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**CONTACT INFORMATION**

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**CITIZENSHIP**

United States of America

**EDUCATION**

2003 Ph.D., Department of Microbiology, University of Washington, Seattle, WA  
Thesis: "Population genetics of human immunodeficiency virus type 1 during within-host chronic infection"

1995 B.S., Department of Microbiology, University of Maryland, College Park, MD  
Graduated summa cum laude

**CONTINUING EDUCATION**

2012: Propensity Score Analysis, October 12–13, 2012, Philadelphia, PA

2009: Large-scale Significance Testing of Genomic Data, July 23, 2009, Webinar course presented by John D. Storey, sponsored by the Biopharmaceutical Section of the American Statistical Association.

2009: The Dark Matter of Genomic Associations with Complex Diseases: Explaining the Unexplained Heritability from Genome-wide Association Studies, February 2–3, 2009, National Human Genome Research Institute, National Institutes of Health, MD

2007: Introduction to Human Population Genetics Theory, August 23–December 4, 2007, University of Alabama at Birmingham, Birmingham, AL

2007: Modeling, Networks and Evolution of Complex Systems, June 18–22, 2007, New England Complex Systems Institute, Cambridge, MA

2007: Statistical Genetics II, January 8–April 26, 2007, University of Alabama at Birmingham, Birmingham, AL

2007: Complex Physical, Biological & Social Systems, January 8–12, 2007, New England Complex Systems Institute, Cambridge, MA

2006: Bayesian Data Analysis, August 22–November 28, 2006, University of Alabama at Birmingham, Birmingham, AL

- 2006: Statistics, Images, and Perceptions of Truth: Detecting Research Bias and Misconduct, September 14–15, 2006, University of Alabama at Birmingham, Birmingham, AL
- 2006: Statistical Bioinformatics, June 1–August 1, 2006, University of Alabama at Birmingham, Birmingham, AL
- 2006: R Fundamentals and Programming Techniques, February 27–28, 2006, University of Alabama at Birmingham, Birmingham, AL
- 2005: Advanced Gene Mapping/Linkage Course, December 12–16, 2005, Rockefeller University, New York, NY
- Awarded travel stipend
- 2005: Missing Data, August 4–5, 2005, University of Alabama at Birmingham, Birmingham, AL
- 2005: 5<sup>th</sup> Annual National Institute of Diabetes & Digestive & Kidney Diseases Short Course on Statistical Genetics, May 16–19, 2005, University of Alabama at Birmingham, Birmingham, AL

## **EXPERIENCE**

- 2012–present Staff Scientist, Center for Research on Genomics and Global Health, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD  
Supervisor: Dr. Charles N. Rotimi
- 2008–2012 Research Fellow, Center for Research on Genomics and Global Health, National Human Genome Research Institute, National Institutes of Health, Bethesda, MD  
Supervisor: Dr. Charles N. Rotimi
- 2005–2008 Postdoctoral Scholar, University of Alabama at Birmingham, Birmingham, AL  
Advisors: Drs. David B. Allison and Nengjun Yi
- 2004–2005 Postdoctoral Fellow, University of Washington, Seattle, WA  
Advisor: Dr. John E. Mittler
- 2003–2004 Postdoctoral Fellow, University of Washington, Seattle, WA  
Advisor: Dr. James I. Mullins
- 1996–2003 Research Assistant, University of Washington, Seattle, WA  
Advisor: Dr. James I. Mullins
- 1995–1996 Teaching Assistant, University of Washington, Seattle, WA
- MICROM 411: Gene Action
  - MICROM 302: General Microbiology Laboratory

1993–1995 Undergraduate Research Assistant, University of Maryland, College Park, MD

Senior thesis: “Recombination in the human immunodeficiency virus: analysis *in vitro* of the influence of specific nucleotide sequences on reverse transcriptase catalyzed recombination”

