

CURRICULUM VITAE

Name: Michael W. Smith, Ph.D.

Citizenship: United States

Education:

- 1979–1983 B.S. (Zoology) and B.S. (Statistics), University of Georgia, Athens, Georgia
1983–1989 Ph.D. (Biology with a Genetics concentration), Johns Hopkins University, Baltimore, Maryland

Brief Chronology of Employment:

- 1989–1991 Post-doc, University of California, San Diego, San Diego, CA
1991–1993 Post-doc, Salk Institute for Biological Studies, San Diego, CA
1993–1994 Staff Scientist/Assistant Director, Human Genome Center, Salk Institute for Biological Studies, San Diego, CA
1994–present Principal Scientist/Principal Investigator, Laboratory of Genomic Diversity, Basic Research Program, SAIC-Frederick, Inc., National Cancer Institute at Frederick, Frederick, MD

Societies:

- American Association for the Advancement of Science
American Society of Human Genetics
Society for Epidemiological Research

Honors and Other Special Scientific Recognition:

- National Cancer Institute Mentor of Merit, 2002
National Cancer Institute Mentor of Merit, 2004
NIH Study Section, Ad hoc reviewer for Genomics Computational Biology and Technology Study Section, 2005
NIH Study Section, Gene, Genomes, and Genetics Fellowships, 2006–2007
NIH Study Section, Shared Instrumentation, 2008

Grants, Scholarships and Fellowships:

- NIH Postdoctoral Traineeship, University of California, San Diego, 1989–1991
Department of Energy Human Genome Distinguished Postdoctoral Fellowship, Salk Institute for Biological Studies, 1992–1994
Co-Investigator on the NIH grant “Mapping and Sequencing the Human Genome,” 1993–1994
Mapping by Admixture Linkage Disequilibrium Genotyping Laboratory for the NIDDK-funded Familial Investigation of Nephropathy of Diabetes (FIND) Study, 1999–present

Patents Issued:

U.S. Patent #5,851,760: Method for generation of sequence sampled maps of complex genomes
U.S. Patent #6,600,030: Delayed progression to AIDS by a missense allele of the *CCR2* gene

Patents Pending:

60/128521: Method of predicting susceptibility to HIV infection or progression of HIV disease
Single nucleotide polymorphisms associate with renal disease (submitted 1/08)

Faculty Appointments:

Adjunct Professor in the Department of Epidemiology, Bloomberg School of Public Health of the Johns Hopkins University, 2002–present

Bibliography:

1. Brisbin Jr., I., Smith, M.W., and Smith, M.H. Feral swine studies at the Savannah River Ecology Laboratory, an overview of program goals and design. In: *Research and Management of Wild Hog Populations*, Wood, G.W. (Ed.), Belle W. Baruch Forest Service Institute, Georgetown, SC, 1977, pp. 71–79.
2. Smith, M.H., Britton, J.C., Burke, P., Chesson, R.K., Smith, M.W., and Hagen, J. Genetic variability in Corbicula, an invading species. In: *Proceedings of the First International Corbicula Symposium*, Britton, J.C., Mattice, J.S., Murphy, C.W., and Newland, L.W. (Eds.), Christian University Research Foundation, Fort Worth, TX, 1979, pp. 243–248.
3. Smith, M.W., Smith, M.H., and Brisbin Jr., I.L. Genetic variability and domestication in swine. *J Mammal* 61: 39–45, 1980.
4. Smith, M.W., Aquadro, C.H., Etges, W.E., Smith, M.H., and Chesson, R.K. *Bibliography of electrophoretic studies of biochemical variation in natural vertebrate populations*, Texas Tech University Press, Lubbock, TX, 1982, pp. 105.
5. Smith, M.W., Smith, M.H., and Chesson, R.K. Biochemical genetics of mosquito fish populations. I. Environmental correlates and temporal and spatial heterogeneity of allele frequency within river drainage. *Copeia* 182–193, 1983.
6. Smith, M.H., Smith, M.W., Scott, S.L., Liu, E.H., and Jones, J.C. Selection in bass populations for malate dehydrogenase variants by natural and elevated water temperatures. *Copeia* 193–197, 1983.
7. Smith, M.W., Teska, W.R., and Smith, M.H. Food as a limiting factor and selective agent for genetic heterozygosity in the cotton mouse *Peromyscus gossypinus*. *Amer Midl Nat* 112: 10–118, 1984.
8. Chesson, R.K., Smith, M.W., and Smith, M.H. Biochemical genetics of mosquito fish populations. Incidence and significance of multiple inseminations. *Genetica* 64: 77–81, 1984.
9. Tolliver, D.K., Smith, M.H., Johns, P.E., and Smith, M.W. Low levels of genetic variability in pikas from Colorado. *Can J Zool* 63: 1735–1737, 1985.

