十一、研究計畫中英文摘要：請就本計畫要點作一概述，並依本計畫性質自訂關鍵詞。

（二）計畫英文摘要。（五百字以內）

Along with the availability of the huge amount of markers (e.g., SNP), association studies that are used to explore potential associations between candidate genes and a disease can be regarded as a tool for fine mapping. For example, a typical family-based association test, the transmission/ disequilibrium test (TDT) is popularly used in genome-wide scan. For complex diseases, the phenotypes assessed in association studies are likely to be continuous measures (quantitative traits). Methods extending the TDT to allow for a quantitative trait were widely addressed as well. These methods, however, do not take into account the genetic model of a quantitative trait, thus may lose substantial power in some situations. In practice, the underlying genetic model is usually unknown. A robust association test that can be applied in this situation is thus required. In this proposal, by using nuclear families with more than one child, I am trying to propose a robust association test. Tasks in this proposal include the theoretical derivation of a robust test, understanding interference of the environment factors, and investigation on the power performances of the robust test under some situations.

Keywords：association test, exponential family, genetic model, quantitative traits, robustness