

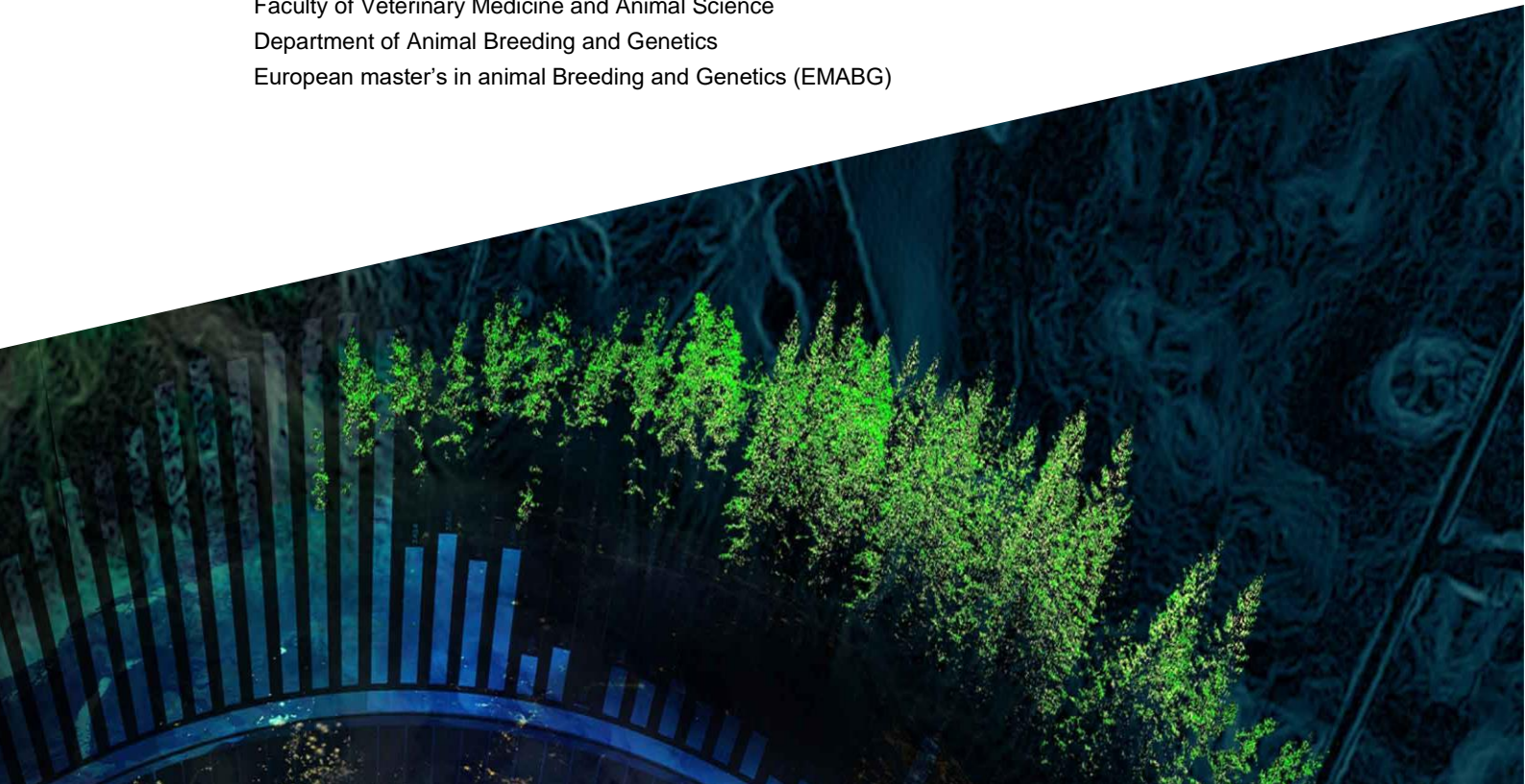


# Heritability of methane emission in Swedish Red cattle in northern Sweden

---

LUCY CHIPONDORO

Degree project/Independent project • 30 hp  
Swedish University of Agricultural Sciences, SLU  
Faculty of Veterinary Medicine and Animal Science  
Department of Animal Breeding and Genetics  
European master's in animal Breeding and Genetics (EMABG)



# Heritability of methane emission in Swedish Red cattle in northern Sweden

Lucy Chipondoro

**Supervisor:** Prof. Erling Strandberg, Swedish University of Agricultural Sciences (SLU), Department of Animal Breeding and Genetics,  
**Assistant supervisor:** Dr. Birgit Jutta Zumbach, University of Göttingen  
**Assistant supervisor:** Dr. Abdulai Guinguina, SLU/LUKE, Department of Animal Nutrition  
**Examiner:** Prof. Lotta Rydhmer, SLU, Department of Animal Breeding and Genetics

**Credits:** 30 credits  
**Level:** Advanced, A2E  
**Course title:** Independent project in Animal Science  
**Course code:** EX0870  
**Programme/education:** European master's in Animal Breeding and Genetics  
**Course coordinating dept:** Department of Animal Breeding and Genetics  
**Place of publication:** Uppsala  
**Year of publication:** 2024

**Keywords:** Methane emission, Heritability, Swedish Red cattle, dairy cow

**Swedish University of Agricultural Sciences**  
Faculty of Veterinary Medicine and Animal Science  
Department of Animal Breeding and genetics  
Unit/section (add if needed or delete row)

## Abstract

Dairy cattle contribute a significant proportion of greenhouse gases (GHG), mainly methane (CH<sub>4</sub>), among other livestock species. Methane has a negative impact on climate; therefore, its reduction is a top priority for a sustainable dairy production system. Genetic selection could be a viable, permanent strategy to reduce methane production in dairy cows. This study aimed to estimate the heritability of CH<sub>4</sub> emission in Swedish Red cattle. Genetic correlations of CH<sub>4</sub> with production traits were also determined as a second objective of the study. A total of 1089 CH<sub>4</sub> records were used in this study, collected from 194 Swedish Red cows from a single herd. The GreenFeed system was used to measure CH<sub>4</sub> emissions. This study examined two specific CH<sub>4</sub> traits: daily CH<sub>4</sub> production (g/d) and CH<sub>4</sub> intensity [g CH<sub>4</sub>/kg energy-corrected milk (ECM)]. The following traits were also analysed in this study: dry matter intake (DMI), ECM, milk yield (MY), and body weight (BW). Heritability estimates and correlations were calculated using univariate and bivariate animal models. The variance components for the calculation of heritability and genetic correlations were obtained using an AI-REML algorithm in the DMU software. The heritability (standard error in brackets) for CH<sub>4</sub> production ranged from 0.24 (0.31) in the first parity to 0.44 (0.20) in the second and later parities. The estimates of heritability for CH<sub>4</sub> intensity were 0.26 (0.35) in the first parity and 0.38 (0.20) in second and later parities. The heritability for ECM, MY, DMI and BW in the first parity were 0.40 (0.28), 0.58 (0.30), 0.80 (0.37), and 0.34 (0.39), respectively. The heritability estimates for ECM and MY were extremely low in the second and later parities: 0.01 (0.12) and 0.05 (0.14), respectively. Genetic correlation of CH<sub>4</sub> with DMI, ECM and MY in the first parity were 0.48 (0.64), 0.23 (0.4), -0.06 (0.41) and 0.92 (0.77), 0.75 (0.64), 0.48 (0.41) in second and later parities respectively. The standard error of estimates was very high for genetic correlations. However, strong positive genetic correlation obtained between CH<sub>4</sub> production and DMI in this study shows that precautions must be taken when selecting for reduced CH<sub>4</sub> production as this may consequently reduce the dry matter intake of animals. The high standard error of estimates signifies the importance of enlarging the data set. The results of this study show that methane is a moderately heritable trait. Hence, it is possible to reduce CH<sub>4</sub> emissions in Swedish Red cows through genetic selection.

*Keywords:* methane emission, heritability, Swedish Red cattle, dairy cow

# Table of contents

<b>List of tables .....</b>	<b>6</b>
<b>List of figures.....</b>	<b>7</b>
<b>Abbreviations .....</b>	<b>8</b>
<b>1. INTRODUCTION.....</b>	<b>9</b>
1.1 Background.....	9
1.2 Statement of the problem.....	10
1.3 Objectives .....	10
<b>2. Literature Review .....</b>	<b>11</b>
2.1 Livestock and methane production .....	11
2.2 Impact of methane emission on global warming.....	11
2.3 Methods of measuring methane .....	11
2.3.1 Respiration chambers.....	12
2.3.2 Automated head chamber system (GreenFeed System) .....	12
2.3.3 Sniffer Technique.....	13
2.3.4 Laser Methane Detector .....	13
2.3.5 Sulfur Hexafluoride Tracer Technique .....	14
2.3.6 General comments .....	14
2.4 Strategies to reduce methane and their pitfalls. ....	15
2.5 Genetics as a potential solution. ....	16
2.6 Heritability and methane .....	16
<b>3. MATERIALS AND METHODS .....</b>	<b>18</b>
3.1 Experimental design .....	18
3.2 Description of the diet .....	18
3.3 Traits measurement .....	19
3.4 Pedigree data.....	20
3.5 Statistical analysis.....	20
3.6 Variance and covariance estimation .....	20
3.7 Calculation of heritability .....	21
3.8 Estimation of Correlation.....	22
<b>4. RESULTS .....</b>	<b>23</b>
4.1 Descriptive statistics of the data .....	23

4.2	Lactation curves for CH <sub>4</sub> production,CH <sub>4</sub> intensity and ECM .....	24
4.3	Variance components and heritability estimates .....	26
4.4	Genetic and permanent environmental correlation.....	30
4.5	Raw correlation of CH <sub>4</sub> and other traits .....	30
<b>5.</b>	<b>DISCUSSION.....</b>	<b>32</b>
<b>6.</b>	<b>Conclusion.....</b>	<b>36</b>
	<b>References .....</b>	<b>Fel! Bokmärket är inte definierat.</b>
	<b>Popular science summary.....</b>	<b>44</b>
	<b>Acknowledgements.....</b>	<b>45</b>
	<b>Publishing and archiving .....</b>	<b>46</b>

# List of tables

Table 1.Descriptive statistics: mean, standard deviation (SD), minimum (Min), maximum (Max) and coefficient of variation (CV%) of CH <sub>4</sub> , CH <sub>4</sub> /ECM, ECM, MY, DMI, BW. ....	23
Table 2. Number of cows and number of records for each trait.....	23
Table 3.Estimates of variance components for Experiment x Diet (ExpD), Experiment x Period (ExpP), experiment (Exp), permanent environmental ( $\sigma^2_{pe}$ ), additive genetic ( $\sigma^2_a$ ), residual variance ( $\sigma^2_e$ ), phenotypic variance ( $\sigma^2_p$ , sum of $\sigma^2_{pe}$ , $\sigma^2_a$ , and $\sigma^2_e$ ), and heritability estimated using a single trait animal model [1] for parity 1. ....	27
Table 4.Variance components and heritability estimate for parity 2+ estimated with a single trait animal model [1]. ....	27
Table 5.Variance components and heritability estimates estimated using a bivariate animal model for parity 1 and 2. ....	29
Table 6.Genetic ( $r_g$ ) and permanent environmental correlation ( $r_{pe}$ ) estimates for methane and other traits between parity 1 and parity 2+ with their corresponding standard errors in brackets. ....	30
Table 7. Raw correlations of CH <sub>4</sub> , g CH <sub>4</sub> / kg ECM, MY, ECM, BW and DMI of combined data set (All parities) .....	31

## List of figures

Figure 1. Illustration of the GreenFeed components for methane measurement in ruminant species (Alexander N. Hristov et al., 2015) .....	19
Figure 2. Lactation curve for methane production fitted using model [1] .....	24
Figure 3. Lactation curve for ECM fitted using model [1] for cows in parity 1 and 2+ .....	25
Figure 4. Lactation curve for g CH <sub>4</sub> /kg ECM fitted using model [1] for cows in parity 1 and parity 2+ .....	26

## Abbreviations

DIM	Days in milk
DMI	Dry matter intake
ECM	Energy corrected milk
CH <sub>4</sub>	Methane
C0 <sub>2</sub>	Carbon dioxide
GHG	Green House Gases
$h^2$	Heritability
MY	Milk yield
$r_g$	Genetic correlation
$r_{pe}$	Permanent environmental correlation



# 1. INTRODUCTION

## 1.1 Background

Swedish Red cattle is one of Sweden's dominant dairy breeds and plays an important role in the provision of milk. Milk and milk products are important food sources rich in essential nutrients for human health (FAO, 2013). The demand for dairy products is expected to rise as the human population continuously increases (Mickiewicz & Volkava, 2022) and an increase in demand of dairy products is expected to result in an increased dairy production.

