

Exploring different definitions of *methane phenotypes* in Holstein cattle *in three European countries*

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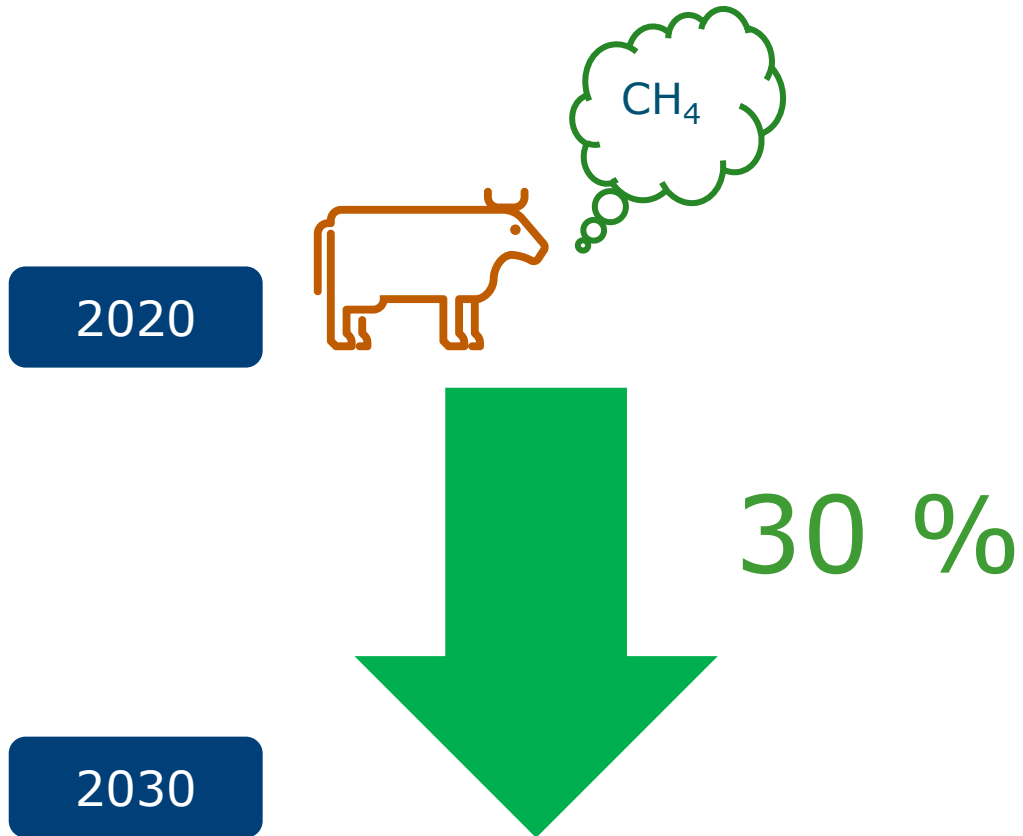


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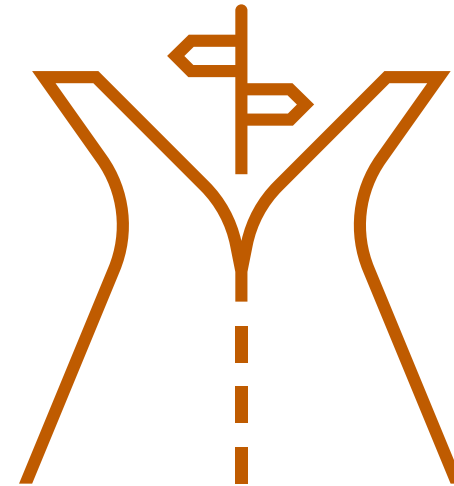


BETTER COWS > BETTER LIFE

Importance



Several countries are introducing or planning to introduce methane breeding values in the coming years



Challenge

There it is **not a common agreement** in terms of chosen **phenotype**, nor **trait definition** (measurement, editing procedures).



