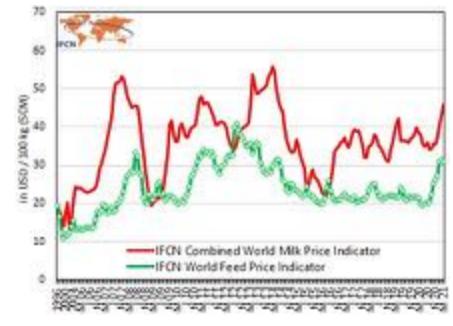
Qualitas.

Building a two-lactation model for feed efficiency in dairy cattle

Patrick Stratz, Adrien Butty and Urs Schnyder

Importance of feed efficiency



Profitability:

- Globally, feed accounts for about 60% of the costs in a dairy farm.
- depending on zone + pasture : feed costs in direct costs in Switzerland around 60-70%.

Source: https://ifcndairy.org/ifcn-milk-price-indicator/, retrieved on 07.05.2021

Definition of feed-efficiency

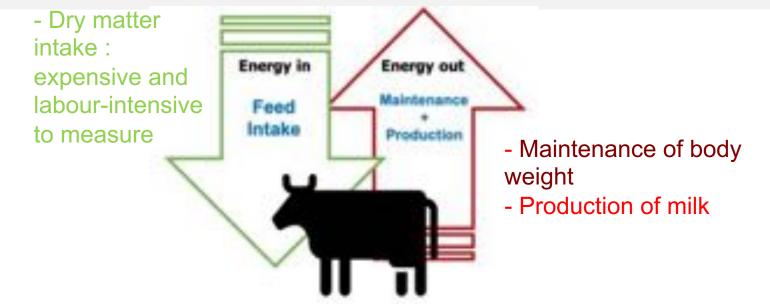


Figure 1: Feed efficiency definition in Canada (Richardson, C. and Van Doormaal B., 2021)

Metabolic efficiency expressed as RFI EBV_{RFI} = EBV_{DMI} - $rk1^* EBV_{ECM} + rk2^* EBV_{MBW}$

Feed efficiency (FE) is complex and influenced by many biological mechanisms. In-depth, detailed records of many traits of the cow is necessary

RDGP-Project

Raw data used from Switzerland (CHE) and several other countries (Australia:

AUS, Canada: CAN, Germany: DEU, Denmark: DNK, Spain :ESP and USA).

- Between 1 and 3 milkings per day
- Daily and Weekly records from research and commercial farms for dry matter

intake and bodyweight depending on the country

--> For more details see van Staaveren et al. (in preparation)

Findings from RDGP data

Simulation study by Houlahan et al. (2021) tailored to the Canadian population:

Expected cumulative response to RFI selection:

→ For first lactation data: After 10 generations, 0.52 kg DM/day or 158 kg DM/305 days lactation more efficient than without selection for RFI.

Canada has already built up a breeding value estimation using data from the first lactation

Jamrozik and Kistemaker (2022) showed that "Inclusion of second lactation data into the genetic evaluation leads to increased reliability in comparison with an evaluation comprising only 1st lactation records"

Aim of this study

We want

- 1. to derive residual feed intake as indicator for feed-efficiency
- 2. to investigate whether residual feed intake in first and second lactation can be modelled as one trait or should be treated separately

Data selection (following Jamrozik et al.,2020a):

- 1. Calving year > 2002
- 2. Age at calving:

first calving: 17 until 40 months

second calving : 28 until 68 months

--> Only data from first / second lactation used

Data selection (Jamrozik et al.,2020a):

- 3. Days in milk from 5 to 305
- 4. Daily milking yield > 4kg
- 5. Daily fat and protein content > 0kg
- 6. Energy corrected milk (10 60 kg)
- 7. Daily dry matter intake (4 50 kg)

Calculation of weekly averages for the traits:

- Energy Corrected Milk (ECM),
- Metabolic body weight (MBW)
- Dry Matter Intake (DMI)

→ 10066 cows (AUS, CAN, CHE, DEU, DNK, ESP and USA)

