



# Genomics Tools for Improving Health and Production Performance of Canadian Pigs

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## INTRODUCTION

- Genomics is promising more benefits than BLUP
  - Production, health and meat quality traits
- Application requirements
  - Dense marker panels, large reference populations and affordable genotyping cost
  - Successful validation models and protocols
    - Selection of genotyping candidates
    - Choosing the appropriate SNP panel density
- Imputation can help to decrease genotyping costs

## OBJECTIVE

- Providing an overview on:
  - Genomic evaluation research in pigs
  - Tools required for application of the technology

## TRADITIONAL BLUP EVALUATIONS

- Genetic progress of litter size as an example
  - No change in litter size despite some herds practicing phenotypic selection before year 2000
  - After implementation of genetic evaluation program for litter size, there has been 2.10 and 2.25 piglets genetic gain for Landrace and Yorkshire breed, respectively, in the last 13 years.

## POWER AND POTENTIAL OF GENOMICS

- Disease resistance: Boddicker et al. (J Anim Sci. 2012. 90:1733-46) reported a SNP associated with porcine reproductive and respiratory syndrome (PRRS) viral load and post-infection weight gain in growing pigs
- Meat quality: Jafarikia et al. (ICoMST. 2012) reported a correlation of about 60% between direct genomics values (DGVs) and EBVs for Minolta L\* and loin marbling score
- Reproduction: Jafarikia et al. (PAG. 2012) found that GEBVs had 20% greater predictive ability than parental average EBVs for litter size

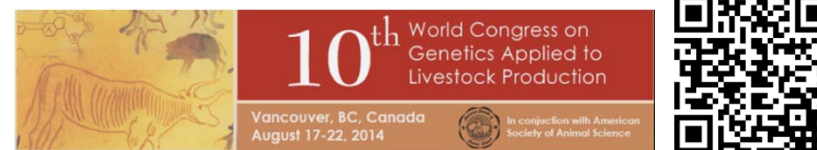
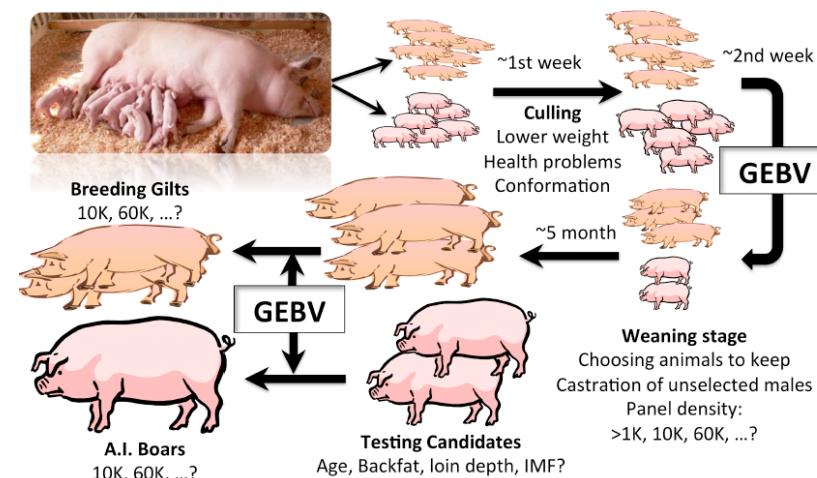
## GENOMIC APPLICATION REQUIREMENTS

- Linkage disequilibrium (LD): Levels of LD in Canadian pigs are high
- Accuracy of imputation: Relatively accurate imputation due to high levels of LD
- Reference population size: Important to estimate the SNP effect in estimation group
  - Thousands of genotyped animals with accurate records are required
- Method of evaluation: Different methods are available to calculate GEBV, however, method of evaluation is not currently a limiting factor

