Faculty of Agriculture and Nutritional Science

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Breeding value estimation for feed intake in German HF cows using single-step genomic evaluation

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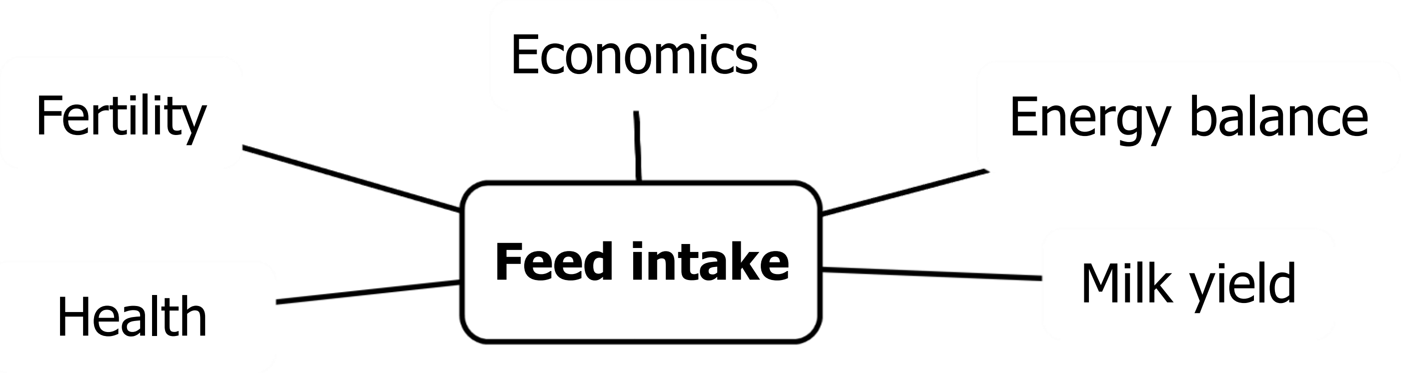
Introduction