However, the production of dairy products has a negative impact on the climate due to CH<sub>4</sub> emissions. According to Gerber et al. (2013b), dairy production accounts for 20% of global livestock sector GHG and 46.5% of total GHG of dairy cattle are from enteric CH<sub>4</sub>. The production of CH<sub>4</sub> from livestock and its impact on climate changes are a major concern worldwide (Martin et al., 2010). In livestock production, CH<sub>4</sub> is a colourless, odourless gas that is produced mainly in the rumen. The other source of CH<sub>4</sub> is manure decomposition. Microbial fermentation in the rumen (enteric) accounts for about 80% of emissions and 20% from manure decomposition (Garnsworthy et al., 2019). Enteric CH<sub>4</sub> contributes significantly to greenhouse gases (Moss et al., 2000; Musa, 2020). Methane is a potent greenhouse gas with a severe impact on climate change. According to Myhre et al. (2014), CH<sub>4</sub> emission is equivalent to 28 times more global warming potential than that of CO<sub>2</sub>. Hence, its mitigation is a top priority for sustainable cattle production.

There have been several efforts to reduce CH<sub>4</sub> for more sustainable livestock farming. Mitigation strategies such as nutritional interventions, microbial solutions, dietary supplements, and effective management practices have been adopted to reduce CH<sub>4</sub> emissions (Black et al., 2021; Cottle et al., 2011). Nutritional strategies reduce CH<sub>4</sub> emissions, but the reduction is only short-term and very expensive to maintain. Microbial use reduces CH<sub>4</sub> emission but negatively affects feed intake and ruminal passage rate. Genetic means could offer an alternative permanent solution to the reduction of CH<sub>4</sub>. This could be done by selecting and breeding for low CH<sub>4</sub>-producing animals.

Heritability is one of the most important genetic parameters for the breeding and selection of animals, contributing to faster genetic progress. Earlier research studies have indicated that heritability of CH<sub>4</sub> emissions in dairy cattle varies from 0.12 to 0.45 (Breider et al., 2019; Lassen & Løvendahl, 2016). The variation depends on the trait under examination and the lactation stage (such as CH<sub>4</sub> intensity, early-to-middle or late lactation). Most research studies have been done on Holstein dairy cows (Breider et al., 2019; Lassen & Løvendahl, 2016), there are no heritability studies on Swedish Red cows. Heritability is a population parameter and thus depend on population-specific parameters and variation attributed to environmental factors. There are also different CH<sub>4</sub> emission traits relevant for selection such as daily CH<sub>4</sub> produced (g/d), CH<sub>4</sub> intensity (grams of methane/kg milk) and CH<sub>4</sub> yield (g methane/kg of dry matter) (Kamalanathan et al., 2023).

## 1.2 Statement of the problem

If we are going to select for cows that produce less CH<sub>4</sub>, we need to know the heritability of the trait, to correctly separate the additive genetic information from the phenotype and to predict an expected genetic gain. In addition, it is important to know the genetic correlations with other important traits, to avoid any undesired genetic changes in those traits.

## 1.3 Objectives

The main objective was to estimate heritability of CH<sub>4</sub> emission in Swedish Red cattle. A secondary objective was to estimate genetic correlations between methane emission traits and production traits (milk yield, body weight and dry matter intake).

## 2. Literature Review

### 2.1 Livestock and methane production

Livestock species are responsible for 7.1 gigatonnes CO<sub>2</sub>e per year of the global anthropogenic gases which is approximately 14.5% of the total Green House Gas (GHG) emissions (Gerber et al., 2013a). Methane from enteric fermentation represents 25% of CH<sub>4</sub> anthropogenic emissions (Wuebbles and Hayhoe, 2002). Over 90% of CH<sub>4</sub> emissions from cattle and 40% of the greenhouse gas emissions from agriculture come from the rumination process (Tubiello et al., 2013). Cattle produce methane from enteric fermentation of feed stuffs (85 to 90%) and fecal excretion. A total of 95% of rumen CH<sub>4</sub> is excreted via eructation and around 1% is excreted via the anus (Murray et al., 1976). Methane production is a natural biological process that occurs in the rumen during fermentation of feedstuffs and it is produced by a group of Archaea known as methanogens (Hook et al., 2010b). Methanogens in the rumen uses carbon dioxide and hydrogen produced through carbohydrate fermentation to produce methane (Hook et al., 2010b).

### 2.2 Impact of methane emission on global warming

Methane is the second most predominant GHG following CO<sub>2</sub> and its ability to trap heat is stronger than CO<sub>2</sub> (MILICH, 1999) and it is increasing in the atmosphere at a rate of 1% annually (Heilig, 1994). An increase in GHG emissions has a negative impact on climate change. The accumulation of GHG in the atmosphere results in elevated global warming. Global warming results in rising sea levels, elevated temperatures, fluctuations in precipitations, heatwaves, and serious drought. Therefore, CH<sub>4</sub> mitigation is important.

### 2.3 Methods of measuring methane

Accuracy of measurement of CH<sub>4</sub> is very important to develop efficient mitigation strategies. The production of CH<sub>4</sub> is influenced by several factors such as feed intake, animal behaviour, feed nutritional composition and general animal management (Goopy et al., 2016). The suitability of the measuring method depends on the measurement objectives and its appropriateness. There are several methods that are used to measure CH<sub>4</sub>. The traditional methods include sulfur hexafluoride (SF<sub>6</sub>), the greenFeed™ system, breath during feeding or milking, and the laser detector methods (Breider et al., 2019; Garnsworthy et al., 2019). Methane is released from different parts of an animal, and each method measures specific output. Respiration chambers are the only method that measures all emissions from an animal through anus, oral and nostrils. Other methods do not measure emissions from the anus but only from the breath.

### 2.3.1 Respiration chambers

This method is mainly used in nutritional studies and physiological studies where few animals are recorded in controlled environments (Lassen et al., 2016). However, this method is less applicable in genetic studies where individual recording of more than a thousand animals is required. In addition to that, respiratory chambers also induce stress which will impact the cows' metabolism and consequently the methane emission. Due to the capacity to regulate the environment and assess the dependability and stability of the equipment, chambers are recognized as the industry standard for estimating the methane emission from ruminants. However, an artificial environment may influence animal behaviour, such as dry matter intake (DMI), which may in turn affect methane output (Tedeschi et al., 2022) .

### 2.3.2 Automated head chamber system (GreenFeed System)

GreenFeed (C-Lock Inc, Rapid City, SD, USA) is an automatic head-chamber equipment designed with a portable feeding station for spot sampling of CH<sub>4</sub> emissions and gaseous exchange in ruminant animals (Hammond, Crompton, et al., 2016). The green feed system combines gas measurement, airflow and feed intake and does automatic animal identification ( Hristov et al., 2015). The system has got an automated gas sampling technique. The green feed system sucks air from the nose and mouth and direct it into a gas analysis system where CH<sub>4</sub> concentration is measured with an infra-red sensor (Zhao et al., 2020). The GF system is designed in such a way that the feed availability is distributed equally for each animal. In addition, it has a built-in program that automatically controls timing and availability of feed for each individual. The measurements are taken over 3 to 7 min when cattle visits the GF unit, and should be distributed evenly over 24 hr or weighted to

eliminate bias due to clustering of visits at specific times (Hammond, Waghorn, & Hegarty, 2016). Methane emissions estimation is done on a cloud-based system developed by the GF manufacturer (Garnsworthy et al., 2019).

A green feed system is a portable, automatic system for estimating individual emissions. The technique can be used in both indoor and outdoor environments. Reliable CH<sub>4</sub> estimates can be obtained through controlling the time of each animal recording. Hristov et al. (2016) and Velazco et al. (2016) highlighted the significance of monitoring the timing and visits of each animal to the GF system to ensure sufficient recordings for each animal throughout the 24-hour feeding period.

However, the system has a limitation of between animal and between days variation. Furthermore, the type of the feed may influence the frequency of an animal's visit to the feeder (Velazco et al., 2014); this can be a limitation as some animals may not go to the system or maybe less frequent.

### 2.3.3 Sniffer Technique

Sniffer methods are developed to measure methane during milking and feeding. The technique is referred to as sniffer method because it used an equipment initially intended to detect hazardous gas leaks. A sampling tube mounted in the feed trough and directly attached to a gas analyzer collects air samples from the nostrils. Different gas analyzers (Nondispersive Infrared (NDIR), Fourier-transform infrared (FTIR), or photoacoustic infrared (PAIR)) and sampling intervals are used by different research centers. (Garnsworthy et al., 2019)

The major advantage of this method is that it is fast and ensures the measurement of many individual animals during milking in a commercial system. The method also distinguishes between low and high-emitting animals. However, its disadvantage is the wide variation between and within cow variability. Additionally, compared to the GF method, it is less accurate in estimating CH<sub>4</sub> out. Several factors, such as animal head movement, feed bin design and the location of sampling points all affect the accuracy of this kind of method. The heritability of methane recorded with this method ranges from 0.12 to 0.45 (Lassen & Løvendahl, 2016).

### 2.3.4 Laser Methane Detector

The Laser Methane detector (LMD) method involves a hand-held device that is pointed towards an animal's nostrils and record methane density. Animals are restrained manually while taking the measurement. The time between methane

eruction events varies between 15 to 25 seconds. A monitoring period of 2 to 4 minutes separates eruction events from breathing cycle. Measurements are taken by an operator at a distance of 1 to 3 m away from the animal. Care must be taken to ensure the laser is pointed exactly to the nostrils throughout the recording period (Garnsworthy et al., 2019).

Several factors, such as distance from the animal, animal's head position, pointing direction, head movement, direction of air movement and temperature in the environment, close animals and the operator can influence the accuracy of the method (Sorg et al., 2017). The operator has the biggest influence since he is in charge of distance and pointing direction (angle). The design of the cattle barn, air circulation in the barn and wind direction and speed are other sources of variation at the point of measurement. Depending on the efficiency of the operator, each LMD can record up to 10 individuals in an hour. Measurements can be taken 3 times a day and for 3 days per each animal. Pickering et al. (2015) estimated heritability of 0.11 for laser based method.