## PUBLICATIONS

### Articles and Letters (\* indicates Joint First Authorship)

1. DeStefano, J. J., Roberts, B., and *Shriner, D.* 1997. The mechanism of retroviral recombination: the role of sequences proximal to the point of strand transfer. *Arch. Virol.* 142(9): 1797–1812.
2. Liu, S.-L., Schacker, T., Musey, L., *Shriner, D.*, McElrath, M. J., Corey, L., and Mullins, J. I. 1997. Divergent patterns of progression to AIDS after infection from the same source: human immunodeficiency virus type 1 evolution and antiviral responses. *J. Virol.* 71(6): 4284–4295. PMID: PMC191644.
3. Liu, S.-L., Mittler, J. E., Nickle, D. C., Mulvania, T. M., *Shriner, D.*, Rodrigo, A. G., Kosloff, B., He, X., Corey, L., and Mullins, J. I. 2002. Selection for human immunodeficiency virus type 1 recombinants in a patient with rapid progression to AIDS. *J. Virol.* 76(21): 10674–10684. PMID: PMC136598.
4. Nickle, D. C., Jensen, M. A., Gottlieb, G. S., *Shriner, D.*, Learn, G. H., Rodrigo, A. G., and Mullins, J. I. 2003. Consensus and ancestral state HIV vaccines. *Science.* 299(5612): 1515–1517.
5. *Shriner, D.*, Nickle, D. C., Jensen, M. A., and Mullins, J. I. 2003. Potential impact of recombination on sitewise approaches for detecting positive natural selection. *Genet. Res.* 81(2): 115–121.
6. Nickle, D. C., *Shriner, D.*, Mittler, J. E., Frenkel, L. M., and Mullins, J. I. 2003. Importance and detection of virus reservoirs and compartments of HIV infection. *Curr. Opin. Microbiol.* 6(4): 410–416.
7. Nickle, D. C., Jensen, M. A., *Shriner, D.*, Brodie, S. J., Frenkel, L. M., Mittler, J. E., and Mullins, J. I. 2003. Evolutionary indicators of human immunodeficiency virus type 1 reservoirs and compartments. *J. Virol.* 77(9): 5540–5546. PMID: PMC153940.
8. Jensen, M. A., Li, F.-S., van ’t Wout, A. B., Nickle, D. C., *Shriner, D.*, He, H.-X., McLaughlin, S., Shankarappa, R., Margolick, J. B., and Mullins, J. I. 2003. Improved coreceptor usage prediction and genotypic monitoring of R5-to-X4 transition by motif analysis of human immunodeficiency virus type 1 *env* V3 loop sequences. *J. Virol.* 77(24): 13376–13388. PMID: PMC296044.
9. *Shriner, D.*, Shankarappa, R., Jensen, M. A., Nickle, D. C., Mittler, J. E., Margolick, J. B., and Mullins, J. I. 2004. Influence of random genetic drift on HIV-1 *env* evolution during chronic infection. *Genetics* 166(3): 1155–1164. PMID: PMC1470792.
10. *Shriner, D.*, Rodrigo, A. G., Nickle, D. C., and Mullins, J. I. 2004. Pervasive genomic recombination of HIV-1 *in vivo*. *Genetics* 167(4): 1573–1583. PMID: PMC1470992.
11. Liu, Y., Nickle, D. C., *Shriner, D.*, Jensen, M. A., Learn, G. H., Jr., Mittler, J. E., and Mullins, J. I. 2004. Molecular clock-like evolution of human immunodeficiency virus type 1. *Virology* 329(1): 101-108.
12. *Shriner, D.*, Liu, Y., Nickle, D. C., and Mullins, J. I. 2006. Evolution of intrahost HIV-1 genetic diversity during chronic infection. *Evolution* 60(6): 1165–1176.
13. Liu, Y., McNevin, J., Cao, J., Zhao, H., Genowati, I., Wong, K., McLaughlin, S., McSweyn, M. D., Diem, K., Stevens, C. E., Maenza, J., He, H., Nickle, D. C., *Shriner, D.*, Holte, S. E., Collier, A. C., Corey, L., McElrath, M. J., and Mullins, J. I. 2006.

