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Promote breed conservation by implementing specific traits for a local sheep breed

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Specific traits for a local sheep breed

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Introduction *(in general)*

- Many local breeds are endangered → Genetic diversity ↓
- Need for genetic diversity → Gene reservoir for future (Boettcher et al., 2010)
- Certain traits of local breeds are not identified or phenotypically recorded in conventional breeding schemes
- Specific traits of local breeds (e.g. traits for specific environments) may get lost over years due to artificial considered traits

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Introduction *(in detail)*

- Farmers want to emphasise breed-specific characteristics under extensive environmental conditions → History of this local breed

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  - Main purpose:
    - Landscape conservation on dykes
    - Make dyke slip-proof
    - Densify soil condition
    - Ensure against floodings
    - Captured outside whole year with progeny under extensive feed

  - Breeding goal:
    - Robust
    - Muscled
    - Well-growing
    - Grazing in maritime climates
    - Various soil conditions

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Test station

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Aims

- Identification and implementation of specific traits for a local sheep breed
- Computation of estimated breeding values (EBVs) for specific traits based on phenotypic information from a field experiment
- Investigation of correlations between specific and conventional EBVs

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Animals and Data

- German White-Headed Mutton (GWM)

- Datasets include:
  - Pedigree information
  - EBVs for several traits and additional information on farm and breeders

- Datasets provided by herdbook associations (LKV SH and LV SH SZZ)

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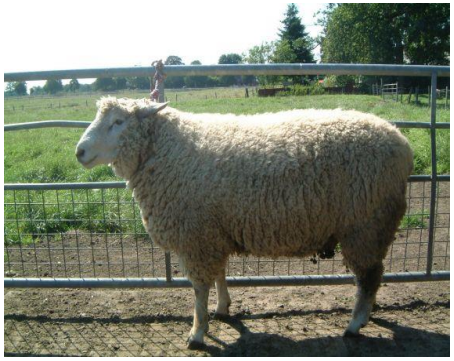
Animals and Data

Phenotypes

- Data were collected in a field experiment on farm during a trial period of 100 days

- 14 GWM reference sires were progeny tested with 47 male for two traits:
  - Average daily gain under extensive conditions (ADG_E)
  - Ultrasonic muscle-fat ratio (UMFR)



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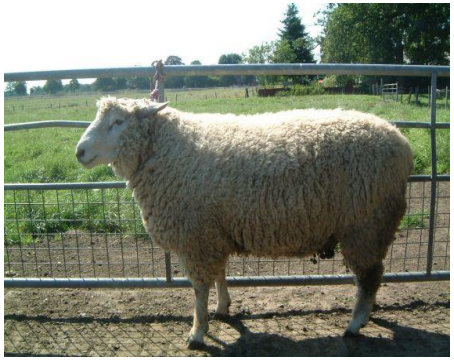

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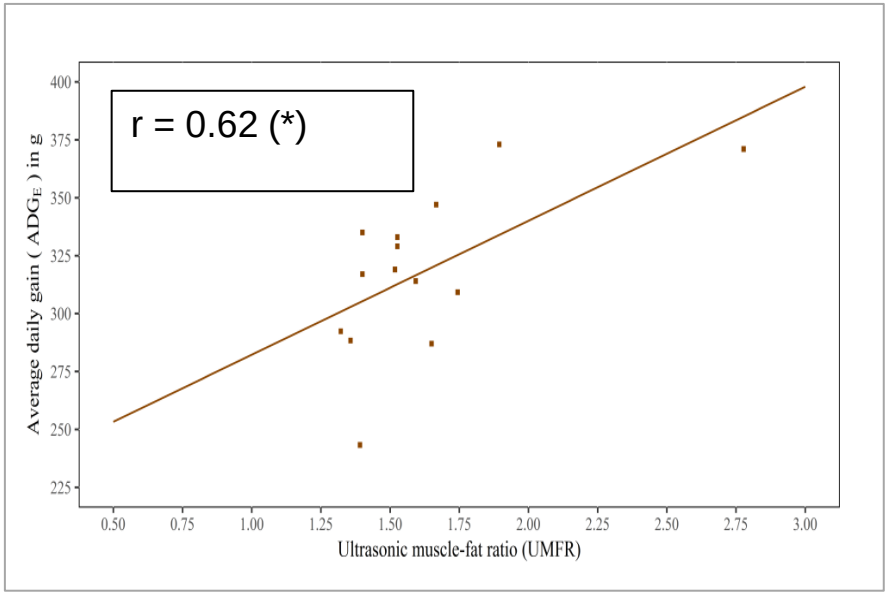
Animals and Data