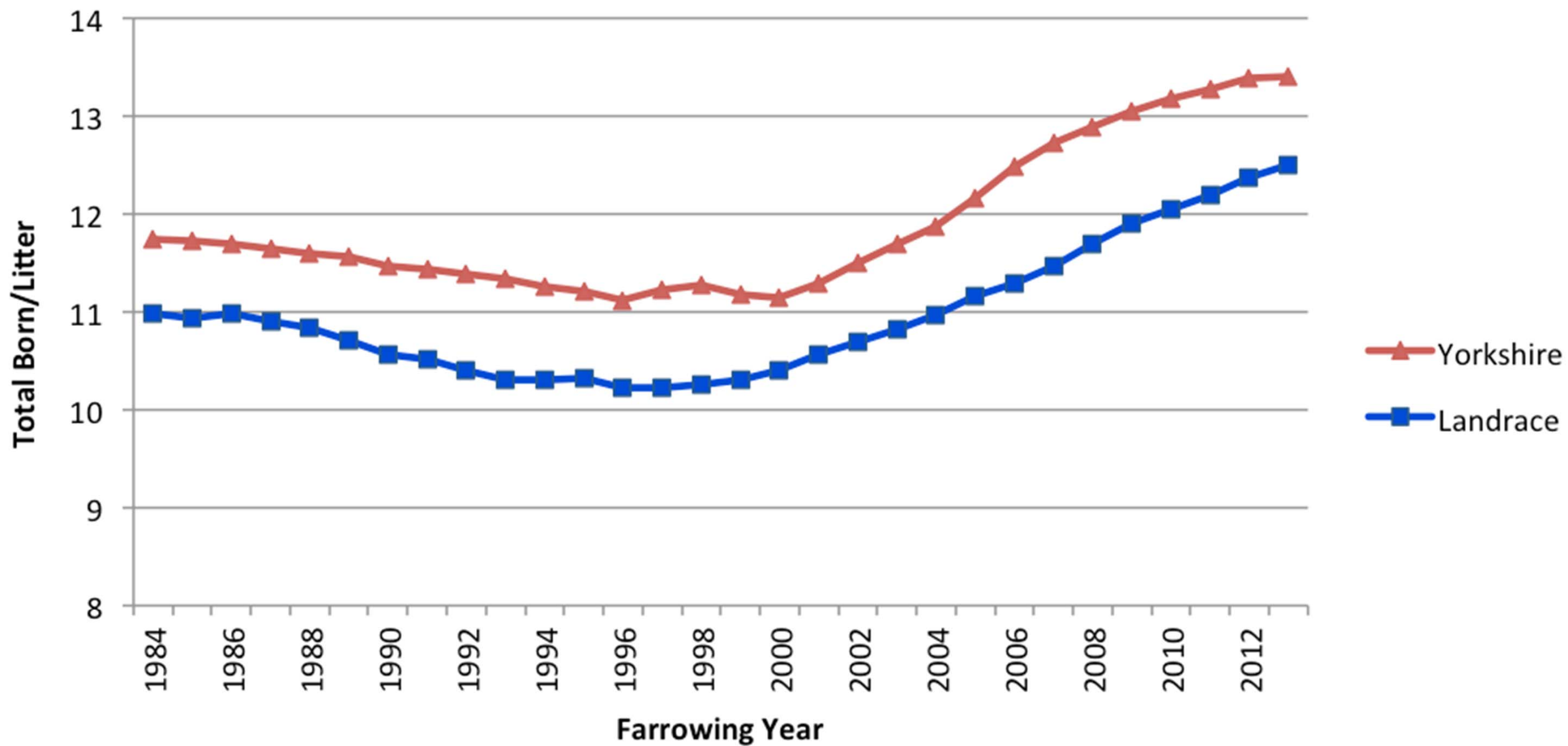
## IMPLICATION

- Very low-density SNP panels can be used to start selecting animals at a very young age (Figure 1)
- Putting the theory into practice requires guidelines and successful validation models
- Low-density panels and protocols for a genomic evaluation program are needed

Figure 1: A schematic view of the application of genomics for selection of the breeding animals at different selection stages