Opportunity

Re-Breeding livestock for resilience



Demonstrate the **potential** of animal **breeding** in climate change **mitigation** and **adaptation**



To improve **accuracy** and **predictive ability** of **EBV** for **mitigation** and **adaptation** traits



To design **breeding strategies** that **reduce** GHG emission and **contribute** to adaptation to climate change



Measurement
standardization

Raw data
processing

Trait
definition

Final
phenotype

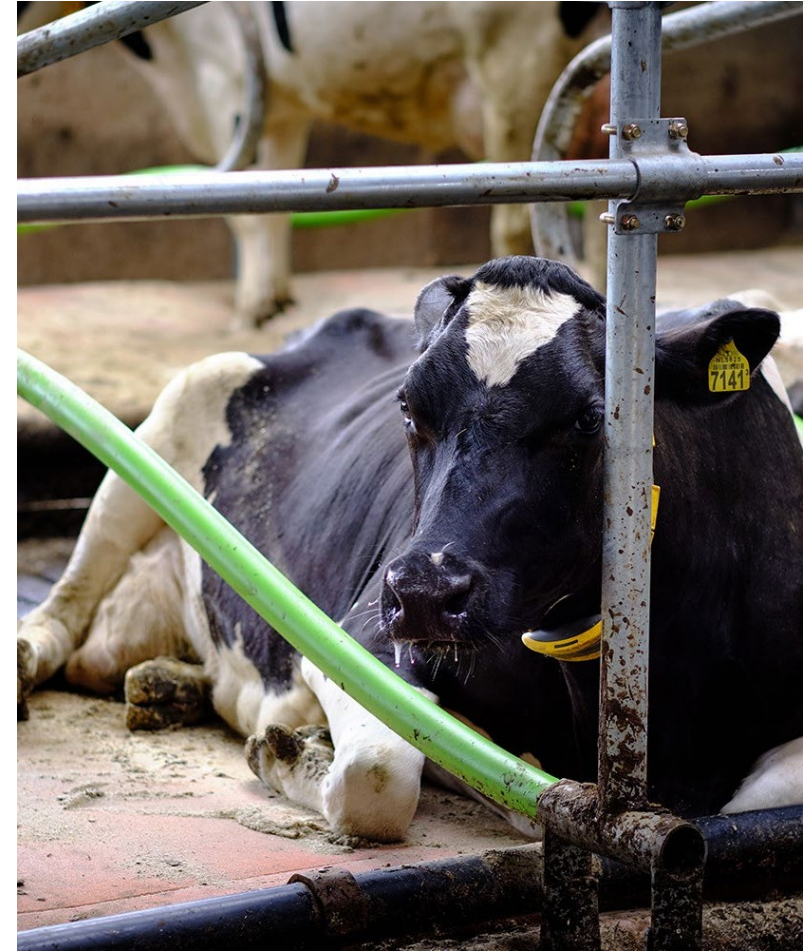


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Session 1: Integrating mitigation and adaptation breeding strategies

Objectives

1. Investigate *six distinct methane phenotypes* across three countries.
2. Estimate *genetic parameters* for these methane phenotypes, including genetic correlations between countries.



Methane phenotypes

METHANE CONCENTRATION

1. **conc** Average *methane concentration* per visit (ppm)
2. **#peaks** *Number of methane peaks* per minute
3. **ratio** between *methane* and *carbon dioxide* concentration

METHANE PRODUCTION (g/d)

4. **Madsen** Methane production based on Madsen equation
5. **Kjeldsen** Methane production based on Kjeldsen equation
6. **Tier2** Methane production based on Tier2 (IPCC) equation



