

# RobustMilk

## An EU-wide programme to improve robustness of dairy cows

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# What is RobustMilk ?

- ▶ EU small collaborative project
- ▶ Started April 2008
- ▶ Completed April 2012
- ▶ 6 Northern European partners



# RobustMilk Partners

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# RobustMilk Objective

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To **develop new practical technologies** to allow breeders to re-focus their selection to include milk quality and **dairy cow robustness** and to evaluate the consequences of selection for these traits taking cognisance of various milk production systems

- ▶ Robustness :
  - ▶ Healthy, fertile, long living cows
  - ▶ Able to handle environmental disturbance

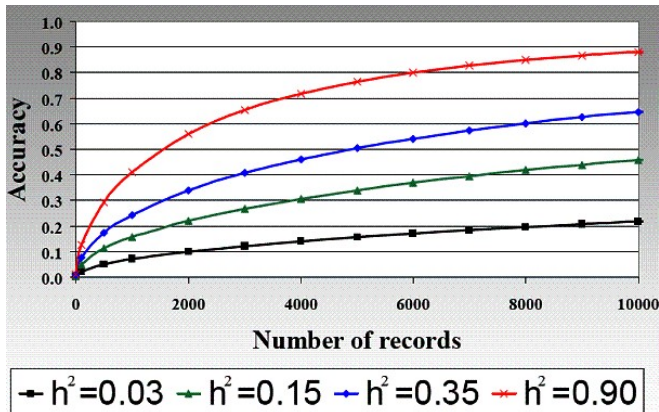
# RobustMilk Outline

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## 6 work packages

1. Common database
2. Phenotypic measurement tools
3. Statistical tools
4. Genomic tools
5. Dissemination
6. Management

## WP-1 Common database



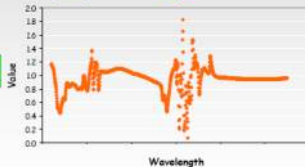
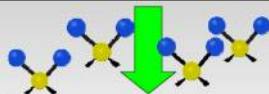
- ▶ Objective : increase power
  - ▶ combine phenotypes, genotypes and pedigree data from all partners into a single database

## WP-2 Phenotypic measurement tools

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- ▶ Objective : Evaluate usefulness of routinely measured milk mid-infrared (MIR) spectra to predict :
  - ▶ Milk quality
  - ▶ Robustness (energy balance)

# What is "mid infrared", MIR ?



Group	Num of Cows	Milk P %	Fat P %	SNF/ D Dap	Milk Solids % Content	Protein % Content	Carbonyl % Content	Shal % Content	Heast % Content	SDR €
Overall Cows	81	38			€ 64	€ 17	€ 154	€ 74	€ 17	
	7.8	8.00	4.7		38.9%	4.9%	34.9%	%	%	€ 63
	7.8	8.08	4.3							
1st Lactation	38	37			€ 61.8	€ 15.5	€ 157	€ 70	€ 15	
	7.7	8.00	4.2		38.6%	4.9%	34.9%	%	%	€ 67
	7.8	8.08	4.4							
2nd Lactation	33	38			€ 67.0	€ 17.2	€ 143	€ 74	€ 11	
	8.0	8.00	4.4		39.2%	%	36.7%	%	%	€ 44
	8.2	8.00	4.4							
3rd Lactation	10	36			€ 62.4	€ 14.0	€ 127	€ 70	€ 15	
	7.8	8.08	4.5		38%	%	36%	%	%	€ 31
	8.7	8.00	6.7							
4th Lactation	14	36			€ 63.3	€ 17.5	€ 131	€ 73	€ 13	
	8.8	8.00	5.2		39.5%	5%	36.9%	%	%	€ 54
	8.8	8.00	4.9							
5th Lactation (v)	10	38			€ 63.0	€ 17.5	€ 130	€ 73	€ 13	
	8.4	8.00	5.9		39.5%	5.0%	36.7%	%	%	€ 67
	8.0	8.00	4.7							



# Prediction of energy balance from milk MIR

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Energy balance was experimentally measured on 418 lactations in the experimental herd in Ireland

- ▶ Calibration on 75% of data
  - ▶ 306 milk samples
  - ▶ estimate prediction equation parameters
- ▶ Validation of other 25% of data
  - ▶ 112 milk samples
  - ▶ predict energy balance
- ▶ Accuracy of prediction
  - ▶ Energy balance : 0.71 - 0.78
  - ▶ Energy intake : 0.82 - 0.85
  - ▶ Body condition score : 0.45 - .48