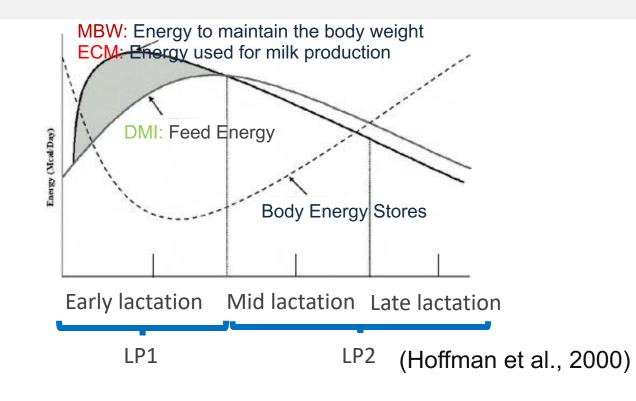
8514 cows with > 1 DMI during lactation (72,6% in lactation 1 and 27,4% in lactation 2)

Definition of the traits:

All traits are defined in two lactation periods.

- **first** lactation period (LP) for DIM 5-60
- second LP for DIM 61-305

trait	lactation 1		lactation 2				
	period 1	period 2	period 1	period 2			
DMI	DMI1_L1	DMI2_L1	DMI1_L2	DMI2_L2			
MBW	MBW1_L1	MBW2_L1	MBW1_L2	MBW2_L2			
ECM	ECM1_L1	ECM2_L1	ECM1_L2	ECM2_L2			



Definition of the traits:

All traits are defined in two lactation periods.

- **first** lactation period (LP) for DIM 5-60
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trait	lactation 1		lactation 2					
	period 1	period 2	period 1	period 2				
DMI	DMI1_L1	DMI2_L1	DMI1_L2	DMI2_L2				
MBW	MBW1_L1	MBW2_L1	MBW1_L2	MBW2_L2				
ECM	ECM1_L1	ECM2_L1	ECM1_L2	ECM2_L2				

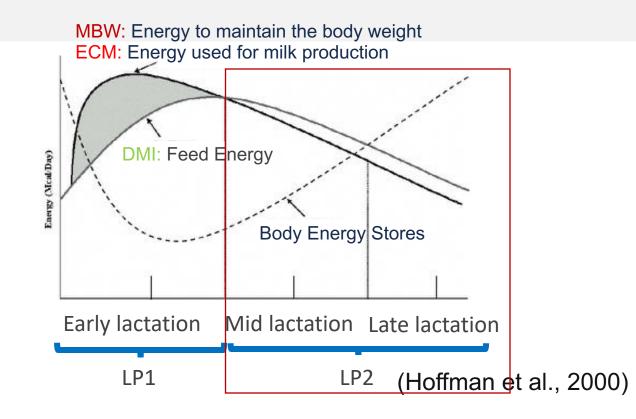


Table 1: Number of records, mean and standarddeviation for eachtrait in lactation L1 and L2 for LP2

Standardized traits*	# Records	Mean	SD
DMI2_L1	90'821	19.12	2.776
MBW2_L1	65'863	124.53	8.616
ECM2_L1	91'623	32.31	6.162
DMI2_L2	58'863	21.69	2.662
MBW2_L2	43'688	130.52	7.502
ECM2_L2	64'662	37.45	8.202

*DMI and MBW were standardized to the mean and standarddeviation of the herd of Agroscope Posieux

The linear animal model which fitted for each of the 12 FE traits was the same:

Factors in the model are:

- 1. Age at calving,
- 2. Week of lactation,
- 3. Year-Season at calving,
- 4. Herd-Year at calving,
- 5. Additive genetic effect,
- 6. Permanet environmental effect
- 7. Residual effect

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- 6. Permanet environmental effect
- 7. Residual effect

Treatment/Diet	AUS	CAN	CHE	DEU	DNK	ESP	USA
PASTURE	-	-	-	-	-	+	-
SILAGE	-	-	+	-	-	+	-
CONCENTRATE	-	-	-	-	-	+	-
TMR	-	+	-	+	+	+	+
Cube	+	-	-	-	-	+	-

+ available, - not available

Effect of Treatment/Diet is well covered by the factors **1.** and **4.** (results from backward elimination, not shown)

The linear animal model which fitted for each of the 12 FE traits was the same:

Factors in the model are:

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- 3. Year-Season at calving,
- 4. Herd-Year at calving,
- 5. Additive genetic effect,
- 6. Permanet environmental effect
- 7. Residual effect

Table 2: Treatments/Diets are shown by country

Treatment/Diet	AUS	CAN	CHE	DEU	DNK	ESP	USA
PASTURE	-	-	-	-	-	+	-
SILAGE	-	-	+	-	-	+	-
CONCENTRATE	-	-	-	-	-	+	-
TMR	-	+	-	+	+	+	+
Cube	+	-	-	-	-	+	-