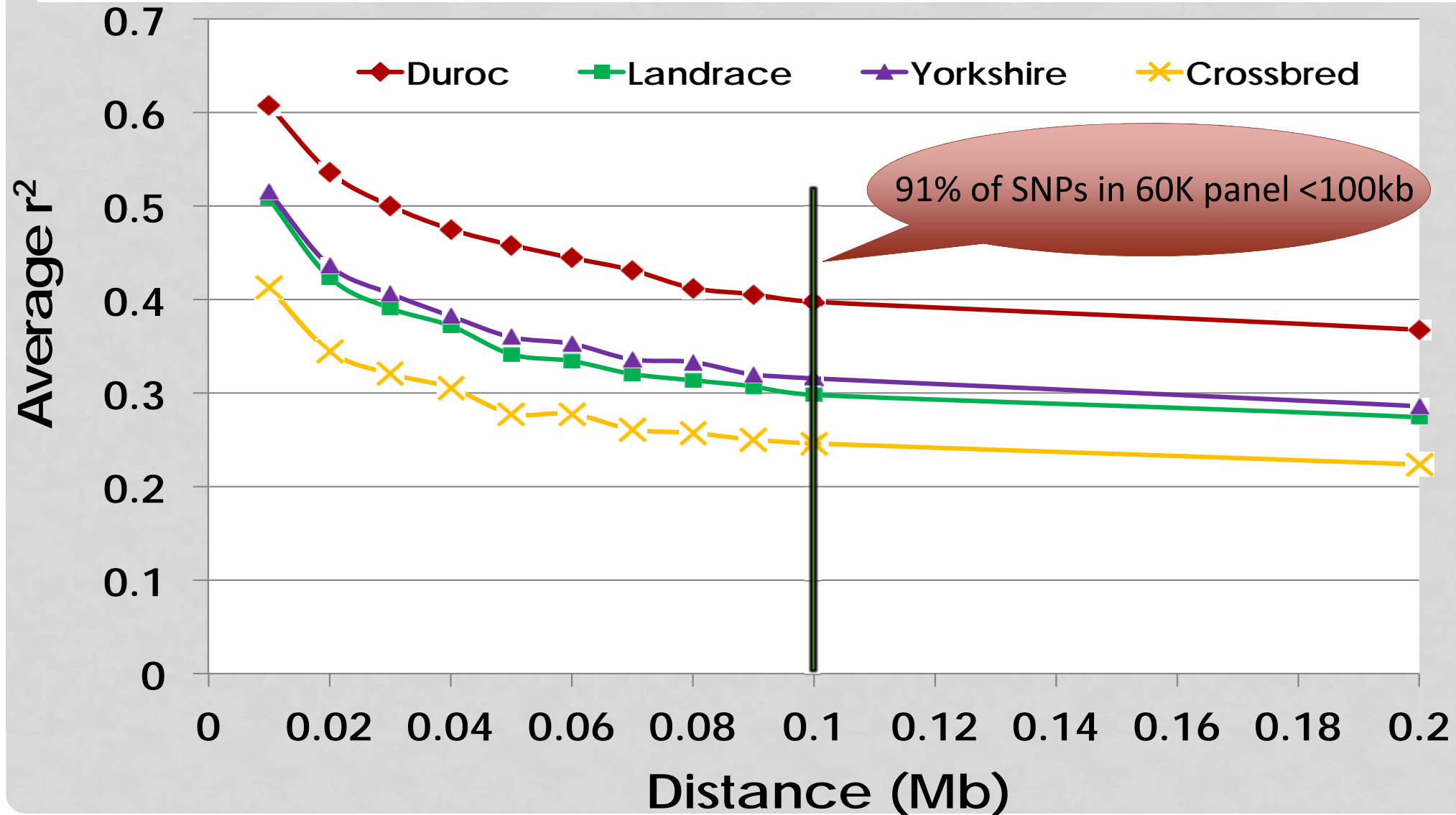


# Genetic Trends on Litter Size



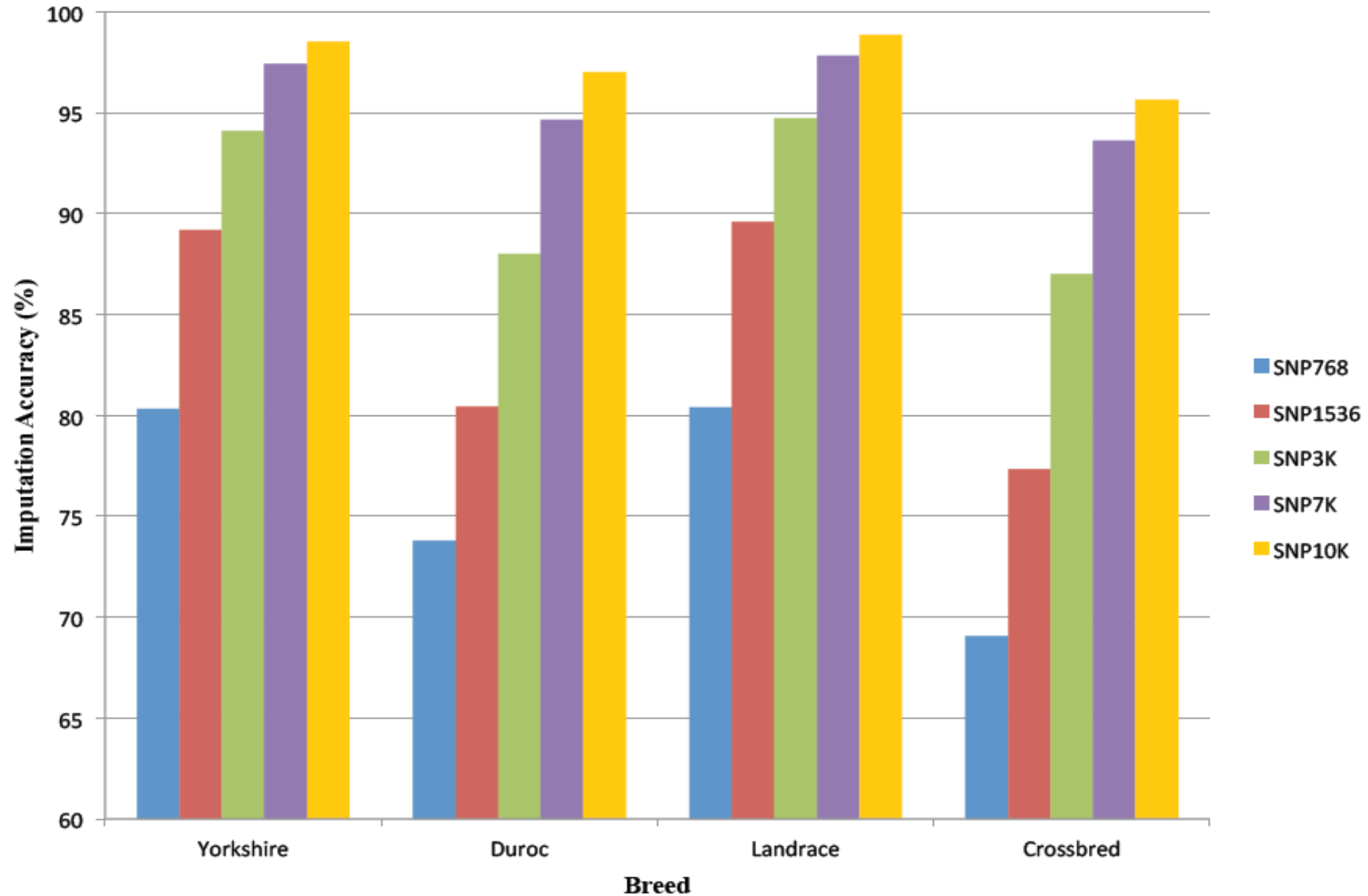
# EXTENT OF LINKAGE DISEQUILIBRIUM

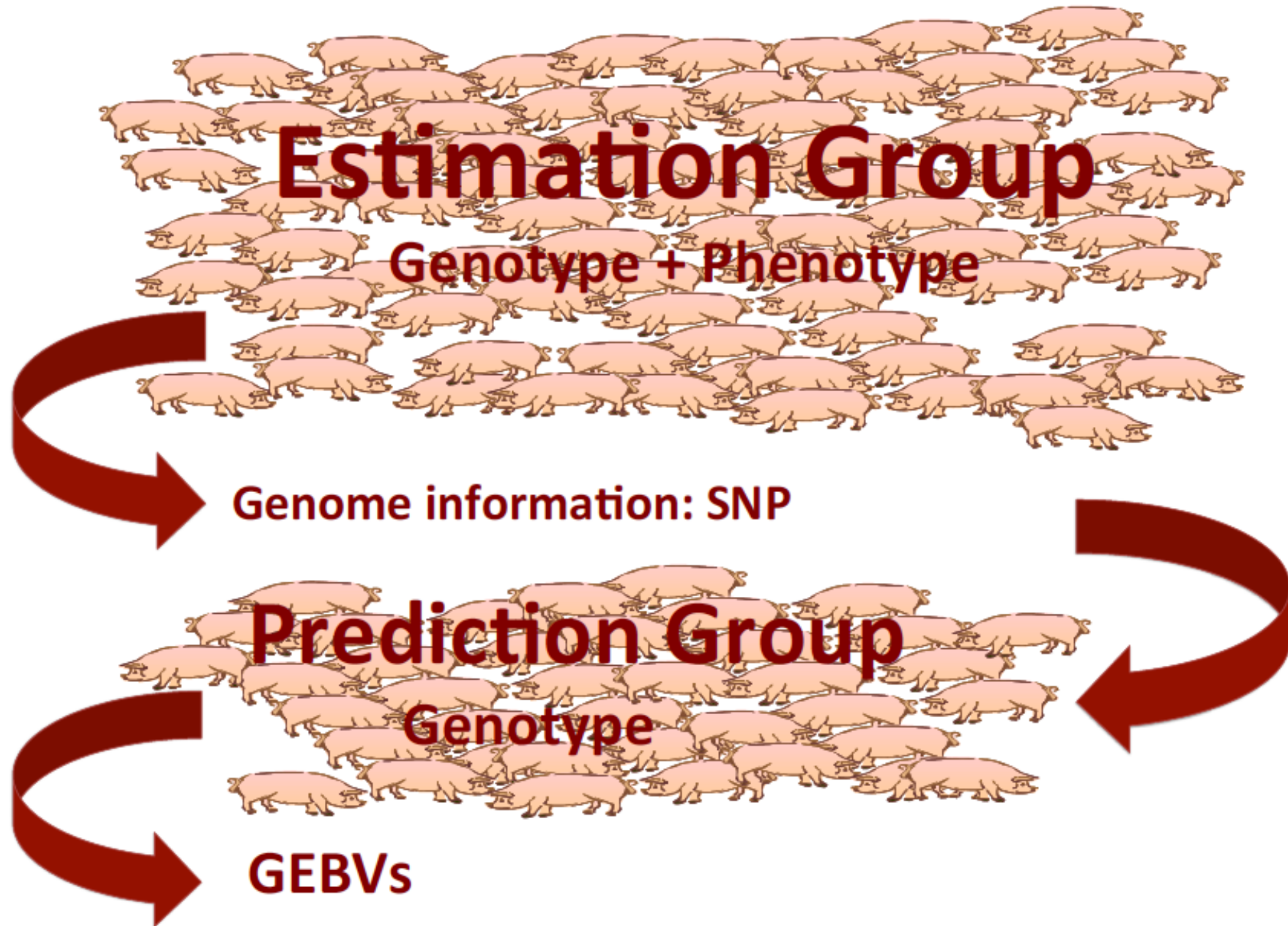
Grossi D. A., M. Jafarikia, M. Sargolzaei, F. S. Schenkel. 2014. Linkage Disequilibrium in Canadian pigs. Manuscript in preparation



# Imputation accuracy of 60K genotypes from 5 alternate LD SNP Panels

Lee, Y-S. (2013). MSc project, University of Guelph, Guelph, Ontario, Canada







**Figure 1: A schematic view of the application of genomics for selection of the breeding animals at different selection stages**