### 2.3.5 Sulfur Hexafluoride Tracer Technique

The Sulfur Hexafluoride (SF<sub>6</sub>) method involves the insertion of a perforated tube containing SF<sub>6</sub> in the rumen. The SF<sub>6</sub> technique is an invasive method, that involves insertion of the rumen, too much animal handling and laboratory analysis of the collected gas (McGinn et al., 2006). Noninvasive methods such as laser guns and infrared based methods are the preferred method used to collected noninvasive, short-term spot samples, which makes it possible to obtain records while cows are in their normal production environment (Hegarty, 2013).

### 2.3.6 General comments

Assessing methane levels in a large population of cows is quite challenging. Although respiration chambers have high throughput, expenses of running the system are high hence less applicable to record huge number of animals. The system is thus suitable for research studies involving small groups of individual animals and not for genetic analysis. Techniques such as SF<sub>6</sub> and GreenFeed offer cost advantages in terms of both initial investment and operational expenses compared to respiration chambers. Additionally, they have higher throughput and potential applicability in extensive grazing systems. However, cost is still a limiting factor for recording large number of animals.

## 2.4 Strategies to reduce methane and their pitfalls

Several methods have been adopted to mitigate CH<sub>4</sub> emissions in ruminant species. These methods include management practices, feeding strategies, enhancing biochemical processes in the rumen through use of feed additives, vaccination of animals, direct alteration of microorganisms in the rumen and genetic approaches (Króliczewska et al., 2023). Nutritional strategies are one of the proposed and researched solutions. This is because CH<sub>4</sub> is predominantly produced in the rumen during the process of digestion.

Several factors such as feed intake, type of carbohydrate and its inclusion rate in the diet, feed processing and addition of fat or ionophores to the ration alter rumen microflora and indirectly affect CH<sub>4</sub> production in cattle (Shibata & Terada, 2010). Therefore, CH<sub>4</sub> emission can be reduced through nutritional strategies.

Several feed additives such as saponins, flavonoids, organic acids, probiotics and tannins are used to alter rumen microflora (Kumar et al., 2014; Patra & Saxena, 2009; Rasmussen & Harrison, 2011). Tannins, saponins and flavonoids have been proven to decrease methane (CH<sub>4</sub>) in the rumen through inhibition of hydrogen producing microflora, and lowers methanogenesis (Króliczewska et al., 2023).

Fats and lipids have the potential to reduce CH<sub>4</sub> in ruminant species ( Patra et al., 2017). Addition of fats and lipids to the diet would result in an increased efficiency of rumen microbes and energy utilization which in turn results in a reduction in CH<sub>4</sub> emission (Beauchemin & McGinn, 2006). Moreover, lipid additives also alter archaeal plasma membrane which results in disturbed membrane potential and leakage of ions, and activation of enzyme reaction leading to the degradation of methanogens and thus reduced CH<sub>4</sub> production (Palangi et al., 2022). However, fats have a negative impact on the digestion process and nutrient absorption ( Patra, 2012). According to Hassanat and Benchaar (2019), high lipid diet above 6% of dry matter reduces fibre and feed digestibility, thus increasing nutrient by-pass and CH<sub>4</sub> production from manure.

In addition to feed additives, direct manipulation of rumen microflora also reduces CH<sub>4</sub> emissions in ruminants. This can be done through defaunation, a process of removing protozoa from the rumen. Defaunation has been shown to reduce methane emissions by 9 to 37% (Hook et al., 2010a; Morgavi et al., 2012). However, the process of defaunation is complex and can result in reduced feed intake and digestibility (Newbold et al., 2015).

Another mitigation strategy is vaccination. Vaccination involves inducing an animal's immune response to suppress the multiplication and growth of

methanogens (Subharat et al., 2016). The effectiveness of this strategy relies on sufficient production of specific antibodies to the methanogen's antigens.

Although the above-mentioned nutritional strategies have been proven to reduce methane emission in ruminants, the potential benefits are not long lasting. There is a need for continuous alterations and management of diet. Diet and rumen microbiota manipulation in ruminants requires specific adjustments that are expensive to implement on a large scale and may not always yield the desired results. Hence there is need to explore other strategies like genetic improvement.

## 2.5 Genetics as a potential solution

Animal breeding involves the application of genetics and selection to improve traits of animals over generations. Breeding involves selection of the best performing animals to become parents of the next generation. Heritability and genetic correlations are critical parameters to consider when selecting a particular trait.

Incorporating methane in a breeding program and giving it an economic weight can reduce methane emissions by 20% in the year 2050 (Haas et al., 2021). Compared to other approaches like feed additives and immunisation, genetic selection is long lasting and have cumulative effects (Knapp et al., 2014; Lassen & Difford, 2020). There are no selection studies that have been done in dairy on methane but selection of low methane lines in sheep have resulted in reduced CH<sub>4</sub> (Jonker et al., 2017). This proves that genetics is a potential solution to mitigate methane emission in ruminants. However, many animals with methane observations are required for genetic studies (Króliczewska et al., 2023), therefore, more effort should be done on improving the methane measurement techniques.

## 2.6 Heritability and methane

Heritability is the proportion of phenotypic variation that is attributed to genetic factors. It is categorised into narrow and broad sense heritability. Broad sense is the proportion of the genetic factors (dominance, epistasis, and additive) to phenotypic variance. Narrow sense heritability is the proportion additive variance of phenotypic variance. Heritability ranges from 0 to 1. Heritability of 0 means the variation observed for a trait is not due to genetic factors.

The heritabilities (standard error given in brackets) of methane (CH<sub>4</sub>) production, calculated on a daily emission basis (grams of CH<sub>4</sub> per day), are moderate, ranges



from 0.12(0.16) to 0.45(0.11) (Breider et al. 2019). However, when assessed on a yield basis (grams of CH<sub>4</sub> per kilogram of dry matter intake), the heritabilities are notably lower, at 0.13 for sheep and 0.19 for cattle (Pickering et al. 2015). Results from a study done by Pszczola et al. (2017), on methane emission from dairy cows over the lactation period, shows that methane heritability varies throughout the lactation period, commencing at 0.23 (SE 0.12), reaching its peak of 0.3 (SE 0.08) at 212 days in milk (DIM), and 0.27 (SE 0.12) at the end of the production cycle. Based on the type of methane characteristic being studied, heritability estimates in dairy cows can range from 0.10 to 0.42, making methane a good option for decrease through genetic selection. (de Haas et al., 2011; Pickering et al., 2015; Lassen and Løvendahl, 2016)

Correlation between methane (CH<sub>4</sub>) production and other economic traits remain mostly unexplored (Basarab et al., 2013). However, a recent study by Breider et al. (2019) revealed genetic correlations ranging from 0.49 to 0.54 between CH<sub>4</sub> production and milk yield. This suggests that genetically favouring lower CH<sub>4</sub> production could lead to a decrease in productivity.

## 3. MATERIALS AND METHODS

### 3.1 Experimental design

Methane observations were obtained from the SLU experimental farm Röbbäcksdalen outside Umeå in the northern part of Sweden. A total of 1089 CH<sub>4</sub> records were collected from 194 Swedish Red cows from a single herd. Data included 12 individual studies conducted using one continuous design and 11 changeover designs (Latin square or switchback). Different treatment diets were offered in each experiment. The experimental period ran for 21 or 28 days. The cow per period observations were considered as experimental units. The number of records per cow depends on the experiment, but generally there were 3-4 periods/records per cow per experiment, except for the continuous experiment with 18 periods representing week of lactation. The number of records for each trait are shown in table 2. The observations available were weekly averages expressed per day and consisted of repeated observations from the same cow over the course of the experiment. Observations were from cows in parity 1 to parity 6 with days in milk ranging from 7 to 232 days.

### 3.2 Description of the diet

The experimental diets consisted of grass silage mixed with protein and energy source concentrates. The forage to concentrate ratio was 56:44 on dry matter basis. Grass silages were produced from primary growth, primary regrowth, and secondary regrowth material, and were wilted before ensiling with application of silage acid-based additive. Cereal grains (maize, wheat, and barley) and agro-industrial by-products (molassed or unmolassed sugar beet pulp, citrus pulp, or molasses) were used as energy source in the main diet, while soybean meal, canola expeller, or meal were incorporated in the diet as protein source. Oil supplements, vitamins and minerals were included to make a complete diet with an adequate supply of nutrients. The exact content of each diet is not within the scope of this paper, but any differences in diets are accounted for in the statistical model.

### 3.3 Traits measurement

The study focused on two CH<sub>4</sub> traits; CH<sub>4</sub> production, which is total produced CH<sub>4</sub> in grams per day and CH<sub>4</sub> intensity (grams of CH<sub>4</sub> produced per trait, e.g., kg of energy corrected milk). A GreenFeed (GF) system was used to measure CH<sub>4</sub> production. GreenFeed is a portable open-circuit head chamber system (GF system, C-Lock Inc., Rapid City, SD). The GF system is shown in Figure 1. The system was in the experimental dairy barn where dairy cows were kept. Dry matter intake (DMI) was recorded on daily basis with Roughage Intake Control feeders (Insentec, B.V., Marknesse, the Netherlands). Milk yield (MY) was documented digitally with gravimetric milk recorders (SAC; S.A. Christensen and Co Ltd, Kolding, Denmark). The cows were milked twice a day at 6 am and 4 pm in a 2 × 8 herringbone-milking parlor. Energy corrected milk (ECM) was estimated according to Sjaunja et al. (1990), using the following equation:

$$\text{ECM (kg)} = \text{Milk production (kg)} \times (383 \times \text{fat \%} + 242 \times \text{protein \%} + 165.4 \times \text{lactose \%} + 20.7) / 3140.$$
 Body weight was recorded on 3 consecutive days at the end of every period after morning milking.

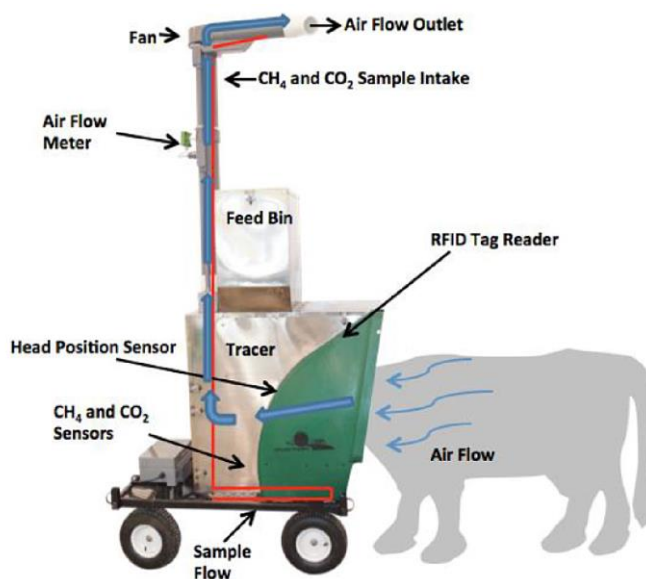


Figure 1. Illustration of the GreenFeed components for methane measurement in ruminant species (Hristov et al., 2015)

### 3.4 Pedigree data

Pedigree data was obtained from Växa. A total of 1816 individuals were included in the pedigree file (503 sires and 1190 dams) over 5 generations.