+ available, - not available

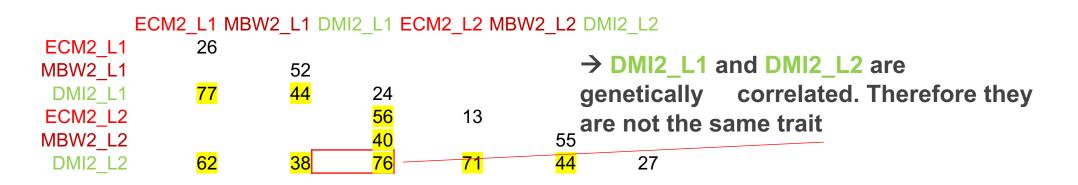
Effect of Treatment/Diet is well covered by the factors **1.** and **4.** (results from backward elimination, not shown)

Estimation of the variance components for 12 traits was done in MiX99 using the Monte Carlo (MC) Expectation Maximization (EM) Restricted Maximum Likelihood (REML) (MC EM REML) algorithm

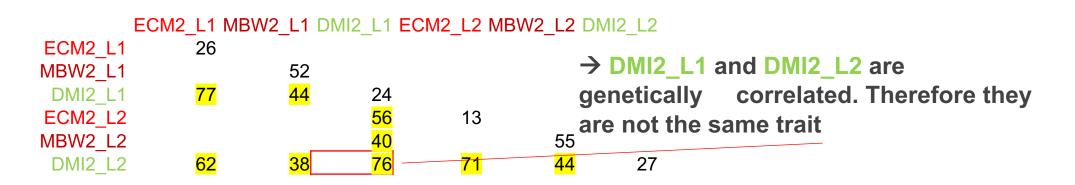
Ratios from the multi-trait model, at the genetic level. On the diagonal: heritabilities, below the diagonal: genetic correlations. All values were multiplied by 100

	ECM2_L1 MB\	N2_L1 DN	II2_L1 EC	M2_L2 MB	W2_L2 DM	112_L2
ECM2_L1	26					
MBW2_L1		52				
DMI2_L1	<mark>77</mark>	<mark>44</mark>	24			
ECM2_L2			<mark>56</mark>	13		
MBW2_L2			<mark>40</mark>		55	
DMI2_L2	<mark>62</mark>	<mark>38</mark>	<mark>76</mark>	<mark>71</mark>	<mark>44</mark>	27

Ratios from the multi-trait model, at the genetic level. On the diagonal: heritabilities, below the diagonal: genetic correlations. All values were multiplied by 100



Ratios from the multi-trait model, at the genetic level. On the diagonal: heritabilities, below the diagonal: genetic correlations. All values were multiplied by 100



 \rightarrow Positive relationship between DMI2_L1 (DMI2_L2) and the energy sinks in LP2

→ Breeding for low DMI2_L1 (DMI2_L2) => Reduction of MBW and ECM in LP2.

Aim: Derivation of DMI which is genetically independent of MBW and ECM (RFI)

```
--> cov(RFI,ECM) = cov(RFI,MBW) = 0
```

Definition of the breeding value of RFI: RFI = DMI - rk1 * ECM - rk2 * MBW

rk1(2) : regression coefficients (recursive coefficients)

Decomposition of cov(RFI,ECM) and cov(RFI,MBW)

- I. cov(RFI,ECM) = -rk1 * var(ECM) + cov(DMI,ECM) rk2 * cov(MBW,ECM) = 0
- II. cov(RFI,MBW) = -rk2 * var(MBW) + cov(DMI,MBW) rk1 * cov(ECM,MBW) = 0

 \rightarrow Solving II to rk2 and inserting it into I, the formula for rk1 can be derived \rightarrow By inserting rk1 into II, the formula for rk2 can be derived

Decomposition of $cov_{(RFI,ECM)}$ and $cov_{(RFI,MBW)}$

 $\rightarrow rk1 = \frac{cov(ECM,MBW)*cov(MBW,DMI)-cov(ECM,DMI)*var(MBW)}{cov(ECM,MBW)^2-var(ECM)*var(MBW)}$

