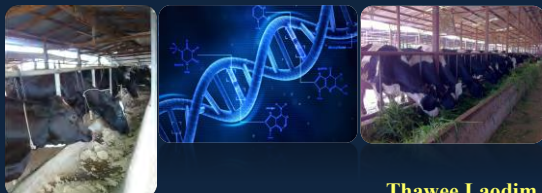


Genome Patterns of SNPs Variation in a Thai Multibreed Dairy Population



Thawee Laodim

Skorn Koonawootrittriron*, Thanathip Suwanasopee* and Mauricio A. Elzo**

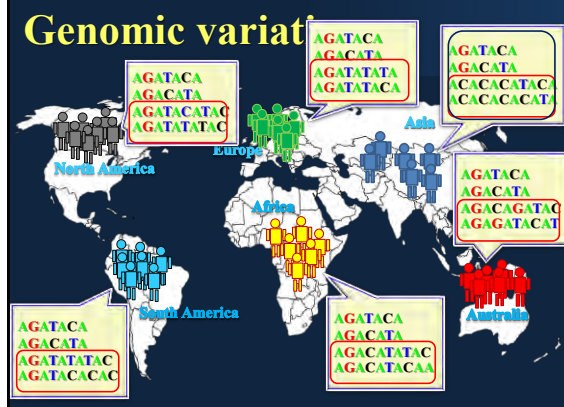
*Department of Animal Science, Kasetsart University, Thailand

** Department of Animal Sciences, University of Florida

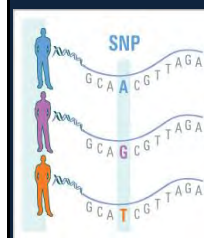
Phenotypic variation



Genomic variation



Single nucleotide polymorphism

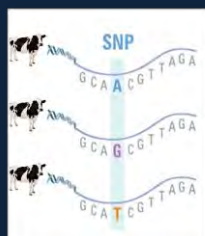


Evolution and mechanism

Medicine and pharmacology

Reduce at time

Single nucleotide polymorphism



Genomic variation

Genome-wide association

Genomic selection

Genomic evaluation

Objective

To study the genome patterns of SNPs variation
in a Thai multibreed dairy population

Dairy datasets

Pedigree

- ID (animal, sire, dam)
- Breed fraction (animal)
- Date of birth

Performance

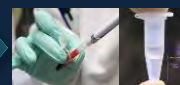
- Calving age
- Milk production (milk, fat and protein yield)

600 dairy cattle from 25 farms
in Thailand

SNPs genotypic data



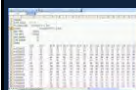
Blood sampling



DNA Extraction & DNA
preparation for genotyping



SNPs genotyping



SNPs genotypic



Call genotypes
from clusters



Hybridize samples on
beads (Bead Chip)

Statistical analysis

SNPs genotype (8,810)

SNPs genotype (8,587)

