

GENETIC ANALYSIS OF PATHOGEN-SPECIFIC MASTITIS

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CLINICAL MASTITIS

- Inflammation of the mammary gland
- Caused by several different pathogens
 - Elicit different part of the cows immune system
 - Contagious and environmental
- Part of breeding goal of Norwegian Red since 1978
 - Veterinary treated cases of clinical mastitis (**CM**)
- Pathogen data from mastitis laboratories since year 2000
 - Not used in genetic analysis until now

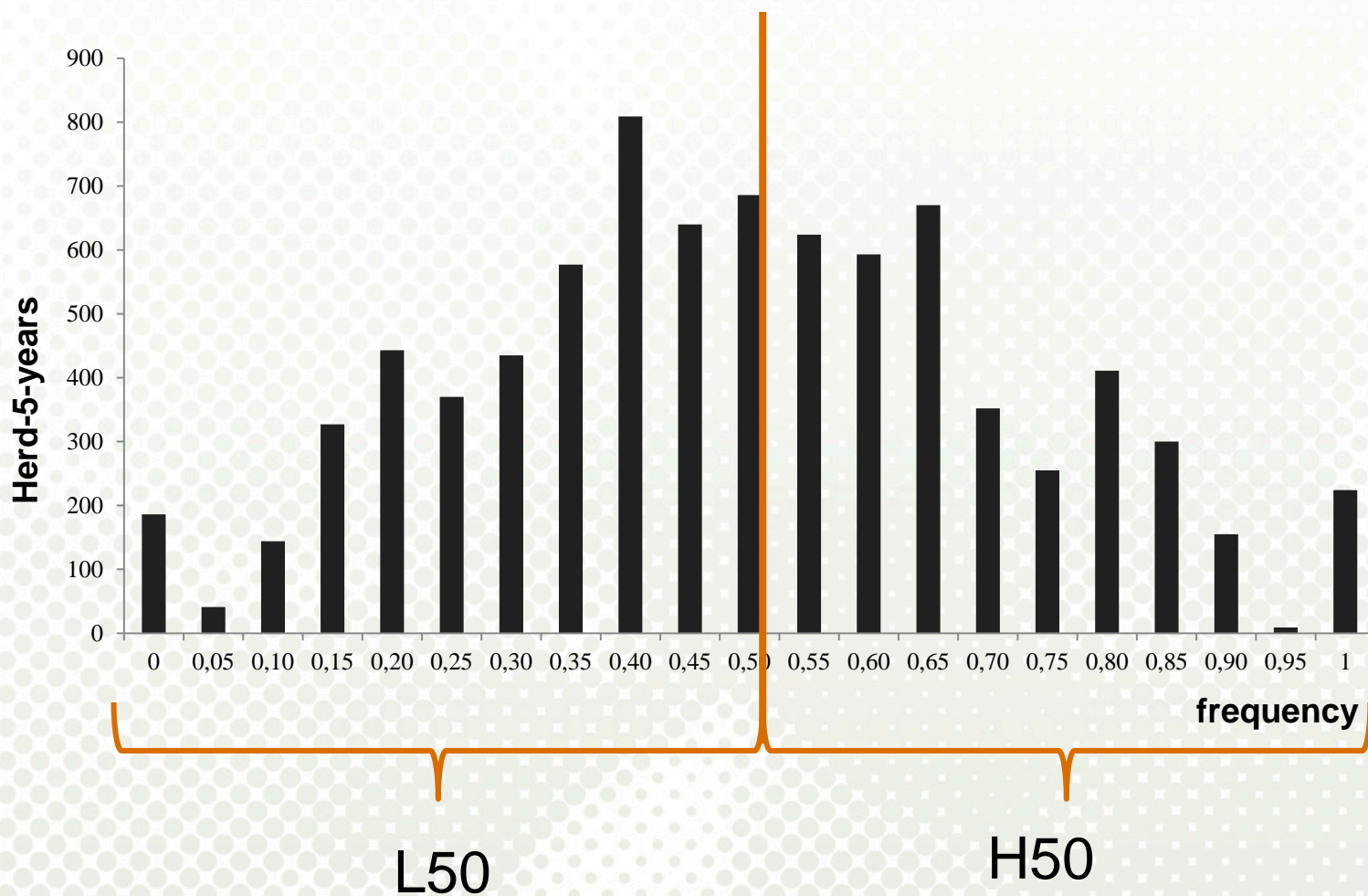
AIMS

- Investigate predictability of genomic breeding values for CM within and between defined environments
 - Herds classified according to mastitis pathogen status
- Assess if a possible interaction between the genotype and environment can affect predictability of a given phenotype