Economics

Fertility

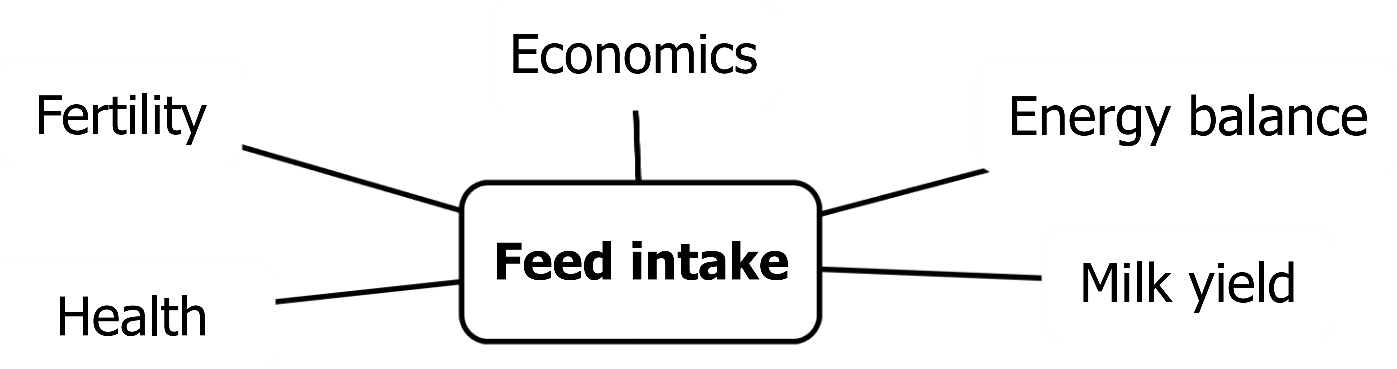
Energy balance

Feed intake

Health

Milk yield

Introduction



Economics

Fertility

Energy balance

Feed intake

Milk yield

Health

Milk yield ↑

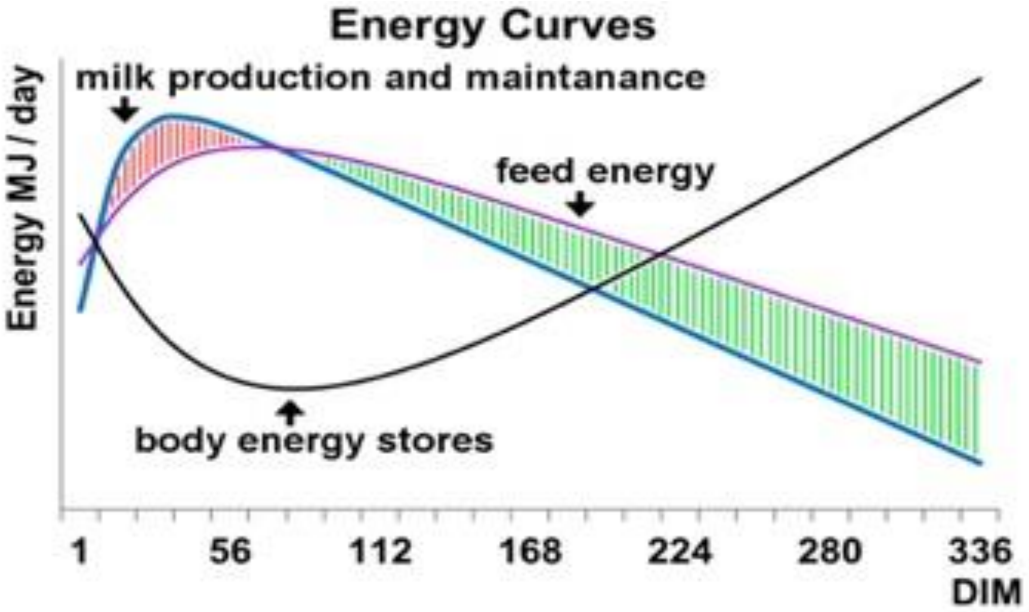
⇩

Energy deficit ↑

⇩

Diseases

Fertility problems ↑



by Strucken et al. 2015

→ Breeding for feed intake at the beginning of lactation

Material and Methods

Phenotypes HF

Trait	No. of Cows	No. of Records	Mean	SD
Feed intake (kg DM/d)	1,341	40,012	21.8	4.25
Milk yield (kg/d)	1,338	39,838	35.5	8.81
Energy balance (MJ NEL/d)	1,322	33,376	3.20	29.4

Genotypes HF

Type of Chip	No. of SNPs after quality control	No. of Cows	Phenotyped
Illumina BovineSNP50K BeadChip	43,455	1,128	✓
		35	✗

Criteria for data editing:

Records: weekly averages
Defined lactation stadium from 8 to 350 DIM
Observations outside of ± 4 sd are excluded
Pedigree information traced 4 generations back

Material and Methods

Model evaluation:

- parametric functions: Ali and Schaeffer (AS),
  Legendre Polynomials 2nd to 4th degree (LP2, LP3, LP4)
- evaluation criteria: AICC und BIC
- procedure: MIXED in SAS
- fixed effects: herd test week or herd group test week, parity (1, 2, 3 ≥4)
  AS function for lactation curve
- random effect: LP (3rd degree) for cow effect

Estimation of variance components and breeding values:

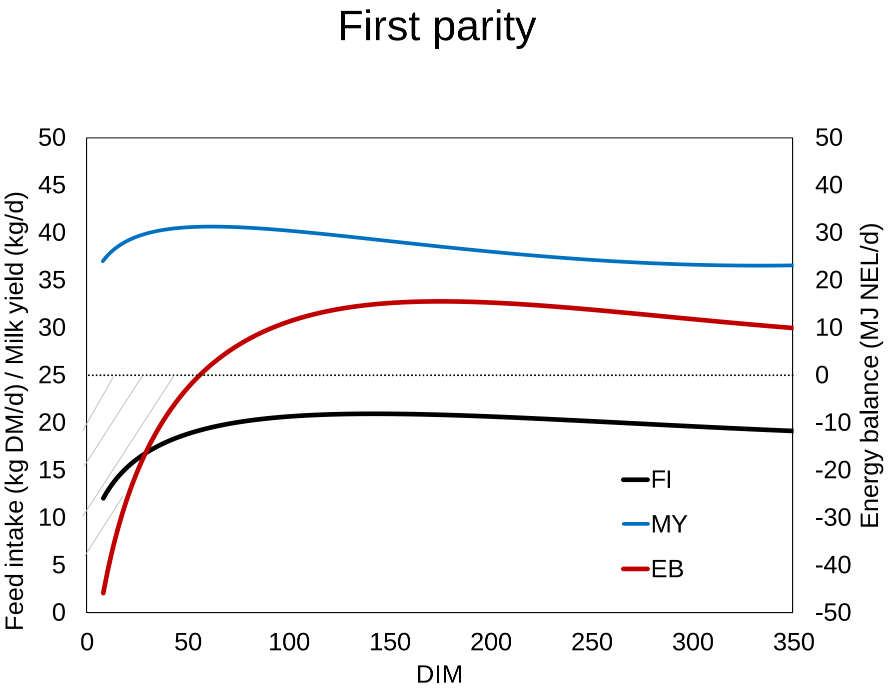
- software packages: G-Matrix und DMU (Madsen et al. 2013)
  part 1: pedigree-based data
  part 2: single-step for combined data (pedigree and genomic)

