GxE and selection response for type traits in a local cattle breed using a reaction norm approach

Cristina Sartori[1], Francesco Tiezzi[2], Nadia Guzzo[1], Roberto Mantovani[1]

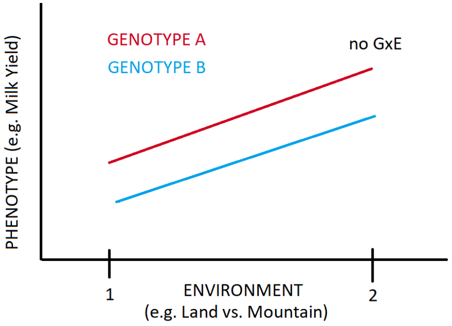
[1]DAFNAE, University of Padua;
[2]Department of Animal Science, NC State University

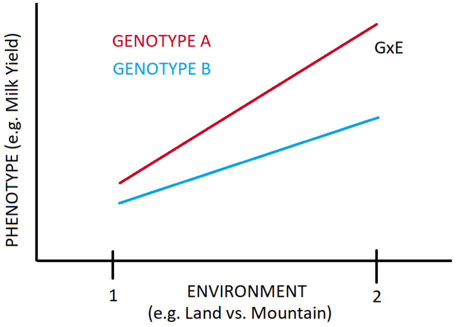
Genotype by Environment (GxE) interactions in local breeds

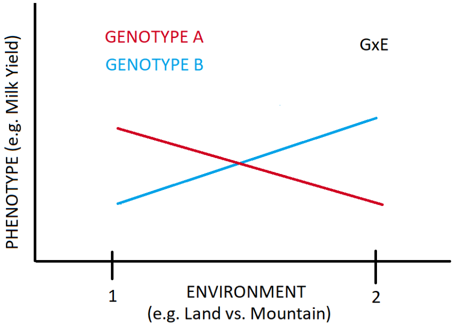
GxE → very common in livestock, may hamper genetic improvement (Mulder 2016)
→ ✓ in most of dairy cattle productive and functional traits (e.g. Hammami et al 2009)

Local breeds → some morphological traits also considered in selection for dual purpose attitude
→ adaptability to environment: variety in breeding areas, herd sizes, farming systems, feeding strategies

→ **GxE MAY BE RELEVANT** !







Aim of the study

To investigate **Genotype by Environment interaction (GxE)** and **response to selection (R)** in **type traits** in various **environmental conditions** in a local cattle breed

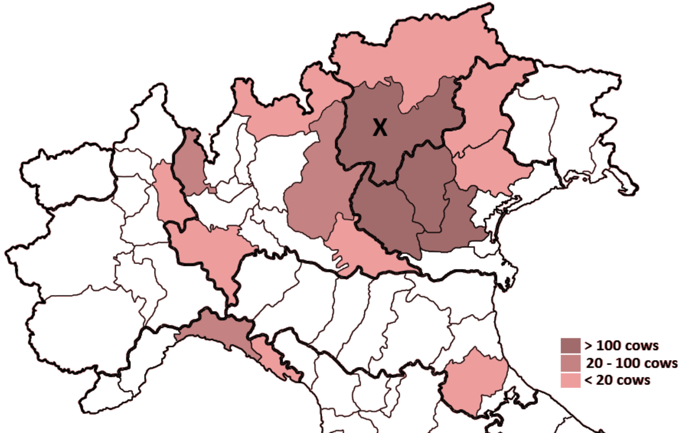
- geographical area *(plain / hill / mountain)*
- type of housing *(tie-stall / loose housing)*
- feeding system *(traditional / total mixed ration)*
- occurrence of summer pasture *(yes / no)*

