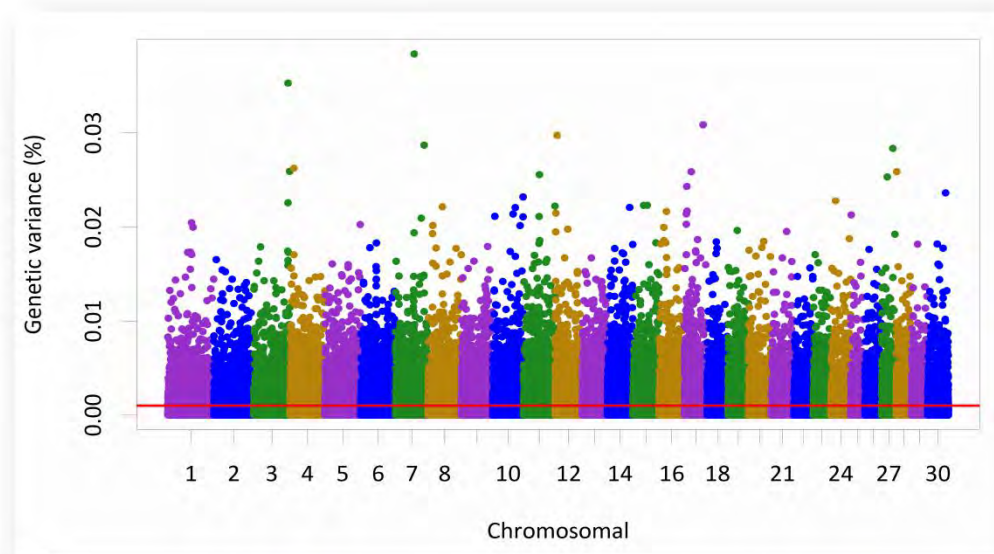




Genome-wide Association Analysis for Milk Yield, Fat Yield, and Age at First Calving in the Thai Multibreed Dairy Population

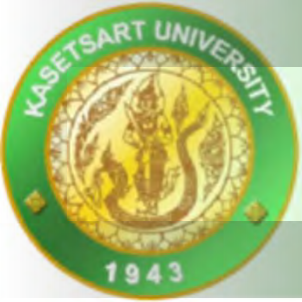


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Genomic Evaluation System in Thailand

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**Pedigree
+
Phenotypic Records**



**Genetic - Genomic
Evaluation**



**Genomic Estimated Breeding Values
(GEBV)**

**Genomic SNPs
Genotyping**

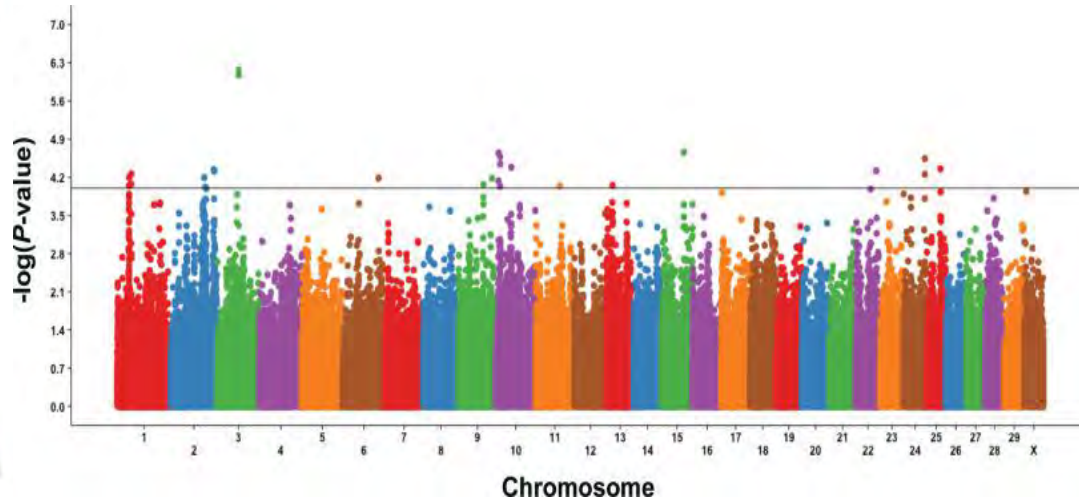
Blood Sample

DNA Preparation



Accuracy of Genomic Prediction

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The utilization of significant SNPs from genome-wide association study (GWAS) help improve the accuracy of genomic selection for dairy economically important traits

