Prevention. 2010. 19:517-24.
20. S-Y. Hu, T. Liu, Z-Z. Liu, E. Ledet, C. Velasco-Gonzalez, **D.M. Mandal**, S. Koochekpour. Identification of a novel germline missense mutation of the androgen receptor in African American men with familial prostate cancer. Asian J. of Andrology. 2010. 12:336-343.
21. P. Liu, P. Yang, X. Wu, H. G. Vikis, Y. Lu, Y. Wang, A. G. Schwartz, S. M. Pinney, M. de Andrade, A. Gazdar, C.Gaba, **D. M. Mandal**, J. Lee, E. Kupert, D. Seminara, J. Minna, J. E. Bailey-Wilson, M. Spitz, C. I. Amos, M. W. Anderson, and M. You. A Second Genetic Variant on Chromosome 15q24-25.1 Associates with Lung Cancer. Cancer Research. 2010. 70:3128-35.
22. C.I. Amos, S.M. Pinney, Y. Li, E. Kupert, J. Lee, M.A. de Andrade, P. Yang, A.G. Schwartz, P.R. Fain, A. Gazdar, J. Minna, J.S. Wiest, D. Zeng, H. Rothschild, **D. M. Mandal**, M. You, T. Coons, C. Gaba, J.E. Bailey-Wilson, M.W. Anderson. A susceptibility locus on chromosome 6q greatly increases lung cancer risk among light and never smokers. Cancer Research. 2010. 70:2359-67.
23. E.M. Ledet, O. Sartor, W. Rayford, J.E. Bailey-Wilson, **D.M. Mandal**. Suggestive evidence of linkage identified at chromosomes 12q24 and 2p16 in African American prostate cancer families from Louisiana. Prostate. 2012. 72:938-47.
24. E.M. Ledet, X. Hu, O. Sartor, W. Rayford, M. Li, **D. M. Mandal**. Characterization of germline copy number variation in high-risk African American families with prostate cancer. Prostate. 2013. 73:614-23.
25. J. Xu, E.M. Lange, L. Lu, S.L. Zheng, Z. Wang, S.N. Thibodeau, L.A. Cannon-Albright, C.C. Teerlink, N. J. Camp, A.M. Ray, K.A. Zuhlke, J. L. Stanford, E.A. Ostrander, K.E. Wiley, S.D. Isaacs, P.C. Walsh, C. Maier, M. Luedeke, W. Vogel, J. Schleutker, T. Wahlfors, T. Tammela, D. Schaid, S.K. McDonnell, M.S. DeRycke, G. Cancel-Tassin, O. Cussenot, F. Wiklund, H. Grönberg, R. Eeles, D. Easton, Z. Kote-Jarai, A.S. Whittemore, C-L. Hsieh, G.G. Giles, J.L. Hopper, G. Severi, W.J.

Catalona, **D.M. Mandal**, E. Ledet, W.D. Foulkes, N. Hamel, L. Mahle, P. Moller , I. Powell, J. E. Bailey-Wilson, J.D. Carpten, D. Seminara, K.A. Cooney, W.B.Isaacs. HOXB13 is a susceptibility gene for prostate cancer: Results from the International Consortium for Prostate Cancer Genetics (ICPCG). Human Genetics. 2013. 132:5-14.

26. C. L. Simpson, A. J. Goldenberg, R. Culverhouse, D. Daley, R. P. Igo, Jr., G. P. Jarvik, **D. M. Mandal**, D. Mascalzoni, C. G. Montgomery, B. Pierce, R. Plaetke, S. Shete, K. A. B. Goddard and C. M. Stein. Practical Barriers and Ethical Challenges in Genetic Data Sharing. Int. J. Environ. Res. Public Health. 2014. 11: 8383-8398.
27. D. Xiong, J-H. Lee, E. Kupert, C. Simpson, S.M. Pinney, C.R. Gaba, **D. M. Mandal**, Y. Wang, A.G. Schwartz, P. Yang, M. de Andrade, F. Ding, P. Cui, H. Jiang, D.D. Stambolian, M.R. Spitz, C.I. Amos, J.E. Bailey-Wilson, M. Anderson, J.H. Jeong, M. You. A recurrent mutation in PARK2 in familial lung cancer. AJHG. 2015. 96:301-308.

C. Research Support

Ongoing Research Support

HHSN268201200007C Mandal(PI) 10/03/2011-11/02/2016
NHLBI/NIH
"Determination of Genetic Susceptibility to Lung Cancer in Families from Southern Louisiana"
The major goal of this project is to localize genes for lung cancer using linkage and association analysis.
Role: PI

2U01CA08960010A1 Thibodeau(PI) 09/01/2013–08/31/2017
NCI
Role: Co-I, 5% effort (Direct Cost Awarded $50,624)
"Prostate cancer Susceptibility: The ICPCG Study"
The major goal of this project is to localize genes for increased prostate cancer risk and aggressiveness using sequencing strategies.
Role: Site PI

1R21CA185213-01A1 Liu(PI) 04/01/2015-03/31/2017
NIH/NCI
Role: Co-I, 5% effort
"Germline mutations in African American families with aggressive prostate cancer"
The major goal of this project is to identify genes that carry risk variants for conferring risk, specifically in AA families and individuals with aggressive PCa.

Completed Research Support (past three years)

LEQSF-EPS(2014)-PFUND-364 Mandal (PI) 01/01/2014–12/31/2014
LA Board of Regents
Role: PI (Direct Cost Awarded $10,000)
"Investigation of germ-line copy number variation [CNV] and whole exome sequencing [WES] data in prostate cancer health disparity"
The major goal of this project is to investigate the genetic variants responsible for health disparity in familial prostate cancer.

LEQSF(2011)-PFUND-250 Mandal (PI) 03/01/2011-02/29/2012
Louisiana Board of Regents
"Germ-line copy number variation in high-risk African American families"
The major goal of this project is to identify the inherited structural variation in families with multiple affected prostate cancer cases.