Approach:
Reaction norm model
Focus on:
Rendena cattle

Study subject

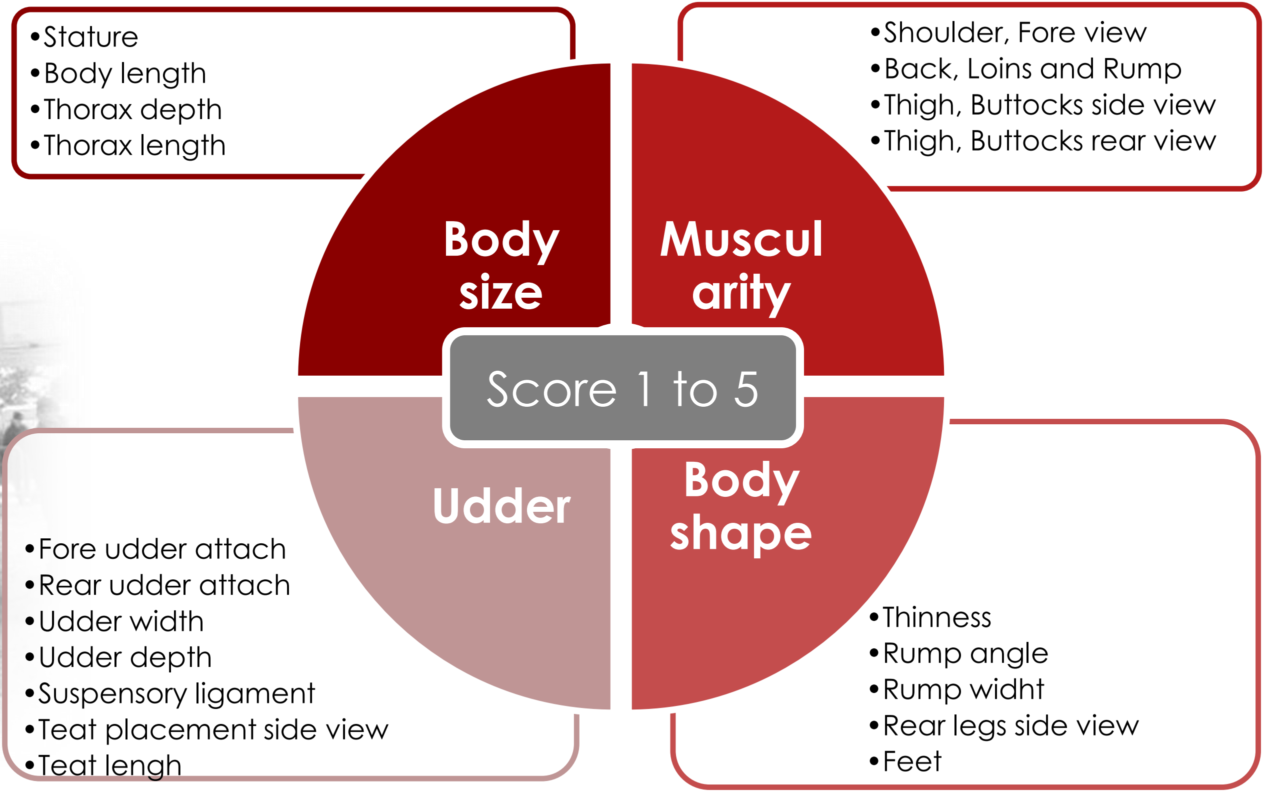
Rendena breed

- Rustic breed, North East Italian Alps & close plains
- Population: ~4000 cows in 200 herds
- Great adaptation to harsh environment & marginal areas
- Dual purpose: milk & meat



Traits: linear type traits

24 linear type traits (20 individual + 4 composite) routinely collected in primiparous cows by trained classifiers



Body size

- Stature
- Body length
- Thorax depth
- Thorax length

Muscularity

- Shoulder, Fore view
- Back, Loins and Rump
- Thigh, Buttocks side view
- Thigh, Buttocks rear view

Score 1 to 5

Udder

- Fore udder attach
- Rear udder attach
- Udder width
- Udder depth
- Suspensory ligament
- Teat placement side view
- Teat lengh

Body shape

- Thinness
- Rump angle
- Rump widht
- Rear legs side view
- Feet

Mazza et al. 2013

Traits: factor scores

3 morphological factor scores:

- Udder volume
- Udder conformation
- Muscularity
- Validated in previous studies (Mazza et al. 2015)

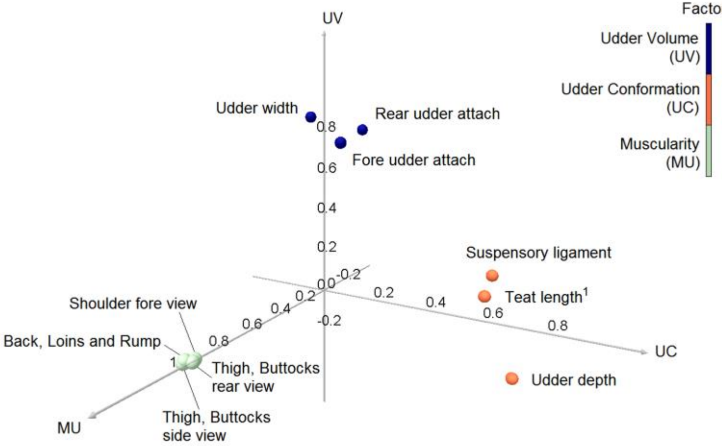
Factor equation

$$x_m = w_{m1}F_1 + w_{m2}F_2 + \dots w_{mn}F_n + w_{mn}U_n + e$$

(Russel, 2002)

Where:

x_m = linear type trait
w_{mn} = loadings of each measurement on the respective factor
F_n = common factors that underlie the measures being analysed
U_n = factors unique to each measurement
e = random measurement error for each trait



(Mazza et al. 2015; Sartori et al. 2018)

Dataset:

15 years of evaluation

8538 cows sired by 807 bulls

Genetic analysis

- **GxE** valued via **reaction norm model**, **2-steps analysis** (Silva *et al*, 2014; Tiezzi *et al*, 2017):

1. Single trait animal model:

$$\mathbf{y = HY + \mathit{fixed} + a + e \quad (M1)}$$

y : individual linear type trait or factor; **HY**: herd year, 1112 levels; ***fixed***: other fixed effects ; **a**: additive genetic; **e**: error term

2. Sire model, derived from (M1):

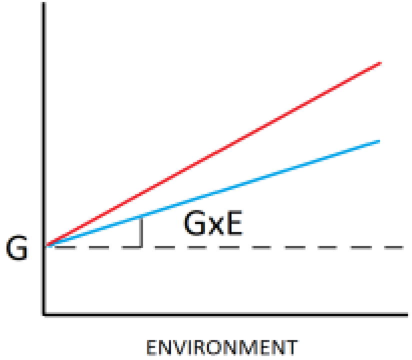
$$\mathbf{y = \mathit{fixed} + \Sigma_{k=0,1}\phi_0 + \Sigma_{k=0,1}\phi_0 s + Pe + e \quad (M2)}$$

$\Sigma_{k=0,1}\phi_0$: Solutions of HY effect from (1), as 1st order Legendre polynomials; **s**: sire effect; **Pe**: permanent environment (cow);
5 classes of residuals (levels of HY)

Program: GIBBS3F90 (Misztal et al., 2008): 120,000 iteration of gibbs sampler; burn –in: 20,000 iteration; thinning: each 100 samples
Posterior distribution analysis: POSTGIBBSF90

Genetic analysis

HY is the environmental gradient considered in the model



E

$\Sigma_{k=0,1}\phi_o$

G **(intercept)**

$\Sigma_{k=0}\phi_o s$

GxE **(slope)**

$\Sigma_{k=1}\phi_o s$

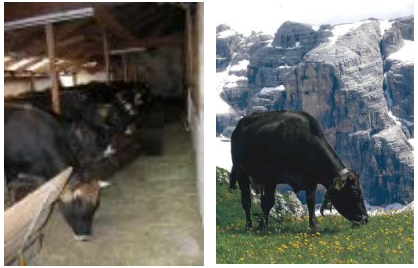
2.

$$y = \mathit{fixed} + \Sigma_{k=0,1}\phi_o + \boxed{\Sigma_{k=0,1}\phi_o s} + Pe + e \quad (M2)$$

$\Sigma_{k=0,1}\phi_o$: Solutions of HY effect from (1), as 1st order Legendre polynomials; **s**: sire effect, **Pe**: permanent environment; 5 classes of residuals (levels of HY)

Genetic analysis

- **Genetic variance in different environments** obtained for $\Sigma_{k=0,1}\phi_0 s$ as $\mathbf{Z'GZ}$ (**Z**: incidence matrix for HY solutions; **G**: genetic (co)variance matrix including **G**, **GxE**, **covGxE**)



