Investigations on GxE interactions at single trait and index level in Brown Swiss dairy cattle

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Dairy production environment in Germany and Austria

- Brown Swiss is a widespread dairy cattle breed in Southern Germany and Austria

- **Broad range of landscapes and topography**
  - ➢ Different regional climates, feeding systems, housing systems
- **Different farming systems**
  - ➢ organic, conventional

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Questions to be answered

Genotype-by-environment interactions (GxE):

- Important variance source of quantitative traits that are strongly influenced by the environment

- Estimated breeding values are environmental sensitive

Are **GxE present in milk production and functional traits** in the German-Austrian Brown Swiss population **and to what extent?**

If GxE is a source of trait variance:
Does it lead to a **re-ranking of bulls on trait level and/or on total merit index level?**

Dataset

- Sample of the **German-Austrian Brown Swiss** population born in Baden-Wuerttemberg (southern Germany)

- **Pedigree** consisting of **185,439** individuals

- **56 - 638 sires** having at least 5 daughters (with at least 7 records) per environment

- **~ 57,000 cows** (daughters of the sires)

- Phenotypes derived from routine animal evaluation
  - **Yield deviations** (YD) and **de-regressed breeding values** (dEBV)

Investigated environments and traits

- Production system
  - Environmental classes: organic, conventional
- Farm location
  - Environmental classes: above 800 m ASL, below 800 m ASL
- Milk energy yield
  - continuous descriptor for reaction norm models

- Milk production traits
  - Milk, fat and protein yield
- 9 functional traits
  - E.g. longevity, non-return-rate, calving ease, …

Univariate analysis (no GxE considered)

$$y = \mu + Zs + e$$

y vector containing trait phenotypes (YD or dEBV)

μ   overall mean

s vector of random sire effects, with $s \sim N(0, A\sigma^2{}_s)$

Z incidence matrix

        (relating cow observations to the corresponding sire effect)

e random residuals, with $N(0, I\sigma^2{}_e)$

The sire models were calculated using **ASReml-R (Butler et al. 2009)**

Investigating GxE

Bivariate model

- Extension of the univariate sire model
- Separate analysis of the environments farm location and production system

Random regression: reaction norm model

- Continuous environmental descriptor: milk energy yield (MEY)

$$y_{ijk} = \mu + \underbrace{b * MEY_k}_{\text{environment (fix)}} + \overbrace{s_{ai}}^{\text{intercept sire } i} + \underbrace{s_{bi}\, MEY_k}_{\text{slope sire } i} + e_{ijk}$$

Genetic correlations of traits measured in different environments (GxE on trait level)

| traits	production system	farm location
milk yield	0.95 (0.03)	0.91 (0.06)
fat yield	0.95 (0.02)	0.93 (0.06)
protein yield	0.93 (0.03)	0.87 (0.08)
longevity	0.96 (0.07)	0.92 (0.09)
non-return-rate 56	0.94 (0.07)	0.98 (0.08)
calving to first insemination	0.99 (0.04)	0.95 (0.11)
first insemination to conception	0.97 (0.05)	0.79 (0.15)
cystic ovaries	0.99 (0.03)	0.90 (0.08)
calving ease maternal	0.84 (0.10)	n.c.
calving ease paternal	0.92 (0.11)	n.c.
stillbirth rate maternal	0.99 (0.04)	0.97 (0.32)
stillbirth rate paternal	0.98 (0.05)	0.94 (0.11)

- No severe GxE

- In agreement with other studies investigating different farming systems in Austria and Switzerland:
  - Brown Swiss (Simianer et al., 2007)
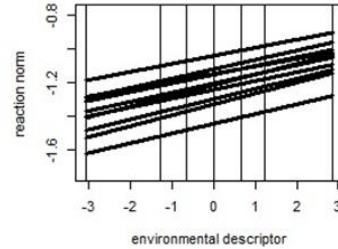 - Simmental (Pfeiffer et al., 2016)

Reaction norms: fat yield (top), cystic ovaries (bottom)
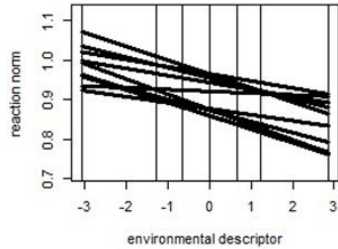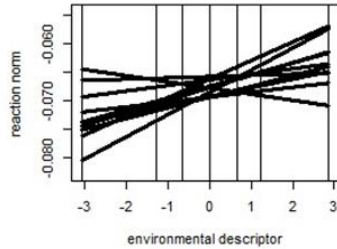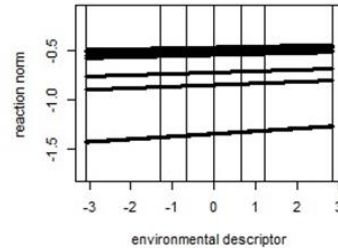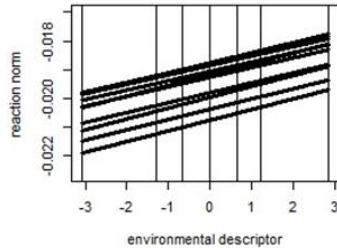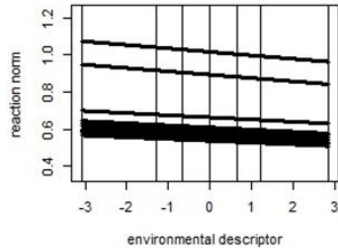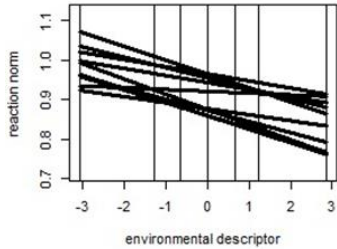