- Selection on the HIV-1 proteome following primary infection. *J. Virol.* **80(19)**: 9519–9529. PMID: PMC1617227.
14. Musani, S. K., *Shriner, D.*, Liu, N., Feng, R., Coffey, C. S., Yi, N., Tiwari, H. K., and Allison, D. B. 2007. Detection of gene × gene interactions in genome-wide association studies of human population data. *Hum. Hered.* **63(2)**: 67–84.
  15. Yandell, B. S., Mehta, T., Banerjee, S., *Shriner, D.*, Venkataraman, R., Moon, J. Y., Neely, W. W., Wu, H., von Smith, R., and Yi, N. 2007. R/qtlbim: QTL with Bayesian interval mapping in experimental crosses. *Bioinformatics* **23(5)**: 641–643.
  16. Yi, N., *Shriner, D.*, Banerjee, S., Mehta, T., Pomp, D., and Yandell, B. S. 2007. An efficient Bayesian model selection approach for interacting QTL models with many effects. *Genetics* **176**: 1865–1877. PMID: PMC1931520.
  17. *Shriner, D.*, Vaughan, L. K., Padilla, M. A., and Tiwari, H. K. 2007. Problems with Genome-Wide Association Studies [Letter to the Editor]. *Science* **316(5833)**: 1840–1841.
  18. Liu, Y., McNevin, J., Zhao, H., Tebit, D. M., Troyer, R. M., McSweyn, M., Ghosh, A. K., *Shriner, D.*, Arts, E. J., McElrath, M. J., and Mullins, J. I. 2007. Evolution of human immunodeficiency virus type 1 cytotoxic T-lymphocyte epitopes: fitness-balanced escape. *J. Virol.* **81(22)**:12179–12188. PMID: PMC2169017.
  19. Yi, N., and *Shriner, D.* 2008. Advances in Bayesian multiple QTL mapping in experimental crosses. *Heredity* **100(3)**:240–252.
  20. *Shriner, D.*, Baye, T. M., Padilla, M. A., Zhang, S., Vaughan, L. K., and Loraine, A. E. 2008. Commonality of Functional Annotation: a method for prioritization of candidate genes from genome-wide linkage studies. *Nucleic Acids Res.* **36(4)**:e26. PMID: PMC2275105.
  21. *Shriner, D.* 2008. Putting Materials and Methods in Their Place [Letter to the Editor]. *Science* **322(5907)**:1463.
  22. Ankra-Badu, G. A., Pomp, D., *Shriner, D.*, Allison, D. B., and Yi, N. 2009. Genetic influences on growth and body composition in mice: multilocus interactions. *Int. J. Obes.* **33(1)**:89–95. PMID: PMC3206648.
  23. *Shriner, D.*, and Yi, N. 2009. Deviance information criterion (DIC) in Bayesian multiple QTL mapping. *Comput. Stat. Data An.* **53(5)**:1850–1860. PMID: PMC2682718.
  24. *Shriner, D.* 2009. Mapping multiple quantitative trait loci under Bayes error control. *Genet. Res.* **91(3)**:147–159. PMID: PMC3205938.
  25. *Shriner, D.*, Adeyemo, A., Gerry, N. P., Herbert, A., Chen, G., Doumatey, A., Huang, H., Zhou, J., Christman, M. F., and Rotimi, C. N. 2009. Transferability and fine-mapping of genome-wide associated loci for adult height across human populations. *PLoS ONE* **4(12)**:e8398. PMID: PMC2792725.
  26. *Shriner, D.*, Adeyemo, A., Chen, G., and Rotimi, C. N. 2010. Practical considerations for imputation of untyped markers in admixed populations. *Genet. Epidemiol.* **34(3)**:258–265. PMID: PMC2912698.
  27. Ankra-Badu, G. A., *Shriner, D.*, Le Bihan-Duval, E., Mignon-Grasteau, S., Pitel, F., Beaumont, C., Duclos, M. J., Simon, J., Porter, T. E., Vignal, A., Cogburn, L. A., Allison, D. B., Yi, N., and Aggrey, S. E. 2010. Mapping main, epistatic and sex-specific QTL for body composition in a chicken population divergently selected for low or high growth rate. *BMC Genomics* **11**:107. PMID: PMC2830984.
  28. Meilleur, K. G., Traoré, M., Sangaré, M., Britton, A., Landouré, G., Coulibaly, S., Niaré, B., Mochel, F., La Pean, A., Rafferty, I., Watts, C., *Shriner, D.*, Littleton-Kearney, M. T., Blackstone, C., Singleton, A., and Fischbeck, K.H. 2010. Hereditary spastic paraplegia and amyotrophy associated with a novel locus on chromosome 19. *Neurogenetics* **11(3)**:313–318.