Environments:

- **geographical area** *(plain / hill / mountain)*
- **type of housing** *(tie-stall (TS)/ loose housing (LH))*
- **feeding system** *(traditional (Trad)/ total mixed ration (TMR))*
- **occurrence of summer pasture** *(yes / no)*

(Average of the genetic variance within level of each environment)

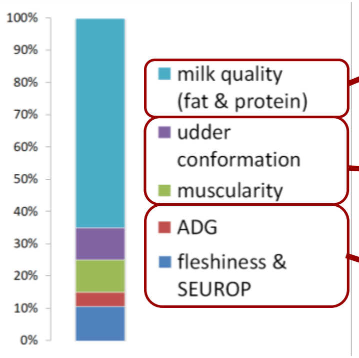
environmental grouping → **18 groups of 24 combinations** → **6 groups**

Cut-off: at least 50 year-heards

Mountain_LH_Trad_No
Mountain_TS_Trad_Yes
Plain_LH_TMR_No
Plain_TS_TMR_No
Plain_TS_Trad_No
Plain_TS_Trad_Yes

Response to selection

Current selection index

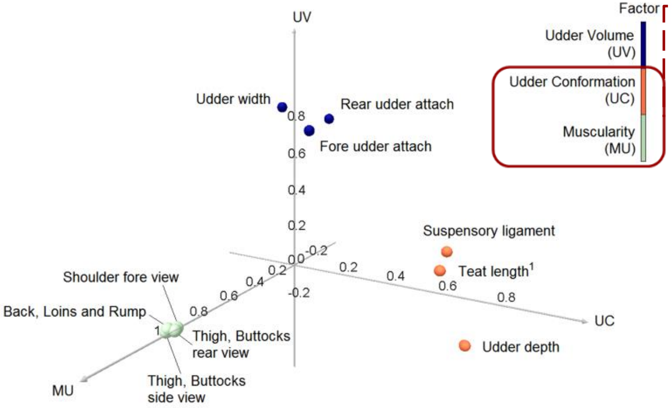


+ milk, udder volume, scs

Routinely test day records
Variances calculated using GxE
(same approach, see ASPA 2019)

Factor scores
Variances calculated using GxE

Performance test traits
Standardized env., no GxE



'Multivariate Breeder's Equation' (Lande, 1979)

$$\mathbf{R = G \cdot S \cdot P^{-1}}$$

$$\mathbf{R = (i/\sigma_i) \cdot b' \cdot P^{-1}}$$ (Kause et al., 2015)

$$\mathbf{\sigma_i = (b'Pb)^{1/2}}$$

$$\mathbf{b = P^{-1}Ga}$$

$$\mathbf{Rds_i = R/\sigma_{Pi}}$$

P= Phenotypic variance matrix
G = Genetic variance matrix
σ_i = Trait's phenotypic standard dev.
i = Selection intensity (here i = 1.755)
a = economic weight of traits

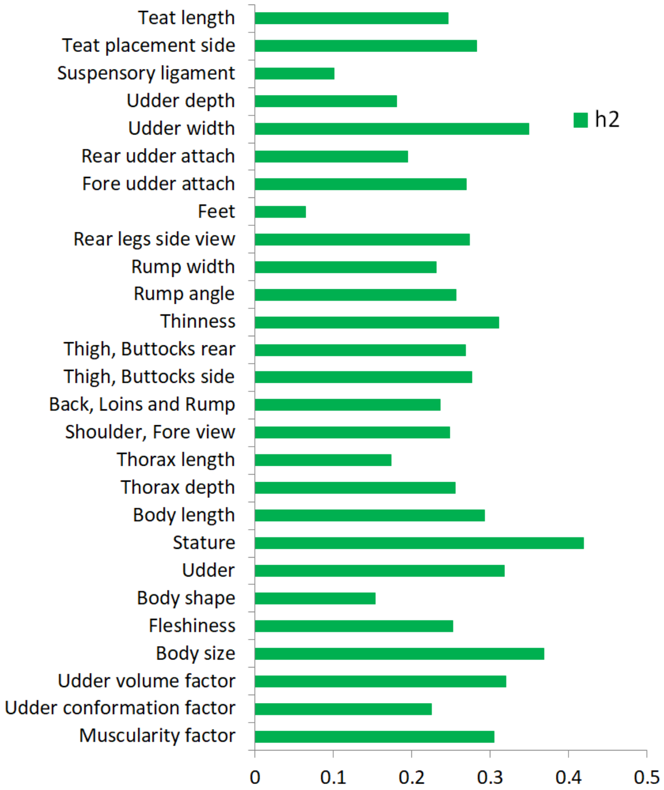
Multivariate response to selection (R) under different environments

Results!

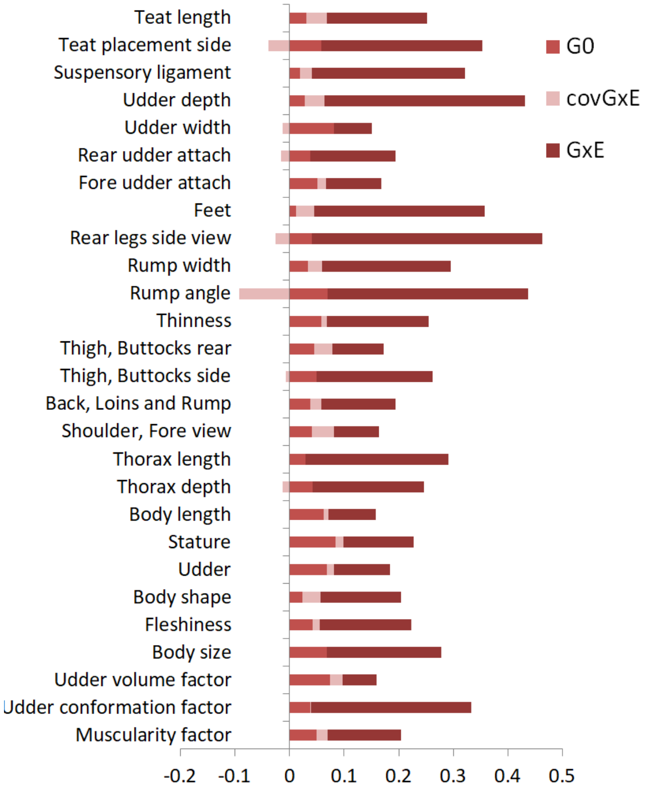
Genetic parameters

- *Heritability of traits*[1]

