MULTI-TRAIT GENOMIC PREDICTION OF METHANE EMISSION IN DANISH HOLSTEIN

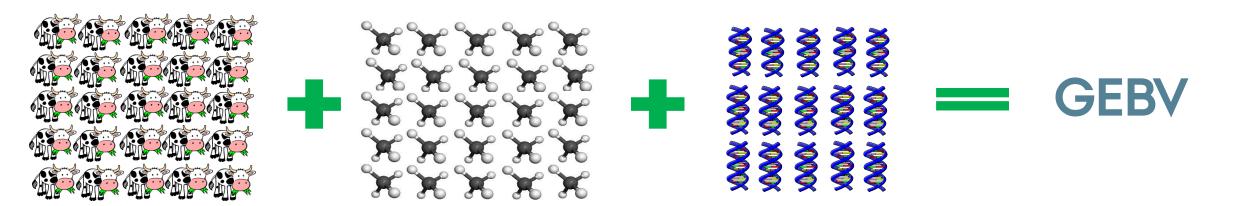


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CHALLENGES



Add information from recorded traits in a multitrait approach could increase the accuracy of prediction of CH₄





OBJECTIVE

Compare accuracies of prediction of GEBV for methane including or not ECM and BW information in a multi trait approach





TRAITS



CH₄ log-ppm



ECM



BW





DATA

- 2 research farms and 10 commercial farms
- 2 methods to measure CH₄ (sniffers)
 - Guardian and Gasmet
- ~2,700 Danish Holstein cows
 - + 60,000 ECM and BW records
 - ~2,300 Danish Holstein cows
 - $\sim 14,000 \text{ CH}_{4} \text{ records}$
 - 1,962 cows with genotypes (50k)

