

Department of Systems Medicine Presents

日時:2017年5月15日(月) 16:30-17:30

場所:総合医科学研究棟1Fラウンジ

1F lounge of Research Park

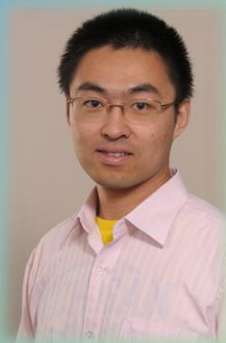
参加自由

“ Bioinformatic assessment of mitochondrial DNA variation and copy number from whole-genome sequence data”

(*This is a talk *in English* /英語での講演)

Abstract:

We have developed a computational algorithm and software to assess variations and copy number of mitochondrial DNA (mtDNA) from whole-genome sequencing data. We have applied the methods to DNA sequence from white blood cells of ~2,000 genome cohort from Sardinia, Italy (SardiNIA Project). We found that heteroplasmy increases with age and also found that mtDNA copy number averages ~110 copies/lymphocyte and is ~54% heritable, implying substantial genetic regulation of the level of mtDNA. The mtDNA copy numbers are significantly associated with waist circumference and waist-hip ratio, but not with body mass index, indicating an association with central fat distribution. To our knowledge, this is the largest population analysis to date of mtDNA dynamics, revealing the age-imposed increase in heteroplasmy and the high heritability of copy number.



Jun Ding, M.S., Ph.D.

Staff Scientist / Facility Head
National Institute on Aging,
National Institutes of Health

Contact: Minoru Ko, Systems Medicine (ko.minoru@keio.jp, #63652)