Phenotypic observations



Phenotypic relation between ADG_E and UMFR

Reference sire	Progeny testing for specific traits	
	ADG_E (g/day)	UMFR
ID 1	309.2	1.74
ID 2	333.0	1.53
ID 3	319.0	1.52
ID 4	329.0	1.53
ID 5	373.0	1.89
ID 6	317.0	1.40
ID 7	292.4	1.32
ID 8	347.0	1.67
ID 9	371.0	2.78
ID 10	287.0	1.65
ID 11	335.0	1.40
ID 12	288.4	1.36
ID 13	243.3	1.39
ID 14	314.0	1.59

Methods

Estimation of genetic parameters and breeding values

- Linear mixed models (LMM) in ‘asreml’ R-package (Butler et al., 2009)
- LMM can be written as: $y = Xb + Z_A a + \sum_k Z_k u_k + e$
- Genetic parameters of repeatability (t), heritability (h^2), genetic (r_G) and phenotypic correlation (r_P) were estimated
- In addition, correlations between EBVs were estimated with function ‘cor.test’ from R-package ‘stats’ (R Core Team, 2018)

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Results

Genetic parameters

t and h^2:

Traits	Linear mixed model (LMM)			
	Repeatability $\hat{t}$ (SE)		Heritability $\hat{h}^2$ (SE)	
ADG_E	0.42	(0.31)	0.70	(0.95)
UMFR	0.46	(0.46)	0.83	(0.59)

	Traits	ADG_E	UMFR
r_P:	ADG_E	-	0.62 (0.30)
r_G:	UMFR	0.61 (0.29)	-

ADG_E= average daily gain under extensive circumstances; UMFR=ultrasonic muscle-fat ratio.

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Results

Correlation between EBVs

EBV	MUSC	WOL	ADG_E	UMFR
ADG_I	**0.60 (*)**	-0.12 (n.s.)	-0.11 (n.s.)	0.04 (n.s.)
MUSC		0.06 (n.s.)	**-0.68 (**)**	-0.31 (n.s.)
WOL			-0.40 (n.s.)	-0.17 (n.s.)
ADG_E				**0.64 (*)**

Estimates were tested for statistical significance: p-value ≥ 0.05 (n.s.), < 0.05 (*), < 0.01 (**), < 0.001 (***); ADG_I = average daily gain under intensive conditions; MUSC = muscularity; WOL = wool; ADG_E = average daily gain under extensive conditions; UMFR = ultrasonic muscle-fat ratio.

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Conclusions

- ADG_E reflects the trait of average daily gain under common environmental conditions
- Slight negative correlation between ADG_I (test station) and ADG_E reflect genotype-environment interactions
- Selection of ADG_E will also improve meat-quality aspects (UMFR)
- Breeding schemes based on ADG_E may the best use of common environment, meat interests of farmers community, and contribute to genetic diversity

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Acknowledgement

This study was funded by the Ministry of Energy, Agriculture, Environment, Nature and Digitalization

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Thank you for your attention

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Back up (1)

Inbreeding coefficient (F)

- Function 'pedInbreeding' from 'optiSel' R-package (Wellmann, 2018)
- Rates of inbreeding calculated as $\Delta F_i = (F_i - F_{i-1})/(1 - F_{i-1})$ between year i and j (ΔF_{i-j}) computed by average of annual inbreeding rates (Lewis and Simm, 2000)