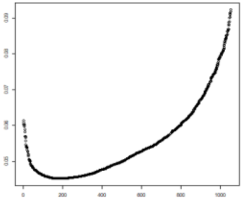
[1] $h^2 = V(a)/V(P)$; $V(a)=4*V(s)$ after calculating $V(s)$ across environments using the reaction norm

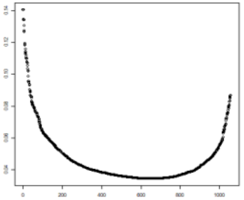


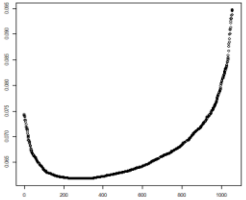
- *Proportion of **G**, **GxE** and **covGxE** on the total phenotypic variance*

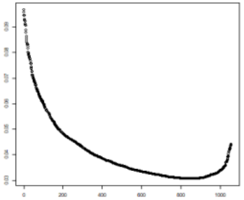


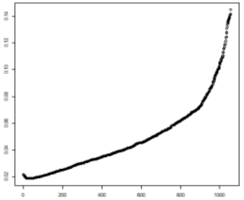
Gradient of Z’GZ variance (sire) in different environments (across herds)

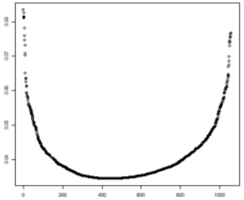

Fore udder attach

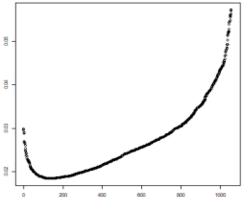

Rear legs side view

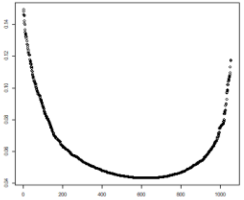

Udder

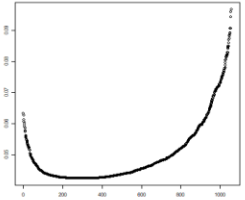

Rear udder attach

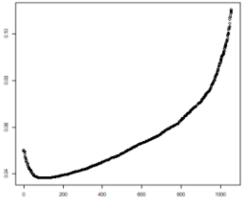

Teat length

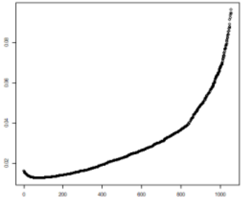

Teat placement side

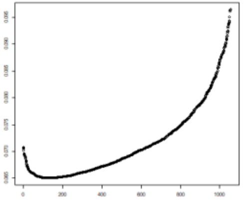

Back, Loins and Rump

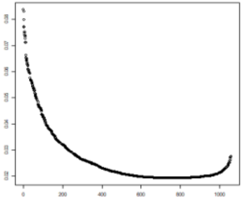

Udder conformation factor

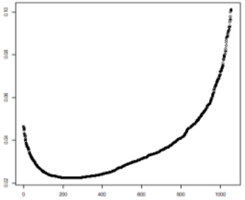

Thinness

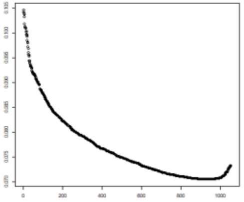

Muscularity factor

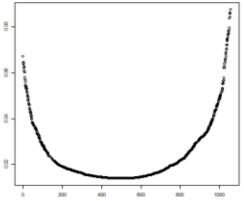

Body shape

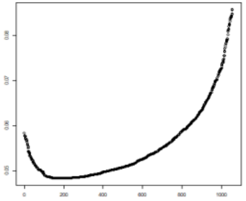

Udder volume factor

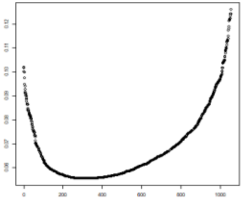

Rump angle

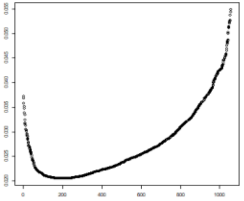

Rump width

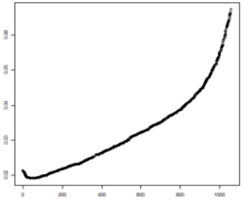

Udder width

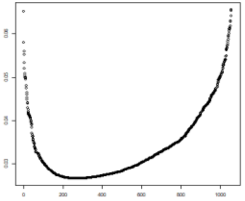

Suspensory ligament

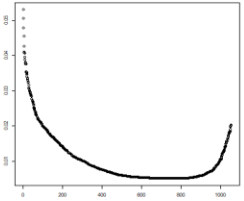

Body length

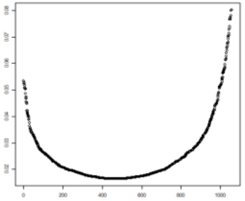

Body size

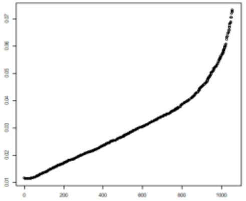

Fleshiness

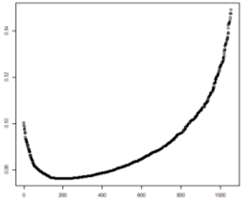

Thigh, Buttocks rear

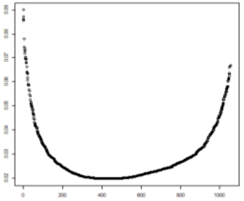

Thigh, Buttocks side

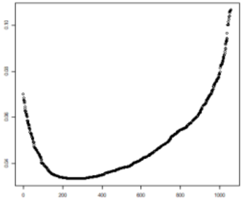

Feet


Udder depth

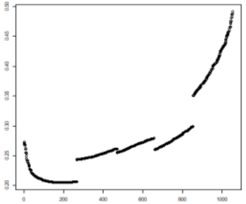

Shoulder, Fore view

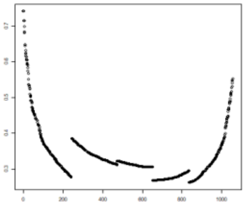

Stature

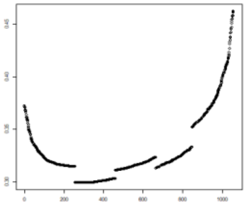

Thorax length

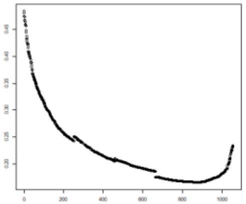

Thorax depth

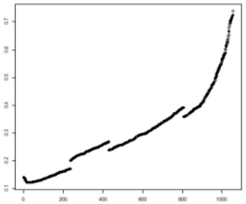
Gradient of heritability in different environments (across herds)

