

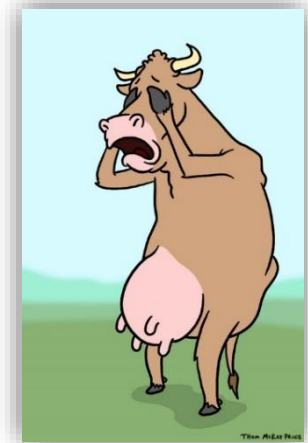
# Investigating potential of multi-breed, across-country genomic prediction using effective number of chromosome segments

Marjanovic J., Yu X., Wallen S., Meuwissen T. H. E., Calus M. P. L.



## WP6: Genomic selection strategies

- **ReDiverse** - Preserve biodiversity within and between ERDB
- ERDB often produce less > increasingly replaced on the farm
- Increase competitiveness
- Accelerate genetic improvement -> **Genomic selection**
- Make ERDB more lucrative for farmers
- **Increase long-term perspectives for ERDB**



# Genomic selection

- Red dairy breeds are often numerically small



- Breed-specific RP is challenging

- Alternative - multi-breed RP



- Choose breeds that are relevant

- **Effective number of chromosome segments ( $M_e$ )**

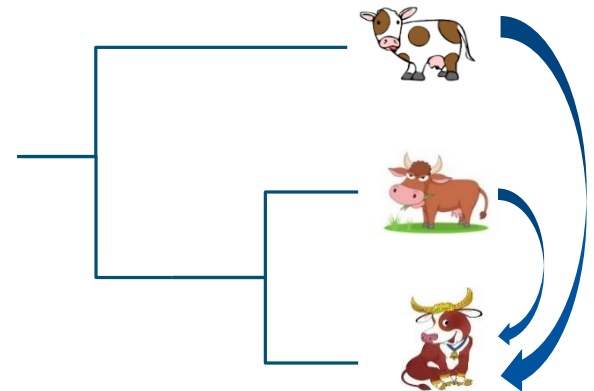
# $M_e$ - effective number of chromosome segments

- Indicator of relatedness & expected accuracy
- $M_e$  - within the population and between two populations
- **Within**  $M_e$  - segments that are segregating independently

$$M_{e,w} = \frac{1}{\text{Var}(G_{ij} - A_{ij})}$$

- **Between**  $M_e$  - consistency of LD between populations/breeds

$$M_{e,b} = \frac{1}{\text{Var}(G_{pop1_i pop2_j} - A_{pop1_i pop2_j})}$$



# Local $M_e$

- $M_e$  in general is computed on a genome-wide basis
- Multi-breed GP may be strongly driven by tagging large effect QTL and assigning appropriate variances to them
- Variation in local  $M_e$  values
- Expected benefits of variable selection models over regular GBLUP

# Objectives

- Investigate relatedness between three European Red cattle breeds
- Estimate  $M_e$  for each RDB and between each pairwise combination of breeds
- Genome-wide and local  $M_e$
- Assess the benefit of multi-breed GP for each of those breeds

# Data & Analysis

- 3 breeds
  - **MRY** (1,177 individuals)
  - **Norwegian Red** (7,243 individuals)
  - **German Red and White** (2,140 individuals)
- MRV – 11k and 50k SNPchip
- German Red and White 50k SNPchip
- Norwegian Red 50k imputed to 777k
- 45,210 common SNPs after QC
- Pedigree
- $M_e$  - calc\_grm
  - Genome wide
  - Per chromosome (local)