OPEN ACCESS Freely available online



Best Linear Unbiased Prediction of Genomic Breeding Values Using a Trait-Specific Marker-Derived Relationship Matrix

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Improving the Accuracy of Whole Genome Prediction for Complex Traits Using the Results of Genome Wide Association Studies

Zhe Zhang^{1,2}, Ulrike Ober², Malena Erbe², Hao Zhang¹, Ning Gao¹, Jinlong He¹, Jiaqi Li^{1*}, Henner Simianer^{2*}

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Proceedings, 10th World Congress of Genetics Applied to Livestock Production

Results of Genome Wide Association Studies Improve the Accuracy of Genomic Selection

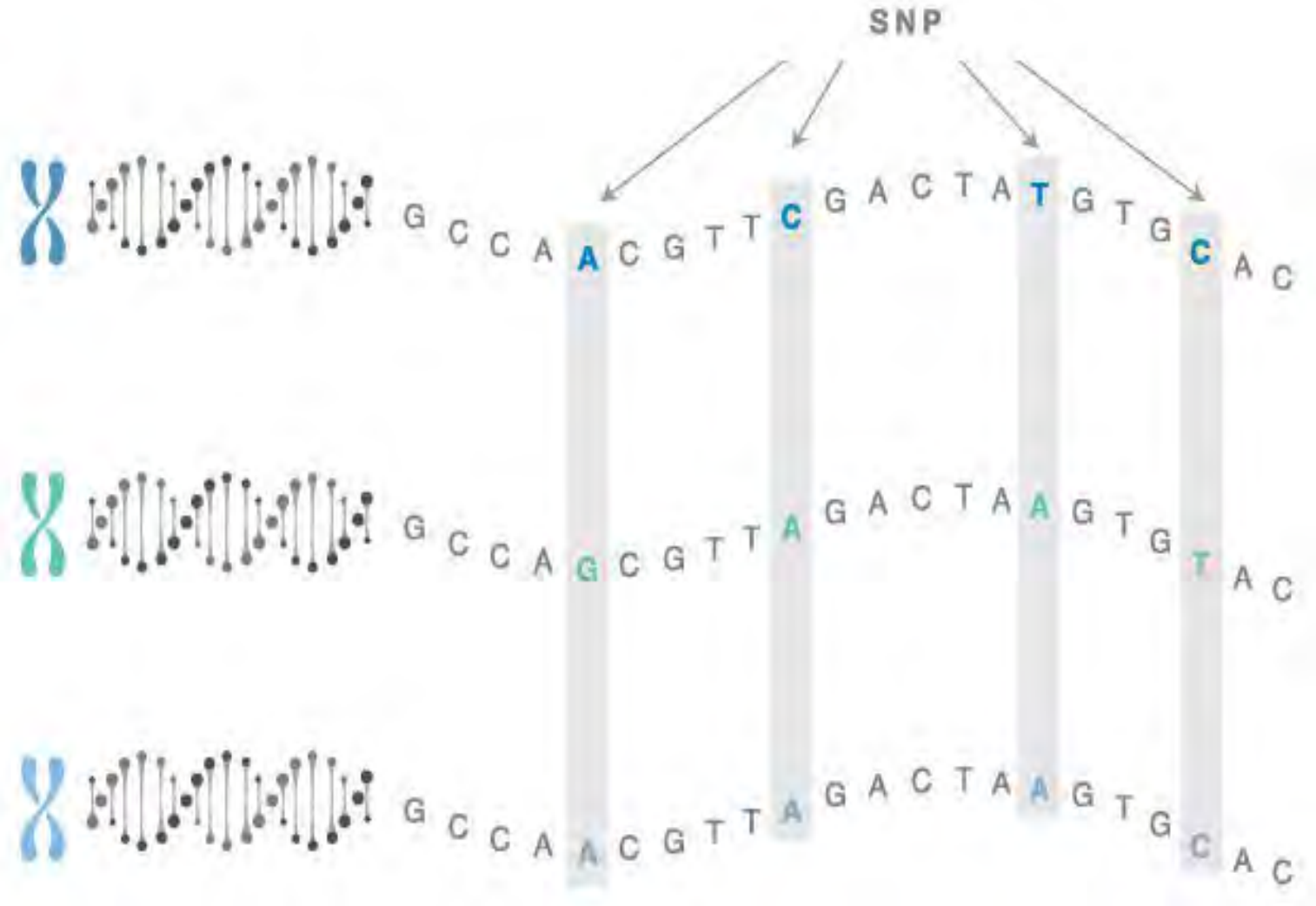
Zhe Zhang¹, Jinlong He¹, Hao Zhang¹, Ping Gao¹, Malena Erbe², Henner Simianer², Jiaqi Li¹