## WP-3 Statistical tools , WP-4 Genomic tools

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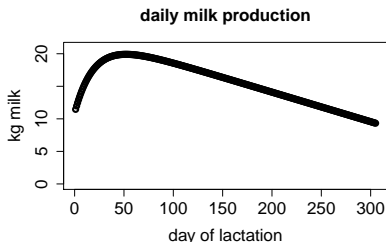
- ▶ WP-3 Objective : Develop statistical tools to model :
  - ▶ Robustness (Sensitivity to environmental disturbance)
  - ▶ Milk Quality (Somatic cell score)
  - ▶ Combined analysis of Robustness and Milk Quality
  
- ▶ WP-4 Objective : Undertake genome wide association studies to find genes for Robustness and Milk Quality
  - ▶ Combine data and DNA samples from research farms in 4 different countries
  - ▶ Genotype 2000 cows for 50,000 Single Nucleotide Polymorphisms (SNP)



# Association study

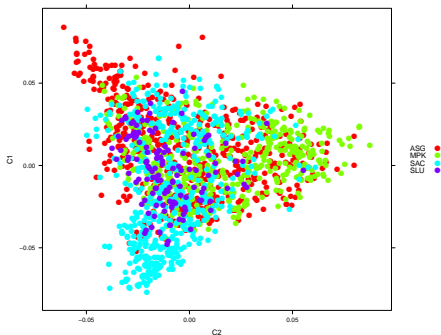
High quality data from research farms, but with diverse backgrounds

- ▶ 1,933 cows born 1980-2007
- ▶ 7 Herds in 4 Countries
  - ▶ 546 : Ireland
  - ▶ 653 : Scotland
  - ▶ 144 : Sweden
  - ▶ 590 : The Netherlands
- ▶ 72,008 Records in first years lactation



# Are populations genetically similar ?

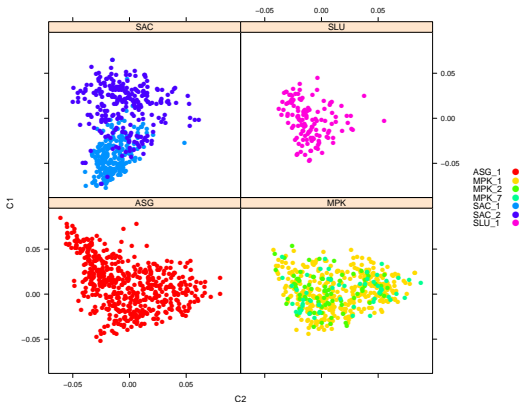
- ▶ Calculate IBS distances between all pairs
- ▶ Apply standard metric 2 dimensional scaling



- ▶ No separate clusters by country
- ▶ Tails for The Netherlands (red) and Scotland (blue)

# Population substructure

- ▶ Same 2D scaling by Country (panel) and Farm (color)

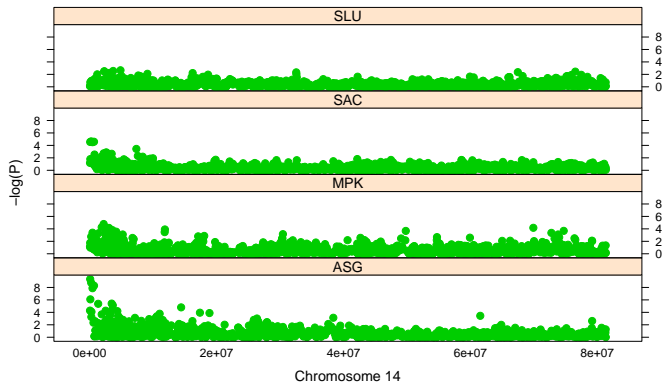


- ▶ Substructure between selection lines in Scotland (blue)