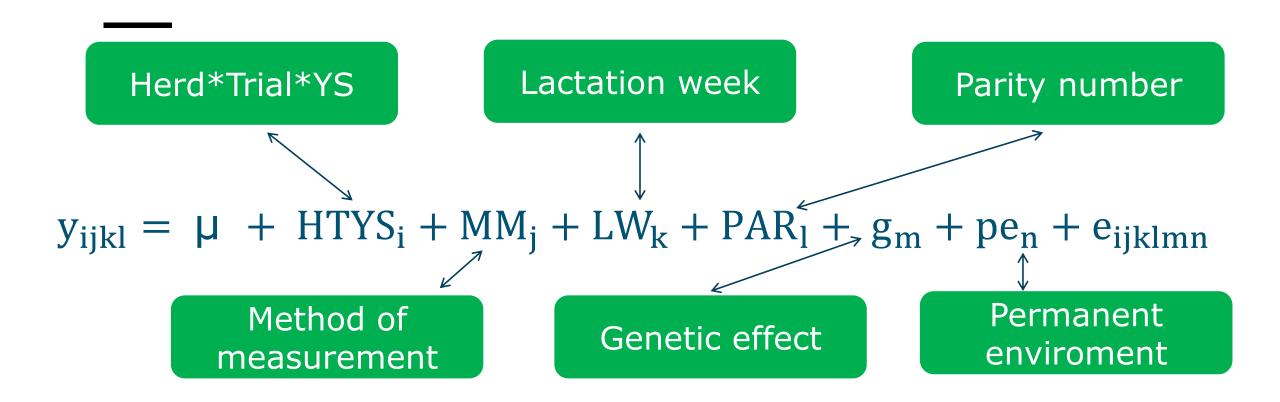








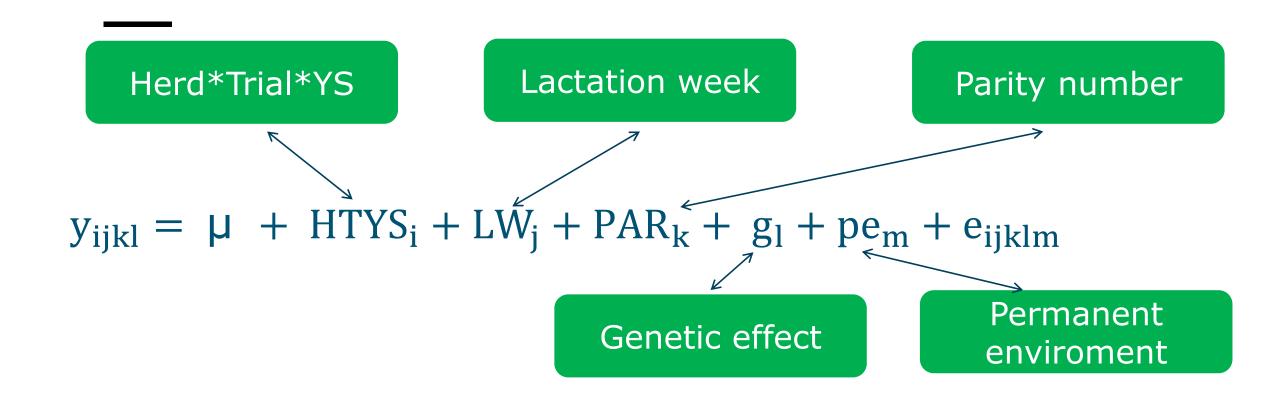
STATISTICAL MODEL FOR CH4







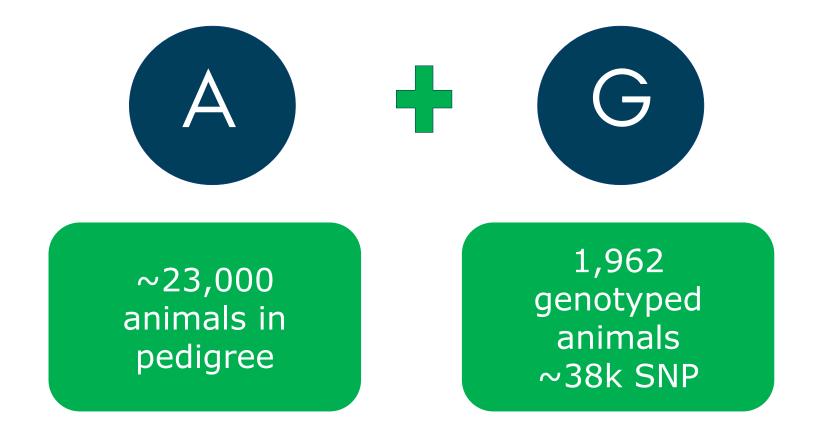
STATISTICAL MODEL FOR BW AND ECM







SINGLE STEP GBLUP





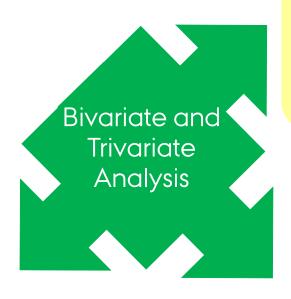


SCENARIOS

BASE SCENARIO CH₄

ONLY IN REFERENCE (OR)

