Announcements[1]

Employment Opportunities

Pre- and Postdoctoral Positions in Statistical Genetic Analysis and Genetic Epidemiology.—The Genetics of Complex Disorders (GCD) training program in the Department of Psychiatry at Columbia University provides pre- and postdoctoral training in the genetic epidemiology and statistical genetic analysis of complex diseases, including psychiatric disorders. Our mission is to train scientists who will be aware of all aspects of genetic studies, including study design, clinical aspects, phenotype definition, molecular laboratory issues, and statistical analysis. Training includes both didactic components (coursework and lab rotations) and research. We seek applicants with training in statistics, epidemiology, and/or genetics and with demonstrated interest in pursuing a career in the genetic analysis of complex disorders. Applicants for postdoctoral positions must have a Ph.D., an M.D., or the equivalent; predoctoral applicants need a master's degree. Further information can be obtained from our Web site (http://cpmcnet.columbia.edu/dept/sph/epi/gcd/) or from the following mailing address: Susan E. Hodge, D.Sc., NYSPI, Unit 24, 1051 Riverside Drive, New York, NY 10032. Columbia University is an affirmative action/equal opportunity employer. Applicants must be U.S. citizens or permanent resident aliens.

Project Scientist.—A research position is available immediately at the Cleveland Clinic Foundation (CCF) Center for Cardiovascular Genetics and Department of Molecular Cardiology and at the Cleveland Clinic College of Medicine at Case Western Reserve University. The CCF cardiovascular medicine program is one of the largest such programs in the United States and has been consistently ranked first for the past 10 years by U.S. News and World Report. We use cutting-edge technologies to clone and functionally characterize genes for various cardiovascular diseases. State-of-the-art research facilities are available for these projects. The CCF Center for Cardiovascular Genetics is directed by Dr. Qing Wang, who has been a key researcher involved in discovering three genes for long QT syndrome, the first gene for Brugada syndrome, the first gene for Klippel-Trenaunay syndrome, and the first nonlipid-related disease-causing gene for coronary artery disease and myocardial infarction. We are recruiting an experienced scientist to expand our research programs into either the molecular genetics of heart failure or stem-cell biology in cardiovascular medicine. Applicants with experience in the genetics of heart failure or stem-cell biology are preferred. Interested applicants should submit a curriculum vitae and the names of and contact information for three references to Dr. Qing Wang, Center for Cardiovascular Genetics, ND40, Lerner Research Institute, The Cleveland Clinic Foundation, 9500 Euclid Avenue, Cleveland, OH 44195; fax: (216) 445-4990; e-mail: wangq2@ccf.org. For more information about our projects, please visit our Web site (http://www.lerner.ccf.org/moleccard/wang/).

Samples Available

Positive Control Samples for Molecular Genetic Testing.—The Centers for Disease Control and Prevention and the Coriell Institute for Medical Research announce the availability of positive control samples derived from transformed cell lines for use in molecular genetic testing. The DNA samples prepared from these validated cell lines are available through the Coriell Cell Repositories (http://ccr.coriell.org/cdc/). Diseases include cystic fibrosis (CF), 5,10-methylenetetrahydrofolate reductase (MTHFR) deficiency, HFE-associated hereditary hemochromatosis, Huntington disease (HD), fragile X syndrome, Muenke syndrome, connexin 26–associated

1. Announcements are published free of charge for members of The American Society of Human Genetics (ASHG). Please e-mail announcements to ajhg@emory.edu. Submission must be received *at least 7 weeks* before the month of issue in which publication is requested. They must be double spaced with a $1\frac{1}{2}$-inch margin on all sides. The maximum length is *250 words,* excluding the address for correspondence. Please include a cover letter indicating the name of the sponsoring ASHG member.

deafness, and α-thalassemia. These validated cell lines contain mutations of public-health importance, some of which were not previously available. The CF samples contain mutations associated with unique populations (394delTT and S1235R), combinations of IVS8 polythymidine tract variants (5T, 7T, and 9T), and muta tions not previously available (I148T and 1078delT). Three DNA samples with homozygous MTHFR-related mutations (A222V/A222V) are available. Hemochromatosis-associated samples include a compound HFE heterozygote (H63D/S65C) as well as other combinations of HFE alleles. DNA samples with triplet repeats at the intermediate range are available for study of HD (31 repeats) and fragile X syndrome (56 repeats). Mutations were confirmed by reference testing and multilaboratory pilot testing in all cell lines from which the DNA has been prepared. Control DNA samples that are negative for all mutations are also available. Information about ordering these samples can be obtained from the Web catalog (http://ccr.coriell.org/cdc/comm/order/order.html). Further information can be obtained from Jeanne C. Beck, Ph.D., Coriell Institute for Medical Research, Coriell Cell Repositories, 403 Haddon Avenue, Camden, NJ 08103.

Database Available

CEPH Genotype Database, Version 10.—The Foundation Jean Dausset–Centre dEtude du Polymorphisme Humain (CEPH) has released version 10 of the CEPH Genotype Database (http://www.cephb.fr/cephdb/). The database contains genotypes for 32,356 DNA markers that have been accumulated since 1985 for 874 individuals from 65 CEPH reference families (Genomics [1990] 6:575–577). Included in the database are genotypes for 21,480 biallelic markers, of which 17,512 are identified in dbSNP by rs or ss numbers. The database contains genotypes for >9,900 microsatellite markers. The mean observed heterozygote frequency is 0.438 for all the loci in version 10 and 0.698 for identifiable microsatellites, of which 56% are highly polymorphic (observed heterozygote frequency $\geqslant$0.70). The CEPH database now manages 6,081,570 genotypes. A total of 25,924,717 LOD scores have been computed between all pairs of syntenic loci. Each of 32,023 markers is assigned to a chromosome by linkage or other means. Genotypes may be downloaded by marker ID, chromosome, family, and observed heterozygote frequency. In addition to genotypes by family, downloadable information includes allele frequencies, lists of close (linked) markers, and graphically represented pedigrees with genotypes. Version 10 links to the National Center for Biotechnology Information (NCBI) Entrez Web site, allowing entry into the current build of dbSNP and other NCBI databases. CEPH collaborators and others who have genotyped CEPH reference families can submit data for markers directly through the CEPH Web server. Marker submissions require a submitter password, which is available by e-mail request (cephdbm@cephb.fr). File submission is also available after consultation with CEPH.