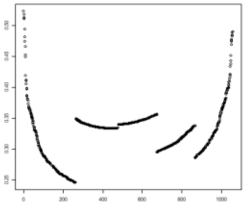

Fore udder attach

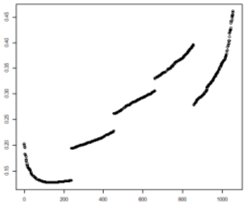

Rear legs side view

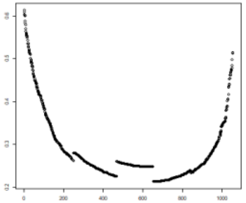

Udder

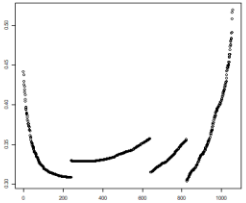

Rear udder attach

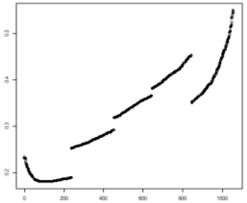

Teat length

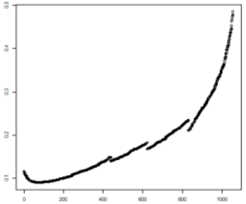

Teat placement side

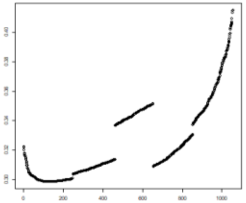

Back, Loins and Rump

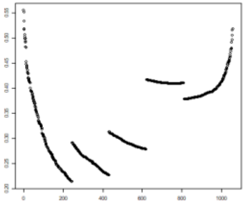

Udder conformation factor

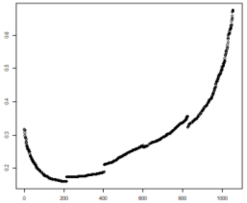

Thinness

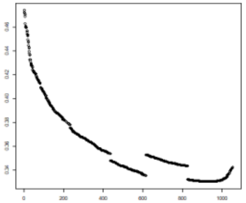

Muscularity factor

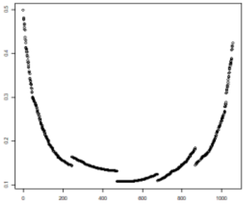

Body shape

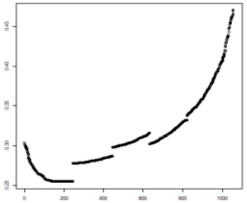

Udder volume factor

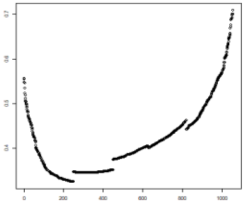

Rump angle

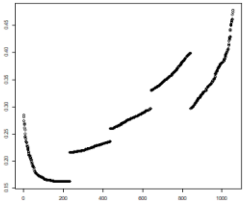

Rump width

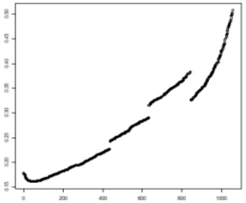

Udder width

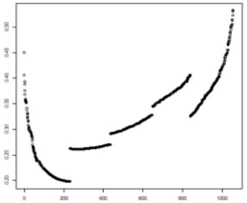

Suspensory ligament

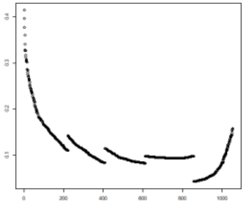

Body length

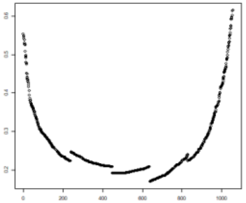

Body size

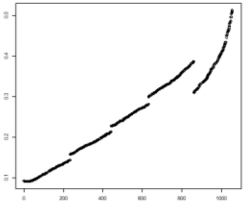

Fleshiness

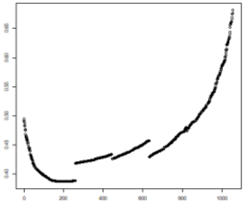

Thigh, Buttocks rear