29. Adeyemo, A., Chen, G., Zhou, J., *Shriner, D.*, Doumatey, A., Huang, H., and Rotimi, C. 2010. *FTO* genetic variation and association with obesity in West Africans and African-Americans. *Diabetes* **59(6)**:1549–1554. PMID: PMC2874717.
30. Kang, S. J., Chiang, C. W. K., Palmer, C. D., Tayo, B. O., Lettre, G., Butler, J. L., Hackett, R., Adeyemo, A. A., Guiducci, C., Berzins, I., Nguyen, T. T., Feng, T., Luke, A., *Shriner, D.*, Ardlie, K., Rotimi, C., Wilks, R., Forrester, T., McKenzie, C. A., Lyon, H. N., Cooper, R. S., Zhu, X., and Hirschhorn, J. N. 2010. Genome wide association of anthropometric traits in African and African derived populations. *Hum. Mol. Genet.* **19(13)**:2725–2738. PMID: PMC2883343.
31. Chen, G., *Shriner, D.*, Zhou, J., Doumatey, A., Huang, H., Gerry, N. P., Herbert, A., Christman, M. F., Chen, Y., Dunston, G. M., Faruque, M. U., Rotimi, C. N., and Adeyemo, A. 2010. Development of admixture mapping panels for African Americans from commercial high-density SNP arrays. *BMC Genomics* **11**:417. PMID: PMC2996945.
32. Meilleur, K. G., Doumatey, A., Huang, H., Charles, B., Chen, G., Zhou, J., *Shriner, D.*, Adeyemo, A., and Rotimi, C. 2010. Circulating adiponectin is associated with obesity and serum lipids in West Africans. *J. Clin. Endocrin. Metab.* **95(7)**:3517–3521. PMID: PMC2928908.
33. Ramos, E., Chen, G., *Shriner, D.*, Doumatey, A., Gerry, N. P., Herbert, A., Huang, H., Zhou, J., Christman, M. F., Adeyemo, A., and Rotimi, C. 2011. Replication of genome-wide association studies (GWAS) loci for fasting plasma glucose in African-Americans. *Diabetologia* **54(4)**:783–788. PMID: PMC3052446.
34. *Shriner, D.*, and Vaughan, L. K. 2011. A unified framework for multi-locus association analysis of both common and rare variants. *BMC Genomics* **12**:89. PMID: PMC3040731.
35. Charles, B. A., *Shriner, D.*, Doumatey, A., Chen, G., Zhou, J., Huang, H., Herbert, A., Gerry, N. P., Christman, M. F., Adeyemo, A., and Rotimi, C. N. 2011. A genome-wide association study of serum uric acid in African Americans. *BMC Med. Genomics* **4**:17. PMID: PMC3045279.
36. Fox, E. R., Young, J. H., Li, Y., Dreisbach, A. W., Keating, B. J., Musani, S. K., Liu, K., Morrison, A. C., Ganesh, S., Kutlar, A., Ramachandran, V. S., Polak, J. F., Fabsitz, R. R., Dries, D. L., Farlow, D. N., Redline, S., Adeyemo, A., Hirschhorn, J. N., Sun, Y. V., Wyatt, S. B., Penman, A. D., Palmas, W., Rotter, J. I., Townsend, R. R., Doumatey, A. P., Tayo, B. O., Mosley, T. H. Jr., Lyon, H. N., Kang, S. J., Rotimi, C. N., Cooper, R. S., Franceschini, N., Curb, J. D., Martin, L. W., Eaton, C. B., Kardia, S. L. R., Taylor, H. A., Caulfield, M. J., Ehret, G. B., Johnson, T., *The International Consortium for Blood Pressure Genome-Wide Association Studies*, Chakravarti, A., Zhu, X., and Levy, D. 2011. Association of genetic variation with systolic and diastolic blood pressure among African Americans: the Candidate Gene Association Resource (CARE) Study. *Hum. Mol. Genet.* **20(11)**:2273–2284. PMID: PMC3090190.
37. Jiao, Y., Jiao, F., Yan, J., Xiong, Q., *Shriner, D.*, Hasty, K., Stuart, J., and Gu, W. 2011. Identifying a major locus that regulates spontaneous arthritis in IL-1ra-deficient mice and analysis of potential candidates. *Genet. Res.*, **93(2)**:95–103. PMID: PMC3245888.
38. *Shriner, D.* 2011. Investigating population structure and admixture using eigenanalysis of dense genotypes. *Heredity*, **107(5)**:413–420. PMID: PMC3128175.
39. *Shriner, D.*, Adeyemo, A., Ramos, E., Chen, G., and Rotimi, C. N. 2011. Mapping of disease-associated variants in admixed populations. *Genome Biol.* **12**: 223. PMID: PMC3219963.
40. Tin, A., Woodward, O. M., Kao, W. H. L., Liu, C.-T., Lu, X., Nalls, M. A., *Shriner, D.*, Semmo, M., Akyzbekova, E. L., Wyatt, S. B., Hwang, S.-J., Yang, Q.,

