Design and Statistical Analysis in a Genome-Wide Association Study: An Example of Chronic HBV Infection and Its Clinical Progression in Male Han-Taiwanese

Su-Wei Chang
Clinical Informatics and Medical Statistics Research Center,
Chang Gung University College of Medicine

Abstract

In this talk, I will focus on essential issues for designing and conducting a case-control genome-wide association study. An analytical work flow starting with data preparation, sample size and power consideration from both statistical and clinical perspectives will be discussed. The choice of genotyping chips, statistical testing and use of imputation will be evaluated. I will also review the strength, challenges and future opportunities of performing second-generation genome-wide association studies. Our previous work in identifying genetic factors associated with chronic HBV susceptibility in male Taiwanese will be used as an example.