BIOGRAPHICAL SKETCH

Michael F. Hammer
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A. Education/Training

Institution	Degree	Year	Field of Study
Lake Forest College, IL	BA	1976	Biology
University of California, Berkeley, CA	PhD	1984	Genetics

B. Personal Statement

Dr. Hammer is a Research Scientist in the Division of Biotechnology at the University of Arizona with appointments in the Department of Ecology and Evolutionary Biology, Bio5, the School of Anthropology, the University of Arizona Cancer Center, and the Steele Children's Research Center. Since 1991 he has been Director of the University of Arizona Genetics Core (UAGC), a facility that provides training and molecular biology services to University and biotechnology communities at large. After receiving his Ph.D. in Genetics at the University of California at Berkeley in 1984, Dr. Hammer performed post-doctoral research at Princeton and Harvard. Over the past two decades, Dr. Hammer headed a productive research lab in human evolutionary genetics, resulting in over 100 published articles documenting the African origin of human diversity, interbreeding between modern humans and archaic forms of the genus *Homo*, and genome diversity in the great apes. His lab was an early adopter of next generation sequencing (NGS) technology and the application of whole genome analysis in humans, and has been a key player in the Gibbon and Baboon Genome Projects, as well as a consortium that has analyzed the genomes of over 100 Great Apes (GAPE Project). In the past 3 years, Dr. Hammer's team has been exploring the use of NGS methods to discover the underlying genetic architecture of neurodevelopmental disorders. This has led to the publication of articles identifying pathogenic variants associated with epileptic encephalopathies in young children.

C. Positions and Honors

1978 to 1984	Graduate Student, Biochemistry Department, University of California, Berkeley, with Dr. Allan C. Wilson. Dissertation**:** "Of Mice and Lysozyme: Evolution and Regulatory Genetics" (1984)
1985 to 1988	Postdoctoral Fellow, Princeton University with Dr. Lee M. Silver Origin and evolution of mouse *t* haplotypes.
1988 to 1991	Postdoctoral Fellow, Harvard University with Dr. Richard C. Lewontin The Y chromosome and human evolution.
1991 to present	Director of the University of Arizona Genetics Core (UAGC) Facility, Assistant Research Scientist, ARL Division of Biotechnology, University of Arizona, Tucson, Arizona (1991) Joint appointment in the Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, Arizona (1992) Associate Research Scientist, ARL Division of Biotechnology, University of Arizona, Tucson, Arizona (1997) Faculty member Graduate Interdisciplinary Program in Genetics (1997) Member of Arizona Cancer Center (1997)

Joint appointment in School of Anthropology, University of Arizona, Tucson, Arizona (1999)
Member of BIO5 (2000)
Full Research Scientist, ARL Division of Biotechnology, University of Arizona, Tucson, Arizona (2002)
Member of Steele Children's Research Center (2013)

Lake Forest College Dean's List, Beta Beta Beta, Phi Beta Kappa 1976
Society of Sigma Xi Commendations in Biology 1976
National Institutes of Health Training Grant GM07127 1978-1984
National Institutes of Health Postdoctoral Fellowship GM10728 1985-1988
Alfred P. Sloan Postdoctoral Fellow 1989-1991
Member of Center for Academic Research and Training in Anthropogeny (CARTA) 2013