Descriptive statistic

Distribution of SNPs
on chromosome

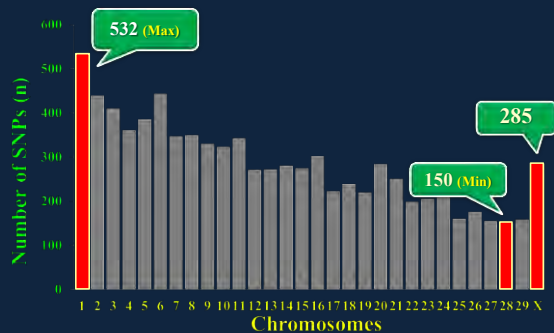
Distribution of MAF
on chromosomes

Physical length of
SNPs on chromosomes

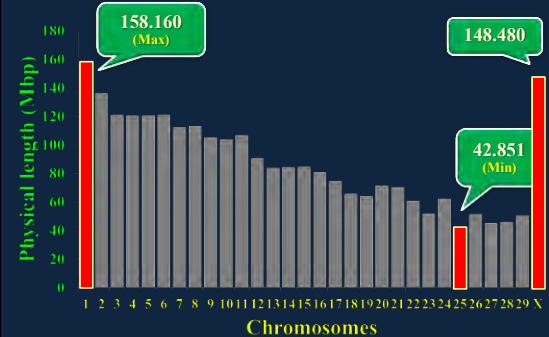
Distance of SNPs on
chromosomes

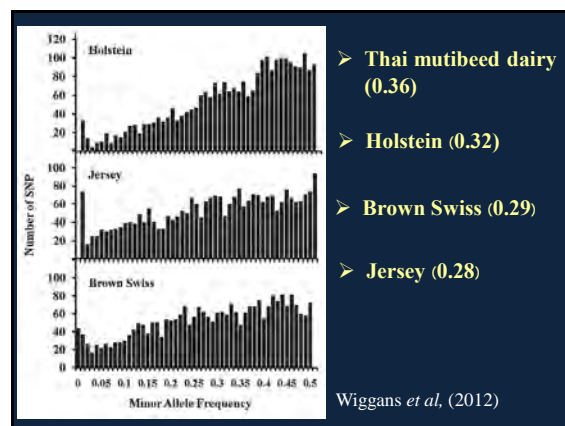
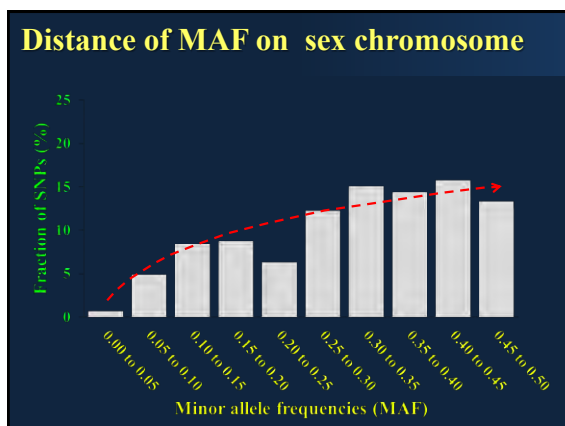
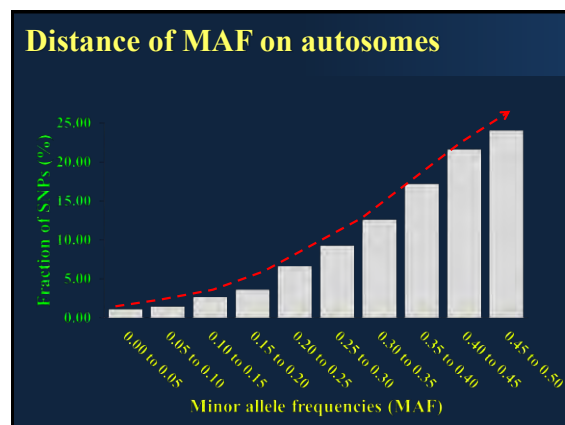
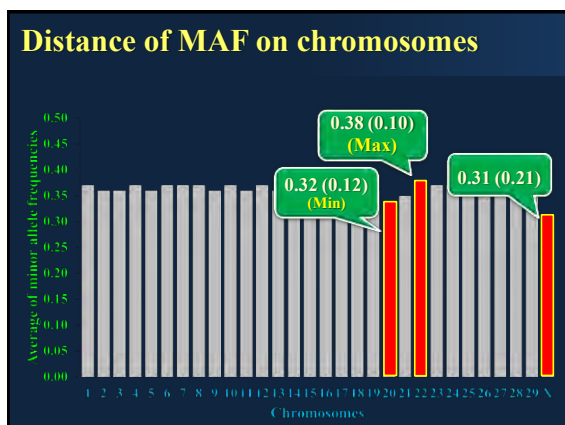
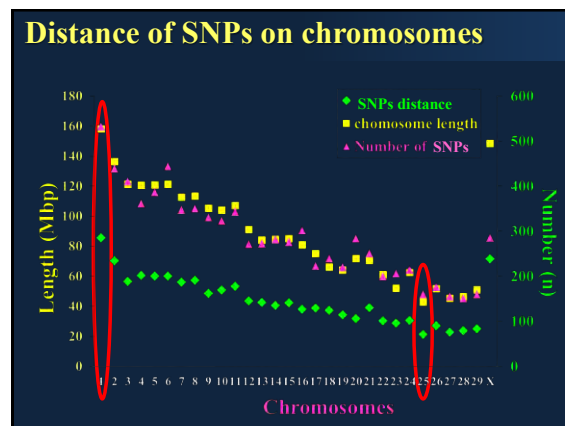
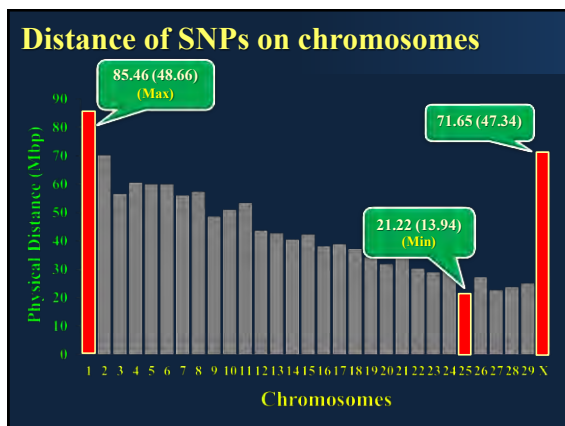
Results and discussion

Distribution of SNPs on chromosomes



Physical length of SNPs on chromosomes





Conclusions

SNPs genotype

- The distribution of SNPs varied among the chromosomes, with chromosome 1 having the highest number of SNPs (532)
- The overall mean MAF was 0.38 (Autosomes) and 0.31 (Sex chromosome)

Acknowledgments



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Dairy Farming Promotion Organization (DPO)

Kasetsart University Research and Development Intitute (KURDI)



Dairy farm in Thailand

Thank you

Minor allele frequency (MAF)

If the number of AA calls is less than the number of BB calls for sample, the frequency for the minor allele A is

$$MAF = AA + \frac{1}{2}AB$$

Where

AA = frequency of AA genotype

AB = frequency of AB genotype