 $\rightarrow \mathsf{rk2} = \frac{\mathit{cov}(\mathit{ECM}, \mathit{MBW}) \ast \mathit{cov}(\mathit{ECM}, \mathit{DMI}) - \mathit{var}(\mathit{ECM}) \ast \mathit{cov}(\mathit{MBW}, \mathit{DMI})}{\mathit{cov}(\mathit{ECM}, \mathit{MBW})^2 - \mathit{var}(\mathit{ECM}) \ast \mathit{var}(\mathit{MBW})}$

 → Four recursive coefficients, due to 2 lactations: 1.lactation: rk1_L1, rk2_L1
2.lactation: rk1_L2, rk2_L2

(Co)variances between RFI and the energy sinks can also be derived from G*, P* and R*

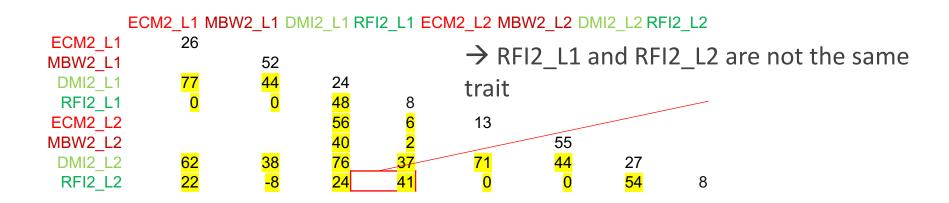
 G*= ΛGΛ', P*= ΛPΛ' and R*= ΛRΛ', where G, P and R are the genetic ,permanent environmental and residual (co)variance Matrices and

$$\Lambda_{6,6} = \begin{bmatrix} 1 & 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 0 & 0 & 0 & 0 \\ -rk1_L1 & -rk2_L1 & 1 & 0 & 0 & 0 \\ 0 & 0 & 0 & 1 & 0 & 0 \\ 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & -rk1_L2 & -rk2_L2 & 1 \end{bmatrix}$$

representing a matrix in the order and the size of G, P and R

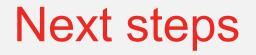
Is feed intake in lactation 1 and 2 the same trait?

Variance components for FE as RFI adjusted for energy sinks, at the genetic level.



Conclusions

- 1. Residual feed intake can be derived as an indicator for feedefficiency
- 2. Residual feed intake is genetically independent of MBW and ECM
- 3. Residual feed intake in first and second lactation must be considered as two different traits



- 1. To study the effect of including genomic information to the evaluation
- 2. To compare the changes in reliability estimates of models with data of one or two lactations included
- 3. To build a feed efficiency index

Literature

Hoffman, K., R. DeClue, and D. Emmick. (2000) Prescribed grazing and feeding management of lactating dairy cows. NYS grazinglands conservation initiative. USDA-NRCS Accessed: Jun. 16, 2017. <u>http://grazingguide.net/documents/cow-feeding-mgt.pdf</u>

Houlahan, Kerry, et al. (2021) "Effects of Incorporating Dry Matter Intake and Residual Feed Intake into a Selection Index for Dairy Cattle Using Deterministic Modeling." *Animals* 11.4 : 1157.

Jamrozik, J., G.J. Kistemaker, T.C.S. Chud, F.S. Schenkel.(2020a) "Genetic evaluation for feed efficiency: progress report." *Research Report to GEB*, pp. 5.

Jamrozik, J. and G.J. Kistemaker (2022). "Including Second Lactation Data in Feed Efficiency Evaluations". Open Insdustry Session. https://lactanet.ca/wp-content/uploads/2022/03/OIS-Presentation-Package-March-3-2022.pdf. Acessed 09.05.2022.

Richardson, C. and B. Van Doormaal (2021) "Is your feed going

to waste?" Lactanet Canada. <u>https://www.cdn.ca/images/uploaded/image/Introducing%20feed%20effecency%20techENG2.JPG</u>. Accessed 09.05.2022.

van Staaveren et al. (unpublished paper). "The Resilient Dairy Genome Project – a general overview of methods and objectives related to feed efficiency and methane emissions".

Thank you for your attention!