D. Peer-Reviewed Publications (10 recent publications)

1. Veeramah KR, Johnstone L, Karafet TM, Wolf D, Sprissler R, Salogiannis J, Barth-Maron A, Greenberg ME, Stuhlmann T, Weinert S, Jentsch TJ, Pazzi M, Restifo LL, Talwar D, Erickson RP, Hammer MF (2013) Exome sequencing reveals new causal mutations in children with epileptic encephalopathies. Epilepsia. doi: 10.1111/epi.12201
2. Veeramah KR, Karafet TM, Wolf D, Samson RA, Hammer MF (2013) The KCNJ8-S422L variant previously associated with J-wave syndromes is found at an increased frequency in Ashkenazi Jews. Eur J Hum Genet. doi: 10.1038/ejhg.2013.78.
3. Hammer MF (2013) Human hybrids. Sci Am 308(5):66-71.
4. Mendez FL, Watkins JC, Hammer MF (2013) Neandertal origin of genetic variation at the cluster of OAS immunity genes. Mol Biol Evol 30(4):798-801.
5. Mendez FL, Krahn T, Schrack B, Krahn AM, Veeramah KR, Woerner AE, Fomine FL, Bradman N, Thomas MG, Karafet TM, Hammer MF (2013) An African American paternal lineage adds an extremely ancient root to the human Y chromosome phylogenetic tree. Am J Hum Genet 92(3):454-459.
6. Prado-Martinez, J., Sudmant, P.H., Kidd, J.M., Li, H., Kelley, J.L., Lorente-Galdos, B., Veeramah, K.R., Woerner, A.E., O'Connor, T.D., Santpere, G., Cagan, A., Theunert, C., Casals, F., Laayouni, H., Munch, K., Hobolth, A., Halager, A.E., Malig, M., Hernandez-Rodriguez, J., Hernando-Herraez, I., Prüfer, K., Pybus, M., Johnstone, L., Lachmann, M., Alkan, C., Twigg, D., Petit, N., Baker, C., Hormozdiari, F., Fernandez-Callejo, M., Dabad, M., Wilson, M.L., Stevison, L., Camprubí, C., Carvalho, T., Ruiz-Herrera, A., Vives, L., Mele, M., Abello, T., Kondova, I., Bontrop, R.E., Pusey, A., Lankester, F., Kiyang, J.A., Bergl, R.A., Lonsdorf, E., Myers, S., Ventura, M., Gagneux, P., Comas, D., Siegismund, H., Blanc, J., Agueda-Calpena, L., Gut, M., Fulton, L., Tishkoff, S.A., Mullikin, J.C., Wilson, R.K., Gut, I.G., Gonder, M.K., Ryder, O.A., Hahn, B.H., Navarro, A., Akey, J.M., Bertranpetit, J., Reich, D., Mailund, T., Schierup, M.H., Hvilsom, C., Andrés, A.M., Wall, J.D., Bustamante, C.D., Hammer, M.F., Eichler, E.E., Marques-Bonet, T. (2013). Great ape genetic diversity and population history. Nature 499, 471-475.
7. Veeramah KR, Wegmann D, Woerner A, Mendez FL, Watkins JC, Destro-Bisol G, Soodyall H, Louie L, Hammer MF (2012) An early divergence of KhoeSan ancestors from those of other modern humans is supported by an ABC-based analysis of autosomal resequencing data. Mol Biol Evol 29(2):617-630.
8. Veeramah KR, O'Brien JE, Meisler MH, Cheng X, Dib-Hajj SD, Waxman SG, Talwar D, Girirajan S, Eichler EE, Restifo LL, Erickson RP, Hammer MF (2012) De novo pathogenic SCN8A mutation identified by whole-genome sequencing of a family quartet affected by infantile epileptic encephalopathy and SUDEP. Am J Hum Genet 90(3):502-510.

9. Meyer M, Kircher M, Gansauge MT, Li H, Racimo F, Mallick S, Schraiber JG, Jay F, Prufer K, de Filippo C, Sudmant PH, Alkan C, Fu Q, Do R, Rohland N, Tandon A, Siebauer M, Green RE, Bryc K, Briggs AW, Stenzel U, Dabney J, Shendure J, Kitzman J, Hammer MF, Shunkov MV, Derevianko AP, Patterson N, Andres AM, Eichler EE, Slatkin M, Reich D, Kelso J, Paabo S (2012) A high-coverage genome sequence from an archaic Denisovan individual. Science 338(6104):222-226.
10. Mendez FL, Watkins JC, Hammer MF (2012) A haplotype at STAT2 Introgressed from neanderthals and serves as a candidate of positive selection in Papua New Guinea. Am J Hum Genet 91(2):265-274.

E. Current Research Support

National Science Foundation (1025266) 09/15/10-08/14/13
Testing Models of Genetic an Linguistic Change in the Caucasus Mountains $347,455
The goals of this project are to use genetic markers to investigate the co-evolution of genes, languages and culture, to explore the history of settlement of the Caucasus Mountains, and the robustness of social structure at the village scale.
Role: Principal Investigator

National Institutes of Health 05/01/10-04/30/14
*Genomic Patterns of Polymorphism in Primates (*5R01HG005226) $1,735,377
A major goal of this proposal is to construct a large whole genome sequence database from 8 primate species using next generation sequencing technologies to elucidate mechanisms of speciation and the evolutionary forces acting within primate populations.
Role: Co-Principal Investigator

Dravet Syndrome Foundation 09/01/13-08/31/15
Identifying modifier genes in patients with SCN1A haploinsufficiency using whole exome sequencing *$187,000*
The major goal of this project is to explore the role that modifier genes may play in altering the phenotype of patients with haploinsufficiency at *SCN1A*
Role: Co-Principal Investigator

National Science Foundation (1203874) 04/01/13-03/31/16
The genetic basis of adaptation to climatic stress in Siberian indigenous populations $295,535
The major goal of this project is to identify genes underlying adaptation to cold climate, or that function in pathways involved to energy metabolism or cold-adapted traits in populations living in the northernmost settlements of Siberia.
Role: Co-Principal Investigator

F. Research Advising and Training

Undergraduates (75)
Graduate Students (20)
Postdoctoral fellows (11)