22-Mouse CSS panel is now available

Pioneering research conducted at Case Western Reserve University, Cleveland, OH has led to a landmark in the study of mouse models of common human diseases. A unique panel of consomic strains has been developed, and is now available for commercial applications. This panel of 22 genetically engineered inbred strains enables researchers to perform experiments that were previously impossible. These strains save enormous time and funds in the study of complex traits because more genes are readily detected in fewer mice than with any other method. Additionally, the same strains can be used simultaneously for both gene discovery and functional studies. The mice can now be purchased as a complete panel or as individual strains for specific chromosomal studies.

Consomic mice have an entire single chromosome from one inbred strain of mice substituted into the inbred genetic background of another inbred strain. Each of the 22 strains in the panel was made by successive backcrossing to the host strain. More than 17,000 mice were genotyped over 7 years to produce these strains. This is the first complete panel in mammals that involves the systematic substitution of every chromosome. With a simple genome structure, consomic strains require a wider and easier array of statistical tools to be used in analysis. In contrast to other methods that are used to detect chromosome location, consomic strains do not require the use of costly, specialized algorithms or software applications. For both the initial genome scan and for subsequent higher resolution mapping, consomic strains are the most cost-effective, time-efficient and reliable method for successful phenotyping and genotyping. In addition, with their unique set of phenotypic properties, consomic strains can be used in powerful ways to test the efficacy, toxicity and side-effects of candidate drugs that may be used to treat particular aspects of disease.

Key Benefits of CSS Mapping:

More powerful than traditional approaches
Detect more genes in fewer mice

Easy replication of results
Validate results with mice from the same strains

Pinpoint chromosome locations quickly
Use crosses with the consomic strains or with congenic strains derived from the consomic strains to rapidly determine the number and location of genes on the substituted chromosome

Gene discovery
Because the DNA of both progenitor strains has been sequenced, genetic variants between the strains are already catalogued in databases. Researchers can therefore proceed directly to functional tests of candidate genes.

Functional tests
Because they are inbred, the same strains that are used for gene mapping and discovery can be used for functional studies to characterize the biological consequences of the genetic variants.

For more information and licensing inquiries, speak with our representative or contact Michael Haag, Case Western Reserve University at mhaag@case.edu or (216) 368-6106.