10. McClenaghan Jr., L.R., Smith, M.W., and Smith, M.H. Biochemical genetics of mosquito fish populations. IV. Changes of allele frequency through time and space. *Evolution* 39: 451–460, 1985.
11. Powers, D.A., Agellon, L.B., Chen, T.T., Van Beneden, R.V., Smith, M.W., Frazier, J., and DiMichelle, L. Genetic engineering of fish. In: *Proceedings of the Pacific Congress on Marine Technology*, MRM 12: 3–4, 1986.
12. Smith, M.W., Chapman, R.W., and Powers, D.A. Mitochondrial DNA analysis of Chesapeake Bay *Fundulus heteroclitus* populations. In: *Understanding the Estuary: Advances in Chesapeake Bay Research*. Chesapeake Research Consortium Publication Number 129, Lynch, M.P. and Krone, E.C., (Eds.), 1988, pp. 36–37.
13. Smith, M.W. Structure of vertebrate genes: a statistical analysis implicating selection. *J Mol Evol* 27: 45–55, 1988.
14. Brisbin Jr., I.L., Breshears, D., Brown, K.L., Ladd, M., Smith, M.H., Smith, M.W., and Towns, A.L. Relationships between levels of radio cesium in components of terrestrial and aquatic food webs of a contaminated streambed and floodplain community. *J Appl Ecol* 26: 173–182, 1989.
15. Powers, D.A., Lauerman, T., Crawford, D., Smith, M.W., Gonzales, I., and DiMichelle, L. The evolutionary significance of genetic variation at enzyme synthesizing loci in the teleost *Fundulus heteroclitus*. *J Fish Biol* 39A: 164–184, 1991.
16. Selleri, L.A., Eubanks, J.H., Giovannini, M., Hermanson, G.G., Romo, A., Djabali, M., Maurer, S., McElligott, D.L., Smith, M.W., and Evans, G.A. Detection and characterization of "chimeric" yeast artificial chromosome clones by fluorescent in situ suppression hybridization. *Genomics* 14: 536–541, 1992.
17. McDonald, M.A., Smith, M.H., Smith, M.W., Novak, J.M., Johns, P.E., and DeVries, A.L. Biochemical systematics of Nototheniooid fishes from Antarctica. *Biochem Syst Ecol* 20: 233–241, 1992.
18. Smith, M.W., Glimcher, M.C., and Powers, D.A. Differential introgression of nuclear alleles between subspecies of the teleost *Fundulus heteroclitus*. *Molec Mar Biol Biotech* 1: 226–238, 1992.
19. Smith, M.W., Feng, D.-F., and Doolittle, R.F. Evolution by acquisition: the case for horizontal gene transfers. *TIBS* 17: 489–493, 1992.
20. Smith, M.W. and Doolittle, R.F. Anomalous phylogeny involving the enzyme glucose-6-phosphate isomerase. *J Mol Evol* 34: 544–545, 1992.
21. Smith, M.W. and Doolittle, R.F. A comparison of evolutionary rates of the two major kinds of super oxide dismutases. *J Mol Evol* 34: 75–184, 1992.
22. Smith, M.W., Clark, S.P., Hutchinson, J.S., Wei, Y., Churukian, A.C., Daniels, L.B., Diggle, K.L., Gen, M.W., Romo, A.J., Lin, Y., Selleri, L., McElligot, D.L., and Evans, G.A. A sequence-tagged site map of human chromosome 11. *Genomics* 17: 699–725, 1993.