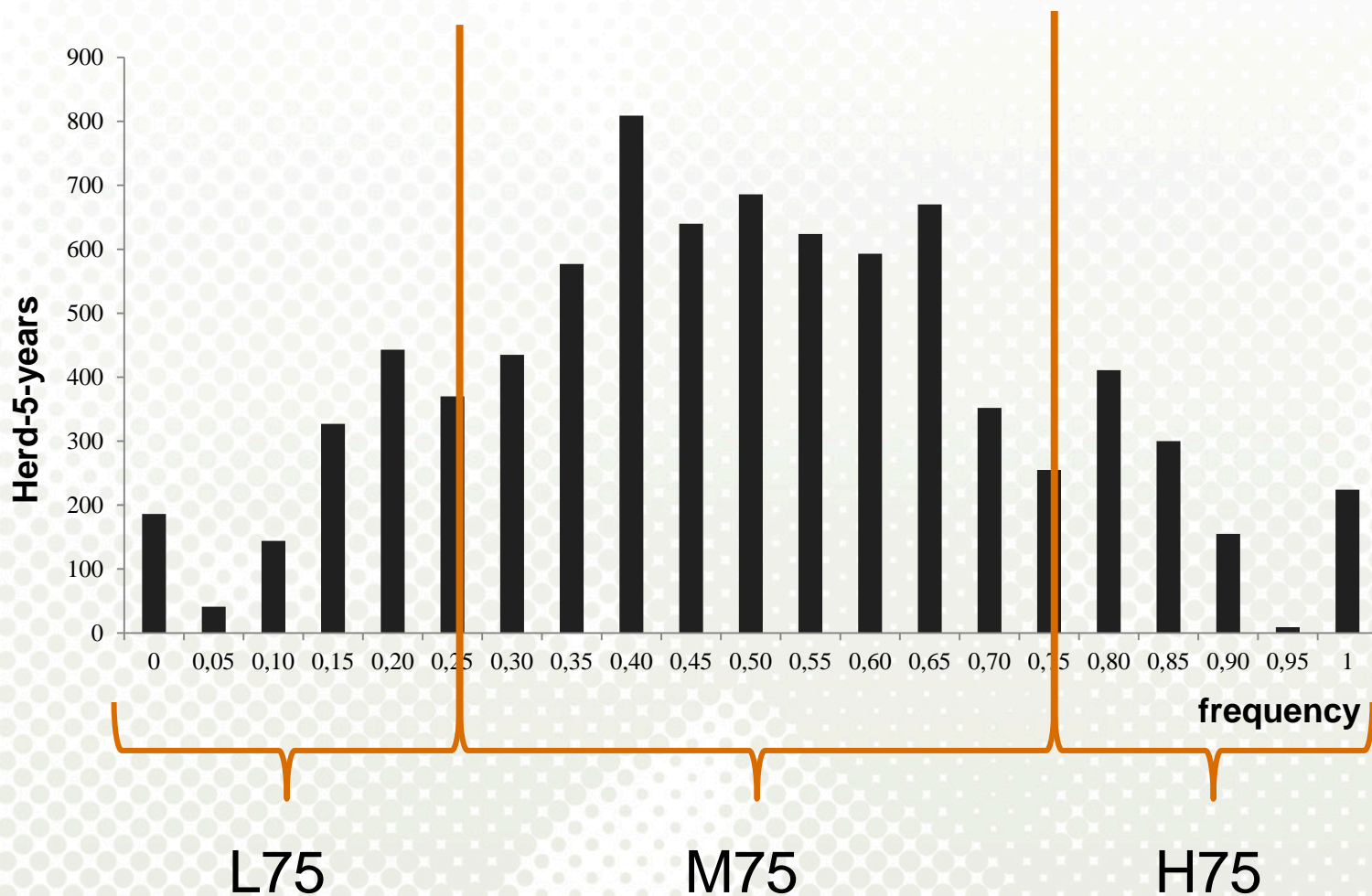
DATA

- All mastitis milk samples used for environmental definition of the herd
- Only herds with milk sample records included
 - Herd-5-year groups
- Proportion of milk samples positive for contagious pathogens
- Contagious pathogens
 - *Staphylococcus aureus*
 - *Streptococcus dysgalactiae*
 - *Streptococcus agalactiae*