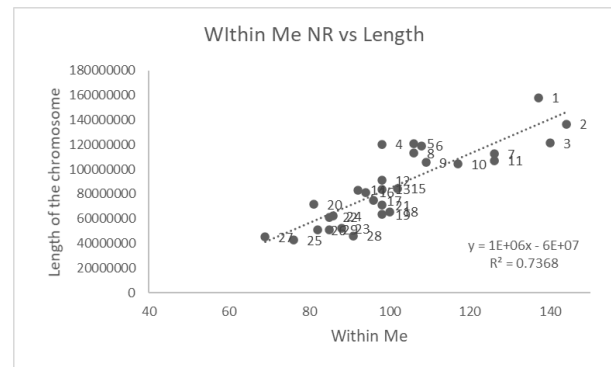
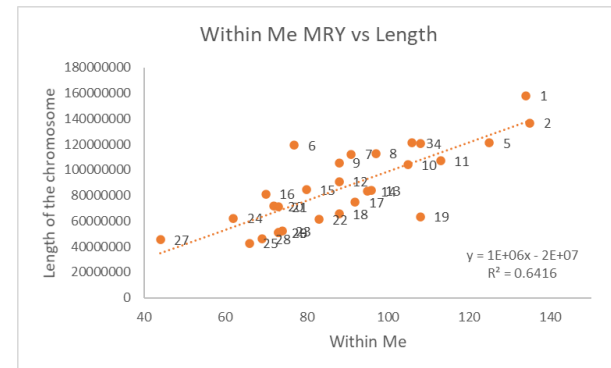
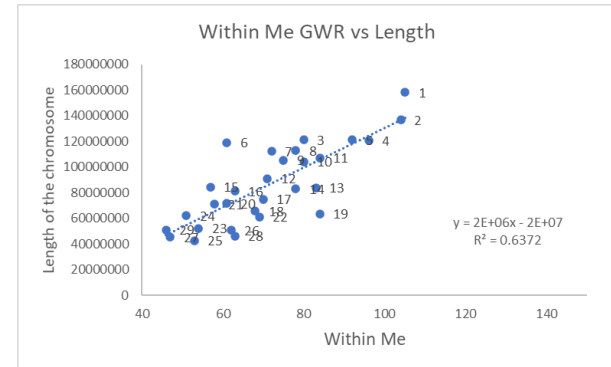
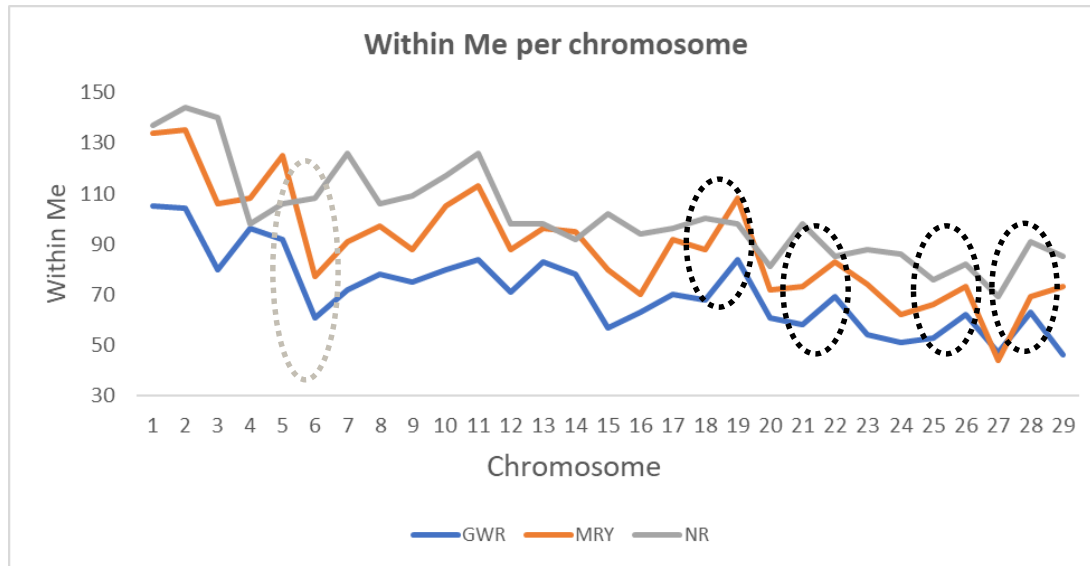
# Results – Genome wide $M_e$

	<b>MRY</b>	<b>Norwegian Red</b>	<b>German RW</b>
<b>MRY</b>	995		
<b>Norwegian Red</b>	55,621	998	
<b>German RW</b>	919	57,023	700

<b>Fst value</b>	<b>MRY</b>	<b>German RW</b>
<b>Norwegian Red</b>	0.084	0.098
<b>MRY</b>		0.013