23. Powers, D.A., Smith, M.W., Gonzales, I., DiMichelle, L., Crawford, D., Lauerman, T., and Bernadi, G. A multidisciplinary approach to the selectionist-neutralist controversy using the model teleost, *Fundulus heteroclitus*. In: *Oxford Surveys*, Futuyma, D. and Antonovics, J. (Eds.), Oxford University Press, New York, 1993, pp. 43–107.
24. Smith, M.W., Holmsen, A.L., Peterson, M., Wei, Y.H., and Evans, G.A. Genomic sequence sample analysis: a rapid strategy for sequence-based physical mapping of complex genomes. *Nat Genet* 7: 40–47, 1994.
25. Kaczor, C.M., Smith, M.W., Sangwan, I., and O'Brian, M.R.: Plant-aminolevulinic acid dehydratase: expression in soybean root nodules and evidence for a bacterial lineage of the *Alad* gene. *Plant Physiol* 104: 1411–1417, 1994.
26. Rozario, C., Smith, M.W., and Muller, M. Primary sequence of a putative pyrophosphate-linked phosphofructokinase gene of *Giardia lamblia*. *Biochem Biophys Acta* 1260: 218–222, 1995.
27. Kupfer, K., Smith, M.W., Quackenbush, J., and Evans, G.A. Physical mapping of complex genomes by sampled sequencing: a theoretical analysis. *Genomics* 27: 90–100, 1995.
28. Selleri, L., Smith, M.W., Holmsen, A.L., Romo, A.J., Thomas, S.D., Paternotte, C., Romberg, L.C.R., Wei, Y.H., and Evans, G.A. High-resolution physical mapping of a 250 kb region of human chromosome 11q24 by genomic sequence sampling. *Genomics* 26: 489–501, 1995.
29. Quackenbush, J., Davies, C., Bailis, J.M., Khristich, J.V., Digge, K., Marchuk, Y., Tobin, J., Clark, S.P., Rodkins, A., Marcano, S., Churukian, A.C., Hutchinson, J.S., Probst, S., Romberg, L., Wei, Y.H., Garner, H.J., Smith, M.W., Selleri, L., and Evans, G.A. An STS content map of human-chromosome-11 localization of 910 YAC clones and 109 islands. *Genomics* 29: 512–525, 1995.
30. Dean, M., Carrington, M., Winkler, C., Huttley, G.A., Smith, M.W., Allikmets, R., Goedert, J., Buchbinder, S.P., Vittinghoff, E., Gomperts, E., Donfield, S., Vlahov, D., Kaslow, R., Saah, A., Rinaldo, C., and Detels, R. Hemophilia Growth and Development Study, Multicenter AIDS Cohort Study, San Francisco City Cohort, ALIVE Study, and O'Brien, S.J. Genetic restriction of HIV-1 infection and progression to AIDS by a deletion allele of the *CKR5* structural gene. *Science* 273: 1856–1862, 1996.
31. Rozario, C., Morin, L., Roger, A.J., Smith, M.W., and Muller, M. Primary structure and phylogenetic relationships of glyceraldehyde-3-phosphate dehydrogenase genes of free-living and parasitic diplomonad flagellates. *J Eukaryot Microbiol* 43: 330–340, 1996.
32. Roger, A.J., Smith, M.W., Doolittle, R.F., and Doolittle, W.F. Evidence for the heterolobosea from phylogenetic analysis of genes encoding glyceraldehyde-3-phosphate dehydrogenase. *J Eukaryot Microbiol* 43: 475–485, 1996.
33. Meng, T., Aley, S.B., Svard, S.G., Smith, M.W., Huang, B., Kim, J., and Gillin, F.D. Immunolocalization and sequence of caltractin/centrin from the early branching eukaryote *Giardia lamblia*. *Mol Biochem Parasitol* 79: 103–108, 1996.