Email Adress: patrick.stratz@qualitasag.ch

Backup slides

Investigation: Impact of BWC on FE (Jamrozik, RDGP-Project)

Canada included BWC as

 3rd sink for FE calculated as regression of BW on day, within weekly intervals (7d)

Investigation: Impact of BWC on FE (Jamrozik, RDGP-Project)

Canada included BWC as

- 3rd sink for FE calculated as regression of BW on day, within weekly intervals (7d)
- 3rd sink for FE calculated as regression of BW on day, within 2 DIM intervals, 5-60 DIM and 61-305 DIM (2int)

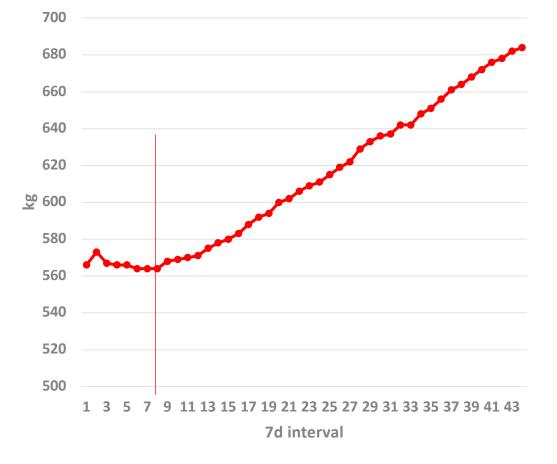


Figure S1: Average BW (kg) by 7d intervals (5 – 305 DIM)

Investigation: impact of BWC on FE (Jamrozik, RDGP-Project)

Drawbacks of using BWC as the 3rd sink for FE (2int):

- 1. FE becomes more like DMI (r_g (DMI, FE) = **0.57** vs 0.37 (Old model))
- 2. Inflated genetic variance of FE (compared with FE with 2 sinks, around 5%)
- 3. Increased computations
- 4. Reduced stability of evaluation (inclusion of **lowly correlated traits**)

DII	M	61 – 305								
Inter	val/	ECM	MBW	ΔBW	DMI	RFI				
Tra	it									
	ECM	32	-2	<mark>-6</mark>	71	0				
61	MB		57	<mark>10</mark>	40	0				
	W									
-	ΔBW			37	<mark>6</mark>	0				
305	DMI				28	57				
	RFI					<mark>13</mark>				

Are we adding useful info or just a noise?

Assumption:

EBV correlation between

- 1. BWC for both definitions should be **high**
- 2. BWC and RFI is lower than BWC and DMI for both definitions
- 3. DMI and RFI decrease when BWC is in the model

Are we adding useful info or just a noise?

Assumption:

EBV correlation between

- 1. BWC for both definitions should be **high**
- 2. BWC and RFI is lower than BWC and DMI for both definitions
- 3. DMI and RFI decrease when BWC is in the model

EBV correlation between

- 1. **BWC** for both definitions is **r=0.18**
- 2. BWC and RFI is 0.17 (0.08) compared to 0.04 (0.06) for BWC and DMI for 7d (2int)
- 3. DMI and RFI is 0.59 (0.57) when BWC is in the model

 \rightarrow Evidence that just noise was added in the model

Table 1: Number of records, weekly mean and standarddeviation for eachtrait and DIM class in lactation L1 and L2

Standardized traits*	# Records	Mean	SD
stdDMI1_L1	26615	17.697	2.5367
stdDMI2_L1	90821	19.117	2.7758
stdMBW1_L1	18830	121.1	8.4133
stdMBW2_L1	65863	124.53	8.616
ECM1_L1	24500	32.124	6.6713
ECM2_L1	91623	32.307	6.1615
stdDMI1_L2	18950	21.805	2.5297
stdDMI2_L2	58863	21.691	2.6621
stdMBW1_L2	14139	129.12	8.0312
stdMBW2_L2	43688	130.52	7.5023
ECM1_L2	18920	42.743	7.595
ECM2_L2	64662	37.447	8.2024

*DMI and MBW were standardized to the mean and standarddeviation of the Posieux herd

Fokus auf RFI2_L1/RFI2_L2 und DMI2_L1/DMI2_L2

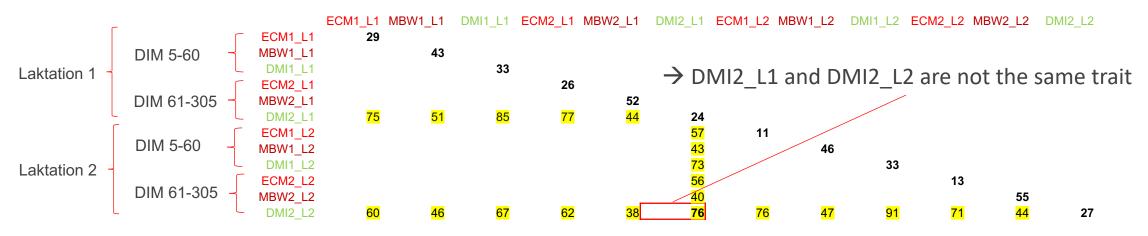
→ Per Definition RFI2_L1/RFI2_L2 genetisch unabh. von den Energiesenken !!!