¹ College of Animal Science, South China Agricultural University, Guangzhou 510642, China, ² Department for Animal Sciences, Animal Breeding and Genetics Group, Georg-August-Universität Göttingen, 37075 Göttingen, Germany



Genome-Wide Association Studies

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Objective of this Study

To identify sets of SNP markers and genes:

☐ **Milk yield**

☐ **Fat yield**

☐ **Age at first calving**

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Animals and Database



❖ Pedigree:

- ☐ Animals ID
(Animal, Sire and Dam)
- ☐ Birth date
- ☐ Breed composition

❖ Phenotypes:

- ☐ Milk production
- ☐ Calving date
- ☐ Date of collected data

**8,361 first-lactation cows from 810 farms
under Thai tropical environmental condition**

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Genomic SNPs Information

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- ❖ **Actual and imputed GGP80k SNPs makers (76,519 SNPs) from 2,661 animals**
- ❖ **29 autosomes and X chromosome**
- ❖ **Quality controls:**
 - ❑ Call rate ($\geq 90\%$)
 - ❑ Minor allele frequencies (≥ 0.01)
- ❖ **74,144 SNPs were used for this study**



Genome-wide Association Analysis

- ❖ **Single-step genomic best linear unbiased prediction**

(Aguilar et al., 2010)

- ❖ **Genomic-polygenic model**

$$y = Xb + Za + e$$

Where

y = vector of phenotypes (milk yield, fat yield, and age at first calving)

b = vector of fixed effects

(herd-year-season, breed group, and heterosis)

a = vector of random animal additive genetic effects

e = vector of random residuals

X = incidence matrix related MY and FY records to elements of vector b

Z = incidence matrix related MY and FY records to elements of vector a

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Percentage of Genetic Variance Explained by Individual SNP

$$\text{Genetic variance (\%)} = \frac{\text{Var}(\text{SNP}_i)}{\sigma_a^2} \times 100$$

Where

$\text{Var}(\text{SNP}_i)$ = genetic variance of the i^{th} SNPs

σ_a^2 = the total genetic variance

(Wang et al., 2014)

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Identification of Molecular Function and Biological Processes of Genes

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- A**
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- U**
- ❑ 0.001% of the genetic variance for milk yield, fat yield or age at first calving were selected
 - ❑ **Map2NCBI** (Hanna and Riley, 2014)
 - ❑ **SNP located inside or at $\leq 2,500$ bp of genes in the NCBI database**
 - ❑ **PANTHER** (<http://www.pantherdb.org/>)
 - ❖ **Molecular function**
 - ❖ **Biological processes**