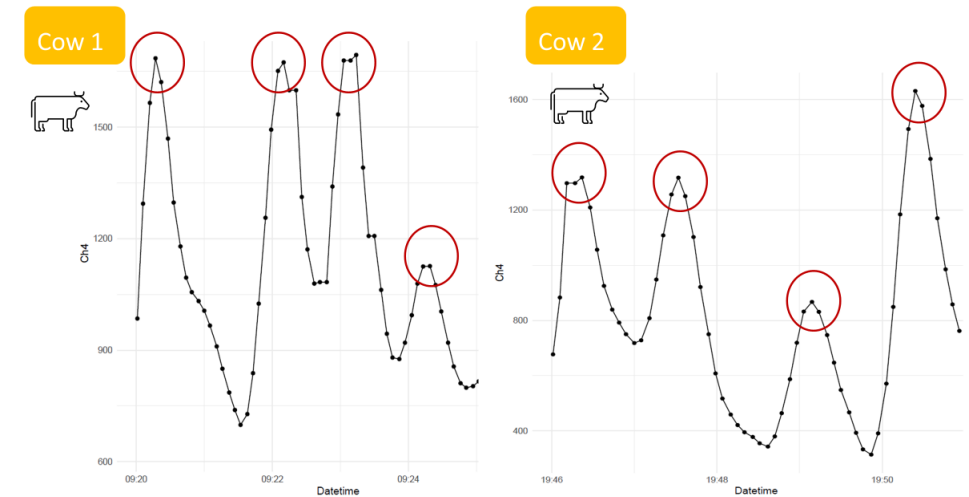
Methane concentration phenotypes

1. Average CH_4 concentration
2. Number of peaks per minute
3. CH_4/CO_2 ratio



baseline

Time



Formulas for Methane Production

Madsen *et al.* (2010) equation

$$\text{CO}_2 = 180 \times 24 \times (5.6 \text{ MBW} + 22 \text{ ECM} + 1.6 \times 10^{-5} \times \text{num days in gestation})$$

Kjeldsen *et al.* (2024) equation

$$\begin{aligned} \text{CO}_2 = & \beta_0 + (\beta_1 \times \text{ECM}) + (\beta_2 \times \text{DIM}) + \text{breed} + \text{parity} + (\beta_{\text{breed}}, \text{parity}) + (\beta_{\text{DIM}}, \text{DietCF} \times \text{DIM} \times \text{DietCF}) \\ & + (\beta_{\text{ECM}}, \text{DIM} \times \text{ECM} \times \text{DIM}) + (\beta_{\text{DIM}}, \text{breed} \times \text{DIM}) + (\beta_{\text{MilkCF}}, \text{parity} \times \text{MilkCF}) \end{aligned}$$

Tier2 *et al.* (2019) equation

$$\text{NE}_m = \text{CF} \times \text{MBW} \quad \text{NE}_1 = \text{Milk} \times (1.47 + 0.4 \times \text{Kg Fat})$$

$$\text{REM} = 1.123 - (0.004092) \times \text{DE} + 0.00001126 \times (\text{DE}^2 - 25.4/\text{DE})$$

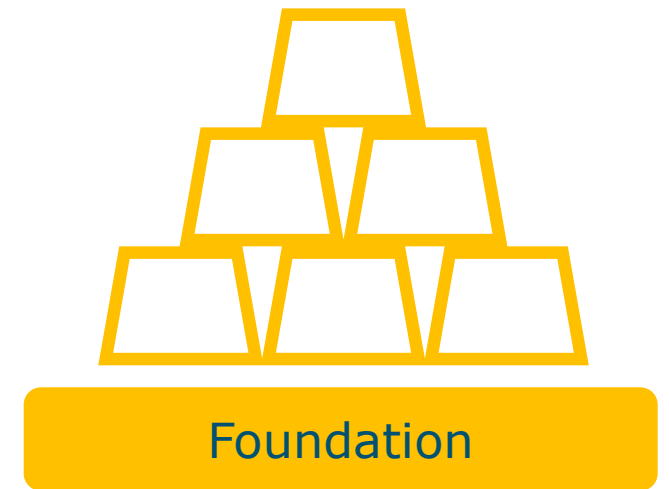
$$\text{GE} = (1000 \times (\text{Nem} + \text{Nea} + \text{NE}_1 + \text{Nep}) / \text{REM} / \text{DE} / 100$$

$$\text{CH}_4 = \text{GE} \times 0.065 / 55.65$$



Data preparation

- **Weekly** records
- Minimum **5 records** (visits) per week
- Use **calendar week**
- Background correction within visit: **average 5** lowest measurements per visit
- Max duration: **5 min**
- Lactation grouping **1, 2, 3+**
- **3 lactation stages**: 0-90, 91-150, 151-365



