STUDIES OF HUMAN FAMILIES FOR GENETIC LINKAGE

One of the most important and exciting activities in human genetics involves the elucidation of man's genetic map by linking gene loci to each other and to specific chromosomes. Knowledge of man's genetic map will form the basis for antenatal and early post-natal detection of many hereditary disorders, will permit us to understand the molecular pathogenesis of the abnormalities resulting from various chromosomal abnormalities and, looking to the future, is fundamental for any attempts at genetic engineering. Linkage information in man is obtained primarily by two types of investigation, one involving in vitro interspecific somatic cell hybridization, and the other involving analysis of segregation of various genetic markers and marker chromosomes in human families. The latter approach, family studies for linkage determinations, has been an important and ongoing activity in the Genetics Laboratory of the Department of Pediatrics at Stanford University School of Medicine. This laboratory has the capability, facilities and experience in testing for a number of human polymorphic gene markers (mostly of blood) including red blood cell antigens, serum proteins and erythrocyte enzymes, and a number of families with disorders determined by x-linked or autosomal dominant genes have been studied for co-segregation of these genes and the various polymorphic marker genes. More recently we have been able, through close collaboration with the Tissue Typing Laboratory (Dr. Rose Payne) at Stanford, to incorporate the highly

polymorphic HL-A system into our family studies, improving the power for detecting linkage. Presently, we are applying techniques for giemsa and fluorochrome banding of human chromosomes to our linkage studies, taking advantage of these highly informative methods to identify specific chromosomes (or portions thereof) and to detect differences between homologous chromosomes within families in order to follow co-segregation of chromosomes and gene markers. Thus, we have expanded our capabilities for detecting linkage between gene loci and between loci and chromosomes, and we willsstudy, in a systematic manner, human families showing evidence of segregation of dominant and x-linked traits or cytogenetic markers. These linkage studies form one of the projects of a recently developed collaborative effort of the Departments of Pediatrics and Genetics at Stanford in human genetics research. We are committed to an ongoing program in genetic linkage studies in man, and we are seeking support for this important activity.