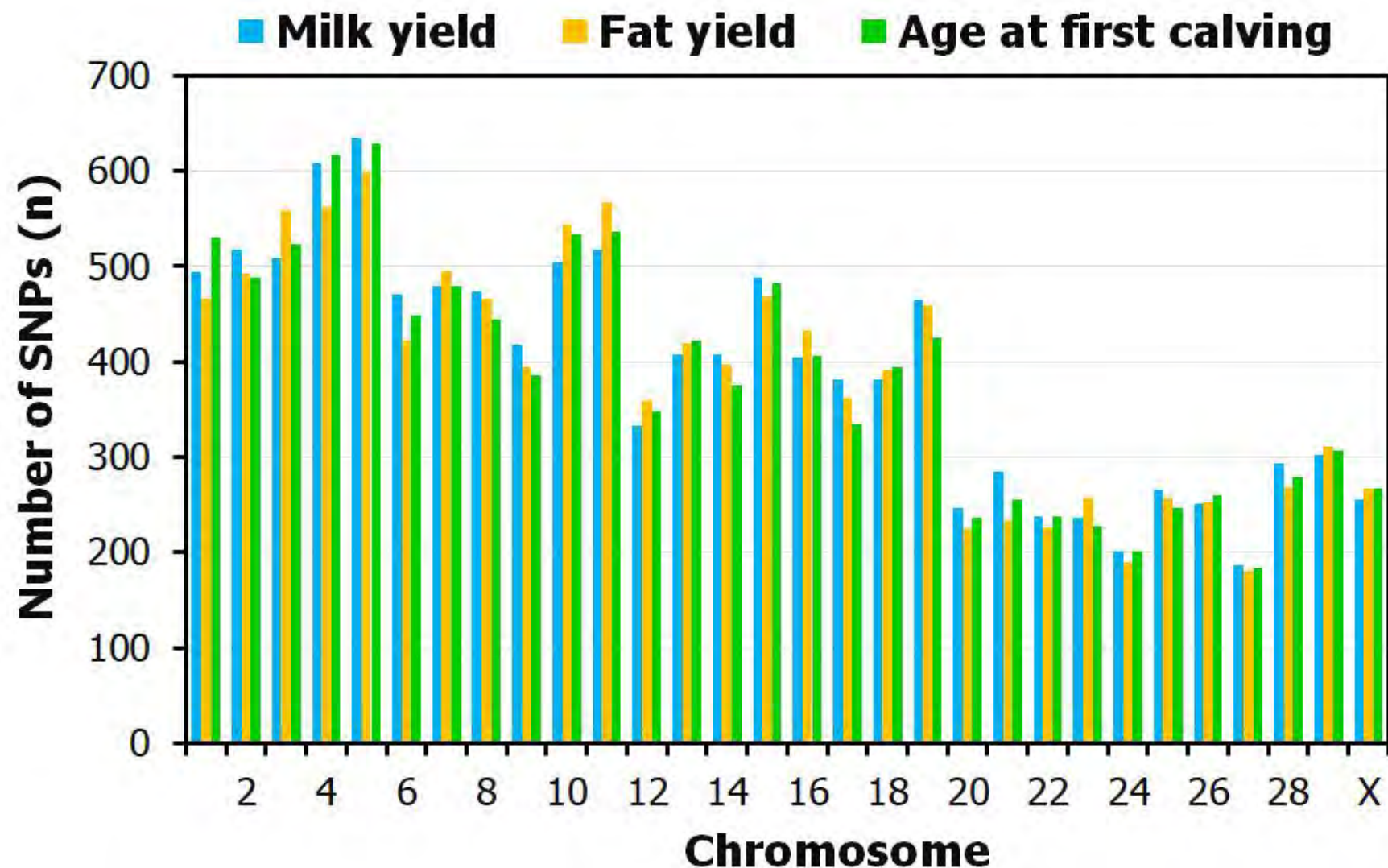


Number of the SNP Markers by Distance between SNP and Genes in the NCBI

Distance between SNP and gene	Milk yield	Fat yield	Age at first calving
Inside gene	10,263	10,119	10,149
≤ 2,500 bp			
	44%	44%	38%
	1,390	1,406	1,360
2,500 bp < distance ≤ 5,000 bp	855	848	878
5,000 bp < distance ≤ 25,000 bp	3,726	3,739	3,713
distance > 25,000 bp	10,342	10,287	10,555
Total	26,576	26,399	26,655