→ Keine unterschiedlichen Merkmale RFI2_L1/RFI2_L2, da cor(RFI2_L1/RFI2_L2)=41

	ECM1_L1 MB	N1_L1 DMI1	L_L1 RFI1_L1	ECM	2_L1 MB	W2_L1 DMI2_	_L1 RFI2_L1	ECM1_L	2 MB	W1_L2 DMI1_L	2 RFI1_L2	ECM2	2_L2 MBW	12_L2 DMI2	L2 RFI2_	L2
ECM1_L1	29	21	51	0	94	2	75	6	63	9	54	23	63	4	60	23
MBW1_L1	21	43	68	0	20	96	51	-9	23	89	50	2	11	87	46	-2
DMI1_L1	51	68	33	63	55	61	85	53	43	60	71	30	44	58	67	30
RFI1_L1	0	0	63	16	12	5	27	62	8	5	36	38	21	6	15	15
ECM2_L1	94	20	55	12	26	3	77	0	62	7	57	29	69	2	62	22
MBW2_L1	2	96	61	5	3	52	44	0	13	92	42	-2	2	91	38	-8
DMI2_L1	75	51	85	27	77	44	24	48	57	43	73	18	56	40	76	24
RFI2_L1	6	-9	53	62	0	0	48	8	8	-1	51	33	6	2	37	41
ECM1_L2	63	23	43	8	62	13	57	8	11	21	63	0	87	12	76	15
MBW1_L2	9	89	60	5	7	92	43	-1	21	46	51	0	7	98	47	-5
DMI1_L2	54	50	71	36	57	42	73	51	63	51	33	67	59	47	91	58
RFI1_L2	23	2	30	38	29	-2	18	33	0	0	67	14	14	2	40	65
ECM2_L2	63	11	44	21	69	2	56	6	87	7	59	14	13	-2	71	0
MBW2_L2	4	87	58	6	2	91	40	2	12	98	47	2	-2	55	44	0
DMI2_L2	60	46	67	15	62	38	76	37	76	47	91	40	71	44	27	54
RFI2_L2	23	-2	30	15	22	-8	24	41	15	-5	58	65	0	0	54	8

_	_	ECM1_L1 ME	W1_L1 DMI	1_L1 ECN	M2_L1 MB\	V2_L1 DMI	2_L1 ECN	M1_L2 MB\	V1_L2 DMI1	_L2 ECN	M2_L2 MBV	N2_L2 DMI2	2_L2
	DIM 5-60		43										
Laktation 1	DMI1_L1	51	68	33									
	DIM 61-305	1 94	20	55	26								
		.1 2	96	61	3	52							
L	DMI2_L1	75	51	85	77	44	24						
	ECM1_L	<mark>2</mark> 63	23	43	62	13	57	11					
	DIM 5-60 - MBW1_L	2 9	89	60	7	92	43	21	46				
Laktation 2	L DMI1_L2	54	50	71	57	42	73	63	51	33			
	ECM2_L	2 63	11	44	69	2	56	87	7	59	13		
	DIM 61-305 - MBW2 L2	2 4	87	58	2	91	40	12	98	47	-2	55	
l	DMI2_L2	60	46	67	62	38	76	76	47	91	71	44	27

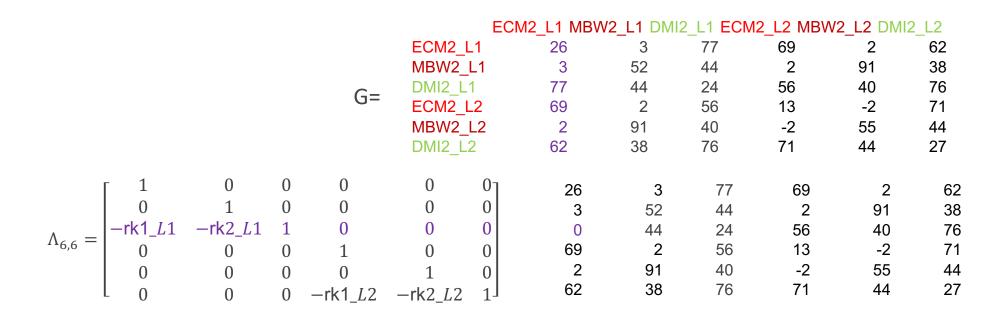
Ratios from the MTM, at the genetic level. On the diagonal: heritabilities, below the diagonal: genetic correlations. All values were multiplied by 100