ENVIRONMENT DEFINITION



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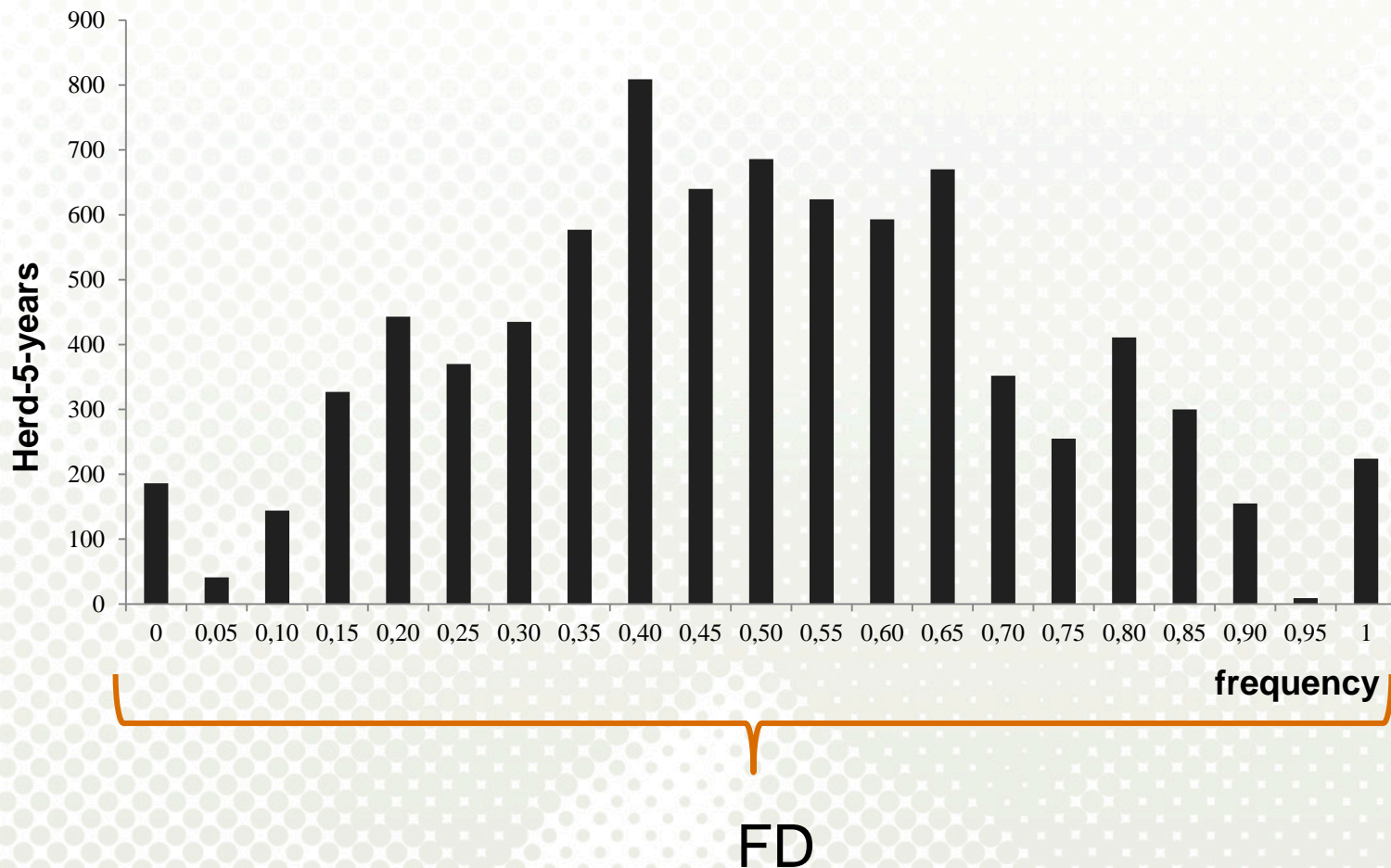
L75