- Zonderman, A. B., Adeyemo, A. A., Palmer, C., Meng, Y., Reilly, M. P., Shlipak, M. G., Siscovick, D., Evans, M. K., Rotimi, C. N., Flessner, M. F., Köttgen, M., Cupples, L. A., Fox, C. S., Köttgen, A., on behalf of the CARE and CHARGE Consortia. 2011. Genome-wide association study for serum urate concentrations and gout among African Americans identifies genomic risk loci and a novel URAT1 loss-of-function allele. *Hum. Mol. Genet.*, **20(20)**:4056–4068. PMID: PMC3177647.
41. The International Consortium for Blood Pressure Genome-Wide Association Studies. 2011. Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. *Nature*, **478(7367)**:103–109. PMID: PMC3340926.
42. Shriver, D. 2011. Approximate and exact tests of Hardy-Weinberg equilibrium using uncertain genotypes. *Genet. Epidemiol.*, **35(7)**:632–637. PMID: PMC4141651.
43. Liu, C.-T., Garnaas, M. K., Tin, A., Kottgen, A., Franceschini, N., Peralta, C. A., de Boer, I. H., Lu, X., Atkinson, E., Ding, J., Nalls, M., Shriver, D., Coresh, J., Kutlar, A., Bibbins-Domingo, K., Siscovick, D., Akyzbekova, E., Wyatt, S., Astor, B., Mychaleckyj, J., Li, M., Reilly, M. P., Townsend, R. R., Adeyemo, A., Zonderman, A. B., de Andrade, M., Turner, S. T., Mosley, T. H., Harris, T. B., The CKDGen Consortium, Rotimi, C. N., Liu, Y., Kardia, S. L. R., Evans, M. K., Shlipak, M. G., Kramer, H., Flessner, M. F., Dreisbach, A. W., Goessling, W., Cupples, L. A., Kao, W. L., and Fox, C. S. 2011. Genetic association for renal traits among participants of African ancestry reveals new loci for renal function. *PLoS Genet.*, **7(9)**:e1002264. PMID: PMC3169523.
44. Charles, B. A., Doumatey, A., Huang, H., Zhou, J., Chen, G., Shriver, D., Adeyemo, A., and Rotimi, C. N. 2011. The roles of IL-6, IL-10, and IL-1RA in obesity and insulin resistance in African Americans. *J. Clin. Endocrin. Metab.*, **96(12)**:E2018–E2022. PMID: PMC3232609.
45. Chambers, J. C., Zhang, W., Sehmi, J., Li, X., Wass, M. N., Van der Harst, P., Holm, H., Sanna, S., Kavousi, M., Baumeister, S. E., Coin, L. J., Deng, G., Gieger, C., Heard-Costa, N. L., Hottenga, J.-J., Kühnel, B., Kumar, V., Lagou, V., Liang, L., Luan, J., Vidal, P. M., Mateo Leach, I., O'Reilly, P. F., Peden, J. F., Rahmioglu, N., Soininen, P., Speliotes, E. K., Yuan, X., Thorleifsson, G., Alizadeh, B. Z., Atwood, L. D., Borecki, I. B., Brown, M. J., Charoen, P., Cucca, F., Das, D., de Geus, E. J. C., Dixon, A. L., Döring, A., Ehret, G., Eyjolfsson, G. I., Farrall, M., Forouhi, N. G., Friedrich, N., Goessling, W., Gudbjartsson, D. F., Harris, T. B., Hartikainen, A.-L., Heath, S., Hirschfield, G. M., Hofman, A., Homuth, G., Hyppönen, E., Janssen, H. L. A., Johnson, T., Kangas, A. J., Kema, I. P., Kühn, J. P., Lai, S., Lathrop, M., Lerch, M. M., Li, Y., Liang, T. J., Lin, J.-P., Loos, R. J., Martin, N. G., Moffatt, M. F., Montgomery, G. W., Munroe, P. B., Musunuru, K., Nakamura, Y., O'Donnell, C. J., Olafsson, I., Penninx, B. W., Pouta, A., Prins, B. P., Prokopenko, I., Puls, R., Ruukonen, A., Savolainen, M. J., Schlessinger, D., Schouten, J. N. L., Seedorf, U., Sen-Chowdhry, S., Siminovitch, K. A., Smit, J. H., Spector, T. D., Tan, W., Teslovich, T. M., Tukiainen, T., Uitterlinden, A. G., Van der Klauw, M. M., Vasani, R. S., Wallace, C., Wallaschofski, H., Wichmann, H.-E., Willemsen, G., Würtz, P., Xu, C., Yerges-Armstrong, L. M., Alcohol Genome-wide Association (AlcGen) Consortium, Diabetes Genetics Replication and Meta-analyses (DIAGRAM+) Study, Genetic Investigation of Anthropometric Traits (GIANT) Consortium, Global Lipids Genetics Consortium, Genetics of Liver Disease (GOLD) Consortium, International Consortium for Blood Pressure (ICBP-GWAS), Meta-analyses of Glucose and Insulin-Related Traits Consortium (MAGIC), Abecasis, G. R., Ahmadi, K. R., Boomsma, D. I., Caulfield, M., Cookson, W. O., van Duijn, C. M., Froguel, P., Matsuda, K., McCarthy, M. I., Meisinger, C., Mooser, V., Pietiläinen, K. H., Schumann, G., Snieder, H., Sternberg, M. J. E., Stolk, R. P., Thomas, H. C., Thorsteinsdottir, U., Uda, M., Waechter, G., Wareham, N. J., Waterworth, D. M., Watkins, H., Whitfield, J. B.,