### 3.5 Statistical analysis

Data editing and descriptive statistics was done in R version 4.3.1. The lactation curves for first and later (2+) parities for various traits were estimated using a polynomial model based on Ali and Schaeffer (1987):

$$y_t = p_0 + p_1 y_1 + p_2 y_t^2 + p_3 w_t + p_4 w_t^2 + c_i + e_t \quad [1]$$
$$y_t = t/(305)$$
$$w_t = \ln\left(\frac{305}{t}\right)$$
$$t = \text{days in milk}(DIM)$$

where

$p_0, p_1, p_2, p_3, p_4$  are the intercept and the 4 regression coefficients;  $p_3, p_4$  are associated with increasing slope of the curve;  $p_1, p_2$  are associated with the decreasing slope;

$c_i$  is the random effect of cow,  $\sim \text{IND}(0, \sigma_c^2)$ , with variance  $\sigma_c^2$ ;

$e_t$  is the residual term for the model,  $\sim \text{IND}(0, \sigma_e^2)$ , where  $\sigma_e^2$  is the residual variance.

Regression analysis was done in R using lme4 package within parity (1, 2+). A maximum of 200 DIM was used instead of 305 days. The data set comprised records up to 235 days, however, the yields after 200 DIM showed an unexpected upward trend, hence these latter observations were excluded.

### 3.6 Variance and covariance estimation

Variance components were determined using univariate and bivariate animal models based on the Average Maximum Restricted Likelihood (AIREML) procedure in the DMU package. Version 6.5.1 (Madsen & Jensen, 2013). The following mixed linear animal model was used to estimate the genetic parameters for single traits:

$$y_{ijklmn} = \text{Parity}_i + (\text{Exp x Diet})_j + (\text{Exp x Period})_k + \text{Exp}_l + \sum_{n=1}^4 \beta, f(DIM) + pe_m + a_m + e_{ijklmn} \quad [2]$$

$y_{ijkl}$  = observation for the given trait;

$\text{Parity}_i$  is the effect of parity 1 or 2+;

$(\text{Exp x Diet})_j$  is the combination effect of experiment and diet

$(\text{Exp x Period})_k$  is the combination effect of experiment and period

$\text{Exp}_l$  is the effect of experiment

$\beta$  = fixed regression coefficients on functions of DIM as described in model [1]

$pe_m$  = random permanent environment effect of cow  $m$ ,  $\sim \text{IND}(0, \sigma_{pe}^2)$ , with variance  $\sigma_{pe}^2$ ;

$a_m$  = random additive genetic effect of cow  $m$ ,  $\sim \text{IND}(0, \mathbf{A}\sigma_a^2)$ , with additive genetic variance  $\sigma_a^2$ , and relationship matrix  $\mathbf{A}$ ; and

$e_{ijkl}$  = the residual term for the model,  $\sim \text{IND}(0, \sigma_e^2)$ , where  $\sigma_e^2$  is the residual variance.

Heritability, genetic correlations, permanent environmental correlation of traits between parity 1 and parity 2+ were estimated using a bivariate model. The fixed effects were the same as those used in the single trait animal model except for random effects. Experiment, diet, and period were combined into a single random effect as shown in the model [3] below:

$$y_{ijkl} = \text{Parity}_i + (\text{Experiment x Diet x Period})_j + \sum_{n=1}^4 \beta, f(DIM) + pe_k + a_k + e_{ijkl} \quad [3]$$

where;  $(\text{Experiment x Diet x Period})_j$  is the combination effect of experiment, diet, and period.

$pe_k$  = random permanent environment effect of cow  $k$ ,  $\sim \text{IND}(0, \sigma_{pe}^2)$ , with variance  $\sigma_{pe}^2$ ;

$a_k$  = random additive genetic effect of cow  $k$ ,  $\sim \text{IND}(0, \mathbf{A}\sigma_a^2)$ , with additive genetic variance  $\sigma_a^2$ , and relationship matrix  $\mathbf{A}$ ; and

$e_{ijkl}$  = the residual term for the model,  $\sim \text{IND}(0, \sigma_e^2)$ , where  $\sigma_e^2$  is the residual variance.

### 3.7 Calculation of heritability

The equation below was used to calculate trait heritability ( $h^2$ ) using variance components estimated in DMU.

$$h^2 = \frac{\sigma_a^2}{\sigma_p^2}$$

$h^2$  = heritability

$\sigma_a^2$  = additive genetic variance

$\sigma_p^2$  = phenotypic variance defined as the sum of the three variances  $\sigma_a^2$ ,  $\sigma_{pe}^2$ , and  $\sigma_e^2$  in the model.

### 3.8 Estimation of Correlation

Raw correlations of traits in the combined data set (all parities) were calculated using Pearson correlation method in R version 4.3.

Genetic correlations between methane emission and other traits were estimated using the equation below:

$$r_g = \frac{\sigma_{aj,ak}}{\sqrt{\sigma_{aj}^2, \sigma_{ak}^2}}$$

$\sigma_{aj,ak}$  = additive genetic covariance between trait j and k

$\sigma_{aj}^2, \sigma_{ak}^2$  = genetic variances estimate for trait j and k, respectively.

Permanent environment correlation was determined using the equation below.

$$r_{pe} = \frac{\sigma_{pej,pek}}{\sqrt{\sigma_{pej}^2, \sigma_{pek}^2}}$$

$\sigma_{pej,pek}$  = permanent environmental covariance between trait j and k

$\sigma_{pej}^2, \sigma_{pek}^2$  = permanent environmental variances estimate for trait j and k, respectively.

## 4. RESULTS

### 4.1 Descriptive statistics of the data

The main aim of this study was to estimate the heritability of methane emission. Genetic correlations were also analysed as second objective of the study. Single trait and bivariate animal models were used to estimate variance components. These variance components were used to calculate heritability and genetic correlations. Data consisted of several nutritional traits, but only a few methane-related traits were analysed, in addition to MY, DMI and BW. Descriptive statistics of the analysed traits are shown in Table 1.

Table 1. Descriptive statistics: mean, standard deviation (SD), minimum (Min), maximum (Max) and coefficient of variation (CV%) of CH<sub>4</sub>, CH<sub>4</sub>/ECM, ECM, MY, DMI, BW.

Trait	Unit	Mean	SD	Min	Max	CV%
CH <sub>4</sub>	g/day	427	68.1	193	655	15
CH <sub>4</sub> /ECM	g/kg	14.1	3.32	4.7	38.3	23
ECM	kg/day	31.2	6.20	10.1	54.6	20
MY	kg/day	29.3	6.17	10.5	48.2	21
DMI	kg/day	20.8	2.87	10.5	29.3	10
BW	kg	615	79.5	433	864	13

Table 2. Number of cows and number of records for each trait

Trait	Number of cows	Number of records
CH <sub>4</sub>	194	1089
ECM	194	1093
MY	194	1095
DMI	194	1100
BW	194	1091

## 4.2 Lactation curves for CH<sub>4</sub> production, CH<sub>4</sub> intensity and ECM

The lactation curves were initially fitted using model [1]. The pattern for methane production showed the same trend for both parity 1 and 2+ (Figure 2. Lactation curve for methane production fitted using model [1]). At the initial stage of lactation, methane production was relatively lower and increased at a fast rate up to 60 days in milk. Methane production was rather stable from 100 day up to the remaining days of lactation in both first and 2+ parities.

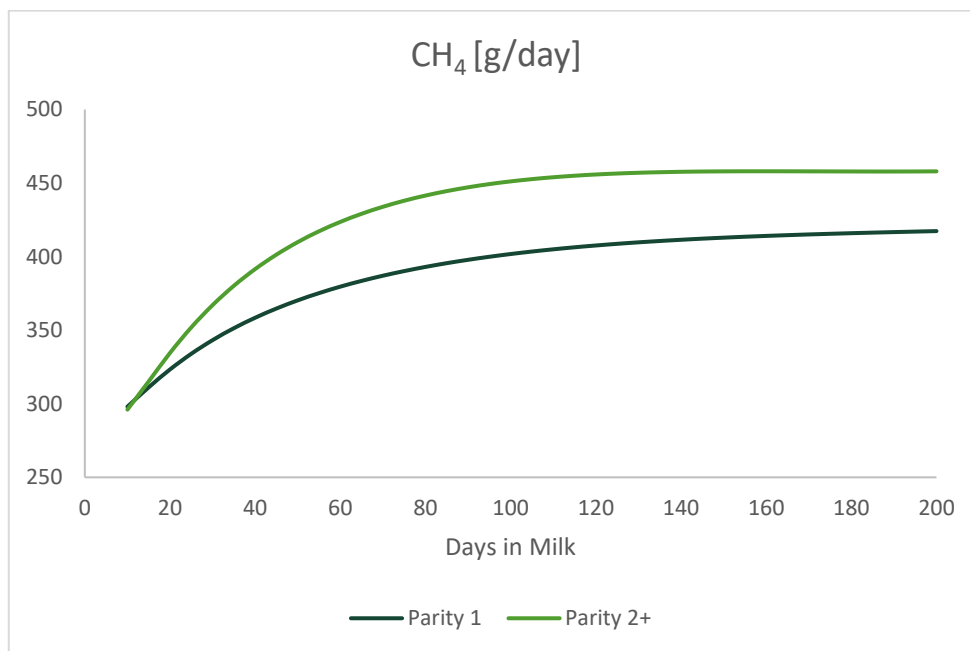


Figure 2. Lactation curve for methane production fitted using model [1]

The lactation curve for ECM in the first parity was different from that in the second and later parities (Figure 3. Lactation curve for ECM fitted using model [1] for cows in parity 1 and 2+). In the first parity, the initial ECM production was relatively less than that in parity 2+, increased up to 20 days and become rather constant for the remaining days of lactation. The ECM production in parity 2+ was high during the first 40 days of lactation and decreases at a faster rate until 140 days then become constant up to 200 days.



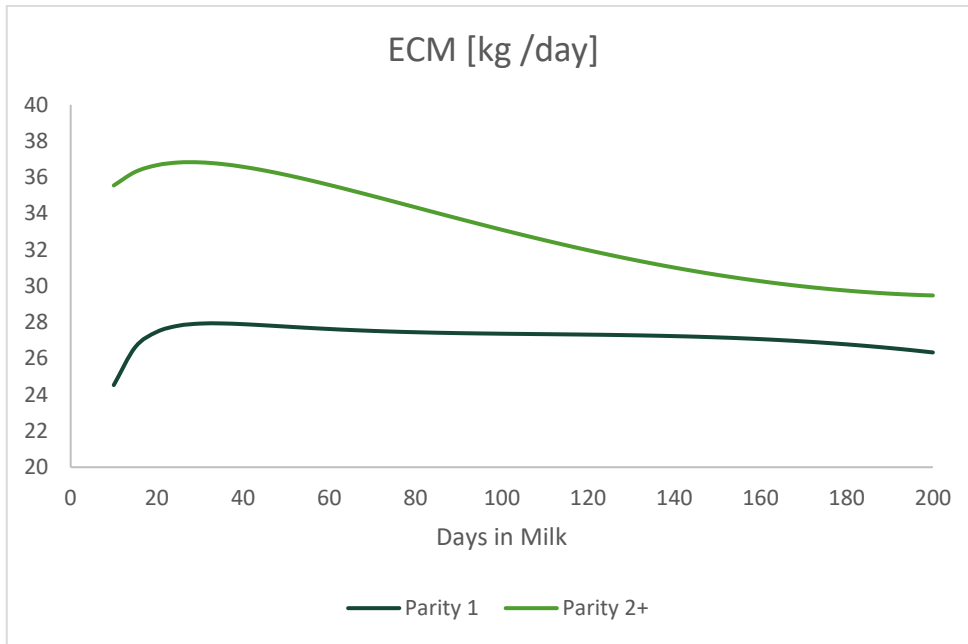


Figure 3. Lactation curve for ECM fitted using model [1] for cows in parity 1 and 2+

The lactation curve for CH<sub>4</sub> intensity (g CH<sub>4</sub>/kg ECM) is shown in Figure 4. Methane intensity was relatively low at the beginning of the lactation and increases at a slower rate until 140 days and become relatively steady until 200 days. Methane intensity for parity 2+ was lower compared to that in first parity but increased at a faster rate than in parity 1.