M75

H75



ENVIRONMENT DEFINITION



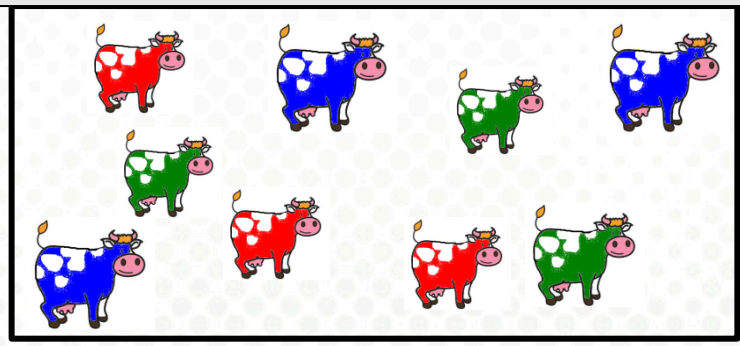
GENOTYPE

- Imputed 25K/54K SNP-data from Norwegian Red AI-bulls
- 47,321 SNP used for analyses after standard editing
- 1,126 sires with phenotypes and genotypes

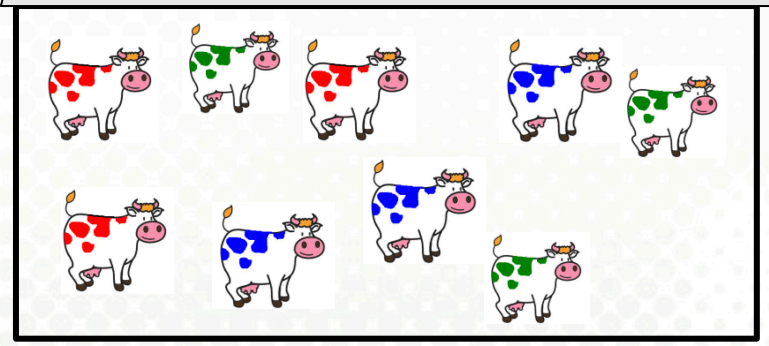
PHENOTYPE

- Daughter-yield-deviation (**DYD**) for CM30
 - CM30 = CM from 15 days before calving to 30 days after calving (frequency 6.93 %)
 - Binary trait (0/1)
- 236,255 first lactation Norwegian Red cows
- 7,858 herd-5-years
- Linear model
 - DMUAI and DMU5 in DMU (Madsen and Jensen, 2007)