Distribution of SNPs on Chromosomes of Thai Multibreed Dairy Population



❖ 6,930 genes
for milk yield

❖ 6,959 genes
for fat yield

❖ 6,922 genes
for age at first
calving

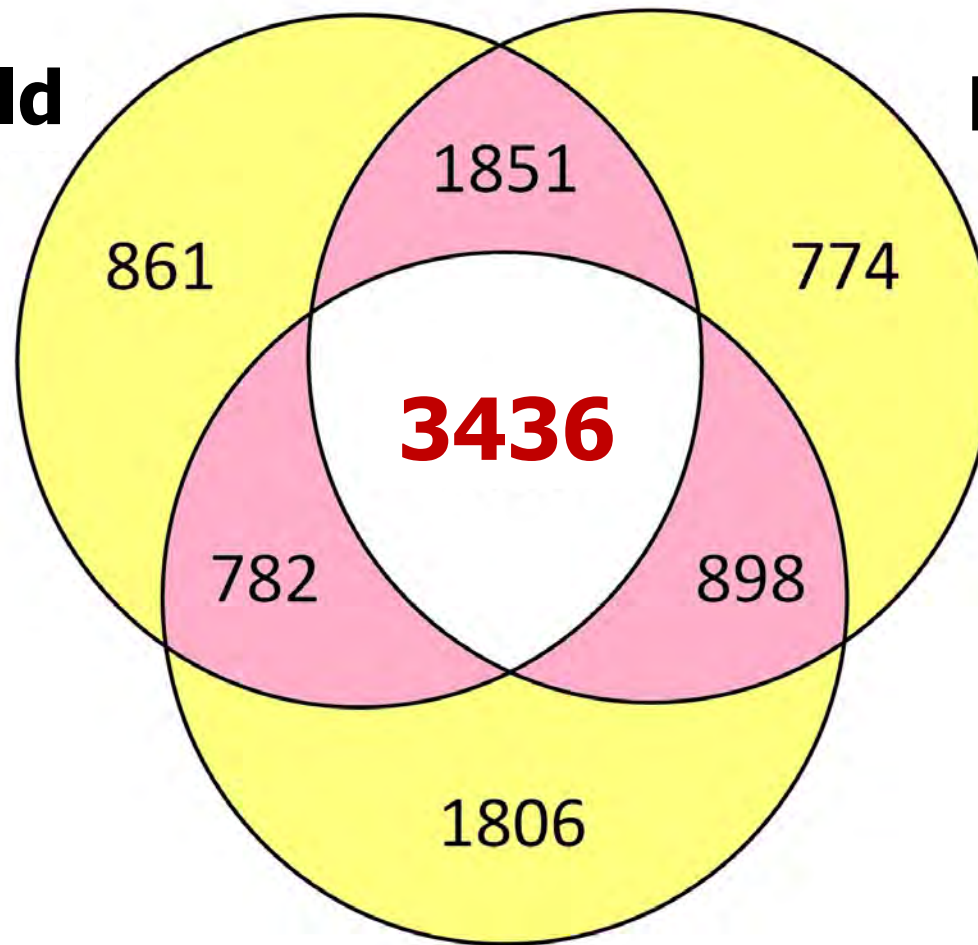


Numbers of Genes Associated with Milk Yield, Fat Yield and Age at First Calving

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Milk yield

Fat yield