34. Smith, M.W., Dean, M., Carrington, M., Winkler, C., Huttley, G.A., Lomb, D.A., Goedert, J.J., O'Brien, T.R., Muñoz, A., Jacobson, L.P., Buchbinder, S., Vittinghoff, E., Vlahov, D., Hoots, K., Hilgartner, M., HGDS, Multicenter AIDS Cohort, Multicenter Hemophilia Cohort Study, San Francisco City Cohort, ALIVE Study, and O'Brien, S.J. Contrasting genetic influence of *CCR2* and *CCR5* receptor gene variants on HIV-1 infection and disease progression. *Science* 277: 959–965, 1997.
35. Shriver, M.D., Smith, M.W., Jin, L., Marcini, A., Akey, J.M., Deka, R., and Ferrell, R.E. Ethnic affiliation estimation using population-specific DNA markers. *Am J Hum Genet* 60: 957–964, 1997.
36. Smith, M.W., Dean, M., Carrington, M., Huttley, G.A., and O'Brien, S.J. *CCR5-Δ32* gene deletion in HIV-1 infected patients. *The Lancet* 350: 741, 1997.
37. Smith, M.W., Carrington, M., Winkler, C.A., Lomb, D., Dean, M., Huttley, G.A., and O'Brien, S.J. *CCR2* chemokine receptor and AIDS progression. *Nature Medicine* 3: 1052–1053, 1997.
38. Winkler, C., Modi, W., Smith, M.W., Nelson, G.W., Wu, X., Carrington, M., Dean, M., Honjo, T., Tashiro, K., Yabe, D., Vittinghoff, E., Buchbinder, S., Goedert, J.J., O'Brien, T.R., Jacobson, L.P., Donfield, S., Willoughby, A., Gomperts, E., Vlahov, D., Phair, J., ALIVE, HGDS, MACS, MHCS, SFCC, and O'Brien, S.J. Genetic restriction of AIDS pathogenesis by an *SDF1* chemokine gene mutation. *Science* 279: 389–393, 1998.
39. Roger, A.J., Svard, S.G., Tovar, J., Clark, C.G., Smith, M.W., Gillin, F.D., and Sogin, M.L. A mitochondrial-like chaperonin 60 gene in *Giardia lamblia*: evidence that diplomonads once harbored an endosymbiont related to the progenitor of mitochondria. *Proc Natl Acad Sci* 95: 229–234, 1998.
40. Stephens, J.C., Reich, D.E., Goldstein, D.B., Shin, H.D., Smith, M.W., Carrington, M., Winkler, C., Huttley, G.A., Allikmets, R., Schriml, L., Gerrard, B., Malasky, M., Ramos, M.D., Morlot, S., Tzetzis, M., Oddoux, C., di Giovine, F.S., Nasioulas, G., Chandler, D., Aseev, M., Hanson, M., Kalaydjieva, L., Glavac, D., Gasparini, P., Kanavakis, E., Claustres, M., Kambouris, M., Ostrer, H., Duff, G., Baranov, V., Sibul, H., Metspalu, A., Goldman, D., Martin, N., Duffy, D., Schmidtke, J., Estivill, X., O'Brien, S.J., and Dean, M.: Dating the origin of the *CCR5-Δ32* AIDS resistance allele by the coalescence of haplotypes. *Amer J Hum Genet* 62: 1507–1515, 1998.
41. Smith, M.W. Discovery of a chemokine receptor gene polymorphism in humans that delays AIDS. *SAIC Science and Technology Trends* 1998, pp. 39–43.
42. Smith, M.W., Aley, S.B., Sogin, M., Gillin, F.D., and Evans, G.A. Sequence survey of the *Giardia lamblia* genome. *Mol Biochem Parasitol* 95: 267–280, 1998.
43. Smith, M.W., Chapman, R.W., and Powers, D.A. Mitochondrial DNA analysis of Atlantic Coast, Chesapeake Bay, and Delaware Bay populations of the teleost *Fundulus heteroclitus* indicates temporally unstable distributions over geologic time. *Mar Biol Biotech* 7: 79–87, 1998.

44. Anzala, A.O., Ball, T.B., Rostron, T., O'Brien, S.J., Plummer, F.A., Rowland-Jones, S.L., Smith, M.W., Dong, T., Njagi, E., Bwayo, J.J., and McMichael, A.J. *CCR2-64I* allele and genotype association with delayed AIDS progression in African women. *The Lancet* 351: 1632–1633, 1998.
45. Martin, M.P., Dean, M., Smith, M.W., Winkler, C., Gerrard, B., Michael, N.L., Margolick, J., Buchbinder, S., Goedert, J.J., O'Brien, T.R., Hilgartner, M.W., Hoots, K., Vlahov, D., O'Brien, S.J., and Carrington, M. Genetic acceleration of AIDS progression by a promoter variant of *CCR5*. *Science* 282: 1907–1911, 1998.
46. Hendel, H., Henon, N., Lebuanec, H., Lachgar, A., Poncelet, H., Caillat-Zucman, S., Winkler, C., Smith, M.W., Kenefic, L., O'Brien, S.J., Lu, W., Andrieu, J.-M., Zagury, D., Schachter, F., Rappaport, J., and Zagury, J.-F. Distinctive effects of *CCR5*, *CCR2* and *SDF-1* genetic polymorphisms in AIDS progression. *J Acquir Immune Defic Syndr Hum Retrovirol* 19: 381–386, 1998.
47. Shriver, M.D., Smith, M.W., and Jin, L. Difficulties in estimation of ethnic affiliation. Reply to Brenner. *Am J Hum Genet* 62: 1560–1561, 1998.
48. Huttley, G.A., Smith, M.W., Carrington, M., and O'Brien, S.J.: A scan for linkage disequilibrium across the human genome. *Genetics* 192: 1711–1722, 1999.
49. Svard, S.G., Rafferty, C., McCaffrey, J.M., Smith, M.W., Reiner, D.S., and Gillin, F.D.: A signal recognition particle receptor gene from the early-diverging eukaryote, *Giardia lamblia*. *Mol Biochem Parasitol* 98: 253–264, 1999.
50. Stephens, J.C., Smith, M.W., and O'Brien, S.J. Tracking linkage disequilibrium in admixed populations with MALD using microsatellite loci. In: *Microsatellites: Evolution and Applications*, Goldstein, D.B. and Schlötterer, C. (Eds.), Oxford University Press, Oxford, 1999, pp. 211–224.
51. Bream, J.H., Young, H.A., Rice, N., Martin, M.P., Smith, M.W., Carrington, M., and O'Brien, S.J. *CCR5* promoter alleles distinguished by specific DNA binding factors. *Science* 284: 283a, 1999.
52. Bream, J.H., Carrington, M., O'Toole, S., Dean, M., Gerrard, B., Shin, H.D., Kosack, D., Modi, W., Young, H.A., and Smith, M.W. Polymorphisms of the human *IFNG* gene noncoding regions. *Immunogenetics* 51: 50–58, 2000.
53. Lautenberger, J.A., Stephens, J.C., O'Brien, S.J., and Smith, M.W. Significant admixture linkage disequilibrium across 30 cM around the *FY* locus in African Americans. *Am J Hum Genet* 66: 969–978, 2000.
54. Shrestha, S., Strathdee, S.A., Brahmbatt, H., Farzadegan, H., Vlahov, D., and Smith, M.W. Short tandem repeat (STR) genotype identification of single-person versus multi-person use of syringes. *AIDS* 14: 1507–1513, 2000.
55. Ping A., Martin, M.P., Nelson, G.W., Carrington, M., Smith, M.W., Gong, K., Vlahov, D., O'Brien, S.J., and Winkler, C.A. Influence of *CCR5* promoter haplotypes on AIDS progression in African Americans. *AIDS* 14: 2117-2122, 2000.