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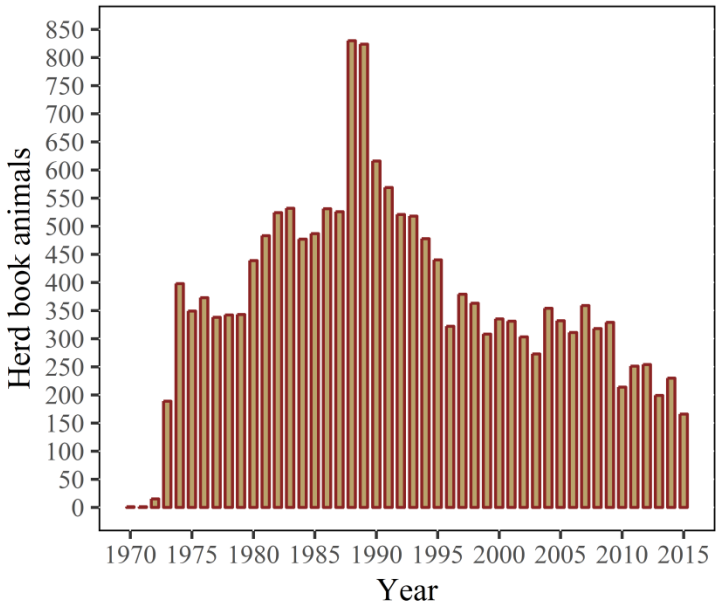
Back up (2)

Population parameters: Herdbook size (a) and Rates of inbreeding (b)

a)



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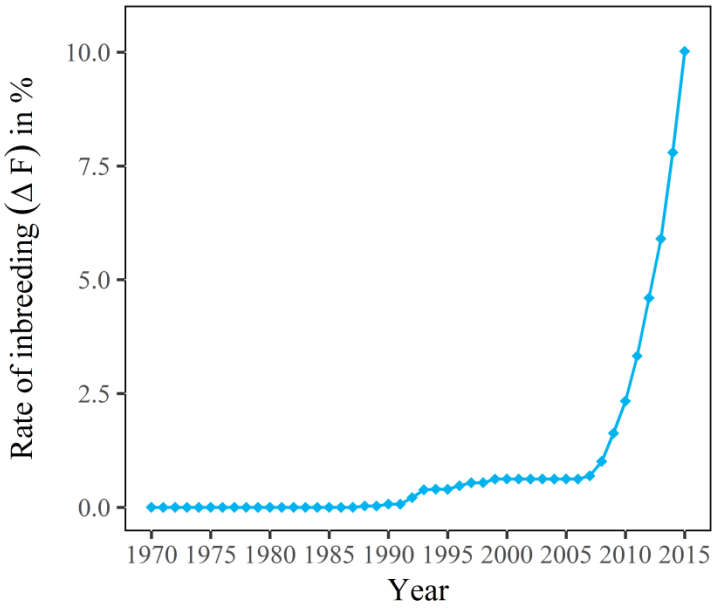

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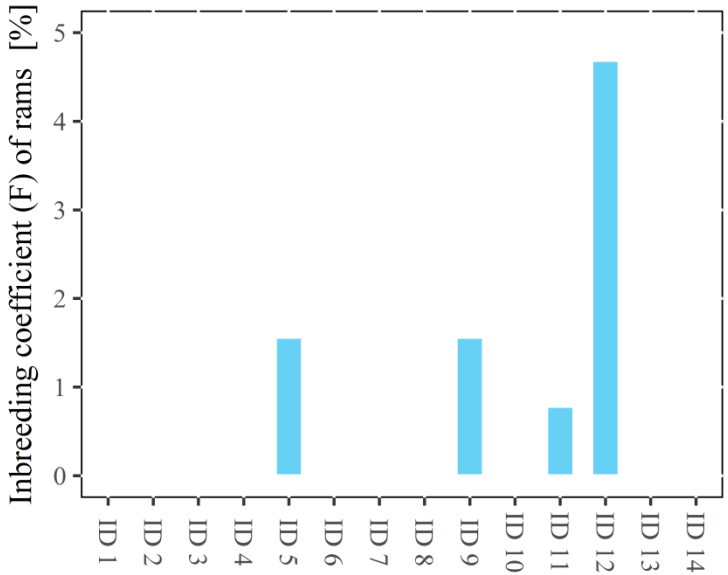
Back up (3)