- Witte man, J. C. M., Wolffenbuttel, B. H. R., Fox, C. S., Ala-Korpela, M., Stefansson, K., Vollenweider, P., Völzke, H., Schadt, E. E., Scott, J., Järvelin, M.-R., Elliott, P., and Kooner, J. S. 2011. Genome-wide association study identifies loci influencing concentrations of liver enzymes in plasma. *Nat. Genet.*, **43(11)**:1131–1138. PMID: PMC3482372.
46. Shri ner, D., Adeyemo, A., and Rotimi, C. N. 2011. Joint ancestry and association testing in admixed individuals. *PLoS Comput. Biol.*, **7(12)**:e1002325. PMID: PMC3245293.
47. Palmer, N. D., McDonough, C. W., Hicks, P. J., Roh, B. H., Wing, M. R., An, S. S., Hester, J. M., Cooke, J. N., Bostrom, M. A., Rudock, M. E., Talbert, M. E., Lewis, J. P., DIAGRAM Consortium, MAGIC Investigators, Ferrara, A., Lu, L., Ziegler, J. T., Sale, M. M., Divers, J., Shri ner, D., Adeyemo, A., Rotimi, C. N., Ng, M. C. Y., Langefeld, C. D., Freedman, B. I., and Bowden, D. W. 2012. A genome-wide association search for type 2 diabetes genes in African Americans. *PLoS ONE*, **7(1)**:e29202. PMID: PMC3251563.
48. Shri ner, D. 2012. Moving towards systems genetics through multiple trait analysis in genome-wide association studies. *Front. Gene.*, **3**:1. PMID: PMC3266611.
49. Shri ner, D. 2012. Improved eigenanalysis of discrete subpopulations and admixture using the minimum average partial test. *Hum. Hered.*, **73**:73–83. PMID: PMC3370671.
50. Chen, G., Ramos, E., Adeyemo, A., Shri ner, D., Zhou, J., Doumatey, A. P., Huang, H., Erdos, M. R., Gerry, N. P., Herbert, A., Bentley, A. R., Xu, H., Charles, B. A., Christman, M. F., and Rotimi, C. N. 2012. UGT1A1 is a major locus influencing bilirubin levels in African Americans. *Eur. J. Hum. Genet.*, **20(4)**:463–468. PMID: PMC3306855.
51. Ayele, F. T., Doumatey, A., Huang, H., Zhou, J., Charles, B., Erdos, M., Adeleye, J., Balogun, W., Fasanmade, O., Johnson, T., Oli, J., Okafor, G., Amoah, A., Eghan, B. A., Jr., Agyenim-Boateng, K., Acheampong, J., Adebamowo, C. A., Herbert, A., Gerry, N., Christman, M., Chen, G., Shri ner, D., Adeyemo, A., and Rotimi, C. N. 2012. Genome-wide associated loci influencing interleukin (IL)-10, IL-1Ra, and IL-6 levels in African Americans. *Immunogenetics*, **64(5)**:351–359. PMID: PMC3418332.
52. Doumatey, A. P., Chen, G., Ayele, F. T., Zhou, J., Erdos, M., Shri ner, D., Huang, H., Adeleye, J., Balogun, W., Fasanmade, O., Johnson, T., Oli, J., Okafor, G., Amoah, A., Eghan, B. A., Agyenim-Boateng, K., Acheampong, J., Adebamowo, C., Gerry, N. P., Christman, M. F., Adeyemo, A., and Rotimi, C. N. 2012. C-reactive protein promoter polymorphisms influence circulating CRP levels in a genome-wide association study of African Americans. *Hum. Mol. Genet.*, **21(13)**:3063–3072. PMID: PMC3373247.
53. Bentley, A. R., Doumatey, A. P., Chen, G., Huang, H., Zhou, J., Shri ner, D., Jiang, C.-Q., Zhang, Z., Liu, G., Fasanmade, O., Johnson, T., Oli, J. M., Okafor, G., Eghan, B. Jr., Agyenim-Boateng, K., Adeleye, J., Balogun, W., Adebamowo, C., Acheampong, J., Amoah, A., Adeyemo, A., and Rotimi, C. N. 2012. Variation in *APOLI* contributes to ancestry-level differences in HDLc-kidney function association. *Int. J. Nephrol.*, **2012:article 748984**. PMID: PMC3438781.
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84. *Shriner, D.* 2015. Mixed Ancestry and Disease Risk Transferability. *Curr. Genet. Med. Rep.*, **3(4)**:151–157.
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87. *Shriner, D.*, Tekola-Ayele, F., Adeyemo, A., and Rotimi, C. N. 2016. Ancient Human Migration after Out-of-Africa. *Sci. Rep.* **6**:26565.
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89. Shriener, D., and Keita, SOY. 2016. Migration route out of Africa unresolved by 225 Egyptian and Ethiopian whole genome sequences. *Front. Genet.*,7:98. PMID: PMC4887474.

### Book Chapters

1. Anderson, J. P., Rain, M., Shriener, D., Rodrigo, A. G., Wang, Y., Nickle, D., Learn, G. H., Naugler, W. E., and Mullins, J. I. 2002. “The Genetics of HIV-1” in *The Human Immunodeficiency Virus: Biology, Immunology, and Therapy*, ed. Emini, E. A. (Princeton University Press, Princeton, NJ).
2. Shriener, D., Musani, S., and Yi, N. 2007. “Statistical methods for multiple QTL mapping in experimental crosses” in *Current Topics in Human Genetics: Studies of Complex Diseases*, eds. Deng, H.-W., Shen, H., Liu, Y., and Hu, H. (World Scientific Publishing Co. Pte. Ltd., Singapore).
3. Shriener, D., Coulibaly, I., Ankra-Badu, G., Baye, T. M., and Allison, D. B. 2012. “Genetic Contribution to the Development of Obesity” in *Textbook of Obesity: Biological, Psychological and Cultural Influences*, eds. Akabas, S. R., Lederman, S. A., and Moore, B. J. (John Wiley & Sons, Ltd., Chichester, United Kingdom).

