



**UNC**  
GILLINGS SCHOOL OF  
GLOBAL PUBLIC HEALTH

## **James E. Grizzle Alumni Award Recipient Lecture**

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**Seoul, Korea**

### **Hidden Heritability and Risk Prediction Based on** **Genome-wide Association Studies**

Although recent genome-wide association studies (GWAS) have led to the discoveries of many susceptibility loci, much of the heritability of the individual traits remain unexplained. We have recently (Park et al., Nature Genetics, 2010) shown that one can use effect-sizes for known susceptibility loci and power for the original discovery samples to estimate the number of undetected susceptibility loci and the distribution of their effect sizes. On the other hand, with a hope to increase predictive power of epidemiologic risk model for diseases, many researchers considered risk models incorporating known published susceptibility SNPs, but the gain in predictive power was very limited for most diseases. In this presentation, we illustrate utility of our tools for improving predictive power of risk models for various traits and diseases by including potential discoveries from future GWAS with a realistic range of sample sizes. The potential utility and limits of various disease risk models are evaluated with new and previously used criteria such as AUC.

**Thursday, April 10, 2014**

**4:00-5:30 PM**

**William and Ida Friday Center for Continuing Education**