56. Shin, H.D., Winkler, C., Stephens, J.C., Bream, J., Young, H., Goedert, J.J., O'Brien, T.R., Vlahov, D., Buchbinder, S., Giorgi, J., Rinaldo, C., Donfield, S., Willoughby, A., O'Brien, S.J., and Smith, M.W. Genetic restriction of HIV-1 pathogenesis to AIDS by promoter alleles of *IL10*. *Proc Natl Acad Sci U S A* 97: 14467–14472, 2000.
57. O'Brien, S.J., Dean, M., Smith, M.W., Winkler, C., Nelson, G.W., Martin, M.P., and Carrington, M. The human genes that limit AIDS. In: *Genes and Resistance to Diseases*, Boulyhenkov, V., Berg, K., and Christen, Y. (Eds.), Springer-Verlag, Berlin, 2000, pp. 9–17.
58. O'Brien, S.J., Nelson G.W., Winkler C.A., and Smith M.W. Polygenic and multifactorial disease gene association in man: Lessons from AIDS. *Ann Rev Genet* 34: 563–591, 2000.
59. Foster, C.B., Shaoxian Z., Erichsen, H.C., Lehrnbecher, T., Hart, E.S., Choi, E., Stein, S., Smith, M.W., Steinberg, S.M., Imbach, P., Kuhne, T., Chanock S. for the Early Chronic ITP Study Group. Polymorphisms in inflammatory cytokines and Fc receptors in childhood chronic immune thrombocytopenic purpura: a pilot study. *Br J Haematol* 113: 596–599, 2000.
60. Smith, M.W., Lautenberger, J.A., Shin, H.D., Gilbert, D.A., and O'Brien, S.J. Markers for mapping by admixture linkage disequilibrium in African Americans and Hispanic populations. *Amer J Hum Genet* 69: 1080–1094, 2001.
61. Oleksyk, T.K., Smith, M.H., Glenn, T.G., Purdue, J.R., Jagoe, C.H., and Smith, M.W. Radioactivity and genetic diversity in populations of *Apodemus flavicollis* from Chornobyl, Ukraine. In: *Proceedings from the International Conference on Radioactivity in the Environment*, Borretzen, P., Jolle, T., and Strand, P. (Eds.), *J Environ Radioact*, 2002, pp. 167–171.
62. Breen, E.C., Boscardin, W.J., Detels, R., Jacobson, L.P., Smith, M.W., O'Brien, S.J., Chmiel, J.S., Rinaldo, C.R., Lai, S., and Martinez-Maza, O. Non-Hodgkin's B cell lymphoma in persons with acquired immunodeficiency syndrome is associated with increased serum levels of *IL10* promoter -592 C/C genotype. *Clin Immunol* 109: 119–129, 2003.
63. Family Investigation of Nephropathy and Diabetes Research Group, Knowler, W.C., Coresh, J., Elston, R.C., Freedman, B.I., Iyengar, S.K., Kimmel, P.L., Olson, J.M., Plaetke, R., Sedor, J.R., and Seldin, M.F. The family investigation of nephropathy and diabetes (FIND): design and methods. *J Diab* 19:1–9, 2003.
64. Patterson, N., Hattangadi, N., Lane, B., Lohmueller, K., Hafler, D.A., Oksenberge, J.R., Hauser, S.L., Smith, M.W., O'Brien, S.J., Atshuler, A., Daly, M.N., and Reich, D. Methods for high-density admixture mapping of disease genes. *Am J Hum Genet* 74:979–1000, 2004.
65. Silverberg, M.J., Smith, M.W., Chmiel, J.S., Detels, R., Margolick, J.B., Rinaldo, C.R., O'Brien, S.J., Munoz, A. Fraction of AIDS cases prevented by the interactions of identified restriction gene variants. *Am J Epidemiol* 159: 232–241, 2004.