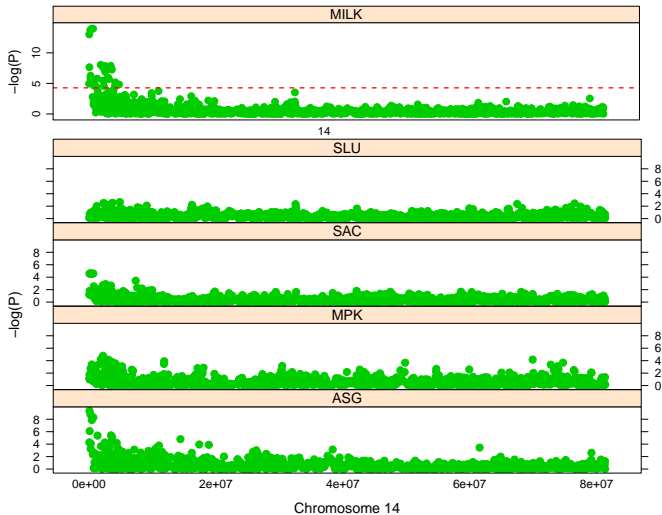
# Association analysis, by individual country

- ▶ Single SNP marker analysis
- ▶ Candidate gene region on chr 14

$$305\text{dayMILK}_{ij} = CHYS_j + \beta_1 \text{age}_{ij} + SNP_{ij} + A + e_{ij} \quad (1)$$

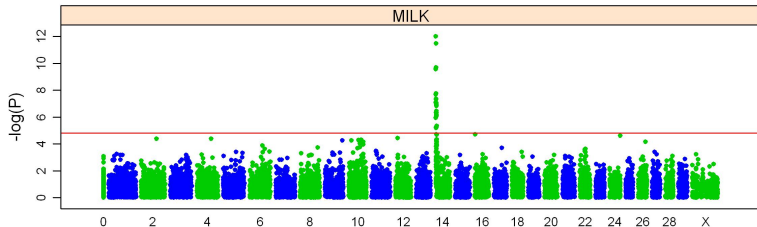


# Association analysis, all countries



# Association analysis, whole genome

- ▶ Markers associated with Milk production
- ▶ 0.05 False Discovery Rate threshold (red line)

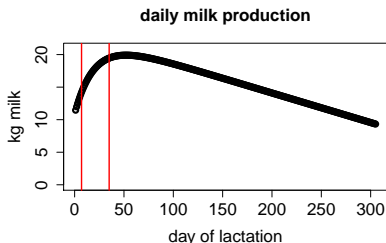




# Robustness phenotypes

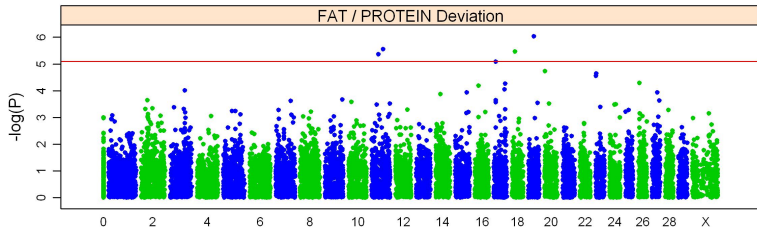
- ▶ calculate Fat yield / Protein yield (FPR) for :
  - ▶ Average over the whole lactation
  - ▶ For each testday in weeks 2 to 5
- ▶ Subtract lactation average FPR from testday FPR (FPRdev)
- ▶ Use maximum FPRdev in association analyses
- ▶ Adjusted phenotypes were used in association analyses :

$$FPRdev_{ij} = CHYS_j + \beta_{1age_i} + SNP_i + A + e_{ij} \quad (2)$$



# Association analysis, whole genome

- ▶ Markers associated with Fat/Protein Ratio
- ▶ 0.05 False Discovery Rate threshold (red line)



# Conclusions

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- ▶ Some genes have measurable effects on Fat/Protein Ratio
  - ▶ promising for selection on Robustness with markers
- ▶ Progress only can be achieved by working together
- ▶ New phenotypes provide huge potential for genetic improvement of difficult traits
- ▶ Significant associations can be detected in combined data from varied sources

# Future work

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- ▶ Add more genotypes and phenotypes to the database
  - ▶ 100's of bulls with accurately estimated genetic values + genotypes
- ▶ Analyse new Robustness and Milk Quality traits
  - ▶ Predictions from MIR spectra
  - ▶ Results from statistical modelling of Robustness and Milk Quality
- ▶ Analyse Genotype by Environment interactions
  - ▶ Does the same gene have different effects in different countries ?
- ▶ Detect regions on the genome affected by selection in populations in Scotland

# Acknowledgements

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More information : <http://www.robustmilk.eu>



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