

Better lives through livestock

Variance components estimation for methane emission in smallholders' dairy farms

Alireza Ehsani, Selam Meseret, Okeyo Mwai, Raphael Mrode.

ILRI, Nairobi, Kenya & SRUC, Edinburgh, UK

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Background information

- Research project into the sustainability of the smallholder dairy system, given climate change
 - Reducing feed costs and greenhouse gas emission in smallholder dairy cattle in Sub-Saharan Africa
 - Multi-facet approach , encompassing not only
 - mitigation strategies
 - adaptive capacity of animals
 - But also ensuring increased productivity and food security.







Research Approach of the project



Selection for direct reduction in methane

Genetic potential for resilience

Improving efficiency

Management





Direct selection for methane reduction

- Herds are small and highly dispersed. Tool needed to capture methane must be
 - Portability and affordability
 - Non-invasive
 - quantify CH4 emission at the animal level
 - Results can digitally stored
- Laser Methane Detector (LMD) seems most suitable
- Measured at several times during life cycle of the cow





Direct selection for methane reduction

- Milk sample are simultaneously captured and analysed by LactoScope 300
 - Mid-infra-red spectrum (MIR)
- Develop prediction equation for CH4 based on the relationship between MIR and CH4
- Predict CH4 emitted by a cow from a milk sample







Data from Ethiopia

- LMD used measure methane from July 2023 to March 2025
- 15723-point LMD measurements of 3-5 minutes duration were recorded on 945 dairy cows and heifers.
- Methane in ppm-m converted to g/day using the equation of Lanzoni et al., (2022)
- Productive data also measured
 - Milk yield, SCC and body weight
 - Fat and protein percentages







Data from Ethiopia

- Cows are crossbreds mostly from Holstein & Jersey crossed with indigenous breeds.
 - Cows were genotyped and admixture analysis used to determine breed proportion
 - Compute percentage exotic (proportion of Holstein and Jersey)







Summary of data

country	trait	No. of animals	No. of records	Mean	SD	Min	Max
Ethiopia	CH4	986	14501	293	122	100	800
	Milk yield	613	6423	12	4.75	1	38
	Fat%	703	7714	2.97	1.44	1.02	7.96
	Protein%	703	7714	3.36	0.6	1.06	7.64
	Body weight	680	9184	440	71	102	680
	MIR	703	7714				
	genotypes	519					







Various factors affecting methane production

parameter	P value	significant
Cow status	< 2.2e-16	***
age	0.03	*
Breed exotic class	6.203e-10	***
Lactation number	0.11	
Lactation stage	3.758e-06	***

• Repeatability was low at about 0.26



Parameter	Effect on CH4 emission (g/day)
mean	233.3
Cow status	
Feeding	100.6
Ruminating	-90.2
Sleeping	-83.1
Standing_idle	-57.3
age	-2.6
Percent Exotic genes	2.55
Lactation number	3.6
Lactation stage	-0.04

Prediction of methane using MIR

- MIR records with ± 15 days from LMD measurements used ۲ to predict CH4
 - 7729 MIR records and corresponding CH4 records from 608 individuals were available for the prediction
- Initial curation spectral data was done using the method of ulletSoyeurt et al., (2011) and smothered by a 3rd order polynomial (Savitzky and Golay, 1964)
- PLS approach using 10 principle components to predict CH4 lacksquareusing R PLS package (Liland et al., 1999).
- The average value of 100 replicates in a 5-fold cross \bullet validation was used to compute the prediction accuracy.



Indirect prediction of methane from MIR

		All data			Feeding time data		
		R	RMSE	Ν	R	RMSE	
MIR + body weight+ milk + fat% + prot%	9872	0.28	48.1	1973	0.42	60.8	
body weight+ milk + fat% + prot%	9872	0.09	94.8	1973	0.17	67.1	
weight + milk	9872	0.03	94.6	1973	0.20	66.7	
MIR	9872	0.25	48.8	1973	0.43	62.7	



Indirect prediction of methane from MIR using mean values of mean methane from LMD

	All data			Feeding data		
	N	R	RMSE	Ν	R	RMSE
MIR + body weight+ milk + fat% + prot%	479	0.45	103.3	296	0.52	104.5
body weight+ milk + fat% + prot%	479	0.26	125.1	296	0.20	138.8
MIR + fat% + prot%	620	0.43	108.4	296	0.51	106.5
MIR	620	0.40	111.9	296	0.52	110.6



Number of records needed for prediction

Based on 464 cows with at least 12 records on methane

Average		
Records	accuracy	RMSE
1	0.24	168
2	0.28	149
3	0.29	133
4	0.37	124
5	0.39	122
6	0.45	116
7	0.47	116
8	0.45	109
9	0.45	107
10	0.45	106
11	0.46	105
12	0.45	106



Genetic parameter estimation

- 945 dairy cows with 15723 methane measurements.
- 90665K SNP cheap was available for 459 cows and 90407 SNPs used after QC
- Pedigree available on 570 cows with observations
- Two models applied
 - Repeatability model
 - Repeatability model with methane averaged by yearseason





Genetic parameter estimation

• Repeatability model

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	HBLUP		PBLUP	
model	h2	ре	h2	ре
Cow status, year-season, avgfarmMY	0.10	0.06	0.09	0.08
(fixed)+ pe	(0.02)	(0.01)	(0.03)	(0.02)

• Repeatability based on year-season means

		HBLUP		PBLUP	
	Model	h2	ре	h2	ре
		0.19	0.12	0.14	0.17
)	year-season, avgfarmIVIY (fixed)+ pe	(0.04)	(0.04)	(0.06)	(0.06)
NA					

Future work

- Further modelling of the data to estimate genetic parameters
- Examine relationship between methane
 - Productivity traits,
 - Body weight to improve maintenance requirement
 - heat tolerance (THI)
- Constructing the Selection index
 - Construction of an index or sub-indexes for selection of bulls and cows with less impact on the environment, better feed utilization and productivity



Conclusions

- Accuracy of prediction of methane from MIR data varied from low to medium but encouraging
- Breed differences influence methane emitted
- It seems that about 4-6 records per cow will be needed for more accurate measurement of methane using LMD and for good prediction of methane from MIR information
- Results indicate low genetic variation but it an be explored through selection.







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