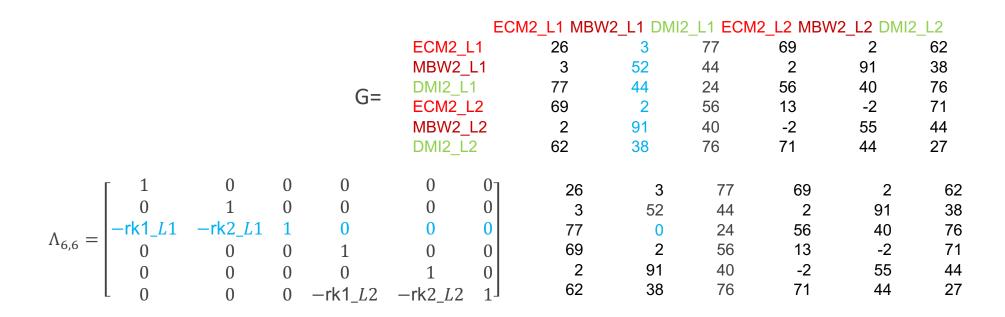


→ positive relationship between DMI2_L1 (DMI2_L2) and the energy sinks in lactation periode DIM 5-60 (LP1) and lactation periode DIM 61-305. (LP2)

 \rightarrow Breeding for low DMI2_L1 (DMI2_L2): Reduction of MBW and ECM in LP1/LP2.

Aim: Reduction of DMI in LP2 genetically independent of MBW and ECM in LP2.





(Co)variances between RFI and the energy sinks can be derived from G*, P* and R*

 G*= ΛGΛ', P*= ΛPΛ' and R*= ΛRΛ', where G, P and R are the genetic ,permanent environmental and residual (co)variance Matrices and

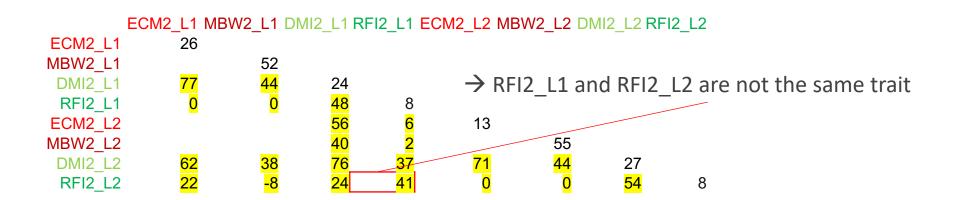
	г 1	0	0	0	0	0	0	0	0	0	0	01
	0	1	0	0	0	0	0	0	0	0	0	0
	$-rk11_L1$	$-rk21_L1$	1	0	0	0	0	0	0	0	0	0
	0	0	0	1	0	0	0	0	0	0	0	0
	0	0	0	0	1	0	0	0	0	0	0	0
۸ —	0	0	0	$-rk12_L1$	$-rk22_L1$	1	0	0	0	0	0	0
$\Lambda_{12,12} =$	0	0	0	0	0	0	1	0	0	0	0	0
	0	0	0	0	0	0	0	1	0	0	0	0
	0	0	0	0	0	0	$-rk11_L2$	$-rk21_L2$	1	0	0	0
	0	0	0	0	0	0	0	0	0	1	0	0
	0	0	0	0	0	0	0	0	0	0	1	0
	L 0	0	0	0	0	0	0	0	0	$-rk12_L2$	$-rk22_L2$	1

representing a matrix in the order and the size of G, P and R

Covariances between DMI and RFI can be derived by using the (co)variance components of the upper triangle of the following matrices:

• ΛG , ΛP and ΛR

Variance Components for FE as RFI (DMI*) adjusted for energy sinks, at the genetic level.



Feedefficiency index, e.g.weighting RFI2_L1 and RFI2_L2 equally: $RFI2 = \frac{RFI2_L1 + RFI2_L2}{2}$