

## UCSF Strategic Asthma Basic Research (SABRE) Center Core Facilities

The UCSF Strategic 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 Sandler-funded research facility that provides service to investigators who are interested in studying the molecular mechanisms of asthma. 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) sensitization and challenge. The core also performs bronchoalveolar lavage to determine total and differential cell counts, prepares frozen and/or fixed lung tissue to evaluate basic morphology, and performs PAS and Sirius Red staining to evaluate mucus cell content and sub-epithelial airway fibrosis. In addition, total and/or OVA-specific serum IgE is evaluated by ELISA. 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 to 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](mailto:xiaozhu.huang@ucsf.edu)**.

### FUNCTIONAL GENOMICS CORE

The UCSF SABRE Center Functional Genomics Core Facility was established in 2000 and facilitates the use of microarray technology by providing state-of-the-art technology and technical expertise. The core offers a comprehensive and integrated approach to array analysis. The multidisciplinary group interacts closely with investigators and offers support for all phases of each study, including experimental design, sample preparation, hybridization, quality control, data analysis, and database maintenance. 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.

In 2006, the core converted from 'home-made' arrays to the Agilent 60mer ink-jet platform. We have very extensive experience with using these arrays for analyzing mRNA and miRNA expression. We can analyze expression in small samples (<1 ng total RNA for mRNA analysis and ~100 ng total RNA for miRNA analysis). We also have some experience with other array-based studies, including ChIP-on-chip analysis. Arrays are available in multiple formats and are easily customizable at no additional cost.

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 Sandler 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 available resources.

**SNP Discovery:** AAF-funded investigators may request for 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 based cohorts 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) Study and the Study of African Americans, Asthma, Genes and Environments (SAGE). 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 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.

**New Cohorts:** We are initiating new recruitment efforts to build replicate cohorts. Recruitment will focus on Latino ethnic groups and African Americans, populations known to have high asthma prevalence, morbidity and mortality. 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 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.

The establishment of the new cohorts will provide important insight into the understanding of genetic and environmental interactions and the impact on racial/ethnic differences in asthma-related and pharmacogenetic traits among Latinos and African Americans. These cohorts will be available to AAF-funded investigators.

To discuss potential collaborative projects for use of this core, contact **Esteban G. Burchard, M.D., M.P.H., Assistant Professor of Medicine and Biopharmaceutical Sciences, core director, esteban @sfgh.ucsf.edu, 415-514-9677.**