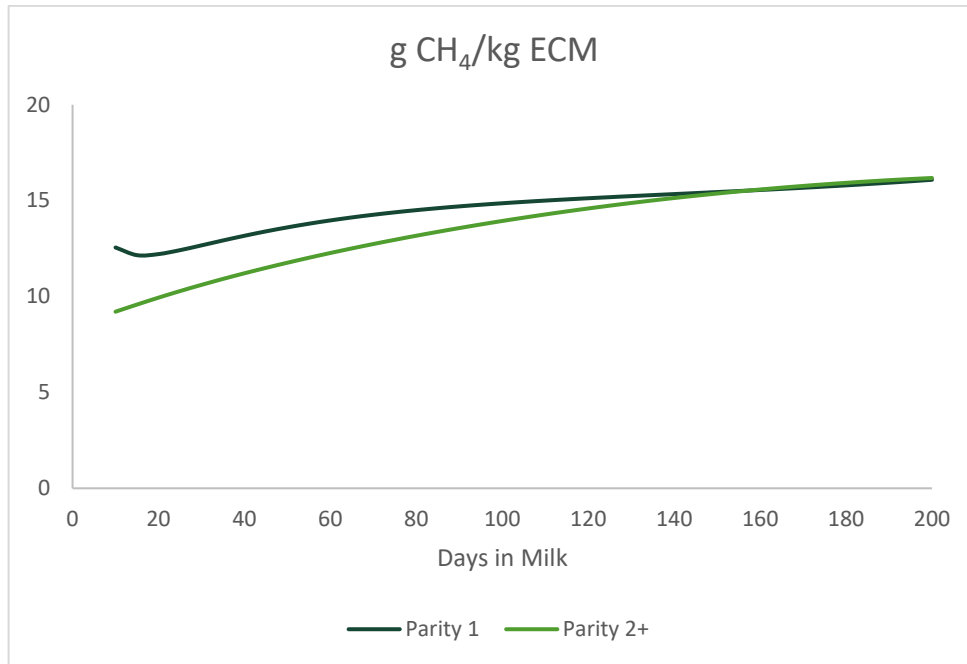


Figure 4. Lactation curve for g CH<sub>4</sub>/kg ECM fitted using model [1] for cows in parity 1 and parity 2+

### 4.3 Variance components and heritability estimates

The variance components and heritability estimates for the first parity are shown in Table 3. and for the second and later parities in Table 4. The heritability for methane production was moderately high in this study, ranging from 0.24 in the first parity to 0.44 in the second and later parities. Heritability for methane intensity (CH<sub>4</sub>/ECM) followed the same pattern, 0.27 in the first parity and 0.38 in the later parities. The heritability of MY, ECM and BW were also moderately high in the first parity, ranging from 0.34 to 0.58. Dry matter intake had the highest heritability estimate of 0.79 in the first parity and moderate heritability of 0.27 in parity 2+. Heritability for all other traits in parity 2+ were lower compared to that in the first parity except for estimates of methane which were comparatively higher than in the first parity. The heritability for DMI and BW were low in second and later parities but still moderate while extremely low for MY and ECM. The standard error of estimates were relatively high in this study.

Table 3. Estimates of variance components for Experiment x Diet (ExpD), Experiment x Period (ExpP), experiment (Exp), permanent environmental ( $\sigma^2_{pe}$ ), additive genetic ( $\sigma^2_a$ ), residual variance ( $\sigma^2_e$ ), phenotypic variance ( $\sigma^2_p$ , sum of  $\sigma^2_{pe}$ ,  $\sigma^2_a$ , and  $\sigma^2_e$ ), and heritability estimated using a single trait animal model [1] for parity 1.

	CH <sub>4</sub>	SE	CH <sub>4</sub> /ECM	SE	ECM	SE	MY	SE	DMI	SE	BW	SE
ExpD	535.93	169.66	1.49	0.70	1.45	0.48	1.01	0.33	1.13	0.55	0.70	1.01
ExpP	144.02	56.92	0.66	0.36	0.27	0.15	0.256	0.12	0.64	0.31	0.45	0.25
Exp	427.03	349.47	2.36	1.59	1.63	1.39	2.98	1.98	2.35	1.71	0.94	2.98
$\sigma^2_{pe}$	857.40	627.86	1.02	1.58	3.85	2.97	3.05	3.27	4.49	2.69	1.70	3.05
$\sigma^2_a$	503.78	671.18	1.27	1.73	4.53	3.32	6.73	3.86	5.97	3.29	1.71	6.73
$\sigma^2_e$	755.98	70.15	2.41	0.43	2.83	0.25	1.73	0.16	1.52	0.27	1.59	1.73
$\sigma^2_p$	2117.15		4.70		11.20		11.5		7.49		5.01	11.50
$h^2$	0.24	0.31	0.27	0.35	0.40	0.28	0.58	0.30	0.80	0.37	0.34	0.58

Table 4. Variance components and heritability estimate for parity 2+ estimated with a single trait animal model [1].

	CH <sub>4</sub>	SE	CH <sub>4</sub> /ECM	SE	ECM	SE	MY	SE	DMI	SE	BW	SE
ExpD	502.36	148.69	0.86	0.45	1.27	0.54	1.22	0.46	2.52	0.90	1.56	0.65
ExpP	95.27	46.45	0.17	0.20	6.78	0.18	1.05	0.13	0.18	0.19	8.34	0.14
Exp	346.12	255.92	0.43	0.53	3.93	2.18	6.97	3.43	0.86	0.98	0.28	0.55
pe	419.72	479.92	2.52	1.90	16.48	4.01	19.45	4.65	4.86	2.40	3.21	1.88
$\sigma^2_{pe}$	1326.07	614.52	3.70	2.20	0.13	3.24	1.30	3.95	3.02	2.57	2.38	2.05
$\sigma^2_a$	1291.67	84.53	3.55	0.40	9.60	0.62	6.60	0.43	3.26	0.39	3.39	0.38
$\sigma^2_p$	3037.45		9.78		26.22		27.35		11.14	6	8.99	
$h^2$	0.44	0.20	0.38	0.20	0.01	0.12	0.05	0.14	0.27	0.22	0.26	0.22

Estimates of heritability ( $h^2$ ), genetic correlation ( $r_g$ ) and permanent environmental correlation ( $r_{pe}$ ) from the bivariate analysis are shown in Table 5. The heritability for methane, milk yield, ECM, and dry matter intake in parity 1 were in range with those estimated using a single trait animal model. Heritability estimates for methane, milk yield, ECM, and dry matter intake in parity 2+ were 0.41, 0.08, 0.07 and 0.07, respectively. For parity 2, the estimates are substantially lower than those for the first parity except for methane, which was slightly higher than that in parity 1. The genetic correlation of milk yield in the first parity and that in the second and later parity was the highest, followed by that of DMI. Methane had a lowest genetic correlation among other traits but still moderate.

Table 5. Variance components and heritability estimates estimated using a bivariate animal model for parity 1 and 2.

	CH <sub>4</sub> _1	CH <sub>4</sub> _2	MY_1	MY_2	ECM_1	ECM_2	DMI_1	DMI_2
$\sigma^2_a$	1037.76	1609.32	6.93	2.44	4.69	2.33	0.72	0.58
$\sigma^2_{pe}$	622	352.2	5.32	18.2	5.22	16	1.26	3.64
VarTreat	390.1	721.6	1.15	3.6	1.36	2.24	0.75	0.96
$\sigma^2_e$	877.6	1258.8	1.60	6.77	2.82	9.63	0.94	2.65
$\sigma^2_p$	2927.46	3941.92	15	31.01	14.08	30.2	3.67	7.83
$h^2$	0.35	0.41	0.46	0.07	0.33	0.08	0.20	0.07
$r_g$	0.27		0.80		0.36		0.54	
$r_{pe}$	1.0		0.50		0.74		0.25	

1: parity 1, 2: parity 2,  $\sigma^2_a$ : additive genetic variance,  $\sigma^2_{pe}$ : permanent environmental variance, VarTreat: treatment variance (Experiment x Diet x Period)

## 4.4 Genetic and permanent environmental correlation

The genetic and permanent environmental correlations of CH<sub>4</sub> and other production traits (ECM, DMI, and MY) are shown in Table 6. The standard error (SE) of genetic and permanent environmental correlations obtained in this study were extremely high, therefore the estimates were not very precise. Only the standard error for permanent environmental correlation of CH<sub>4</sub> with DMI in the second parity was low (0.09). The genetic correlation of CH<sub>4</sub> with DMI and ECM was positive, moderate in the first parity and strong in parity 2+. Methane had a weak negative genetic correlation with MY in the first parity and a moderate positive genetic correlation in parity 2+. The results show that CH<sub>4</sub> has a strong positive genetic correlation with DMI compared to other traits. The bivariate analysis for methane intensity trait did not run.

*Table 6. Genetic ( $r_g$ ) and permanent environmental correlation ( $r_{pe}$ ) estimates for methane and other traits between parity 1 and parity 2+ with their corresponding standard errors in brackets.*

Parity	Estimate	CH <sub>4</sub> -DMI	CH <sub>4</sub> -ECM	CH <sub>4</sub> -MY
1	$r_g$	0.48 (0.64)	0.23 (0.40)	-0.06 (0.41)
	$r_{pe}$	0.36 (0.51)	0.54 (0.65)	0.91 (1.00)
2	$r_g$	0.92 (0.77)	0.75 (0.64)	0.48 (0.41)
	$r_{pe}$	0.60 (0.09)	0.32 (0.14)	-0.17 (0.14)

## 4.5 Raw correlation of CH<sub>4</sub> and other traits

The correlations of CH<sub>4</sub>, g of CH<sub>4</sub>/ kg ECM, MY, ECM, and BW are presented in Table 6. The results showed that CH<sub>4</sub> production is positively correlated with all traits, with a strong correlation with DMI, moderate correlation with g CH<sub>4</sub>/ kg ECM and a weak correlation ECM and MY. Methane intensity had a moderate positive correlation with CH<sub>4</sub> production, weak positive correlation with BW and weak negative correlation with ECM, DMI and MY.