66. Smith, M.W., Patterson, N., Lautenberger, J.A., Truelove, A.L., McDonald, G.J., Waliszewska, A., Kessing, B.D., Malasky, M.J., Scafe, C., Le, E., De Jager, P.L., Mignault, A.A., Yi, Z., de The, G., Essex, M., Sankale, J.L., Moore, J.H., Poku, K., Phair, J.P., Goedert, J.J., Vlahov, D., Williams, S.M., Tishkoff, S.A., Winkler, C.A., De La Vega, F.M., Woodage, T., Sninsky, J.J., Hafler, D.A., Atshuler, D., Gilbert, D.A., O'Brien, S.J., and Reich, D. A high-density admixture map for disease gene discovery in African Americans. *Am J Hum Genet* 74: 1001–1013, 2004.
67. Oleksyk, T.K., Goldfarb, L.G., Sivtseva, T., Danilova, A.P., Osakovskiy, V.L., Shrestha, S., O'Brien, S.J., and Smith, M.W. Evaluating association and transmission of eight inflammatory genes with Viliuisk encephalomyelitis susceptibility. *Euro J Immunogen* 31: 121–128, 2004.
68. Goldstein, A.M., Struewing, J.P., Fraser, M.C., Smith, M.W., and Tucker, M.A. Prospective risk of cancer in *CDKN2A* germline mutation carriers. *J Med Genet* 41:421–424, 2004.
69. Winkler, C.A., Hendel, H., Carrington, M., Smith, M.W., Nelson, G.W., O'Brien, S.J., Phair, J., Vlahov, D., Jacobson, L.P., Rappaport, J., Vasilescu, A., Bertin-Maghit, S., An, P., Lu, W., Andrieu, J.M., Schachter, F., Therwath, A., and Zagury, J.F. Dominant effects of *CCR2-CCR5* haplotypes in HIV-1 disease progression. *J Acquir Immune Defic Syndr* 37: 1534–1538, 2004.
70. Shrestha, S., Smith, M.W., Beaty, T.H., and Strathdee, S.A. Theory and methodology for utilizing genes as biomarkers to determine potential biological mixtures. *Ann Epidemiol* 15: 29–38, 2005.
71. Oleksyk, T.K., Thio, C.L., Truelove, A.L., Goedert, J.J., Donfield, S.M., Kirk, G.D., Thomas, D.L., O'Brien, S.J., and Smith, M.W. Single nucleotide polymorphisms and haplotypes in the *IL10* region associated with HCV clearance. *Genes Immun* 6: 347–357, 2005.
72. Liu , Y.M., Berthier-Schaad, , Y., Fink, N.E., Fallin, M.D., Tracy, R.P., Klag, M.J., Smith, M.W., and Coresh, J. Beta fibrinogen haplotypes and the risk of cardiovascular disease in a dialysis cohort. *Amer J Kid Dis* 46: 78–85, 2005.
73. Smith, M.W., and O'Brien, S.J. Mapping by admixture linkage disequilibrium: advances, limitations and guidelines. *Nat Rev Genet* 6: 623–662, 2005.
74. Shrestha, S., Strathdee, S.A., Galai, N., Oleksyk, T., Fallin, D., Mehta, S., Schaid, D., Vlahov, D., O'Brien, S.J., and Smith, M.W. Behavioral risk exposure and host genetics of susceptibility to HIV-1 infection. *J Infect Dis* 193: 16–26, 2006.
75. Laud, K., Marian, C., Avril, M.F., Barrois, M., Chompret, A., Goldstein, A.M., Tucker, M.A., Clark, P.A., Peters, G., Chaudru, V., Demenais, F., Spatz, A., Smith, M.W., Lenoir, G.M., and Bressac-de Paillerets, B. Comprehensive analysis of *cdkn2a* (p16ink4a/p14arf) and *cdkn2b* genes in 53 melanoma index cases considered to be at heightened risk of melanoma. *J Med Genet* 43: 39–47, 2006.
76. Shrestha, S., Strathdee, S.A., Broman, K., and Smith, M.W. Unknown biological mixtures evaluation using STR analytical quantification. *Electrophoresis* 27: 409–415, 2006.