Population parameters: Inbreeding (a) and Relatedness (b)

a)



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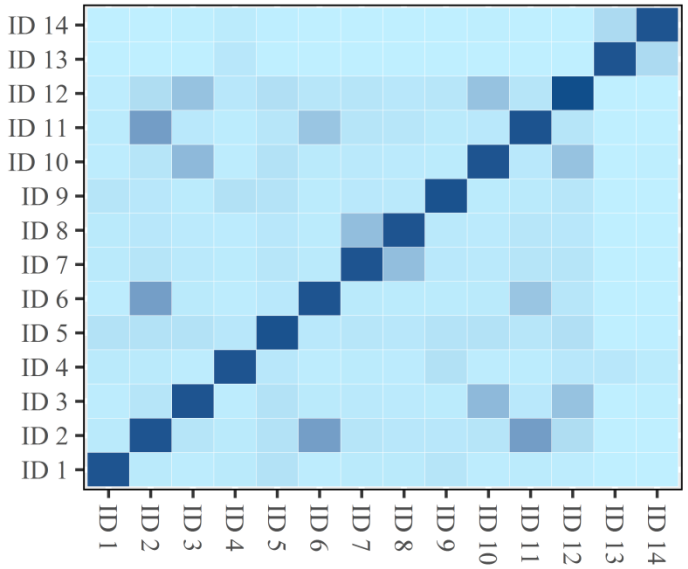

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Back up (4)

Trait implementation

- Selection on specific traits was simulated over 10 years
- Estimation of genetic response with $\Delta G = \frac{i * r_{BV} * \sigma_A}{L}$ (Rendel and Robertson, 1950)
- Four different selection intensities (i):

  (1) p50% → i_1 = 0.798

  (2) p36% → i_2 = 1.039

  (3) p21% → i_3 = 1.372

  (4) p14% → i_4 = 1.590

- Generation intervall (L) was 3.1 (Lewis and Simm, 2000) and accuracy (r_{BV}) was 0.725