H50 herds



L50 herds



$$DYD_{H50} \text{ [green cow] } = \text{£ [green cow] } /n$$

$$DYD_{L50} \text{ [green cow] } = \text{£ [green cow] } /n$$

$$DYD_{H50} \text{ [blue cow] } = \text{£ [blue cow] } /n$$

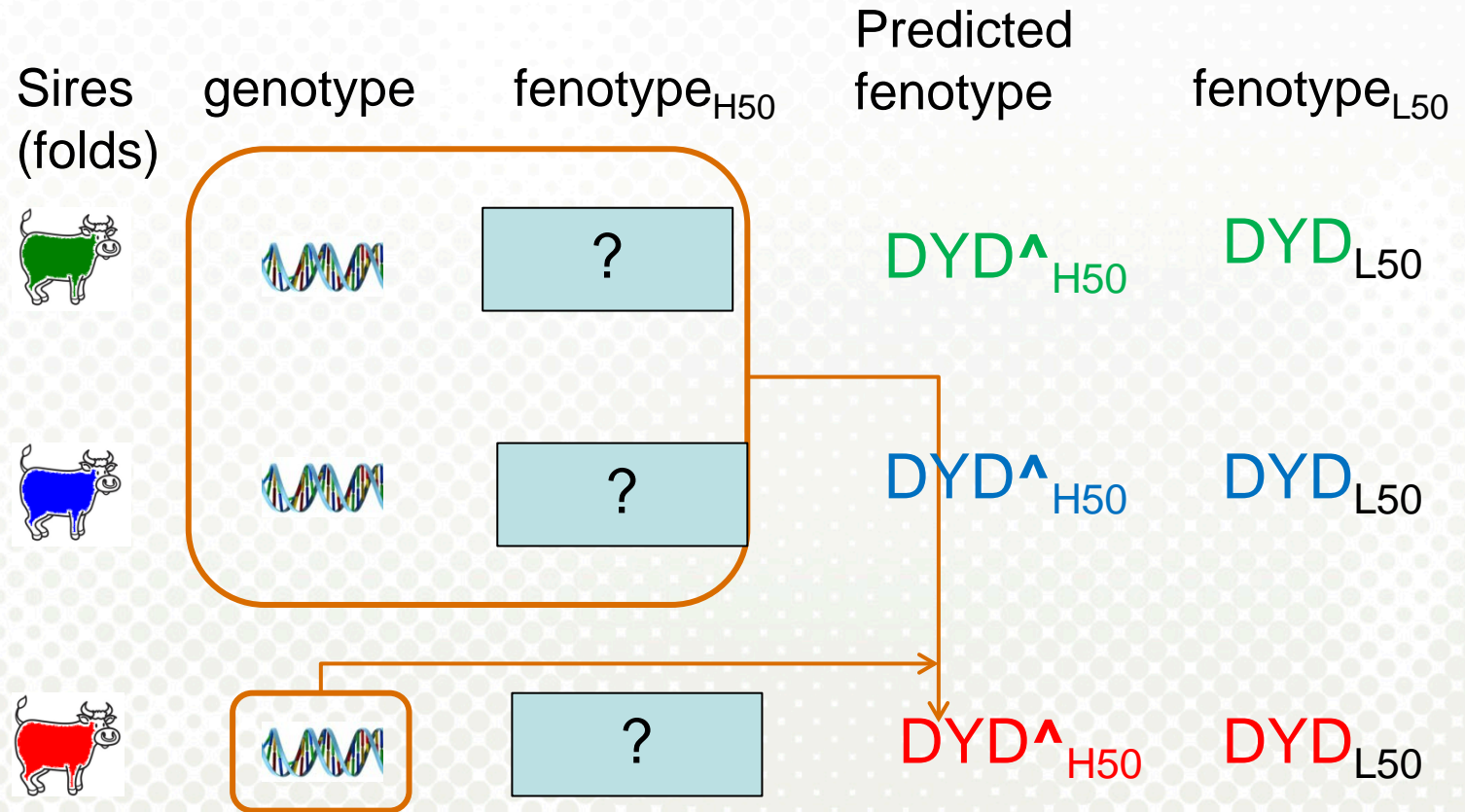
$$DYD_{L50} \text{ [blue cow] } = \text{£ [blue cow] } /n$$

$$DYD_{H50} \text{ [red cow] } = \text{£ [red cow] } /n$$

$$DYD_{L50} \text{ [red cow] } = \text{£ [red cow] } /n$$



CROSS VALIDATION



$$\text{Predictability}_{\text{within}} = \text{corr} (DYD_{H50}; DYD^{\wedge}_{H50})$$

$$\text{Predictability}_{\text{between}} = \text{corr} (DYD_{L50}; DYD^{\wedge}_{H50})$$

MODEL

- Bayesian Ridge Regression (**BRR**) using the BLR (Bayesian Linear Regression; de los Campos and Perez, 2010) package in R.

$$DYD_l = \mu + \sum_{g=1}^p x_{lg} \beta_g + e_l$$

RESULTS

Predictability within and between environments

Testing	Training	
	L50	H50
L50	<u>0.12</u>	0.14
H50	0.12	<u>0.13</u>

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Predictability
FD: 0.19

Testing	Training		
	L75	M75	H75
L75	<u>0.04</u>	0.08	0.10
M75	0.06	<u>0.13</u>	0.10
H75	0.06	0.10	<u>0.15</u>



DISCUSSION

- Small daughter groups
 - Average: 209 daughters/bull
 - FD: 65 % of the bulls <100 daughters
- 137 bulls with >150 daughters
 - Predictability FD = 0.46
 - Predictability subdataset = 0.20 to 0.35

CONCLUSIONS

- Similar predictions within and between environments
- No indications of interaction between the genotypes and the environment groups.

Thank you for your attention