77. Liu, Y.M., Berthier-Schaad, Y., Fallin, M.D., Fink, N.E., Tracy, R.P., Klag, M.J., Smith, M.W., and Coresh, J. IL-6 haplotypes, inflammation, and risk for cardiovascular disease in a multiethnic dialysis cohort. *J Am Soc Neph* 17: 863–870, 2006.
78. Zhang, L., Kao, W.H.L., Berthier-Schaad, Y., Liu, Y.M., Plantinga, L., Jaar, B., Fink, N., Powe, N., Klag, M., Smith, M.W., and Coresh, J. Haplotype of signal transducer and activator of transcription 3 gene predicts cardiovascular disease in dialysis patients. *J Am Soc Neph* 8: 2285–2292, 2006.
79. Chretien, J.-P., Coresh, J., Berthier-Schaad, Y.B., Kao, W.H.L., Fink, N.E., Klag, M.J., Marcovina, S.M., Giaculli, F., and Smith, M.W. Three single-nucleotide polymorphisms in *LPA* account for most of the increase in lipoprotein(a) level elevation in African Americans compared with European Americans. *J Med Genet* 43: 917–923, 2006.
80. Liu, Y.M., Berthier-Schaad, Y., Plantinga, L., Fink, N.E., Tracy, R.P., Kao, W.H., Klag, M.J., Smith, M.W., and Coresh, J. Functional variants in the lymphotoxin-alpha gene predict cardiovascular disease in dialysis patients. *J Am Soc Neph* 17: 3158–3166, 2006.
81. Shrestha, S., Smith, M.W., Broman, K.W., Homayoon, F., Vlahov, D., and Strathdee, S. Multiperson use of syringes among injection drug users in a needle exchange program: a gene-based molecular epidemiological analysis. *J AIDS* 43: 335–343, 2006.
82. Lind, J.M., Hutcheson-Dilks, H.B., Williams, S.M., Moore, J.H., Essex, M., Ruiz-Pesini, E., Wallace, D.C., Tishkoff, S.A., O'Brien, S.J., and Smith, M.W. Elevated male European and female African contributions to the genomes of African American individuals. *Hum Genet* 120: 713–722, 2007.
83. Zhang, L., Kao, W.H.L., Berthier-Schaad, Y., Plantinga, L., Fink, N., Smith, M.W., Coresh, J. C-reactive protein (*CRP*) haplotype predicts longitudinal serum CRP levels but not cardiovascular disease risk in a dialysis cohort. *Am. J. Kidney Dis* 49:118–126, 2007.
84. Berthier-Schaad, Y., Kao, W.H.L., Corest, J., Zhang, L., Ingersoll, R.G., Stephens, R., and Smith, M.W. Reliability of high throughput genotyping of whole genome amplified DNA in SNP genotyping studies. *Electrophoresis* 28:2812–2827, 2007.
85. Iyengar, S.K., Abboud, H.E., Goddard, K.A.B., Saad, M.F., Adler, S.G., Arar, N.H., Bowden, D.W., Duggirala, R., Elston, R.C., Hanson, R.L., Ipp, E., Kao, W.H.L., Kimmel, P.L., Klag, M.J., Knowler, W.C., Meoni, L.A., Nelson, R.G., Nicholas, S.B., Pahl, M.V., Parekh, R.S., Quade, S.R.E., Rasooly, R.S., Rich, S.S., Rotter, J.I., Scavini, M., Schelling, J.R., Sedor, J.R., Sehgal, A.R., Shah, V.O., Smith, M.W., Taylor, K.D., Winkler, C.A., Zager, P.G., and Freedman, B.I. on behalf of the Family Investigation of Nephropathy and Diabetes Research Group. Genome-wide scans for diabetic nephropathy and albuminuria in multiethnic populations: the family investigation of nephropathy and diabetes (FIND). *Diabetes* 56:1577–85, 2007.
86. Parekh, R.S., Kao, W.H.L., Meoni, L.A., Ipp, E., Kimmel, P.L., La Page, J., Fondran, C., Knowler, W.C., Klag, M.J., and the Family Investigation of Nephropathy and Diabetes Research Group. Reliability of urinary albumin, total protein, and creatinine assays after prolonged storage: the family investigation of nephropathy and diabetes. *Clin J Am Soc Nephrol* 2: 1156-1162 2007.

