

Invited Talk

**Linkage Disequilibrium Sharing and
TagSNP Portability Between Populations**

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The discovery of block-like structure of linkage disequilibrium (LD) in human populations holds the promise in delineating etiology of common diseases. However, understanding of the magnitude, mechanism, and utility of between-population LD sharing are critical for future genome-wide association studies. In this study, substantial LD sharing between six non-African populations was observed, though much less between African and non-African, based on 20,000 SNPs of chromosome 21. We also demonstrated the respective roles of recombination and demographic events in shaping LD sharing. Furthermore, we showed that the tagSNPs chosen from one population are portable to the others in East Asia. Therefore, we concluded that the magnitude of LD sharing between human populations justifies the use of representative populations for selecting tagSNPs in genome-wide association studies of complex diseases.