The UCSF Sandler Asthma Basic Research (SABRE) Center operates core facilities that are available to investigators funded by the American Asthma Foundation (AAF).

FUNCTIONAL GENOMICS CORE

The UCSF SABRE Center Functional Genomics Core Facility offers a comprehensive and integrated approach to next-generation sequencing. The multidisciplinary group interacts closely with investigators and offers support for all phases of each study, including experimental design, quality control, sample preparation, and data analysis. We have considerable experience with analyses of human samples and samples from various animal and cell culture model systems frequently used for asthma-related research.

Services Offered:
- Study design consultation
- RNA quality assessment
- Transcript profiling (RNA-Seq)
- micro-RNA profiling (small RNA-Seq)
- ChIP-Seq
- Data analysis

Information about the core is available at http://www.arrays.ucsf.edu.
David Erle, MD, Professor of Medicine, core director, david.erle@ucsf.edu, (415) 514-4370
Andrea Barczak, associate director, andrea.barczak@ucsf.edu, (415) 514-4373

GENETICS CORE

The UCSF SABRE Center Asthma Genetics Core Facility was established to foster genetic research in asthma. We offer AAF-funded investigators a “full service of SNP discovery, genetic testing and analyses.” We analyze promising candidate genes identified by AAF investigators using biologic material (DNA and plasma) from four large well-phenotyped cohorts of ethnically diverse subjects with asthma. Although we do not send out DNA or other biologic material, we have made the cohorts described below widely available to AAF-funded investigators. Projects will be prioritized based on a first come first serve basis. Depending upon available resources a recharge rate may be applied.

SNP Discovery: AAF-funded investigators may request SNP (sequence variant) discovery within asthma candidate genes. The Genetics Core will perform sequencing of coding regions using our SNP discovery panel which consists of 100 individuals (200 chromosomes) from African American, Latino and Caucasian subjects with asthma. Tagged SNPs and linkage disequilibrium patterns will be determined. Representative SNPs will then be genotyped in our existing cohorts of subjects with asthma.

Population of well phenotyped subjects with asthma: The Asthma Genetics Core makes use of four large asthma study populations: For Latino populations these include the Genetics of Asthma in Latino Americans (GALA I) Study and the Genes-environments & Admixture in Latino Asthmatics (GALA II). For African American populations these include the Study of African Americans, Asthma, Genes and Environments (SAGE I and SAGE II). Latinos and African Americans were selected because in the U.S. these populations have the highest asthma
prevalence, morbidity and mortality rates. Paradoxically, some Latino ethnic groups (Mexicans) have the lowest asthma prevalence and morbidity rates in the U.S.

The GALA I Study consists of 700 well-phenotyped Mexican and Puerto Rican families with asthma. Each family consists of an asthmatic proband and both biologic parents. The SAGE Study is a cross-sectional case-control study consisting of 470 well-phenotyped African American asthma cases and controls. Each asthmatic proband has undergone extensive phenotyping including drug responsiveness.

Replication populations: We are actively recruiting subjects for replicate cohorts. All subjects (cases and controls) will complete a comprehensive environmental, demographic and asthma questionnaire. All asthmatics will complete spirometry. In addition, phenotypic assessment in these cohorts will include environmental measures, methacholine challenge and allergen skin testing. GALA II includes more than 4000 asthma cases and controls and SAGE II includes 2000 African Americans (1000 cases and 1000 controls).

These study populations are intended to help AAF sponsored investigators test and validate important findings that will lead to a better understanding of genetic and environmental interactions related to asthma-related and pharmacogenetic traits.

To discuss potential collaborative projects for use of this core, contact Esteban G. Burchard, MD, MPH, Professor of Medicine and Biopharmaceutical Sciences, core director, esteban.burchard@ucsf.edu, (415) 514-9677.

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CALIFORNIA NATIONAL PRIMATE RESEARCH CENTER RESPIRATORY DISEASES CENTER

Scientists at the Respiratory Diseases Center located on the California National Primate Research Center (CNPRC) UC Davis campus provide assistance to outside investigators interested in conducting interventional studies using nonhuman primate models of human lung disease. In 2001, we were the first to report the development of a novel rhesus monkey model of allergic asthma using the common human allergen, house dust mite. Investigators interested in research projects using nonhuman primate models of asthma or other lung diseases (acute or chronic) may conduct studies using CNPRC Cores, which includes the Inhalation Exposure Core, Pulmonary Function Testing Laboratory, Multimodal Imaging Core, as well as Clinical Laboratories. Scientists and staff associated with each of the Cores provide consultation in experimental design, sample collection, data analysis, and offer assays that utilize species-specific reagents wherever possible. Scientists can also work with users to develop new assays to meet research needs.

Animal models offered at the CNPRC:
- Rhesus monkey pediatric allergic asthma
- Rhesus monkey adult allergic asthma
- Rhesus monkey non-atopic asthma
- Rhesus monkey cutaneous allergy
- Rhesus monkey airways inflammation (endotoxin, air pollutants, tobacco smoke)
- Rhesus monkey influenza
- Mouse models of allergic asthma and airways inflammation
- Mouse models of influenza

Information about the CNPRC is available at http://cnprc.ucdavis.edu
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