87. Schelling, J.R., Abboud, H.E., Nicholas, S.B., Pahl, M.V., Sedor, J.R., Adler, S.G., Arar, N.H., Bowden, D.W., Elston, R.C., Freedman, B.I., Goddard, K.A.B., Guo, X., Hanson, R.L., Ipp, E., Iyengar, S.K., Jun, G., Kao, W.H.L., Kasinath, B.S., Kimmel, P.L., Klag, M.J., Knowler, W.C., Nelson, R.G., Parekh, R.S., Quade, S.R., Rich, S.S., Saad, M.F., Scavini, M., Smith, M.W., Taylor, K., Winkler, C.A., Zager, P.G., Shah, V.O. on behalf of the Family Investigation of Nephropathy and Diabetes Research Group. Genome-wide scan for estimated glomerular filtration rate in multiethnic populations: the family investigation of nephropathy and diabetes (FIND). *Diabetes* 57:235–243, 2007.
88. Oleksyk, T.K., Zhao, K., De La Vega, F.M., Gilbert, D.A., O'Brien, S.J., and Smith, M.W. Identifying selected regions from heterozygosity and divergence using a light-coverage genomic dataset from two human populations. *PLoS One* 3:1–15, 2008.
89. Truelove, A.L., Oleksyk, T.K., Shrestha, S., Thio, C.L., Goedert, J.J., Donfield, S.M., Kirk, G.D., Thomas, D.L., O'Brien, S.J., and Smith, M.W. Evaluation of *IL10*, *IL19*, and *IL20* gene polymorphisms, and chronic hepatitis B infection outcome. *Intl J Immunogenet* 35:255-264, 2008.
90. Hutcheson, H.B., Lautenberger, J.A., Nelson, G.W., Pontius, J.U., Kessing, B.D., Winkler, C.A., Smith, M.W., Johnson, R., Stephens, R., Phair, J., Goedert, J.J., Donfield, S., and O'Brien, S.J. Detecting AIDS restriction genes: From candidate genes to genome-wide association discovery. *Vaccine* 26:2451-2465. 2008.

In Press:

1. Kottgen, A., Hsu, C.C., Coresh, J., Shuldiner, A.R., Berthier-Schaad, Y., Gambhir, T.R., Smith, M.W., Boerwinkle, E., Kao, W.H. The association of podocin R229Q polymorphism with increased albuminuria or reduced estimated GFR in a large population-based sample of U.S. adults. *Am J Kidney Dis.*, 2008.

Submitted:

1. Kopp, J.B., Smith, M.W., Johnson, R.C., Freedman, B.I., Bowden, D.W., Oleksyk, T., McKenzie, L.M., Ahuja, T.S., Cho, M.E., Dart, R.A., Kimmel, P.L., Korbet, S.M., Michael, D.M., Mokryzcki, M.H., Schelling, J.R., Simon, E., Trachtman, H., Vlahov, D., Kajiyama, H., Nelson, G.W., and Winkler, C.A. Genome-wide admixture mapping identifies *MYH9* as a major effect risk gene for focal segmental glomerulosclerosis and hypertensive end-stage kidney disease in African Americans. *Nat Genet*, Revised June 2008.
2. Kao, W.H.L., Klag, M., Meoni, L.A., Reich, D., Bethier-Schaad, Y., Li, M., Coresh, J., Patterson, N., Powe, N.R., Fink, N.E., Sadler, J., Weir, M., Adler, S., Divers, J., Iyengar, S., Freedman, B.I., Kamp, K., Kohn O.F., Leehey, D.J., Nicholas, S., Pahl, M., Schelling, J., Sedor, J.R., Thornley-Brown, D., Winkler, C., Smith, M.W., and Parekh, R.S. A genome-wide admixture scan identifies *MYH9* as a candidate locus associated with non-diabetic end stage renal disease in African Americans. *Nat Genet*, Revised June 2008.
3. Oleksyk, T.K., Shrestha, S., Truelove, A., O'Brien, S.J., and Smith, M.W. Association of extended *IL10* haplotypes with HIV progression to AIDS. *Genes Immun*, June 2008.
4. Volfovsky, N., Oleksyk, T.K., Cruz, K.C., Truelove, A.L., Stephens, R.M., and Smith, M.W. Chimpanzee chromosome 23 vs. human 22: genomic insertion, deletion and ancestral indel polymorphisms. *BMC Genomics*, June 2008