- CH₄ + BW
- CH₄ + ECM
- CH₄ + BW + ECM



NO CH₄

- BW
- ECM
- BW + ECM

VALIDATION AND REFERENCE

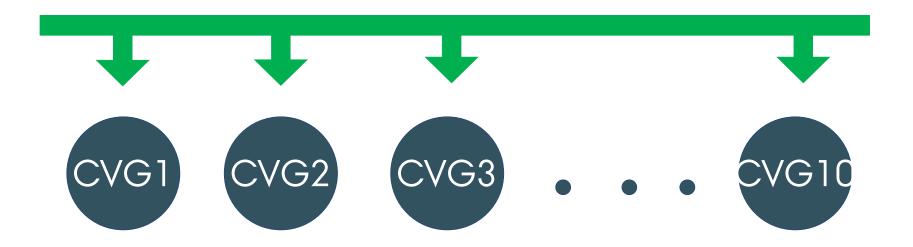
- CH₄ + BW
- CH₄ + ECM
- CH₄ + BW + ECM





CROSS VALIDATION GROUPS









ACCURACY AND BIAS CALCULATION

$$r_{HI} = \frac{r}{\sqrt{\frac{nh^2}{1 + (n-1)rep}}} = r / 0.45$$

Slope = Adjusted phenotype ~ GEBV

r = Adjusted phenotype/GEBV

n = average number of repeated records per CVG

 h^2 = heritability of CH₄

rep = repeatability CH_4

$$rep = \frac{\sigma_a^2 + \sigma_{pe}^2}{\sigma_p^2}$$





DESCRIPTIVE STATISTICS

Trait	Unit	Mean	SD	Min	Max
CH ₄	Log(ppm)*100	572.6	47.1	450	699
BW	kg	641.0	75.4	387	900
ECM	kg/d	32.9	8.5	10	65