### PROFESSIONAL ACTIVITIES

- 1995–2006, member, American Society for Microbiology
- 1997–2014, member, American Association for the Advancement of Science
- 2006–2010, member, American Statistical Association
- 2006–2012, member, The Obesity Society
- 2007–2010, member, American Society for Nutrition
- 2010–2012, member, American Society of Human Genetics
- 2010–present, member, International Genetic Epidemiology Society
  
- Invited Referee: *Evolution, Journal of Leukocyte Biology, Journal of Molecular Evolution, Journal of Theoretical Biology, Molecular Biology and Evolution, Physiological Genomics, Journal of the American Medical Association, Computational Statistics and Data Analysis, PLoS Computational Biology, American Journal of Human Genetics, Molecular Ecology, International Journal of Immunogenetics, Molecular Phylogenetics and Evolution, BMC Genetics, Statistical Applications in Genetics and Molecular Biology, PLoS Genetics, Heredity, Behavior Genetics, International Journal of Plant Genomics, Human Genetics, Bioinformatics, BMC Bioinformatics, Journal of Heredity, Genetics, Genetic Epidemiology, European Journal of Human Genetics, Human Heredity, Molecular Genetics & Genomic Medicine, Bioessays, Statistics in Medicine, Arthritis & Rheumatology, Immunologic Research*
- Reviewer: 2006 Computational Systems Bioinformatics Conference, 2008 Computational Systems Bioinformatics Conference, 12<sup>th</sup> International Congress of Human Genetics/61<sup>st</sup> Annual Meeting of The American Society of Human Genetics, 13<sup>th</sup> International Congress of Human Genetics
- 2010–present, Associate Editor, *Frontiers in Systems Biology*
- 2014, Guest Associate Editor, *PLOS Genetics*
  
- April 15, 2011, Poster Judge, Howard University Health Sciences Research Day 2011
- 2012–present, member of the International Genetic Epidemiology Society Ethical, Legal, and Social Issues Committee

- 2013–present, member of the National Human Genome Research Institute Scientific Review Committee
- 2016–present, Chair of the International Genetic Epidemiology Society Ethical, Legal, and Social Issues Committee
- 2016–present, member of the National Human Genome Research Institute Advisory Committee for the Bioinformatics and Scientific Computing Core
- 2008–2014, organizer of the Center for Research on Genomics and Global Health Journal Club
- 2014–present, website coordinator for the Center for Research on Genomics and Global Health
- 2015–present, organizer of the Metabolic, Cardiovascular and Inflammatory Disease Genomics Branch Journal Club
- 2009, chair, Center for Research on Genomics and Global Health Postdoctoral Fellow Search Committee

## CONFERENCES

- 7<sup>th</sup> Annual HIV Dynamics and Evolution Conference, Seattle, WA, April 2000: “Inferring phylogenies for large, serially sampled data sets” and “Phylogenetic evidence for recombination within an HIV-1 singly infected individual”
- Joint Statistical Meetings, Seattle, WA, July 2006: “Inferring Quantitative Trait Loci Using a Bayesian Variable Selection Model and Markov Chain Monte Carlo Convergence Diagnostics”
- Annual Scientific Meeting of NAASO, The Obesity Society, Boston, MA, October 2006: “Bayesian Mapping of Obesity-related Quantitative Trait Loci in *Drosophila melanogaster*”
- 6<sup>th</sup> Annual Meeting of the Complex Traits Consortium, Braunschweig, Germany, May 26–29, 2007: “Bayes Error Control for Multiple QTL Mapping”
- Annual Scientific Meeting of NAASO, The Obesity Society, New Orleans, LA, October 2007: “Commonality of Functional Annotation: A Method for Prioritization of Candidate Genes from Genome-Wide Linkage Studies”
- Genome-wide Association: *Analyze This!*, National Institutes of Health, Bethesda, MD, August 4–5, 2008: “Powerful, Flexible, and Efficient Multi-locus Genome-wide Association Testing Reveals Pathways Involved in Parkinson Disease”
- 18<sup>th</sup> Annual International Genetic Epidemiology Society Meeting, Oahu, Hawaii, October 18–20, 2009: “Practical Considerations for Imputation of Untyped Markers in Admixed Populations”
- 59<sup>th</sup> Annual Meeting of the American Society of Human Genetics, Honolulu, Hawaii, October 20–24, 2009: “Transferability and fine-mapping of genome-wide associated loci for adult height across human populations”
- 27<sup>th</sup> Annual Meeting of The Obesity Society, Washington, D.C., October 24–28, 2009: “Sizing Up the Design of Genome-wide Association Studies for Adiposity”
- 19<sup>th</sup> Annual International Genetic Epidemiology Society Meeting, Boston, Massachusetts, October 10–12, 2010: “Factor Analysis of Population Structure and Admixture”
- 60<sup>th</sup> Annual Meeting of the American Society of Human Genetics, Washington, D.C., November 2–6, 2010: “GWAS in African Americans: findings, replication, fine-mapping, and implications for imputation”

