**MULTIDISCIPLARY APPROACH TO GWAS FOR HEART FAILURE BASED ON THE VARIOUS ETIOLOGY AND ETHNICITY**

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Background: HF is one of the most serious syndromes with divergent background.

A part is heritable, though the genetic factors remain elusive. Genome-wide association study (GWAS) is promising for identifying not only the causative gene (Kato *et al., Lancet* 1995) but also modifier genes that aggravate or ameliorate the clinical course *via* final common pathway (Toyo-oka *et al., PNAS,* 2004).

Objectives: We intentionally mixed HF carrying various causes (congenital, rheumatic, infectious, ischemic, or degenerative *etc*) to cover whole HF spectrum and to examine prevalence in different ethnicity. This study also aimed personalized medicine to clarify the responses to several therapeutic options.

Methods, Results and Conclusion: Our institute prohibits disclosure of methods and results before publication. With using hand-made microarray, we started genotyping of SNP/SNV/CNV in DNA isolated from peripheral blood (n=200) or cardiac specimens (n=19) after heart transplantation (Tanaka *et al., Nature Genet,* 2002). In total, four thousand SNPs were related to HF. When p values <10-4 was defined significant after χ2 test and about 200 SNPs were found in dominant or recessive inheritance. Whole sequence of mitochondrial genome added to determine the precise identification of etiology and ethnicity (Shin *et al., Am J Hum Genet,* 2000) showed East Asians without pathogenicity. Manhattan plot confirmed the SNP accumulation to specific genes. These SNPs consisted of variable mutations with biological relevancy or unknown progression mechanism of HF. We conclude that modern GWAS presents us incomparable strategy for clinical science, when sufficient bioinformatics data are combined with high throughput machinery.