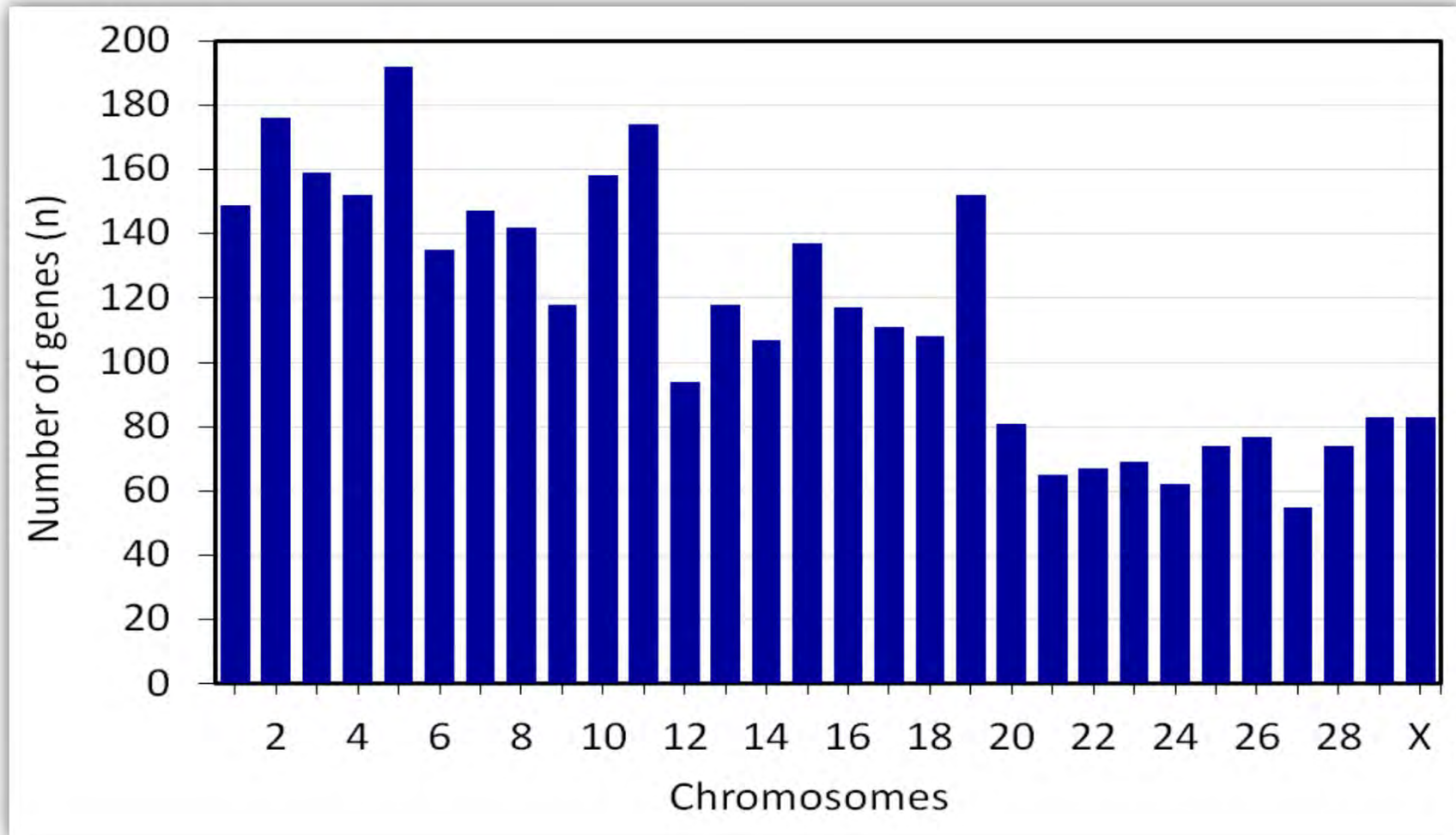


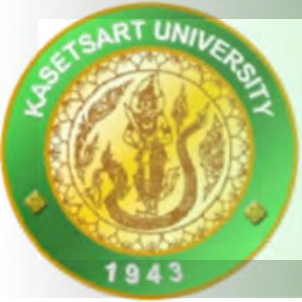
Age at first calving



Distribution of 3,436 Genes Associated with Milk Yield, Fat Yield and Age at First Calving

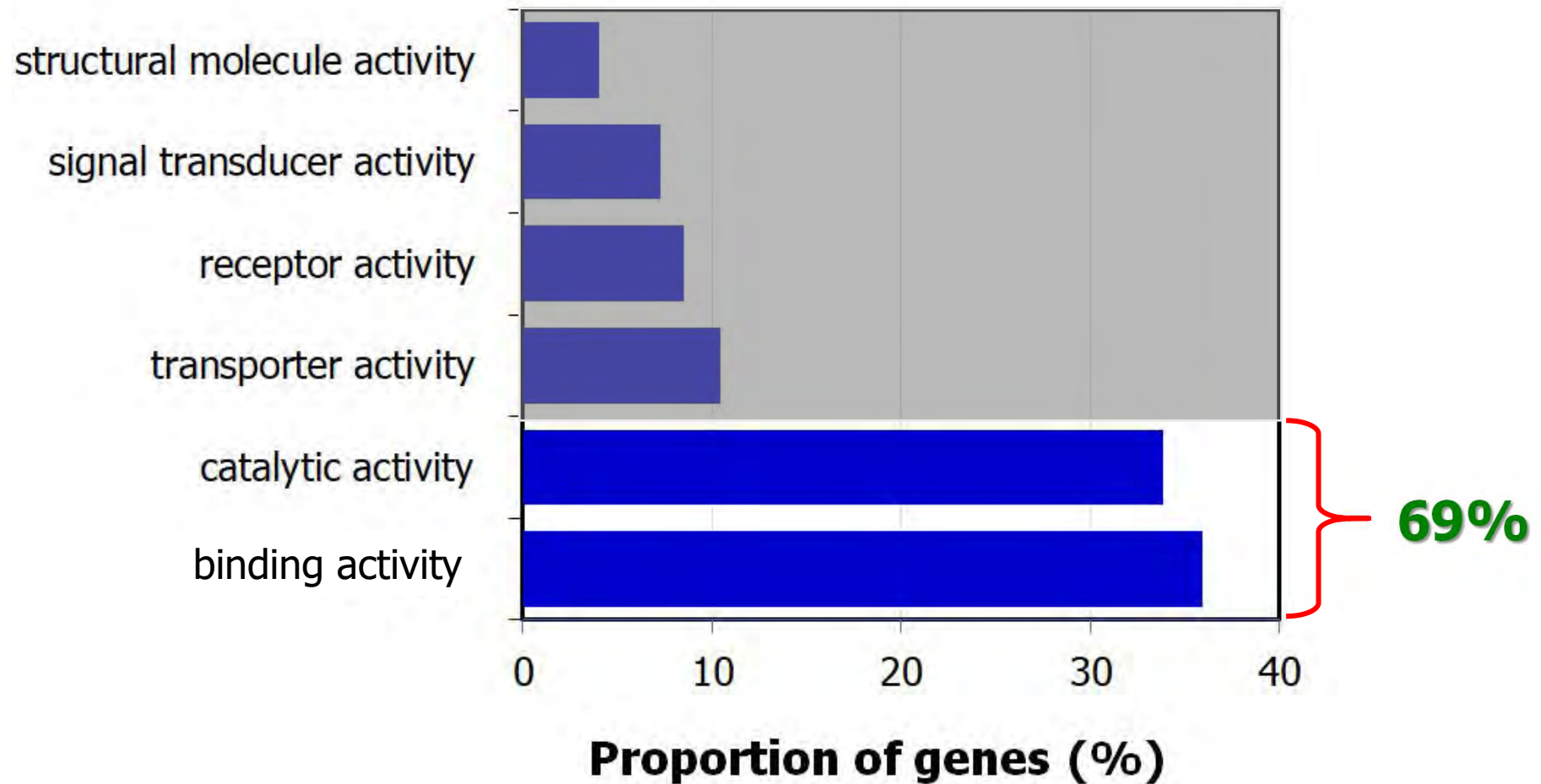
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Proportion of 3,436 Genes Associated with Three Traits based on Molecular Function