- Joint International Conference of the African and Southern African Societies of Human Genetics, Cape Town, South Africa, March 6–9, 2011: “Patterns of structural variation in admixed African Americans and Southern Africans”
- 12<sup>th</sup> International Congress of Human Genetics, Montreal, Canada, October 11–15, 2011: “Joint ancestry and association testing in admixed individuals”
- Genetics of the Peoples of Africa and the Transatlantic African Diaspora, Chapel Hill, North Carolina, March 19–20, 2012
- 21<sup>st</sup> Annual Conference of the International Genetic Epidemiology Society, Stevenson, Washington, October 18–20, 2012: “Trans-ethnic mapping in admixed African Americans”
- Making Sense of the Sequence: Applications in Population Sciences, National Cancer Institute, Rockville, Maryland, May 15–16, 2013: “Lessons and Considerations for Analysis in Diverse Populations”
- 2<sup>nd</sup> Meeting of the H3Africa Consortium, Accra, Ghana, May 16–18, 2013: “The African Genome Variation Project”
- 8<sup>th</sup> Meeting of the African Society of Human Genetics, Accra, Ghana, May 19–21, 2013: “The African Genome Variation Project”
- 22<sup>nd</sup> Annual Conference of the International Genetic Epidemiology Society, Chicago, Illinois, September 15–17, 2013: “Testing Hardy-Weinberg equilibrium conditional on admixture reveals natural selection in admixed populations”
- 23<sup>rd</sup> Annual Conference of the International Genetic Epidemiology Society, Vienna, Austria, August 28–30, 2014: “Genome-wide genotype and sequence-based reconstruction of the 140,000 year history of modern human ancestry”
- 24<sup>th</sup> Annual Conference of the International Genetic Epidemiology Society, Baltimore, Maryland, October 4–6, 2015: “Phenotypic variance explained by local ancestry in admixed African Americans”
- 9<sup>th</sup> Meeting of the African Society of Human Genetics, Dakar, Senegal, May 15–17, 2016: “Ancient Human Migration after Out-of-Africa”

### **INVITED SEMINARS**

- Section on Statistical Genetics Lecture Series, Department of Biostatistics, University of Alabama at Birmingham, December 6, 2006: “Bayes Error Control for Multiple QTL Mapping”
- University of Maryland Bioscience Day, November 13, 2007: “Developing a Comprehensive Research Toolkit”
- Department of Epidemiology, Johns Hopkins Bloomberg School of Public Health, February 27, 2012: “Mapping Disease Loci in Admixed Populations”

### **TEACHING**

- 2009–2014, Bashira A. Charles, Ph.D., NHGRI Intramural Health Disparities Postdoctoral Fellow
- 2010–2014, Amy R. Bentley, Ph.D., Postdoctoral Fellow
- 2010–2014, Fasil Tekola Ayele, Ph.D., Postdoctoral Fellow
- 2015–present, Jennifer L. Baker, Ph.D., Postdoctoral Fellow
- August 2–7, 2009, Instructor, National Human Genome Research Institute Summer Workshop in Genomics, Bethesda, MD
- 8<sup>th</sup> Meeting of the African Society of Human Genetics, Accra, Ghana, May 19–21, 2013: “An Introduction to the Analysis of GWAS”

- Guest Lecturer, Johns Hopkins Bloomberg School of Public Health, Principles of Genetic Epidemiology 4, April 17, 2014
- Guest Lecturer, Johns Hopkins Bloomberg School of Public Health, Principles of Genetic Epidemiology 4, April 9, 2015

### **HONORS AND AWARDS**

- 1994–1995, Howard Hughes Medical Institute Undergraduate Research Fellow
- 1995–present, The Phi Beta Kappa Society
- 1995, P. Arne Hanson Award for the Outstanding Departmental Honors Student, Department of Microbiology, University of Maryland at College Park
- 1995, Honorable Mention, National Science Foundation Graduate Research Fellowship Program
- 1996, Honorable Mention, National Science Foundation Graduate Research Fellowship Program
- 1996–2001, Howard Hughes Medical Institute Predoctoral Fellow in Biological Sciences
- 2006, Finalist for the Ethan Sims Young Investigator Award, The Obesity Society
- Spring 2007, Career Enhancement Award, Office of Postdoctoral Education, University of Alabama at Birmingham

### **REFERENCES**

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- Donald W. Bowden, Ph.D., Center for Genomics and Personalized Medicine Research, Center for Diabetes Research, Department of Biochemistry, Wake Forest School of Medicine, Winston-Salem, NC 27157 USA, E-mail: [dbowden@wakehealth.edu](mailto:dbowden@wakehealth.edu)
- Michèle Ramsay, Ph.D., Division of Human Genetics, National Health Laboratory Service, School of Pathology, Faculty of Health Sciences, University of the Witwatersrand, Johannesburg, South Africa, E-mail: [michele.ramsay@wits.ac.za](mailto:michele.ramsay@wits.ac.za)