Table 7. Raw correlations of CH<sub>4</sub>, g CH<sub>4</sub>/kg ECM, MY, ECM, BW and DMI of combined data set (all parities).

	g CH <sub>4</sub> /kg ECM	ECM	BW	DMI	MY
CH <sub>4</sub> g/d	0.45	0.24	0.39	0.54	0.22
g CH <sub>4</sub> /kg ECM	1	-0.69	0.16	-0.05	-0.66
ECM		1	0.18	0.47	0.92
BW			1	0.31	0.16
DMI				1	0.45
MY					1

CH<sub>4</sub> g/d: methane production per day, g CH<sub>4</sub>/kg ECM: grams of methane per kg of energy corrected milk, MY: Milk yield, BW: body weight, DMI: dry matter intake, ECM: energy corrected milk

## 5. DISCUSSION

The main aim of this study was to estimate the heritability of CH<sub>4</sub> emission in Swedish Red cattle using a data set collected in northern Sweden. Genetic and phenotypic correlations were also estimated as the second objective. Heritability was estimated using both a single trait and bivariate animal models. Most research studies on heritability of CH<sub>4</sub> were in Holstein cows (Breider et al., 2019; Ghavi Hossein-Zadeh, 2022; Kamalanathan et al., 2023; Lassen & Løvendahl, 2016). There are no published studies on heritability for Swedish Red cattle.

The average CH<sub>4</sub> production in this study is within the range of that reported by Kamalanathan et al. (2023) in Holstein cattle using the GreenFeed system. However higher than 352 g/day reported by Huhtanen et al. (2019) using the same measuring system but in grazing system. Furthermore, the average CH<sub>4</sub> yield in this study is even higher than averages previously published using other measurement techniques. For instance, Grainger et al. (2007) obtained an average of 333 g using a SF<sub>6</sub> tracer technique and 322 g with respiration chamber in Holstein cattle under controlled environment. The average CH<sub>4</sub> intensity in this study is similar to that published by Martínez-Marín et al. (2023)

Very few studies have published results on lactation curves for CH<sub>4</sub> production. The pattern for CH<sub>4</sub> production over the course of lactation observed in this study was relatively similar to that published by Pszczola et al. (2017) although using a different model. However, CH<sub>4</sub> production was continuously increasing up to 100 days in milk which is opposite from a study by Lassen and Løvendahl (2016). Generally, there is a similar trend in both parities but relatively higher production in second and later parities. The lactation curve pattern for CH<sub>4</sub> intensity in this study is similar to that modelled using a Wilmink term for CH<sub>4</sub>/corrected milk by Martínez-Marín et al. (2023).

The heritability estimate of CH<sub>4</sub> emission per day obtained from this study for methane in the first parity (0.23-0.27) was slightly higher than that previously recorded for Holstein dairy cattle at 0.16 (Kamalanathan et al., 2023). However, these estimates are also within the range of 0.12 and 0.45 reported by Breider et al. (2019) on a smaller data set of 184 Holstein-Friesian cows. The estimated



heritability for CH<sub>4</sub> intensity of 0.27 is the same as that recorded in a similar study by Kamalanathan et al. (2023), but slightly lower than the 0.33 presented by Richardson et al. (2021) for Australian dairy cows.

Heritability in this study were moderate in the first parity and high in the second and later parities, that is increasing from first parity to later parities. This trend is opposite to the findings of Kandel et al. (2017), where the heritability estimates decrease with parity. Heritability estimates of 0.40 to 0.43 for CH<sub>4</sub> production obtained in this study for second and later parities are among the highest recorded in previous studies. High heritability estimates obtained in this study could result from averaging observations. Methane observations used in this study were weekly averages. It has been previously reported that averaging CH<sub>4</sub> observations can result in high heritability and reduced residual variance (van Breukelen et al. 2022)

Although the estimates for CH<sub>4</sub> emissions are within the range of those previously reported, the standard error of estimates was relatively high in this study. High standard errors could be attributed to challenges separating animal variance into permanent environmental and additive genetic variances with few numbers of observations. Hence, the extremely low or high estimates.

The heritability of 0.01 for ECM in parity 2+ was significantly lower than that in the first parity (0.40). This low heritability was substantially lower than the range of 0.14 to 0.21 recorded for Iranian Holsteins (Hossein-Zadeh 2012). Although the heritability estimates for ECM were extremely low in parity 2+, the decreasing trend over parities has been observed in a previous study by Hossein-Zadeh (2012). Extreme low heritability estimates could occur by chance owing to the smaller data set.

The heritability of 0.80 for dry matter intake in the first parity was extremely high compared to 0.33 recorded for Australian dairy cows (Richardson et al., 2021), 0.46 recorded by Polizel et al. (2018) and 0.2 to 0.6 in Swedish Red Holstein (Tarekegn et al., 2021). However, the heritability estimates in the second parity estimated by the bivariate model were 0.07 and significantly lower than 0.27 estimated by the univariate model. The estimate from the bivariate model are even lower than the lowest 0.10 recorded by Toshniwal et al. (2008). Cavani et al. (2023) obtained heritability estimates of 0.20 to 0.40 for Holstein, 0.17 to 0.42 for Jersey and 0.25 to 0.41 for Nordic Red. Therefore, the results obtained in this study are closer to those reported in the literature, although high in the first parity.

A heritability of 0.40 for energy corrected milk yield in the first parity was slightly higher than that previously published 0.23 in the first parity of Holstein cows

(Liinamo et al. 2012) but still within the range of 0.12 to 0.62 reported by Spurlock et al. (2012). Heritability for MY in the second parity was 0.047, estimated by a single trait animal model, and 0.07 by a bivariate animal model. Despite the estimates being lower than those previously published in literature 0.20 to 0.33 (Abe et al., 2009; Breider et al., 2019; González-Recio et al., 2006; Zink et al., 2012), a decrease in heritability for milk yield across lactation has been reported by Zink et al. (2012).

Previous studies have shown that body weight is a moderate to highly heritable trait, with heritability estimates ranging from 0.48 to 0.57 (Toshniwal et al., 2008). The heritability estimates obtained from this study for body weight align with those previously published.

The bivariate animal model results generally showed the same trend as observed using the univariate animal model. However, the heritability for ECM and MY estimated using a single trait animal model were substantially lower than those obtained using a bivariate animal model. The genetic correlation of traits in the bivariate model were positive. This implies that selection for reduced CH<sub>4</sub> in the first parity will result in reduced CH<sub>4</sub> in second and later parities. This supports the claim that genetic improvement has an advantage of cumulative effects in CH<sub>4</sub> reduction. The bivariate analysis did not work for methane intensity trait. This could be due to variance components close to 0.0.

To effectively introduce CH<sub>4</sub> as the breeding goal, in a breeding program, it is critical to know how it correlates with other traits (Wall et al., 2010). Hence, genetic correlations were also evaluated as a second objective in this study. Genetic correlation of CH<sub>4</sub> and other traits has not been extensively studied, only few research studies are documented (Lassen & Løvendahl, 2016; Pszczola et al., 2017; Zetouni et al., 2018). The results for genetic correlations from this study were unfavourable. All genetic correlations of CH<sub>4</sub> with other traits had high standard errors, making the estimates less reliable. Generally, the results despite of high standard errors showed a strong genetic correlation of methane with DMI and low to moderate correlation with MY and ECM. Methane is strongly correlated with DMI and low to moderate with other traits.

Raw correlations of CH<sub>4</sub> production with CH<sub>4</sub> intensity, DMI, MY and ECM were positive. Methane production was strongly correlated with DMI, moderately correlated with CH<sub>4</sub> intensity and low to moderately with other traits. The strong correlation of CH<sub>4</sub> with DMI is attributed to the fact that methane is predominantly produced in the rumen as by product of fermentation of feed stuffs.

Methane intensity is a very promising CH<sub>4</sub> trait that can be incorporated into a selection index (Lassen & Løvendahl, 2016). However, before incorporating CH<sub>4</sub> traits in a selection index there are various parameters to consider. The trait must be heritable, well defined, recordable, be affordable and its genetic correlation with other traits in the index must be known (Hazel, 1943). Results from this study shows that both CH<sub>4</sub> production and CH<sub>4</sub> intensity are heritable traits, therefore can be included in the selection index. However, opting for few cows that produce more ECM per gram of CH<sub>4</sub>, through selecting for methane intensity is more advantageous than having more cows that emits less CH<sub>4</sub> but produce less ECM. Methane intensity can be included in the selection index together with other production traits, health, longevity and reproduction traits (Haas et al., 2021). Unfortunately, the bivariate analysis was not able to estimate the variance components for estimation of genetic correlation of CH<sub>4</sub> intensity and other traits in this study but CH<sub>4</sub> production was positively correlated with DMI, therefore, selecting for CH<sub>4</sub> production leads to a decrease in in DMI. Incorporating CH<sub>4</sub> in a breeding program with an economic value could reduce CH<sub>4</sub> intensity by 24% by year 2050 (Haas et al., 2021). The economic value of CH<sub>4</sub> traits can be determined using a carbon tax value or a proportional cost of energy lost exhaling CH<sub>4</sub> (González-Recio et al., 2020). Haas et al. (2021) obtained an economic weight of -€0.37 g/d for a year using the formula; Economic value = -1\* (shadow price of CO<sub>2</sub> \* 28/1 000 000) \* 365 where; -1 is the direction of selection, 28 is the global warming potential of CH<sub>4</sub>, division by 1000 000 to convert grams to tonnes and multiplication by 365 to calculate gain per year.

Although CH<sub>4</sub> reduction is a debatable political topic, it has not been incorporated into any breeding program to date, therefore, there is need for strong government support through incentives for including CH<sub>4</sub> in a breeding program and international collaborations.

## 6. Conclusion

Heritability estimates for CH<sub>4</sub> production and intensity obtained from this study were moderate in the first parity and high in the second and later parities. The heritability estimates of CH<sub>4</sub> production and intensity obtained using univariate animal model were similar to those estimated using a bivariate model. Therefore, results obtained from this study suggest that it is possible to select animals for lower CH<sub>4</sub> production and CH<sub>4</sub> intensity for genetic improvement in any parity. The strong positive genetic correlation obtained between CH<sub>4</sub> and DMI in this study shows that precautions must be taken when selecting for reduced CH<sub>4</sub> as this may consequently reduce the DMI of animals. Reduced DMI can affect the cow's health and production. The low to moderate positive genetic correlation of CH<sub>4</sub> with ECM and MY suggests that selecting for CH<sub>4</sub> reduction may not have substantial impact on MY and ECM. However, the standard errors of estimates were very high for genetic correlations in this study. This was a limitation of a relatively small data set. Therefore, I recommend the expansion of the data set to obtain more reliable estimates.