top10 sires   medium sires   flop10 sires

- Minor GxE detected for fat yield

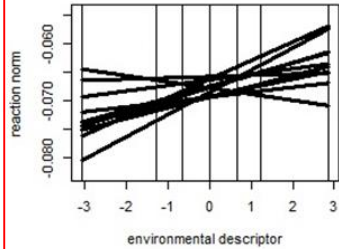- **Across all bulls: rank correlation of EBVs in different environments close to 1**

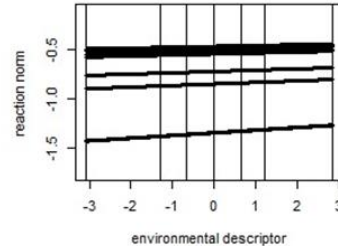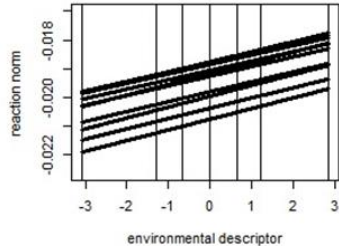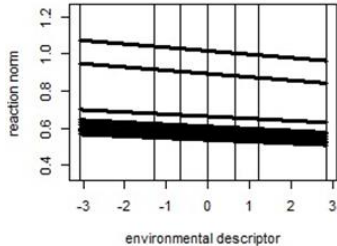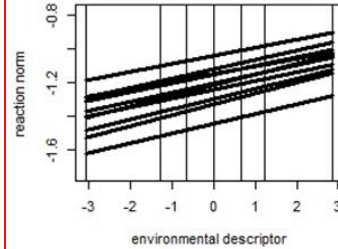# Reaction norms: fat yield (top), cystic ovaries (bottom)

top10 sires   medium sires   flop10 sires

- Sires having EBVs (intercept, no GxE consieded) close to the mean (zero):
- Even minor GxE (slope) led to obvious re-ranking since the EBVs (almost) completely relied on the GxE term

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GxE on total merit index (TMI) level

$$TMI_{con} = \sum_{t=i}^{10} EBV_{con,t} * REW_{con,t}$$

conventional

$$TMI_{org} \sum_{t=i}^{10} EBV_{org,t} * REW_{org,t}$$

organic

- Calculated with the estimated breeding values (**EBV**) obtained from either the **univariate** or the **bivariate** model → i.e. 4 TMIs per bull

- 10 traits (t) → milk traits 0.54 (0,36), functional traits 0.40 (0.56),calving traits 0.06 (0.08) in the conventional (organic) TMI

- **relative economic weights (REW)** derived from the routine animal evaluation index (**conventional**) and studies about breeder preferences (**organic**) (e.g. Just et al., 2018)

Spearman rank correlations between the 4 TMIs

	TMI_{uo}	TMI_{uc}	TMI_{bo}	TMI_{bc}
TMI_{uo}	1			
TMI_{uc}	0.972	1		
TMI_{bo}	0.983	0.966	1	
TMI_{bc}	0.970	0.998	0.965	1

TMI_{uo} (EBVs from univariate estimation, organic weighting)
TMI_{uc} (EBVs from univariate estimation, conventional weighting)
TMI_{bo} (EBVs from bivariate estimation, organic weighting)
TMI_{bc} (EBVs from bivariate estimation, conventional weighting)

Spearman rank correlations between the 4 TMIs

	TMI_{uo}	TMI_{uc}	TMI_{bo}	TMI_{bc}
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- No severe re-ranking at index level when GxE was considered

- Almost no re-ranking due to different weightings

- No noticeable differences between TMIs when they were based on EBVs estimated with the uni- or bivariate model (i.e. GxE was considered or not)

- The little re-ranking observed concerned bulls with high TMI values

Discussion points

- Significant GxE effects are expected when the range of environmental descriptors are large or class differences are extreme, e.g. across country evaluation (Hayes et al. 2016)

  → small differences/variation across the investigated environments in the observed sample

- To reflect real data structure: no further preselection to obtain balanced data in bivariate analyses

  → often large differences between environmental classes regarding the number of individuals

  → few data from farms in extreme environments (e.g. >800 m ASL)

Implications

- No severe GxE at trait and index level were found

- No substantial re-ranking of bulls at trait and total merit index level

- EBVs and selection decisions might not be influenced by GxE especially if sire selection is based on the total merit index

- Notable compromises regarding the efficiency of breeding schemes without considering GxE are not to expect for the environments and traits investigated

Thank you!