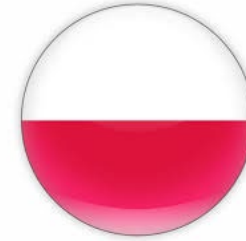
Data Description



- 116,369 records
- 7,129 cows
- 63 farms
- 2019-2024



- 12,455 records
- 3,211 cows
- 34 farms
- 2018-2023



- 7,134 records
- 475 cows
- 2 farms
- 2014-2016

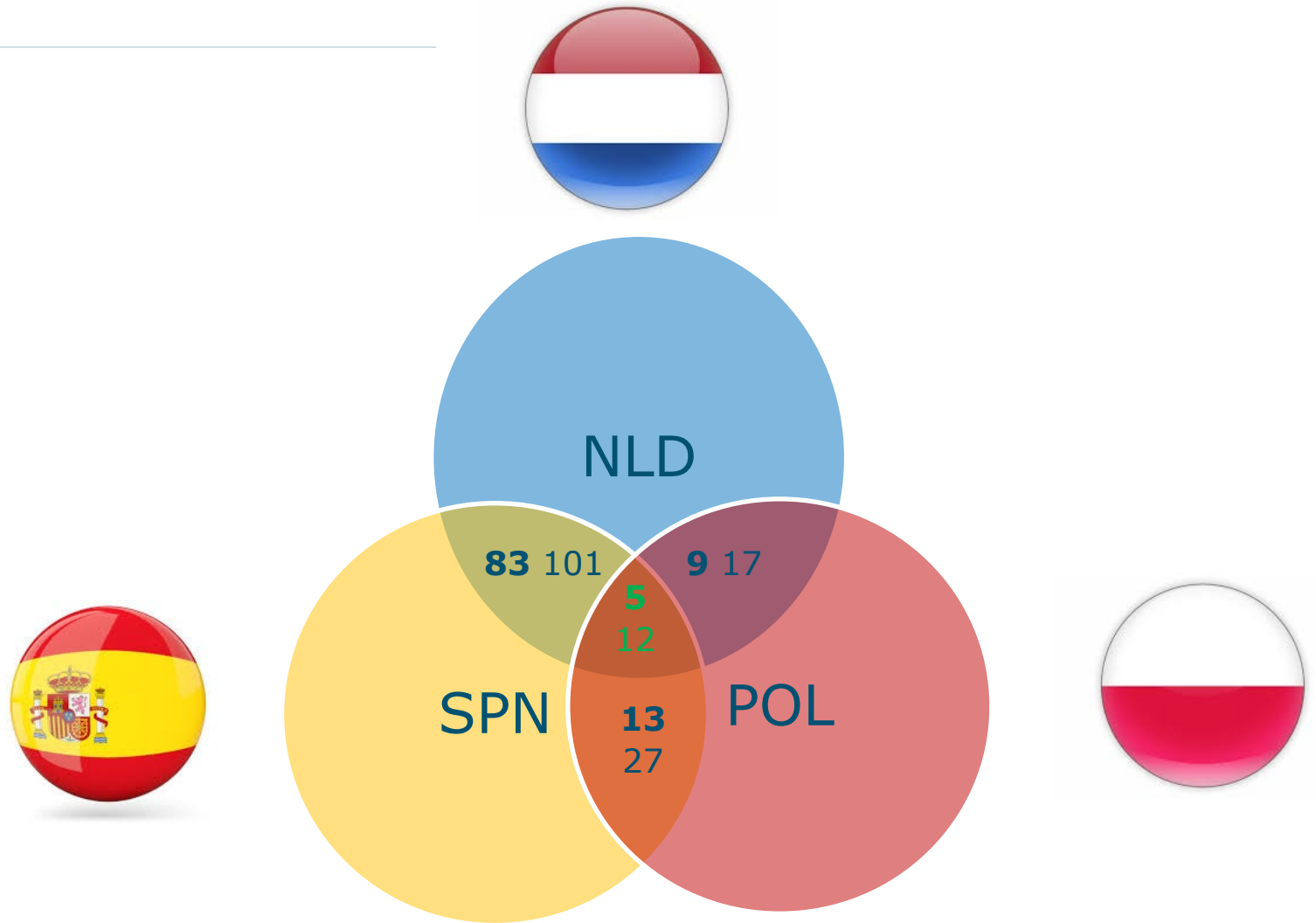
1-3+ parities
405 DIM



Pedigree Description

- 140,515 individuals
- 92,821 individuals after pruning
- 22 generations on average