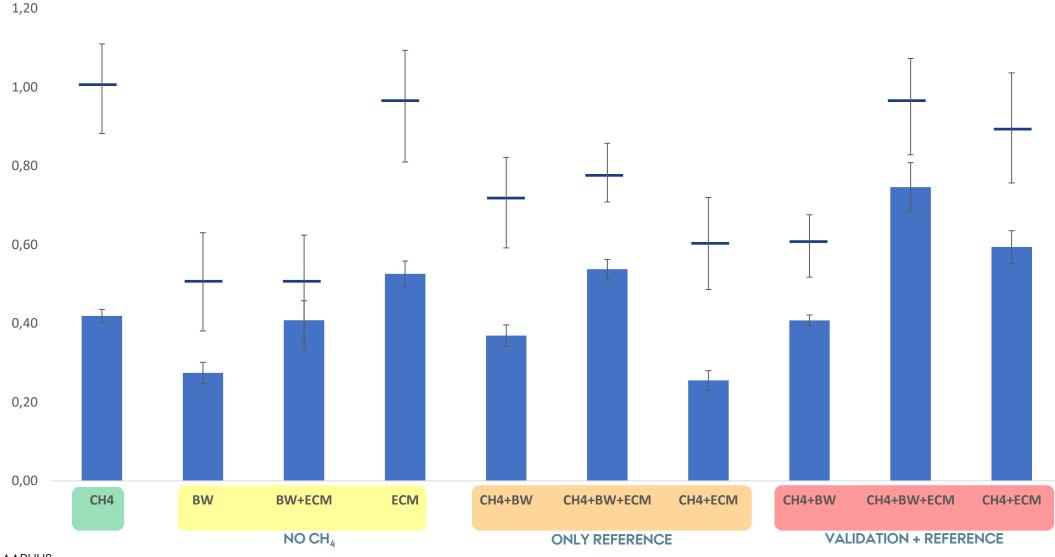
VARIANCE COMPONENTS

Trait	rep	h^2 and r_a
CH_4	0.51	0.14
BW	0.86	0.50 0.58
ECM	0.62	0.59 0.26 0.37





GENOMIC PREDICTION FOR METHANE



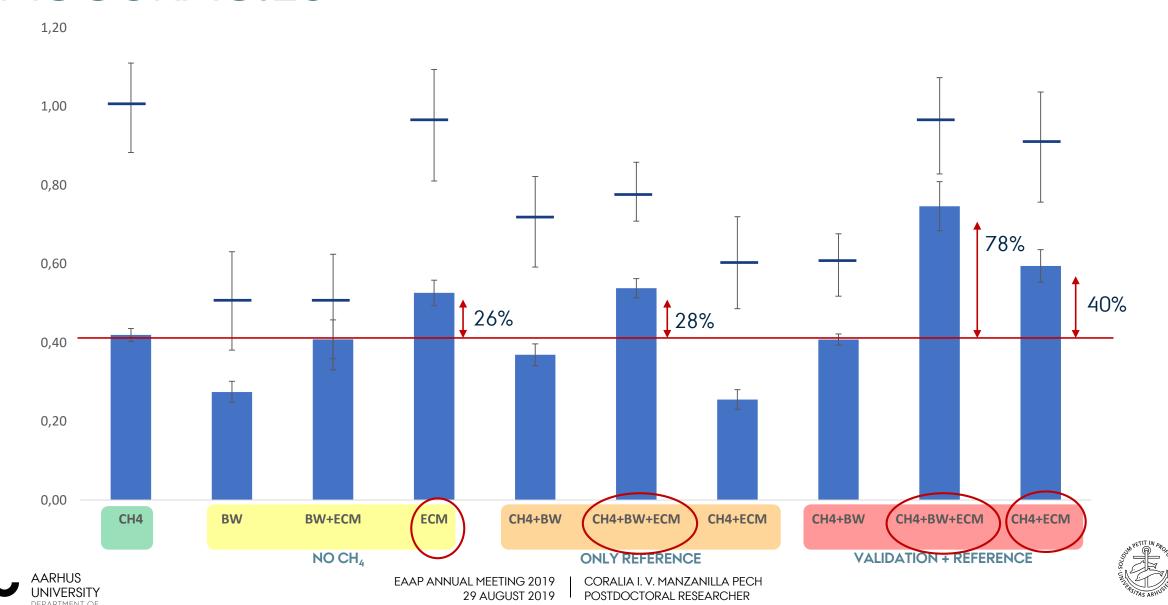


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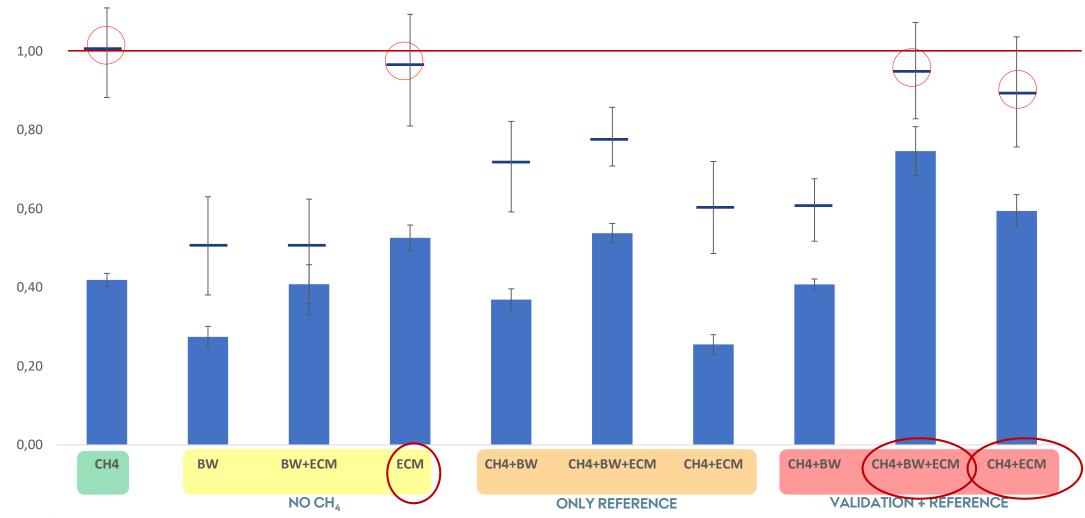
ACCURACIES

MOLECULAR BIOLOGY AND GENETICS



SLOPE (BIAS)







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CONCLUSIONS

- Multitrait genomic prediction can increase the accuracies from 26 to 78%
- In absence of CH₄ information, ECM records can help to predict CH₄ with an acceptable accuracy
- Including **BW and ECM** in both, reference and validation population can almost **double the accuracy** of prediction of CH₄ without affect the bias







