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**RESEARCH PROGRESS SUMMARY:**

**Research directions:**

1. Disease predisposition genes and variants: to identify prevalent genetic variants causing common diseases in Han Chinese; 
2. Population genetics: to characterise the population genetic structure of these disease-predisposition alleles and to analyse these variants in the perspective of population genetics; 
3. Functional analysis of such variants: to determine the functional consequence of these disease predisposition variants; and 
4. Analysis of variation of the transcriptome using the latest technology of next generation sequencing.

The mission of the Genetics of Disease Susceptibility (GDS) Laboratory is to identify disease predisposition genes for common diseases in the locality. Predisposition to many common diseases (for example Alzheimer disease, breast cancer and asthma) are due to alleles in multiple genes in addition to environmental risk factors. This rapidly evolving field of genetic research requires new research methods (for example genome-wide association study (GWAS)), new statistical skills and international multi-centre consortium approaches. We are part of international consortia in studies of healthy aging (including bone and other phenotypes), breast cancer, and genetic susceptibility to tuberculosis.

A new initiative of the Laboratory is to examine the determinants of gene expression in tissues and their variations between individuals.
The origin of polymorphic coding VNTR in this gene has been studied in a pan-ethnic sample of 145 individuals. We found that all common repeat alleles had existed before the dispersion of modern humans out of Africa [Li 2012]. The observed allelic diversity could be arisen simply due to the effect of migration and neutral evolution. The figure was published in *PLoS One*, 7(1), e30268.