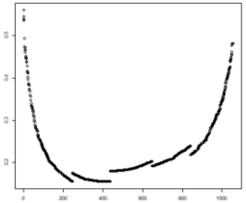

Thigh, Buttocks side

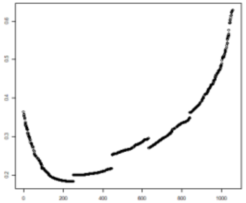

Feet


Udder depth


Shoulder, Fore view


Stature


Thorax length

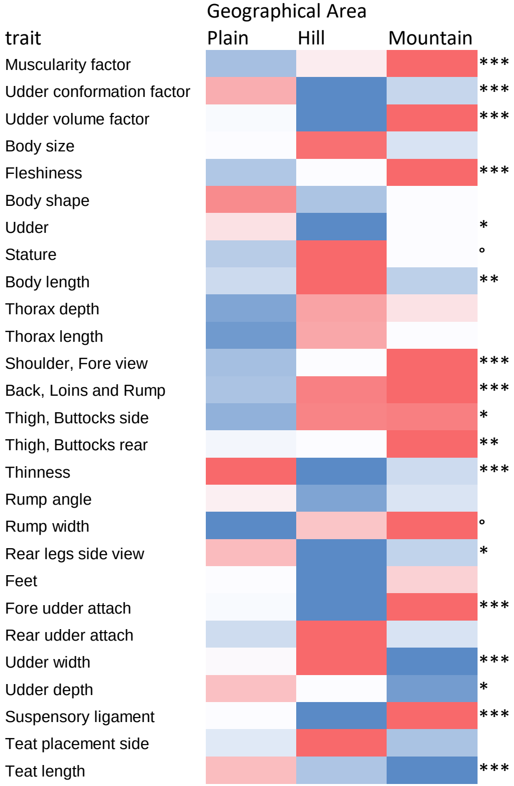

Thorax depth

5 classes of residual variance considered

Results

Variance components of traits

- *Least square means of **Z'GZ** in different environments*



trait	Plain	Hill	Mountain	
	Geographical Area			
Muscularity factor	🟦	⬜	🟥	***
Udder conformation factor	🟥	🟦	🟦	***
Udder volume factor	⬜	🟦	🟥	***
Body size	⬜	🟥	🟦	
Fleshiness	🟦	⬜	🟥	***
Body shape	🟥	🟦	⬜	
Udder	🟥	🟦	⬜	*
Stature	🟦	🟥	⬜	°
Body length	🟦	🟥	🟦	**
Thorax depth	🟦	🟥	🟥	
Thorax length	🟦	🟥	⬜	
Shoulder, Fore view	🟦	⬜	🟥	***
Back, Loins and Rump	🟦	🟥	🟥	***
Thigh, Buttocks side	🟦	🟥	🟥	*
Thigh, Buttocks rear	⬜	⬜	🟥	**
Thinness	🟥	🟦	🟦	***
Rump angle	🟥	🟦	🟦	
Rump width	🟦	🟥	🟥	°
Rear legs side view	🟥	🟦	🟦	*
Feet	⬜	🟦	🟥	
Fore udder attach	⬜	🟦	🟥	***
Rear udder attach	🟦	🟥	🟦	
Udder width	⬜	🟥	🟦	***
Udder depth	🟥	⬜	🟦	*
Suspensory ligament	⬜	🟦	🟥	***
Teat placement side	🟦	🟥	🟦	
Teat length	🟥	🟦	🟦	***

🟦 Greater

🟥 Lower

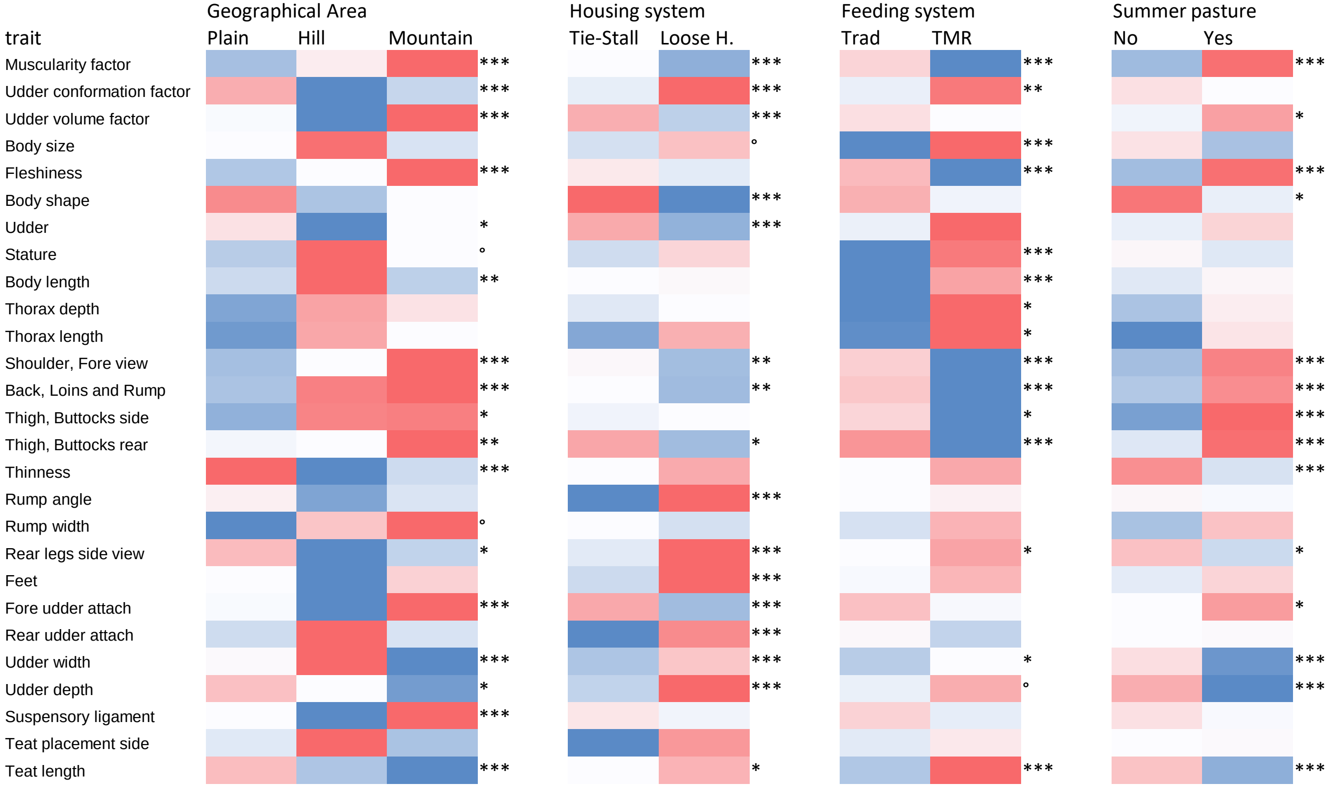
- Different amount of genetic variance in different environments, depending on traits