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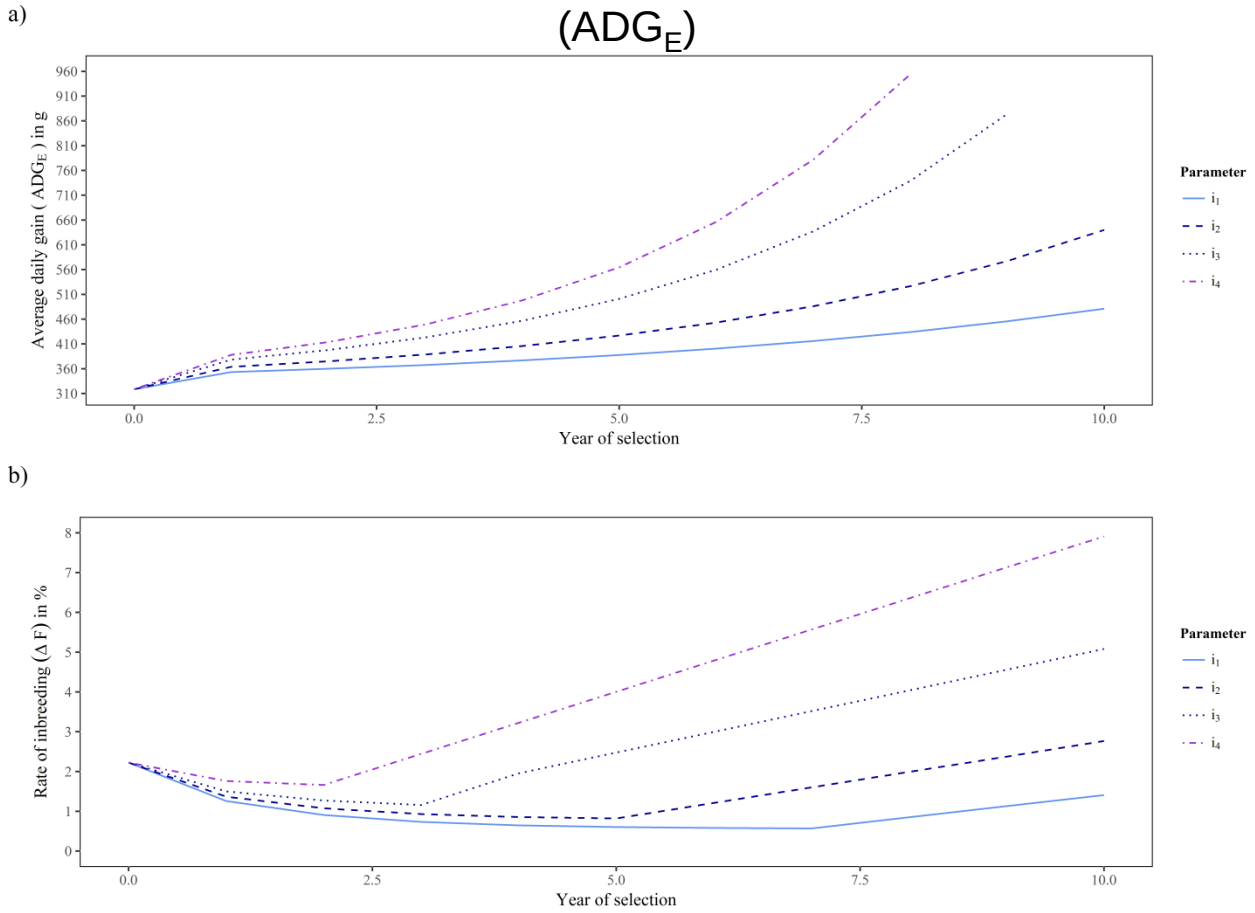
Back up (5)

Trait implementation: Genetic gain (a) vs. Rates of inbreeding (b)



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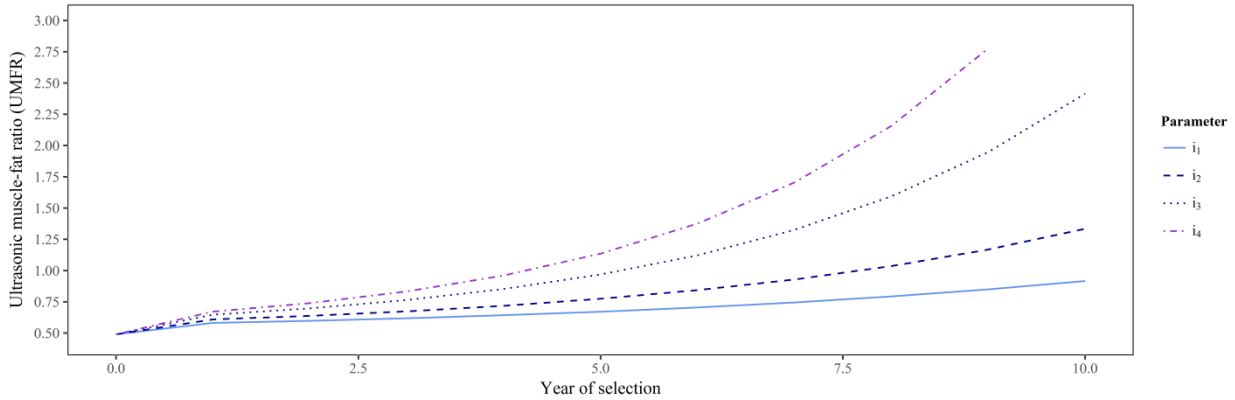
Back up (6)

Trait implementation: Genetic gain (a) vs. Rates of inbreeding (b)

a)



b)