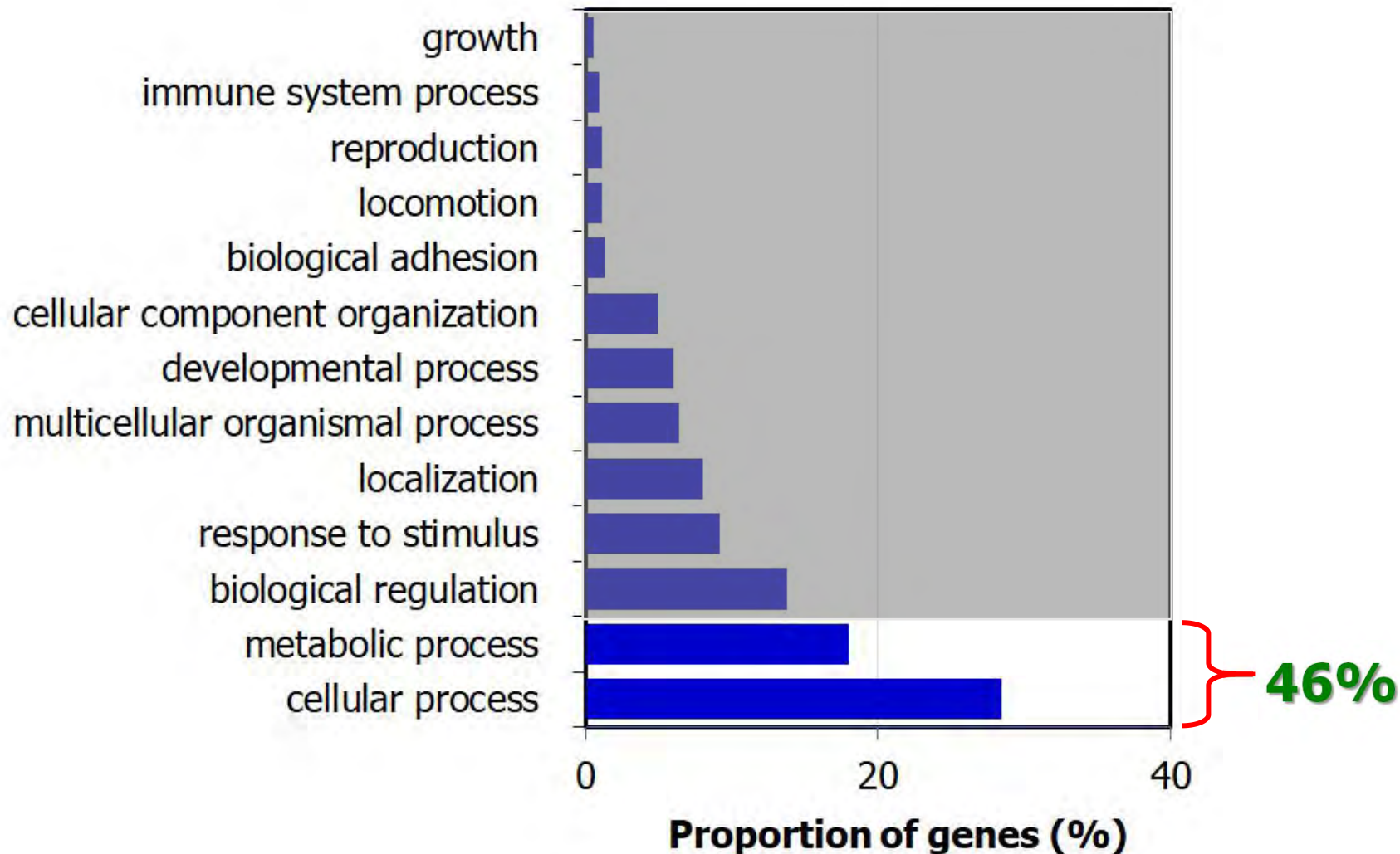
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Proportion of 3,436 Genes involved in Various Biological Processes for All Three Traits