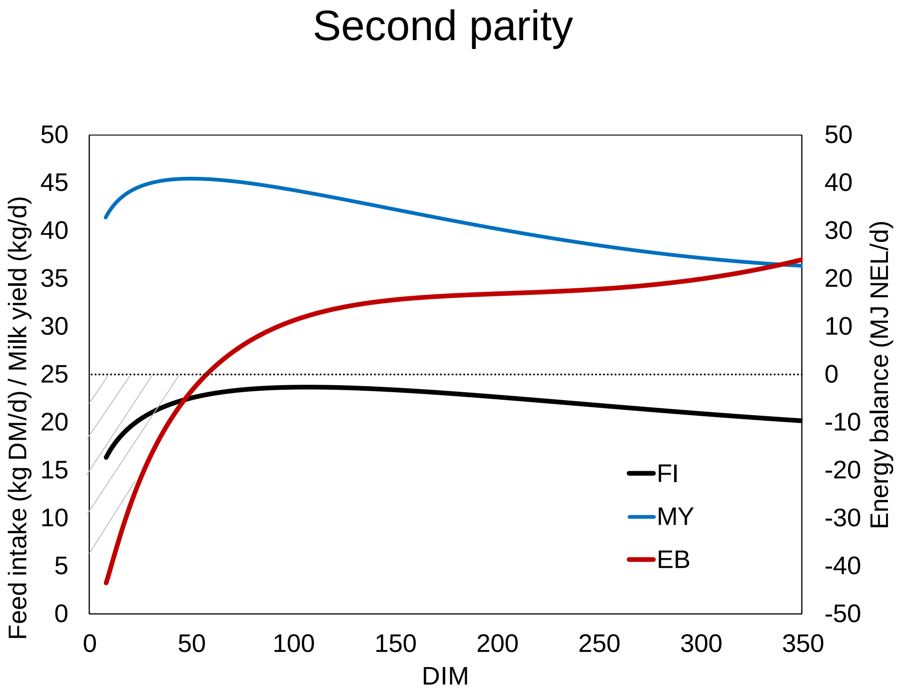
Final computation:

- software packages: SAS
  heritabilities
  genetic correlations
  reliabilities of breeding values

