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1974	Bachelor of Statistics (Honors), Indian Statistical Institute, Calcutta, India
1974–1979	Graduate Assistant and Research Technician II, Center for Demographic and Population Genetics University of Texas Health Science Center at Houston, TX
1979	Ph.D., University of Texas Health Science Center at Houston, TX
1979–1980	Research Fellow, Department of Epidemiology, University of Washington, Seattle, WA
1980–1985	Assistant Professor of Human Genetics and Biostatistics, Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA
1982–1988	Member, Center for Multivariate Analysis, University of Pittsburgh, Pittsburgh, PA
1985–1989	Associate Professor of Human Genetics and Biostatistics, Department of Biostatistics, University of Pittsburgh, Pittsburgh, PA
1986–1991	Adjunct Associate Professor of Anthropology, Department of Anthropology, The Pennsylvania State University
1987–1993	Member, Pittsburgh Cancer Institute, University of Pittsburgh, Pittsburgh, PA
1988–1993	Associate Professor of Psychiatry, Associate Director, Molecular Neurobiology and Genetics Program, Department of Psychiatry, University of Pittsburgh School of Medicine, Pittsburgh, PA
1989–1991	Associate Professor of Human Genetics, Department of Human Genetics, University of Pittsburgh, Pittsburgh, PA
1991–1993	Professor of Human Genetics and Psychiatry, Department of Human Genetics, Department of Psychiatry, University of Pittsburgh, Pittsburgh, PA
1994	Adjunct Professor of Psychiatry, Department of Psychiatry, University of Pittsburgh Professor of Genetics, Department of Genetics , Member, Center for Human GeneticsMember, Ireland Cancer Center, Case Western Reserve University
1998	James H. Jewell Professor of Genetics, Department of Genetics, Case Western Reserve University

Identifying disease alleles by genome sharing

All of genetics is concerned with associating specific trait alleles with specific phenotypes. The challenge is to find the trait alleles in a vast genome given a phenotype. Whether one chooses linkage or association studies for tracking such alleles, the essential problem is detection of those segments of the genome shared identical-by-descent (IBD) between a group of affecteds. The current discussions, and sometimes disagreements, of the relative utility of each method depends on our elucidating the nature of human genetic variation. I shall describe empirical observations of sequence variation in genes and genomic segments that provide insights into measuring IBD segments in unrelateds, and thus how association studies can be designed.