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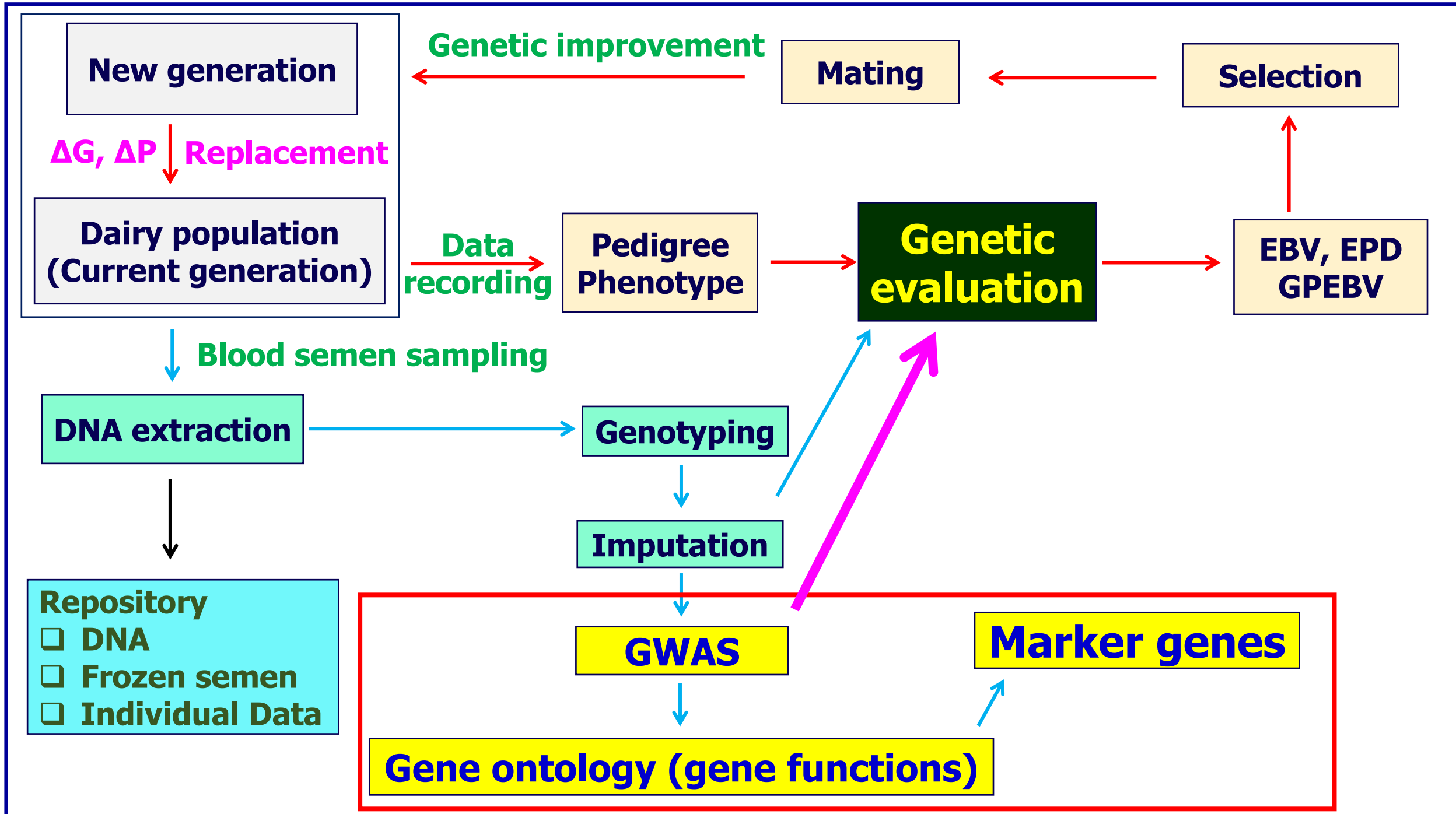




Conclusion

- ❖ Markers and genes associated with milk yield, fat yield, or age at first calving were located across chromosomes
- ❖ Genes were mostly involved in binding and catalytic activities as well as in cellular and metabolic processes

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Acknowledgments



Thailand Research Fund through
the Royal Golden Jubilee Ph.D. Program



Kasetsart University, University of Florida



Development of a Dairy Genetic-Genomic Evaluation System
in Thailand Project

Dairy farmers in Thailand

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*Thank You
For Your Attention*