Results and Discussion

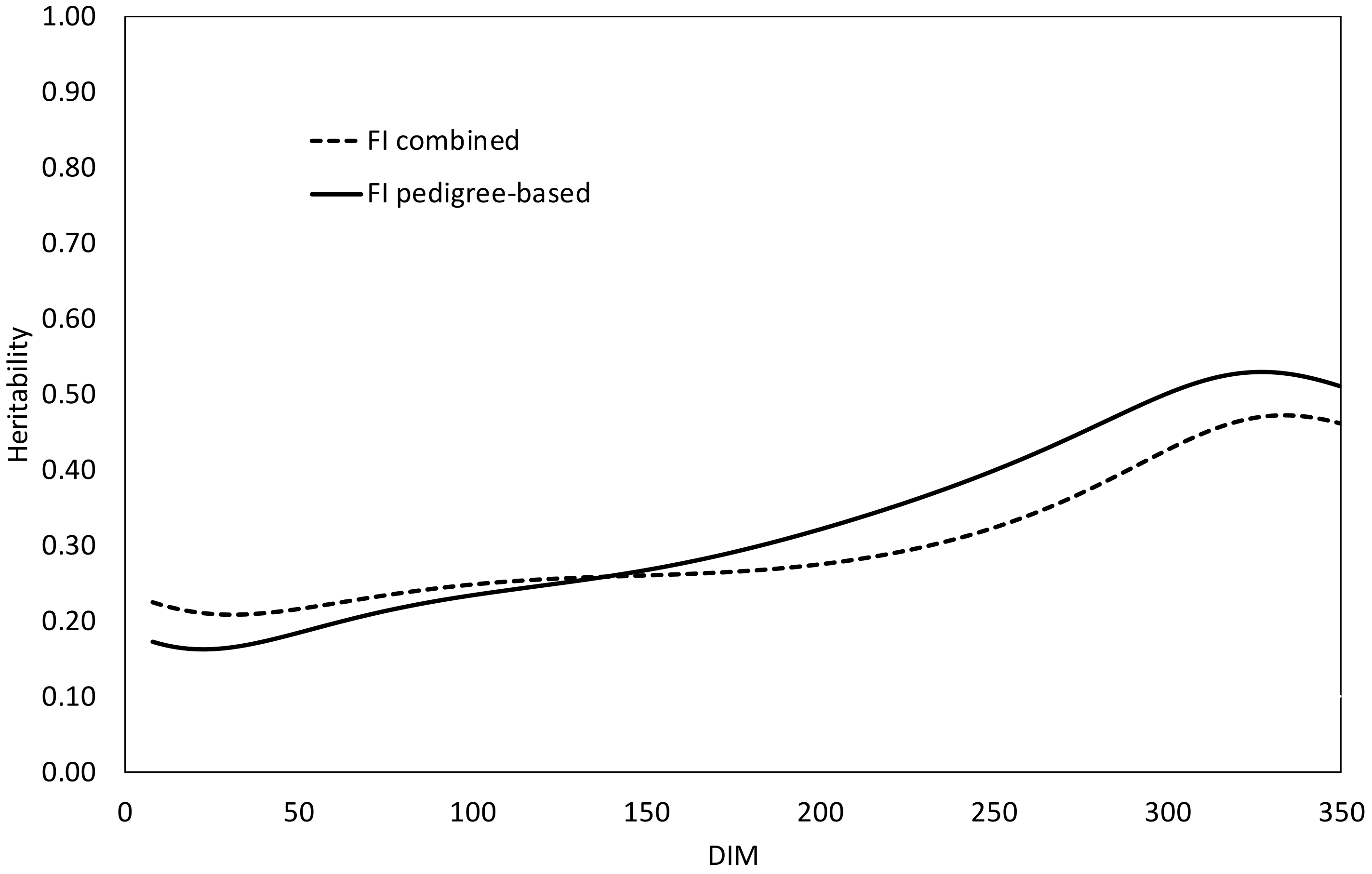
Lactation curves modeled with Ali and Schaeffer function





