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Genome wide association study and genomic prediction for methane emission in Danish Holstein cattle

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”With genomic selection it will be possible to select for scarsely measured traits such as feed efficiency and methane emission”

Phenomics

- ”New” phenotypes
- Feed intake
- Rumen microbial composition
- Methane

- ”Data that you cannot just get provided for free with hardly any effort”

Large scale genotypings

- Full herds gets genotyped
- 10000s animals available
- Phenomics on these cows

Aim of study

- Perform genomic breeding values with including accuracies for methane emission and compare with BLUP EBVs
- Perform GWAS to identify SNPs with major effect on methane emission

Laser

Quantifying methane production

- Measure methane and carbon dioxide concentrations
- Heat producing units (HPU) = 5.6 *live weight^{0,75} + 22*FPCM + 1.6*10^{-5}*days carried calf
- CH4_LITERS = CH4_RATIO*180*24*HPU
- Highly influenced by milk production
- Ignoring variation in CO_2 production

Madsen et al., 2010

Danish data

Trait	Units	#	Mean	SD	Min	Max
CH4_RATIO		3121	0.087	0.012	0.043	0.109
CH4_LITERS	L/ day	1745	381	41.2	283	548
CH4_MILK	L/kg/day	1745	10.41	1.34	8.43	13.7
FPCM	L/ day	3121	36.6	7.9	19.2	62.7
Weight	Kg	1745	647	68.4	467	890

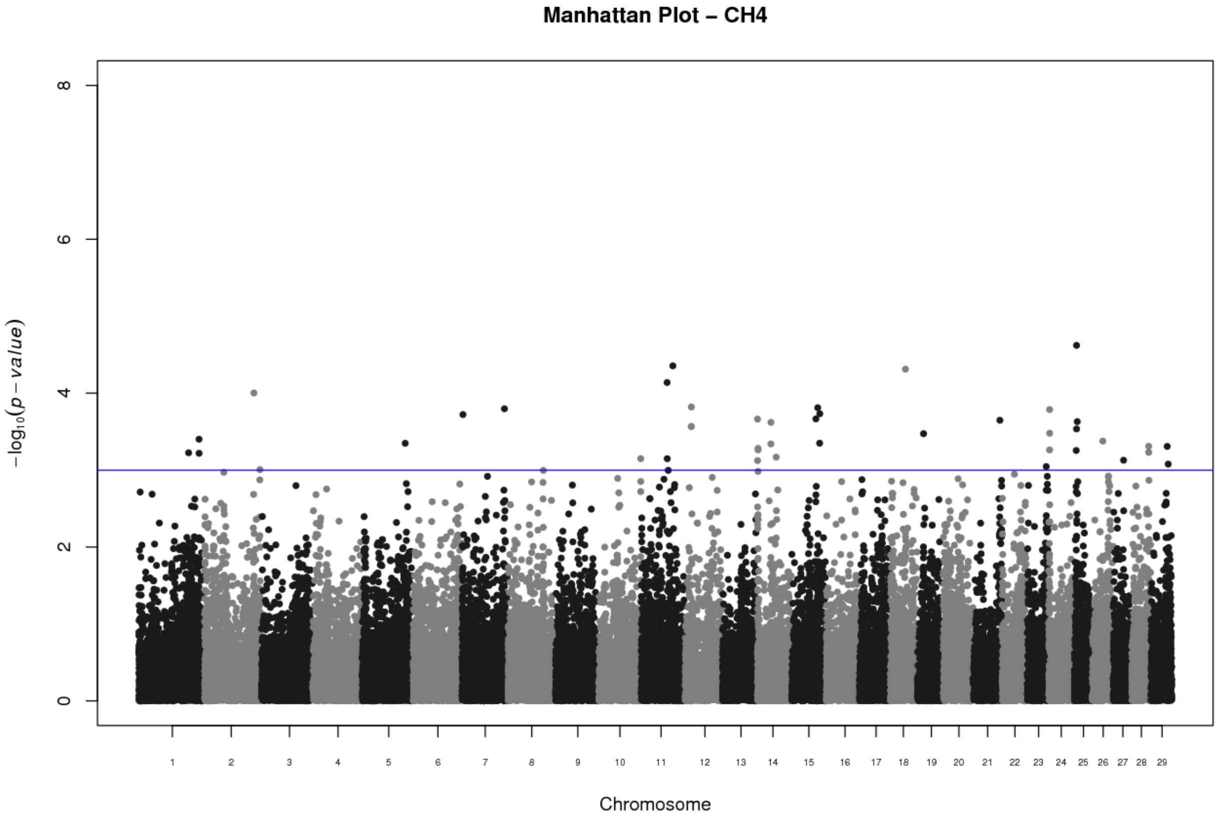
Genomic prediction and GWAS

- 1739 Holstein cows
- Illumina 50 K SNP beadchip
- 44007 SNPs after cleaning

Statistical model for GWAS

Methane	=	mean	
	+	herd-year	fixed
	+	season	fixed
	+	parity	fixed
	+	dim	fixed reg
	+	SNP	fixed reg
	+	animal	random
	+	residual	random

Genome wide association study



Genomic prediction using GBLUP

- Five-fold cross validation procedure
- Whole data randomly into five subsets
- Reliability = $(r_{ebv,y_c})^2/h^2$
- Regression of y_c on estimated breeding values

- Compares BLUP, GBLUP and $GBLUP_w$

Statistical model for genomic prediction

Methane	=	mean	
	+	herd-year	fixed
	+	season	fixed
	+	parity	fixed
	+	dim	fixed reg
	+	animal	random
	+	residual	random

Covariance structure for genomic prediction

1 $\mathbf{a} \sim N(\mathbf{0}, \mathbf{A}\sigma_a^2)$

2 $\mathbf{a} \sim N(\mathbf{0}, \mathbf{G}\sigma_a^2)$

3 $\mathbf{a} \sim N(\mathbf{0}, \mathbf{G}_w\sigma_a^2)$

Genomic prediction

Model	**Validation set**	
	Reliability	Regression
BLUP	0.171	1.025
GBLUP	0.175	1.002
GBLU$_w$	0.183	1.003

Discussion

- Stagnation in the development of the methane phenotype
- No incentive for the farmer to select for lower methane emission
- A company with a business plan is needed
- International collaborations are needed (gCH4, Genome Canada, METHAGENE)

Conclusion

› Scarsely measured traits are still complicated to evaluate and include in a breeding programme

› Genetic variation exists for methane emission

› Limited evidence of any SNP with an effect on methane emission

› Limited difference in reliability between GBLUP and BLUP models