GLM analysis to test the difference among environments

Results

Variance components of traits

- *Least square means of **Z’GZ** in different environments*



trait	Geographical Area Plain Hill Mountain	Housing system Tie-Stall Loose H.	Feeding system Trad TMR	Summer pasture No Yes
Muscularity factor	***	***	***	***
Udder conformation factor	***	***	**	
Udder volume factor	***	***		*
Body size		°	***	
Fleshiness	***		***	***
Body shape		***		*
Udder	*	***		
Stature	°		***	
Body length	**		***	
Thorax depth			*	
Thorax length			*	
Shoulder, Fore view	***	**	***	***
Back, Loins and Rump	***	**	***	***
Thigh, Buttocks side	*		*	***
Thigh, Buttocks rear	**	*	***	***
Thinness	***			***
Rump angle		***		
Rump width	°			
Rear legs side view	*	***	*	*
Feet		***		
Fore udder attach	***	***		*
Rear udder attach		***		
Udder width	***	***	*	***
Udder depth	*	***	°	***
Suspensory ligament	***			
Teat placement side				
Teat length	***	*	***	***

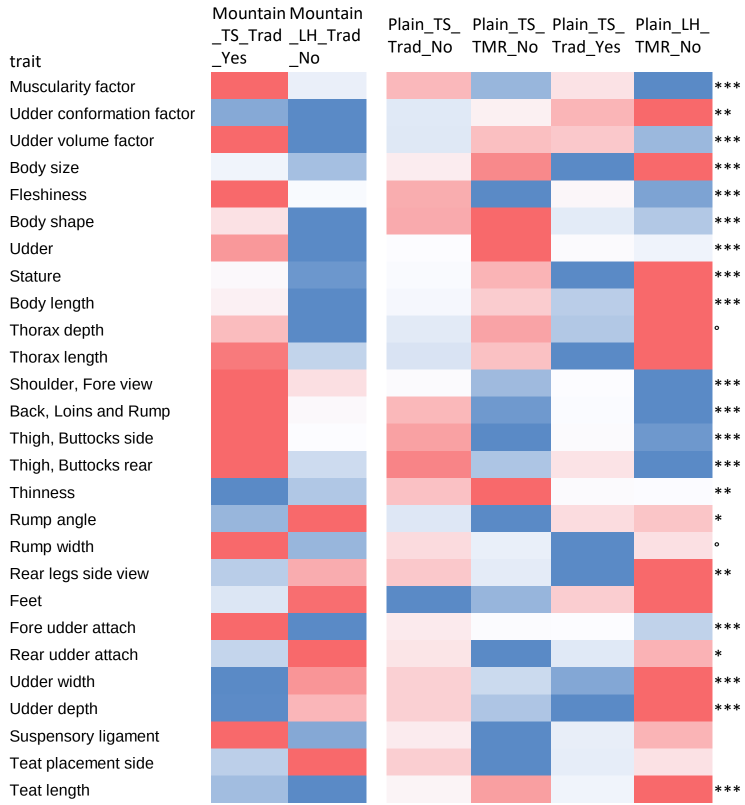
- Different amount of genetic variance in different environments, depending on traits

GLM analysis to test the difference among environments

Results

Variance components of traits

- *Least square means of **Z'GZ** in different environmental groups*



trait	
Muscularity factor	***
Udder conformation factor	**
Udder volume factor	***
Body size	***
Fleshiness	***
Body shape	***
Udder	***
Stature	***
Body length	***
Thorax depth	°
Thorax length	
Shoulder, Fore view	***
Back, Loins and Rump	***
Thigh, Buttocks side	***
Thigh, Buttocks rear	***
Thinness	**
Rump angle	*
Rump width	°
Rear legs side view	**
Feet	
Fore udder attach	***
Rear udder attach	*
Udder width	***
Udder depth	***
Suspensory ligament	
Teat placement side	
Teat length	***

TS = Tie-Stall
LH = Loose housing
Trad = Traditional
TMR = Total Mixed Ration

Greater

Lower

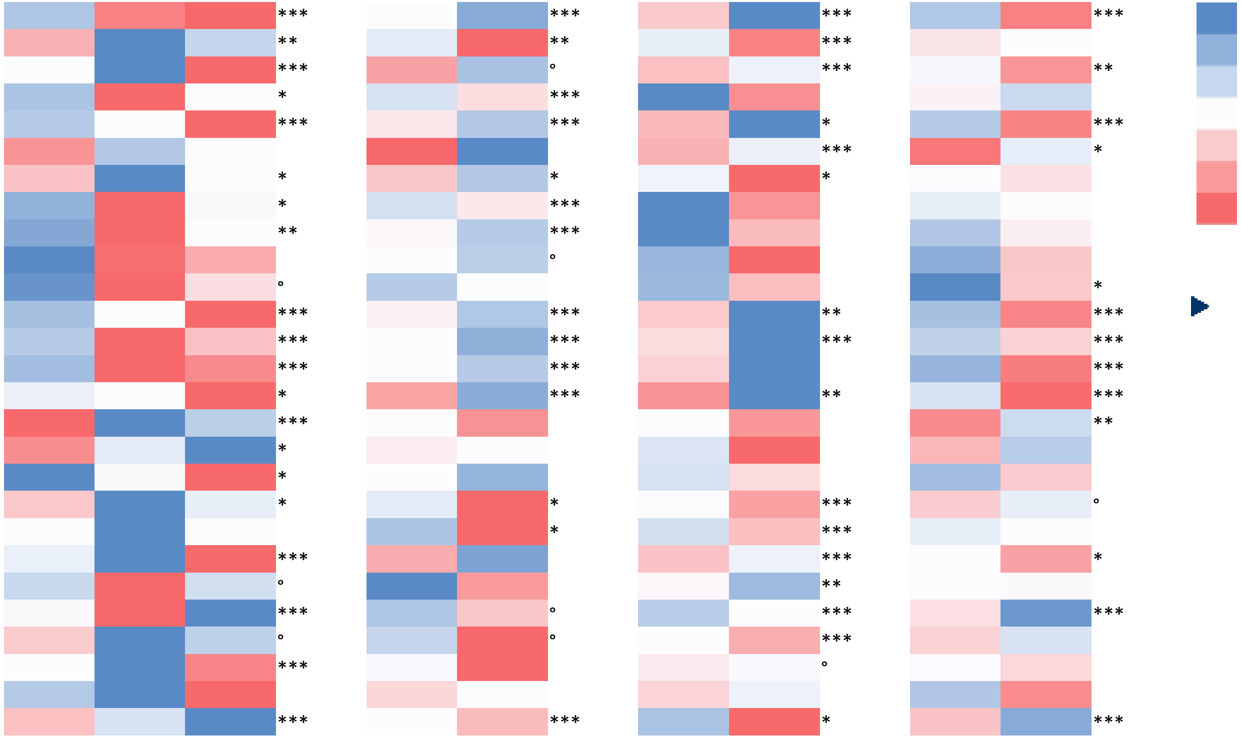
- Different amount of genetic variance in different groups of environments
- The same environment can have a different levels of G depending on the other env. conditions