## References

- Abe, H., Masuda, Y., & Suzuki, M. (2009). Relationships between reproductive traits of heifers and cows and yield traits for Holsteins in Japan. *Journal of Dairy Science*, *92*(8), 4055–4062. <https://doi.org/10.3168/jds.2008-1896>
- Beauchemin, K. A., & McGinn, S. M. (2006). Methane emissions from beef cattle: Effects of fumaric acid, essential oil, and canola oil. *Journal of Animal Science*, *84*(6), 1489–1496. <https://doi.org/10.2527/2006.8461489x>
- Black, J. L., Davison, T. M., & Box, I. (2021). Methane Emissions from Ruminants in Australia: Mitigation Potential and Applicability of Mitigation Strategies. *Animals*, *11*(4), 951. <https://doi.org/10.3390/ani11040951>
- Breider, I. S., Wall, E., & Garnsworthy, P. C. (2019). Short communication: Heritability of methane production and genetic correlations with milk yield and body weight in Holstein-Friesian dairy cows. *Journal of Dairy Science*, *102*(8), 7277–7281. <https://doi.org/10.3168/jds.2018-15909>
- Cottle, D. J., Nolan, J. V., & Wiedemann, S. G. (2011). Ruminant enteric methane mitigation: A review. *Animal Production Science*, *51*(6), 491. <https://doi.org/10.1071/AN10163>
- FAO. (2013). *Milk and dairy products in human nutrition*. <https://ds.amu.edu.et/xmlui/bitstream/handle/123456789/14990/milk%20and%20dairy%20products%20in%20human%20nutrition%20-%20404%20pages.pdf?sequence=1&isallowed=y>
- Garnsworthy, P. C., Difford, G. F., Bell, M. J., Bayat, A. R., Huhtanen, P., Kuhla, B., Lassen, J., Peiren, N., Pszczola, M., Sorg, D., Visker, M. H. P. W., & Yan, T. (2019). Comparison of Methods to Measure Methane for Use in Genetic Evaluation of Dairy Cattle. *Animals*, *9*(10), 837. <https://doi.org/10.3390/ani9100837>
- Gerber, P. J., Steinfeld, H., Henderson, B., Mottet, A., Opio, C., Dijkman, J., Falcucci, A., & Tempio, G. (2013). Tackling climate change through livestock: A global assessment of emissions and mitigation opportunities. *Tackling Climate Change Through Livestock: A Global Assessment of Emissions and Mitigation Opportunities*.
- Ghavi Hossein-Zadeh, N. (2022). Estimates of the genetic contribution to methane emission in dairy cows: A meta-analysis. *Scientific Reports*, *12*(1), 12352. <https://doi.org/10.1038/s41598-022-16778-z>

- González-Recio, O., Alenda, R., Chang, Y. M., Weigel, K. A., & Gianola, D. (2006). Selection for female fertility using censored fertility traits and investigation of the relationship with milk production. *Journal of Dairy Science*, *89*(11), 4438–4444. [https://doi.org/10.3168/jds.S0022-0302\(06\)72492-4](https://doi.org/10.3168/jds.S0022-0302(06)72492-4)
- González-Recio, O., López-Paredes, J., Ouatahar, L., Charfeddine, N., Ugarte, E., Alenda, R., & Jiménez-Montero, J. A. (2020). Mitigation of greenhouse gases in dairy cattle via genetic selection: 2. Incorporating methane emissions into the breeding goal. *Journal of Dairy Science*, *103*(8), 7210–7221. <https://doi.org/10.3168/jds.2019-17598>
- Goopy, J. P., Chang, C., & Tomkins, N. (2016). A Comparison of Methodologies for Measuring Methane Emissions from Ruminants. In T. S. Rosenstock (Ed.), *Methods for measuring greenhouse gas balances and evaluating migration options in smallholder agriculture* (pp. 97–117). Springer Science+Business Media. [https://doi.org/10.1007/978-3-319-29794-1\\_5](https://doi.org/10.1007/978-3-319-29794-1_5)
- Grainger, C., Clarke, T., McGinn, S. M., Auldist, M. J., Beauchemin, K. A., Hannah, M. C., Waghorn, G. C., Clark, H., & Eckard, R. J. (2007). Methane emissions from dairy cows measured using the sulfur hexafluoride (SF<sub>6</sub>) tracer and chamber techniques. *Journal of Dairy Science*, *90*(6), 2755–2766. <https://doi.org/10.3168/jds.2006-697>
- Haas, Y. de, Veerkamp, R. F., Jong, G. de, & Aldridge, M. N. (2021). Selective breeding as a mitigation tool for methane emissions from dairy cattle. *Animal*, *15* Suppl 1, 100294. <https://doi.org/10.1016/j.animal.2021.100294>
- Hammond, K. J., Crompton, L. A., Bannink, A., Dijkstra, J., Yáñez-Ruiz, D. R., O’Kiely, P., Kebreab, E., Eugène, M. A., Yu, Z., Shingfield, K. J., Schwarm, A., Hristov, A. N., & Reynolds, C. K. (2016). Review of current in vivo measurement techniques for quantifying enteric methane emission from ruminants. *Animal Feed Science and Technology*, *219*, 13–30. <https://doi.org/10.1016/j.anifeedsci.2016.05.018>
- Hammond, K. J., Waghorn, G. C., & Hegarty, R. S. (2016). The GreenFeed system for measurement of enteric methane emission from cattle. *Animal Production Science*, *56*(3), 181. <https://doi.org/10.1071/AN15631>
- Hassanat, F., & Benchaar, C. (2019). Methane emissions of manure from dairy cows fed red clover- or corn silage-based diets supplemented with linseed oil. *Journal of Dairy Science*, *102*(12), 11766–11776. <https://doi.org/10.3168/jds.2018-16014>
- Hazel, L. N. (1943). The Genetic Basis for Constructing Selection Indexes. *Genetics*, *28*(6), 476–490. <https://doi.org/10.1093/genetics/28.6.476>
- Heilig, G. K. (1994). The greenhouse gas methane (CH<sub>4</sub>): Sources and sinks, the impact of population growth, possible interventions. *Population and Environment*, *16*(2), 109–137. <https://doi.org/10.1007/BF02208779>

- Hook, S. E., Wright, A.-D. G., & McBride, B. W. (2010a). Methanogens: Methane producers of the rumen and mitigation strategies. *Archaea*, 2010, 945785. <https://doi.org/10.1155/2010/945785>
- Hook, S. E., Wright, A.-D. G., & McBride, B. W. (2010b). Methanogens: Methane producers of the rumen and mitigation strategies. *Archaea*, 2010, 945785. <https://doi.org/10.1155/2010/945785>
- Hristov, A. N., Oh, J., Giallongo, F., Frederick, T., Harper, M. T., Weeks, H., Branco, A. F., Price, W. J., Moate, P. J., Deighton, M. H., Williams, S. R. O., Kindermann, M., & Duval, S. (2016). Short communication: Comparison of the GreenFeed system with the sulfur hexafluoride tracer technique for measuring enteric methane emissions from dairy cows. *Journal of Dairy Science*, 99(7), 5461–5465. <https://doi.org/10.3168/jds.2016-10897>
- Hristov, A. N., Oh, J., Giallongo, F., Frederick, T., Weeks, H., Zimmerman, P. R., Harper, M. T., Hristova, R. A., Zimmerman, R. S., & Branco, A. F. (2015). The Use of an Automated System (GreenFeed) to Monitor Enteric Methane and Carbon Dioxide Emissions from Ruminant Animals. *JoVE (Journal of Visualized Experiments)*(103), e52904. <https://doi.org/10.3791/52904>
- Huhtanen, P., Ramin, M., & Hristov, A. N. (2019). Enteric methane emission can be reliably measured by the GreenFeed monitoring unit. *1871-1413*, 222, 31–40. <https://doi.org/10.1016/j.livsci.2019.01.017>
- Jonker, A., Hickey, S., Pinares-Patiño, C., McEwan, J., Olinga, S., Díaz, A., Molano, G., MacLean, S., Sandoval, E., Harland, R., Birch, D., Bryson, B., Knowler, K., & Rowe, S. (2017). Sheep from low-methane-yield selection lines created on alfalfa pellets also have lower methane yield under pastoral farming conditions<sup>1,2</sup>. *Journal of Animal Science*, 95(9), 3905–3913. <https://doi.org/10.2527/jas.2017.1709>
- Kamalanathan, S., Houlahan, K., Miglior, F., Chud, T. C. S., Seymour, D. J., Hailemariam, D., Plastow, G., Oliveira, H. R. de, Baes, C. F., & Schenkel, F. S. (2023). Genetic Analysis of Methane Emission Traits in Holstein Dairy Cattle. *Animals*, 13(8). <https://doi.org/10.3390/ani13081308>
- Knapp, J. R., Laur, G. L., Vadas, P. A., Weiss, W. P., & Tricarico, J. M. (2014). Invited review: Enteric methane in dairy cattle production: Quantifying the opportunities and impact of reducing emissions. *Journal of Dairy Science*, 97(6), 3231–3261. <https://doi.org/10.3168/jds.2013-7234>
- Króliczewska, B., Pecka-Kiełb, E., & Bujok, J. (2023). Strategies Used to Reduce Methane Emissions from Ruminants: Controversies and Issues. *Agriculture*, 13(3), 602. <https://doi.org/10.3390/agriculture13030602>
- Kumar, S., Choudhury, P. K., Carro, M. D., Griffith, G. W., Dagar, S. S., Puniya, M., Calabro, S., Ravella, S. R., Dhewa, T., Upadhyay, R. C., Sirohi, S. K., Kundu, S. S., Wanapat, M., & Puniya, A. K. (2014). New aspects and strategies

- for methane mitigation from ruminants. *Applied Microbiology and Biotechnology*, 98(1), 31–44. <https://doi.org/10.1007/s00253-013-5365-0>
- Lassen, J., & Difford, G. F. (2020). Review: Genetic and genomic selection as a methane mitigation strategy in dairy cattle. *Animal*, 14(S3), s473-s483. <https://doi.org/10.1017/S1751731120001561>
- Lassen, J., & Løvendahl, P. (2016). Heritability estimates for enteric methane emissions from Holstein cattle measured using noninvasive methods. *Journal of Dairy Science*, 99(3), 1959–1967. <https://doi.org/10.3168/jds.2015-10012>
- Madsen, P., & Jensen, J. (2013). *DMU*. Springer-Verlag. [https://doi.org/10.1007/springerreference\\_5456](https://doi.org/10.1007/springerreference_5456)
- Martin, C., Morgavi, D. P., & Doreau, M. (2010). Methane mitigation in ruminants: From microbe to the farm scale. *Animal*, 4(3), 351–365. <https://doi.org/10.1017/s1751731109990620>
- Martínez-Marín, G., Toledo-Alvarado, H., Amalfitano, N., Gallo, L., & Bittante, G. (2023). Lactation modeling and the effects of rotational crossbreeding on milk production traits and milk-spectra-predicted enteric methane emissions. *Journal of Dairy Science*. Advance online publication. <https://doi.org/10.3168/jds.2023-23551>
- McGinn, S. M., Beauchemin, K. A., Iwaasa, A. D., & McAllister, T. A. (2006). Assessment of the sulfur hexafluoride (SF<sub>6</sub>) tracer technique for measuring enteric methane emissions from cattle. *Journal of Environmental Quality*, 35(5), 1686–1691. <https://doi.org/10.2134/jeq2006.0054>
- Mickiewicz, B., & Volkava, K. (2022). Global consumer trends for sustainable milk and dairy production. *VUZF Review*, 7(2), 183–192. <https://doi.org/10.38188/2534-9228.22.2.19>
- MILICH, L. (1999). The role of methane in global warming: where might mitigation strategies be focused? *Global Environmental Change*, 9(3), 179–201. [https://doi.org/10.1016/S0959-3780\(98\)00037-5](https://doi.org/10.1016/S0959-3780(98)00037-5)
- Morgavi, D. P., Martin, C., Jouany, J.-P., & Ranilla, M. J. (2012). Rumen protozoa and methanogenesis: Not a simple cause-effect relationship. *The British Journal of Nutrition*, 107(3), 388–397. <https://doi.org/10.1017/s0007114511002935>
- Moss, A. R., Jouany, J.-P., & Newbold, J. (2000). Methane production by ruminants: Its contribution to global warming. *Annales De Zootechnie*, 49(3), 231–253. <https://doi.org/10.1051/animres:2000119>
- Musa, A. A. (2020). Contribution of Livestock Production to Global Greenhouse Gas Emission and Mitigation Strategies. *Journal of Zoological Research*, 1(3). <https://doi.org/10.30564/jzr.v1i3.2006>
- Myhre, G., Shindell, D., & Pongratz, J. (2014). *Climate change 2013 : the physical science basis: Working Group I contribution to the fifth assessment report of the Intergovernmental Panel on Climate Change. Climate change 2013: The physical science basis : Working group, contribution to the fifth assessment report of the*