- 64,813 NLD
- 45,408 SPN
- 13,676 POL



Statistical Model

$$y = \textit{Fixed Effects} + a + pe + e$$



$$\textit{Herd} * \textit{year} * \textit{season} * \textit{robot} + \textit{Lact}_{stage} + \textit{parity}$$

ASReml 4.2

BIV and TRI analyses



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Number of observations and *animals* per country

	TRAIT		conc	#peaks	ratio	Madsen	Kjeldsen	Tier2
	NLD		116208 7110	116369 7129	101367 6945	10763 806	74729 6608	14809 855
	SPN		12223 3204	12403 3210	7330 1693	6058 1405	7289 1682	10273 2663
	POL		7121 475	7076 474	7078 475	7134 475	7134 475	7134 475

Mean and (standard deviation) per country

	TRAIT	conc	#peaks	ratio	Madsen	Kjeldsen	Tier2
	NLD	401.3 (178.9)	1.47 (0.44)	0.06 (0.02)	290.5 (125.5)	316.6 (124.1)	355.5 (69.1)
	SPN	357.6 (197.7)	0.57 (0.15)	0.07 (0.02)	341.6 (100.5)	353.4 (101.1)	459.6 (77.8)
	POL	534.8 (142.2)	0.99 (0.12)	0.08 (0.01)	379.3 (94.5)	358.2 (61.4)	334.5 (54.8)



Heritabilities and permanent environmental ratio with (SE)

Parameter	conc	#peaks	ratio	Madsen	Kjeldsen	Tier2	
	h^2	0.19 (0.02)	0.34 (0.05)	0.10 (0.01)	0.06 (0.06)	0.10 (0.02)	0.10 (0.01)
	pe	0.28 (0.01)	0.13 (0.03)	0.14 (0.01)	0.33 (0.04)	0.18 (0.01)	0.14 (0.01)
	h^2	0.18 (0.04)	0.14 (0.06)	0.15 (0.05)	0.21 (0.07)	0.12 (0.05)	0.15 (0.08)
	pe	0.27 (0.02)	0.74 (0.06)	0.25 (0.03)	0.31 (0.05)	0.34 (0.04)	0.25 (0.03)
	h^2	0.36 (0.09)	0.21 (0.11)	0.28 (0.08)	0.32 (0.09)	0.25 (0.09)	0.28 (0.08)
	pe	0.23 (0.07)	0.53 (0.10)	0.23 (0.06)	0.28 (0.07)	0.37 (0.07)	0.23 (0.06)



Heritabilities and permanent environmental ratio with (SE)



h^2

0.19
(0.02)

0.34
(0.05)

0.10
(0.01)

0.06
(0.06)

0.10
(0.02)

0.10
(0.01)

pe

0.28
(0.01)

0.13
(0.03)

0.14
(0.01)

0.33
(0.04)

0.18
(0.01)

0.14
(0.01)



h^2

0.18
(0.04)

0.14
(0.06)

0.15
(0.05)

0.21
(0.07)

0.12
(0.05)

0.15
(0.08)

pe

0.27
(0.02)

0.74
(0.06)

0.25
(0.03)

0.31
(0.05)

0.34
(0.04)

0.25
(0.03)



h^2

0.36
(0.09)

0.21
(0.11)

0.28
(0.08)

0.32
(0.09)

0.25
(0.09)

0.28
(0.08)

pe

0.23
(0.07)

0.53
(0.10)

0.23
(0.06)

0.28
(0.07)

0.37
(0.07)

0.23
(0.06)



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Moderate heritabilities for most of the traits

Genetic correlations and (standard errors)

Trait		conc	#peaks	ratio	Madsen	Kjeldsen	Tier2
		0.65 (0.31)	-0.29 (0.22)	0.79 (0.54)	0.85 (+1)	0.37 (0.64)	0.48 (0.53)
		-0.05 (0.64)	NC	0.08 (0.64)	-0.59 (+1)	0.48 (0.76)	0.92 (0.81)
		0.45 (0.50)	0.79 (0.59)	0.35 (0.92)	-0.45 (0.59)	0.49 (1.0)	0.69 (1.0)