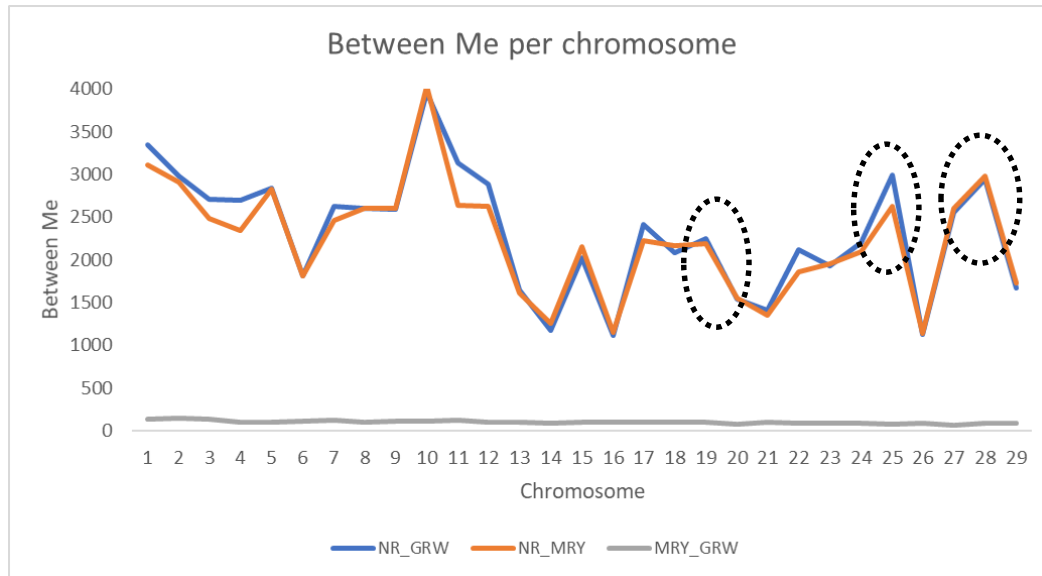


# Results – Local within $M_e$

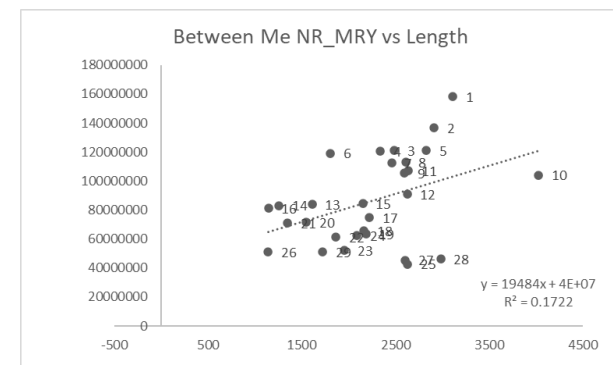
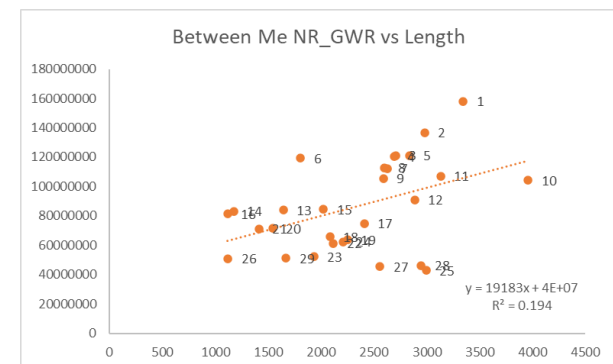
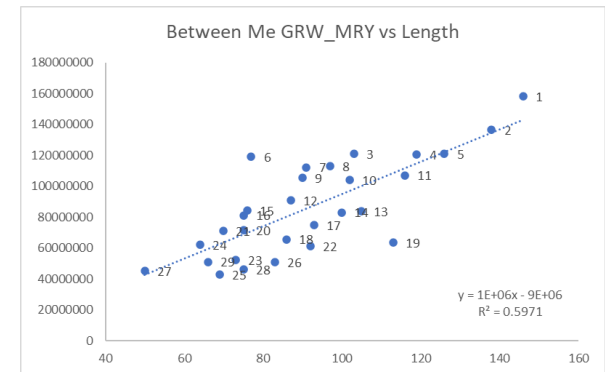


- Variation in  $M_e$  per chromosome
- Number of chromosome segments correlated with length of the chromosome
- 0.80 - 0.85

# Results – Local between $M_e$



- Correlation with the length of the Ch
- MRY\_GRW 0.77
- NR\_MRY & NR\_GWH  $\sim 0.20$



# Number of individuals

- Adding individuals from other breed
- To obtain the same increase in accuracy

$$n_{P,2} = \frac{M_{e_{1,2}}}{M_{e_1}} n_{P,1}$$

		Population 2		
Population 1		MRY	Norwegian Red	German RW
	MRY	1	55	1
	Norwegian Red	55	1	57
	German RW	1.3	81	1

# Conclusions

- Possibilities for multi-breed GP
- MRY and GRW show high relatedness
- More benefit for smaller MRY and GRW breed than for NR
  
- Several interesting regions in within and between local  $M_e$
- May indicate advantage of variable selection models over regular GBLUP