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Korean Genome Analysis Project (KoGAP)

PARK Chan
Division of Genome and Proteome Research, NGRI, Seoul, Korea

After the release of genome analysis data from HUGO at March 2000, Korea NIH immediately made a plan to establish the infrastructure for Korean genome research. By the decision of National Science and Technology Committee at October 2000, the National Genome Research Institute (NGRI) at Korea NIH was founded to facilitate genome research and support the hospital- and national-based genome centers in Korea. The institute is focusing on Korean genome research to identify disease-related genes of human complex diseases such as diabetes, asthma, hypertension, osteoporosis and so on. NGRI is currently collaborating 2 cohort-based and 12 disease-based genome centers to collect Korean genome resources (100,000 persons), including normal and patient samples and epidemiological information since March 2001. NGRI searches disease-related candidate genes and the relationship between disease and various factors including genotype, environments, and lifestyle, etc. Especially, to investigate the genetic effects on disease development and progression, several approaches are used such as SNP discovery, haplotype analysis, genome-wide scan and LD block analysis, etc. Also NGRI proceeds the collaboration with 'International Haplotype Map Consortium' through 'Korean Haplotype Consortium' composed with nation-wide genome scientists. The Korean Genome Analysis Project will provide a lot of infra-structural informations and resources for biomedical research in Korea and stimulate the development of prevention, diagnosis, and treatment for complex trait disorders by elucidating the disease-genes relationship.

S6-2

Single Nucleotide Polymorphisms Associated with Asthma

PARK Choon Sik
Genome Research Center for Allergy and Respiratory Diseases, Soonchunhyang University Bucheon Hospital, Bucheon, Korea

Asthma is an inflammatory airway disease associated with intermittent airflow obstruction and bronchial hyperresponsiveness (BHR) based on eosinophilic airway inflammation. Patterns of clustering and segregation analyses in asthma families have confirmed a genetic component to asthma. Although much progress has been made toward defining the molecular genetics of asthma over the past decade, the intricacy of the numerous genetic and environmental factors involved has made genetic dissection of this and other complex disease difficult. Genome-wide scanning has revealed that multiple loci on several chromosomes (1p, 2p, 2q, 5p, 6p, 9q, 12q, 13q, 14q, 17q, 19q, 21q) are linked to asthma and related phenotypes. The precise definition of which genes in these regions are responsible for the reported linkages to asthma and the phenotypes may await completion of high- resolution physical maps of the human genome. The number of biologically plausible candidate genes that might be involved in the determination of asthma and associated trait is very large. To date, research into the molecular genetics of asthma has generously focused on candidate genes with clearly defined roles in the allergic process. This review summarizes the genetic approach to evaluate multicomplex disorder such as asthma and potential future contributions of one type of DNA sequence variant, single nucleotide polymorphisms (SNPs), to our understanding of asthma pathobiology.