Genetic correlations and (standard errors)

	conc	#peaks	ratio	Madsen	Kjeldsen	Tier2
 	0.65 (0.31)	-0.29 (0.22)	0.79 (0.54)	0.85 (+1)	0.37 (0.64)	0.48 (0.53)
 	-0.05 (0.64)	NC	0.08 (0.64)	-0.59 (+1)	0.48 (0.76)	0.92 (0.81)
 	0.45 (0.50)	0.79 (0.59)	0.35 (0.92)	-0.45 (0.59)	0.49 (1.0)	0.69 (1.0)

Moderate to high positive correlations

Conclusions

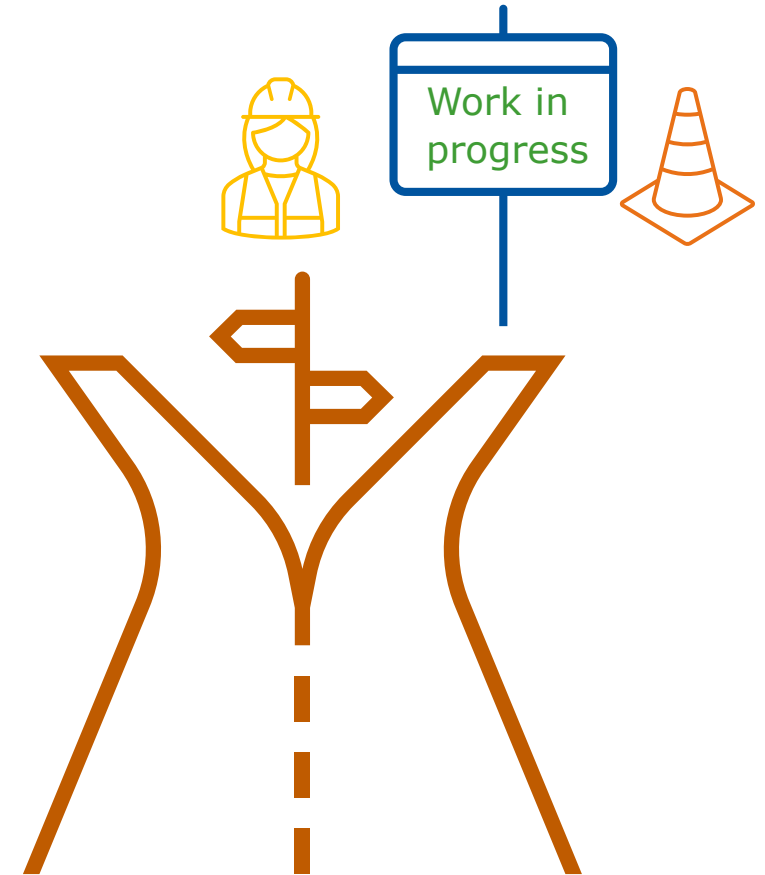
- **Low-moderate genetic links** between the countries (some dozens of sires)
- **Moderate heritabilities** for all traits in the 3 countries
- **Positive moderate genetic correlations** among countries (despite the high standard errors)

- First **inter-country correlations** for several methane phenotypes
- First step towards **international, standardization, evaluation and implementation**



Next

- Add **genomic information** to the analyses
- Investigate the **data structure** further
- Run **country-specific** model



Acknowledgements



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**Integraal
aanpakken**

Samen werken aan duurzame &
klimaatverantwoorde veehouderij

Project: From Breeding Values to Bull
Selection



BETTER COWS > BETTER LIFE



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**Ministerie van Landbouw,
Natuur en Voedselkwaliteit**

Thank you for your
attention



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Genetic Correlations and Phenotypic Correlations

Trait	conc	#peaks	ratio	Madsen	Kjeldsen	Tier2
conc		0.04 (0.01)		0.65 (0.01)	0.68 (0.01)	0.06 (0.02)
#peaks	0.41 (0.06)			0.02 (0.02)	0.05 (0.02)	-0.04 (0.02)
ratio	NE			0.90 (0.00)	0.94 (0.01)	0.02 (0.02)
Madsen	0.70 (0.14)	0.86 (0.48)	0.74 (0.09)		0.98 (0.00)	0.33 (0.02)
Kjeldsen	0.86 (0.11)	0.86 (0.31)	0.96 (0.01)	0.92 (0.02)		0.24 (0.02)
Tier2	0.20 (0.16)	-0.28 (0.14)	0.02 (0.18)	0.49 (0.27)	0.16 (0.37)	

