UCSF Sandler Asthma Basic Research (SABRE) Center
Core Facilities

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

MOUSE AIRWAY PHYSIOLOGY AND MICROSCOPY CORE

The mouse airway physiology and microscopy core is a SABRE-funded research facility that provides service to investigators who are interested in studying the molecular mechanisms of asthma, including AAF Awardees. The core laboratory is equipped with two Scireq FlexiVent pulmonary mechanics analyzers for the measurement of airway responsiveness in anesthetized, ventilated animals.

The core has developed several different protocols for antigen sensitization and challenge appropriate to different strains of commonly used mice (including C57BL/6, 129, BALB/c and FVB), and the core can perform both acute and chronic antigen challenge. The protocols can be modified according to the investigators' needs. Routine studies include acetylcholine concentration response curves in anesthetized/ventilated animals at baseline and after antigen (ovalbumin or aspergillus extract or house dust mite) sensitization and challenge. The core also performs bronchoalveolar lavage to determine total and differential cell counts, prepares fixed lung tissue to evaluate basic morphology, and performs PAS staining to evaluate mucus cell content. In addition, total and/or OVA-specific serum IgE is evaluated by ELISA. Special procedures (special staining, weekend treatment etc) are available at different rate. The core also provides training to students, technicians and post-doctoral fellows in techniques relevant to the animal models and their analysis.

If you are interested in utilizing this facility, or in having someone from your lab learn how to perform these studies or set them up in your own institution, please contact the **laboratory director, Dr. Xiaozhu Huang at 415-514-4272 or e-mail to xiaozhu.huang@ucsf.edu.**

FUNCTIONAL GENOMICS CORE

The UCSF SABRE Center Functional Genomics Core Facility offers a comprehensive and integrated approach to microarray and high throughput sequencing services. The multidisciplinary group interacts closely with investigators and offers support for all phases of each study, including experimental design, sample preparation, quality control, 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
- Messenger RNA (mRNA), micro-RNA (miRNA), ChIP-chip and CGH array analysis
- Illumina next generation sequencing
- Data analysis

Information about the core is available at http://www.arrays.ucsf.edu.
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GENETICS CORE

The 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 two 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 and on available resources.

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 two large asthma cohorts: the Genetics of Asthma in Latino Americans (GALA 1) Study and the Study of African Americans, Asthma, Genes and Environments (SAGE 1). In addition, we have two independent replicate populations: Genes-environments & Admixture in Latino Asthmatics (GALA 2) and SAGE 2. 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 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. Recruitment goals are for 4000 Latino subjects (2000 cases and 2000 controls) as part of the Genes-environments & Admixture in Latino Asthmatics (GALA 2) Study, and 1000 African Americans (500 cases and 500 controls) as part of SAGE 2.

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, M.D., M.P.H., Associate Professor of Medicine and Biopharmaceutical Sciences, core director, esteban@sfgh.ucsf.edu, 415-514-9677.**