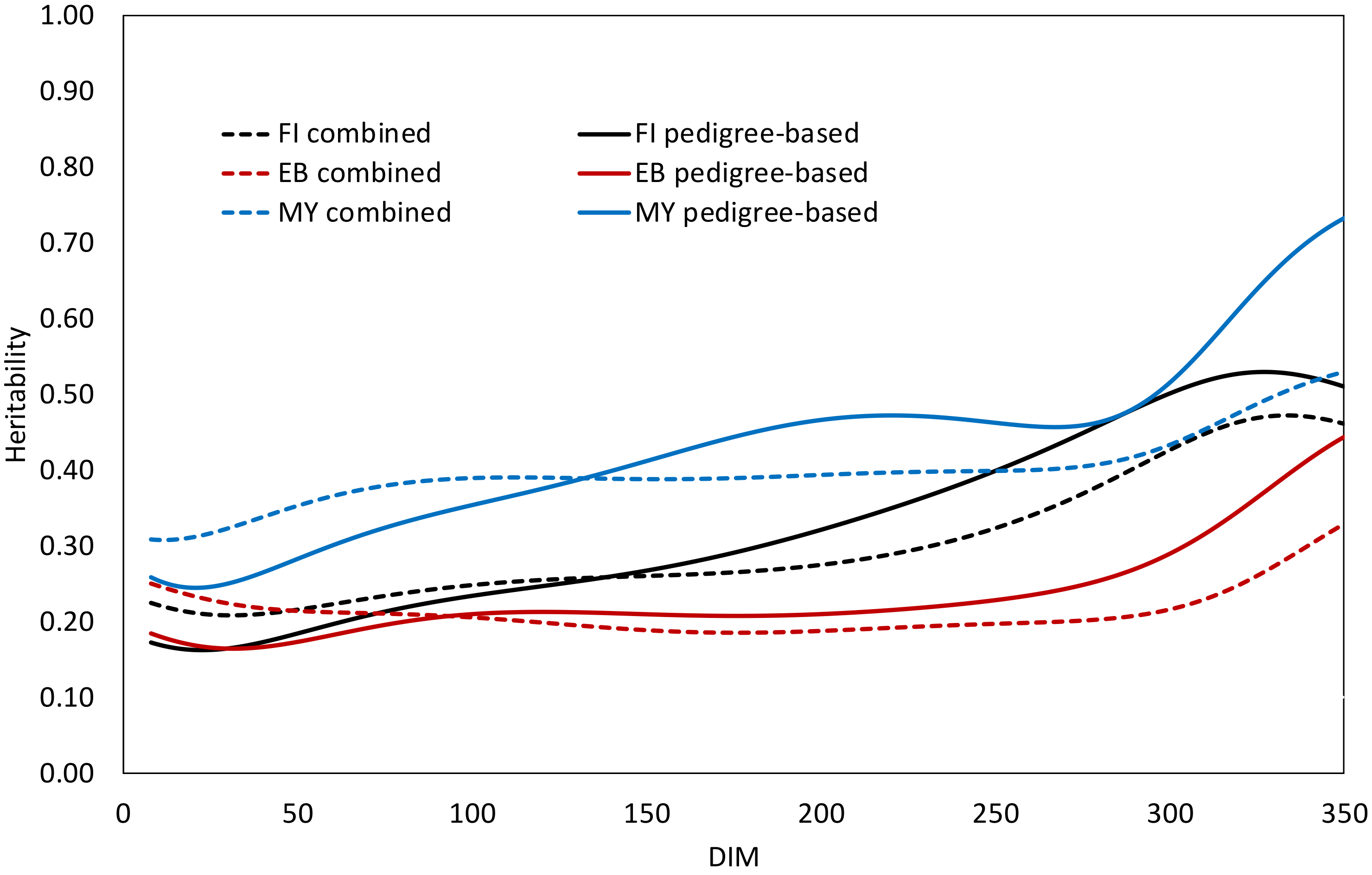
Results and Discussion

Estimated heritabilities of feed intake across the first 350 DIM



Results and Discussion

Estimated heritabilities of FI, MY and EB across the first 350 DIM

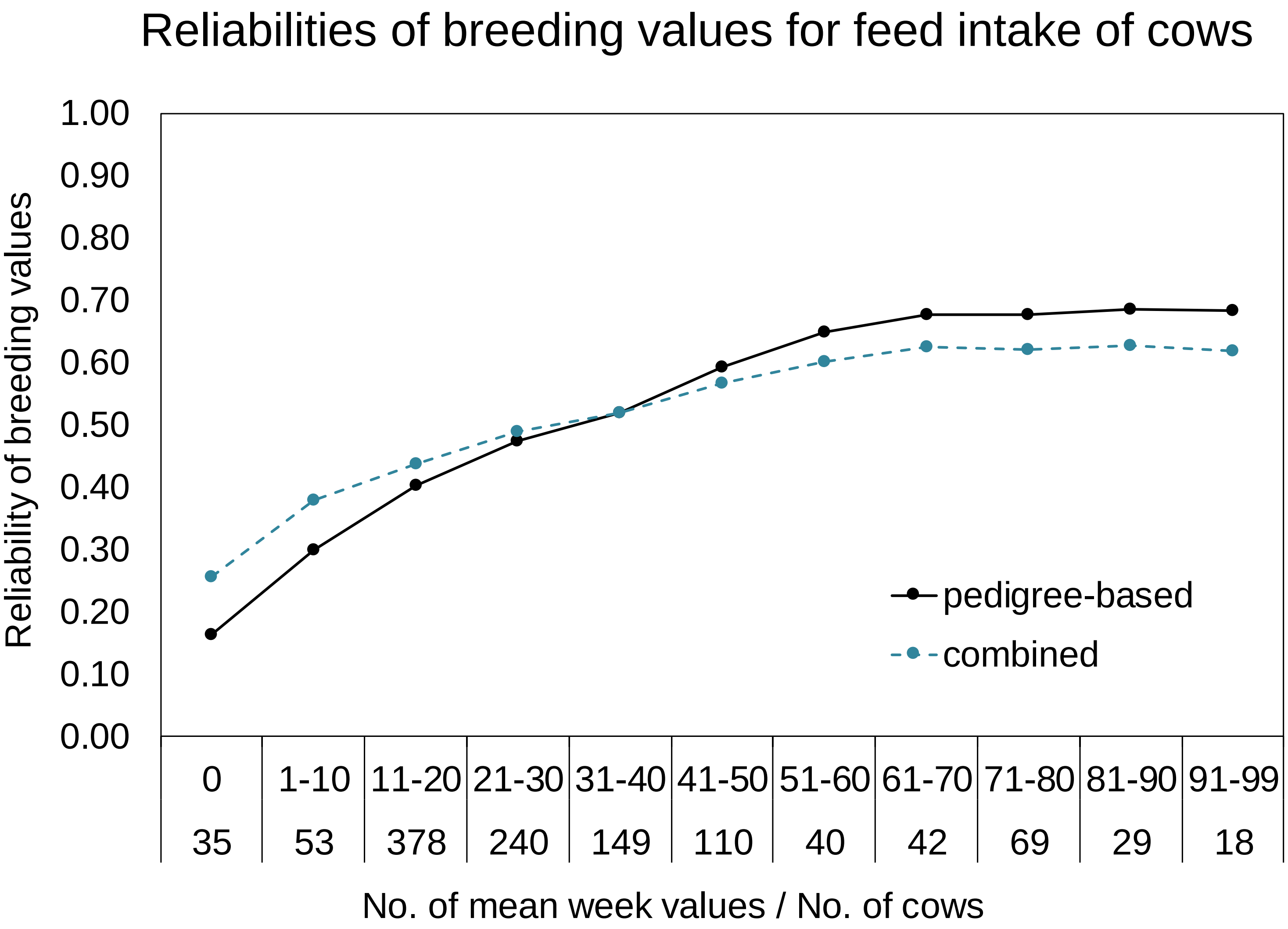


Results and Discussion

Genetic correlations for feed intake in course of lactation

	DIM	10	40	70	100	130	160	190	220	250	280	310
FI	40	0.85										
	70	0.60	0.93									
	100	0.44	0.83	0.97								
	130	0.34	0.74	0.92	0.98							
	160	0.28	0.65	0.83	0.92	0.98						
	190	0.24	0.56	0.73	0.84	0.93	0.98					
	220	0.22	0.49	0.65	0.76	0.87	0.95	0.99				
	250	0.21	0.46	0.61	0.73	0.84	0.92	0.98	1.00			
	280	0.20	0.47	0.64	0.75	0.84	0.92	0.96	0.98	0.99		
	310	0.18	0.51	0.69	0.80	0.87	0.92	0.93	0.94	0.95	0.98	
	340	0.14	0.54	0.74	0.83	0.87	0.87	0.85	0.83	0.84	0.90	0.97

Results and Discussion



Summary

- Unique data set of feed intake measurments across lactation
- Fixed lactation curve: Ali and Schaeffer
  Random lactation curve: Legendre Polynomial (3rd degree)
- Heritabilities ranged between 0.17 and 0.49 (FI) and
  0.19 and 0.33 (EB) along the trajectory
- Low genetic correlations between beginning and end of lactation
- Promising reliabilities of genomic breeding values
  for the trait feed intake

→ Need to increase the number of phenotyped and genotyped animals to improve reliabilities of future breeding values

Outlook

next steps

- Including genotyped sires in the computation

long-term objective

- Follow-up project: eMissionCow

→ Genome based selection of cows with high feed intake at the beginning of lactation

Thank you for your attention!

Attachment

Repeatability of FI, EB and MY for HF and SI