- intergovernmental panel on climate change* (T. Stocker, Ed.). Cambridge University Press. <https://doi.org/10.1017/CBO9781107415324.018>
- Newbold, C. J., La Fuente, G. de, Belanche, A., Ramos-Morales, E., & McEwan, N. R. (2015). The Role of Ciliate Protozoa in the Rumen. *Frontiers in Microbiology*, *6*, 1313. <https://doi.org/10.3389/fmicb.2015.01313>
- Palangi, V., Taghizadeh, A., Abachi, S., & Lackner, M. (2022). Strategies to Mitigate Enteric Methane Emissions in Ruminants: A Review. *Sustainability*, *14*(20), 13229. <https://doi.org/10.3390/su142013229>
- Patra, A. K., & Saxena, J. (2009). The effect and mode of action of saponins on the microbial populations and fermentation in the rumen and ruminant production. *Nutrition Research Reviews*, *22*(2), 204–219. <https://doi.org/10.1017/S0954422409990163>
- Patra, A., Park, T., Kim, M., & Yu, Z (2017). Rumen methanogens and mitigation of methane emission by anti-methanogenic compounds and substances. *Journal of Animal Science and Biotechnology*, *8*(1), 13. <https://doi.org/10.1186/s40104-017-0145-9>
- Patra, A. K. (2012). Enteric methane mitigation technologies for ruminant livestock: A synthesis of current research and future directions. *Environmental Monitoring and Assessment*, *184*(4), 1929–1952. <https://doi.org/10.1007/s10661-011-2090-y>
- Pickering, N. K., Chagunda, M. G. G., Banos, G., Mrode, R., McEwan, J. C., & Wall, E. (2015). Genetic parameters for predicted methane production and laser methane detector measurements. *Journal of Animal Science*, *93*(1), 11–20. <https://doi.org/10.2527/jas.2014-8302>
- Polizel, G. H. G., Grigoletto, L., Carvalho, M. E., Rossi Junior, P., Ferraz, J. B. S., & Santana, M. H. d. A. (2018). Genetic correlations and heritability estimates for dry matter intake, weight gain and feed efficiency of Nellore cattle in feedlot. *Livestock Science*, *214*, 209–210. <https://doi.org/10.1016/j.livsci.2018.06.013>
- Pszczola, M., Rzewuska, K., Mucha, S., & Strabel, T. (2017). Heritability of methane emissions from dairy cows over a lactation measured on commercial farms. *Journal of Animal Science*, *95*(11), 4813–4819. <https://doi.org/10.2527/jas2017.1842>
- Rasmussen, J., & Harrison, A. (2011). The benefits of supplementary fat in feed rations for ruminants with particular focus on reducing levels of methane production. *ISRN Veterinary Science*, *2011*, 613172. <https://doi.org/10.5402/2011/613172>
- Richardson, C. M., Nguyen, T. T. T., Abdelsayed, M., Moate, P. J., Williams, S. R. O., Chud, T. C. S, Schenkel, F. S, Goddard, M. E., van den Berg, I., Cocks, B. G., Marett, L. C., Wales, W. J., & Pryce, J. E. (2021). Genetic parameters for methane emission traits in Australian dairy cows. *Journal of Dairy Science*, *104*(1), 539–549. <https://doi.org/10.3168/jds.2020-18565>

- Shibata, M., & Terada, F. (2010). Factors affecting methane production and mitigation in ruminants. *Animal Science Journal*, *81*(1), 2–10. <https://doi.org/10.1111/j.1740-0929.2009.00687.x>
- Sorg, D., Mühlbach, S., Rosner, F., Kuhla, B., Derno, M., Meese, S., Schwarm, A., Kreuzer, M., & Swalve, H. (2017). The agreement between two next-generation laser methane detectors and respiration chamber facilities in recording methane concentrations in the spent air produced by dairy cows. *Computers and Electronics in Agriculture*, *143*, 262–272. <https://doi.org/10.1016/j.compag.2017.10.024>
- Subharat, S., Shu, D., Zheng, T., Buddle, B. M., Kaneko, K., Hook, S., Janssen, P. H., & Wedlock, D. N. (2016). Vaccination of Sheep with a Methanogen Protein Provides Insight into Levels of Antibody in Saliva Needed to Target Ruminant Methanogens. *PLOS ONE*, *11*(7), e0159861. <https://doi.org/10.1371/journal.pone.0159861>
- Tarekegn, G. M., Karlsson, J., Kronqvist, C., Berglund, B., Holtenius, K., & Strandberg, E. (2021). Genetic parameters of forage dry matter intake and milk produced from forage in Swedish Red and Holstein dairy cows. *Journal of Dairy Science*, *104*(4), 4424–4440. <https://doi.org/10.3168/jds.2020-19224>
- Tedeschi, L. O., Abdalla, A. L., Álvarez, C., Anuga, S. W., Arango, J., Beauchemin, K. A., Becquet, P., Berndt, A., Burns, R., Camillis, C. de, Chará, J., Echazarreta, J. M., Hassouna, M., Kenny, D., Mathot, M., Mauricio, R. M., McClelland, S. C., Niu, M., Onyango, A. A., . . . Kebreab, E (2022). Quantification of methane emitted by ruminants: A review of methods. *Journal of Animal Science*, *100*(7). <https://doi.org/10.1093/jas/skac197>
- Toshniwal, J. K., Dechow, C. D., Cassell, B. G., Appuhamy, J. A. D. R. N., & Varga, G. A. (2008). Heritability of electronically recorded daily body weight and correlations with yield, dry matter intake, and body condition score. *Journal of Dairy Science*, *91*(8), 3201–3210. <https://doi.org/10.3168/jds.2007-0627>
- Tubiello, F. N., Salvatore, M., Rossi, S., Ferrara, A., Fitton, N., & Smith, P. (2013). The FAOSTAT database of greenhouse gas emissions from agriculture. *Environmental Research Letters*, *8*(1), 15009. <https://doi.org/10.1088/1748-9326/8/1/015009>
- Velazco, J. I., Mayer, D. G., Zimmerman, S., & Hegarty, R. S. (2016). Use of short-term breath measures to estimate daily methane production by cattle. *Animal*, *10*(1), 25–33. <https://doi.org/10.1017/s1751731115001603>
- Wall, E., Simm, G., & Moran, D. (2010). Developing breeding schemes to assist mitigation of greenhouse gas emissions. *Animal*, *4*(3), 366–376. <https://doi.org/10.1017/s175173110999070x>
- Zetouni, L., Kargo, M., Norberg, E., & Lassen, J. (2018). Genetic correlations between methane production and fertility, health, and body type traits in Danish Holstein

- cows. *Journal of Dairy Science*, *101*(3), 2273–2280.  
<https://doi.org/10.3168/jds.2017-13402>
- Zhao, Y., Nan, X., Yang, L., Zheng, S., Jiang, L., & Xiong, B. (2020). A Review of Enteric Methane Emission Measurement Techniques in Ruminants. *Animals*, *10*(6). <https://doi.org/10.3390/ani10061004>
- Zink, V., Lassen, J., & Štípková, M. (2012). Genetic parameters for female fertility and milk production traits in first-parity Czech Holstein cows. *Czech Journal of Animal Science*, *57*(3), 108–114. <https://doi.org/10.17221/5562-cjas>

## Popular science summary

Dairy cows play an important role in the provision of milk, which is essential for human health. Dairy cows thrive on a diet primarily composed of grass, a fibrous material indigestible to humans. Microbes present in the rumen aids the digestion of grass into valuable nutrients which can be absorbed by the cow. However, some of these microbes produce methane, as a byproduct of digestion of feedstuffs in the rumen. Methane has a negative impact on climate change; hence it is among the recently studied traits of ruminants. Dairy cows emit a large amount of methane among other livestock species. Reduction of methane results in a more sustainable dairy production. There have been many efforts in attempt to reduce methane emissions from cattle such as nutrition and management practices. However, genetics and breeding strategies could be a long term, permanent strategy. For genetic improvement of a particular trait, it is important to know its heritability as well as genetic correlation with other production traits to access its potential for genetic gain. Heritability is the proportion of phenotypic variance that is due to additive (heritable) genetic effects. A high heritability is desired for fast genetic progress. Low heritable traits are difficult to improve through genetics. Therefore, this study has mainly focused on estimating heritability of methane as well as genetic correlations in Swedish Red cows. We used 1089 methane records from 194 Swedish Red cows from a single herd in Northern Sweden, collected using a GreenFeed system. This study examined two specific methane traits: daily methane production (g/d) and methane intensity (g methane/kg energy-corrected milk). We estimated heritability for other productions traits associated with methane: dry matter intake (i.e., feed intake), energy-corrected milk, milk yield, and body weight. The results from this study proves that methane is a moderately heritable trait, therefore it is possible to reduce methane production and intensity in Swedish Red cattle through genetic selection. However, the results also show a strong genetic correlation of methane with dry matter intake. This means if we select for reduction of methane, dry matter intake will also be reduced. However, reduction in dry matter intake has a negative effect on cow's productivity and its overall health, hence precautions must be taken when selecting for reduced methane for a balanced genetic gain. Although estimates in this study are in line with those previously published, the standard error of estimates were high. Another analysis with a huge dataset could validate the results.

## Acknowledgements

I would like to extend my sincere gratitude to Professor Erling Strandberg, my main supervisor, for allowing me to extend my knowledge in quantitative genetics under his supervision. He has guided me through every step, helping me to understand concepts and he was always available to assist me.

I also want to express my thanks to my co-supervisors, Dr. Birgit Zumbach and Dr. Abdulai Guinguina, for their support and insightful ideas that significantly contributed to the success of this research.

I am also grateful to Växa for providing pedigree information and VHI/Lövsta for the methane observation data.

I appreciate Dr. Anna Maria Johansson, our academic coordinator, for her efforts in organizing workspace, and all the administrative work for the success of this thesis.

I thank God, our creator, for the wisdom and strength to complete this thesis and my family and friends for their emotional support and encouragement during moments of doubt.

Finally, I deeply appreciate the EMABG scholarship not only for financial support but for giving me opportunity to be taught by world class experts and gain international exposure.

## Publishing and archiving

Approved students' theses at SLU are published electronically. As a student, you have the copyright to your own work and need to approve the electronic publishing. If you check the box for **YES**, the full text (pdf file) and metadata will be visible and searchable online. If you check the box for **NO**, only the metadata and the abstract will be visible and searchable online. Nevertheless, when the document is uploaded it will still be archived as a digital file. If you are more than one author, the checked box will be applied to all authors. You will find a link to SLU's publishing agreement here:

- <https://libanswers.slu.se/en/faq/228318>.

YES, I/we hereby give permission to publish the present thesis in accordance with the SLU agreement regarding the transfer of the right to publish a work.

NO, I/we do not give permission to publish the present work. The work will still be archived and its metadata and abstract will be visible and searchable.