- e.g., in Mountain Traditional farms G is on average greater when Loose Housing is adopted and Without Summer Pasture

GLM analysis to test the difference among environments

Variance components of traits

- *Least square means of* ***heritability*** *in different environments*



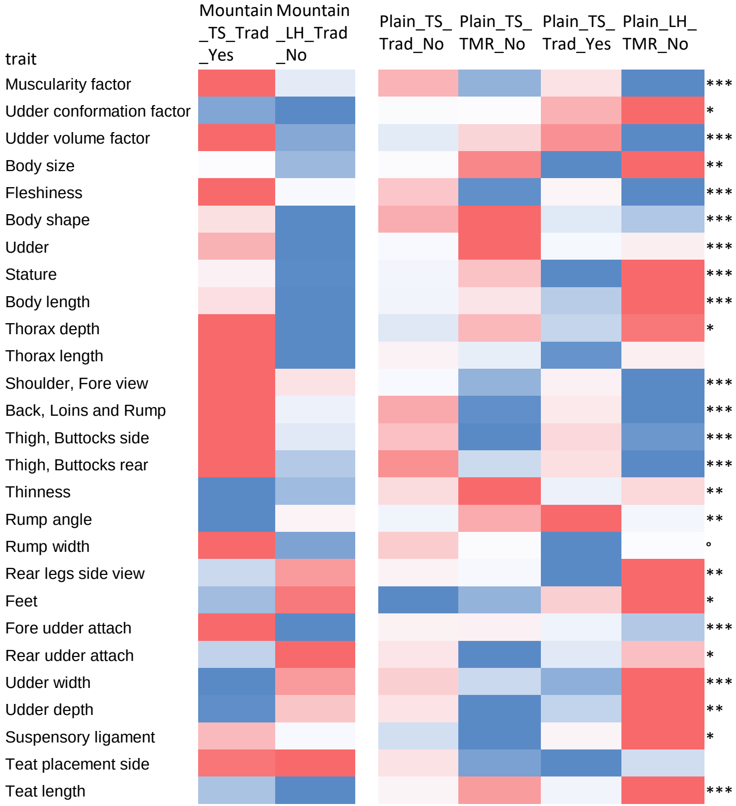
trait	Geographical Area: Plain	Hill	Mountain		Housing system: Tie-Stall	Loose H.		Feeding system: Trad	TMR		Summer pasture: No	Yes	
Muscularity factor				***			***			***			***
Udder conformation factor				**			**			***			
Udder volume factor				***			°			***			**
Body size				*			***						
Fleshiness				***			***			*			***
Body shape										***			*
Udder				*			*			*			
Stature				*			***						
Body length				**			***						
Thorax depth							°						
Thorax length				°									*
Shoulder, Fore view				***			***			**			***
Back, Loins and Rump				***			***			***			***
Thigh, Buttocks side				***			***						***
Thigh, Buttocks rear				*			***			**			***
Thinness				***									**
Rump angle				*									
Rump width				*									
Rear legs side view				*			*			***			°
Feet							*			***			
Fore udder attach				***						***			*
Rear udder attach				°						**			
Udder width				***			°			***			***
Udder depth				°			°			***			
Suspensory ligament				***						°			
Teat placement side													
Teat length				***			***			*			***

- Different levels of heritability in different environments, depending on traits

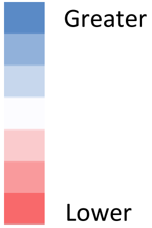
GLM analysis to test the difference among environments

Variance components of traits

- *Least square means of **heritability** in different groups*



TS = Tie-Stall
LH = Loose housing
Trad = Traditional
TMR = Total Mixed Ration

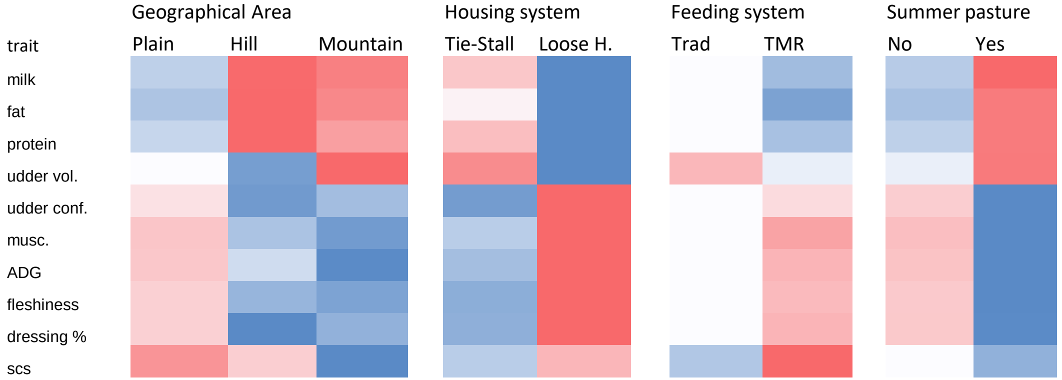


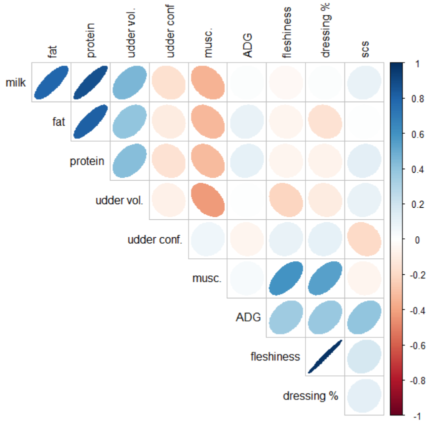
- Different levels of heritability in different environments combinations
- (e.g. look at the 4 env. combinations for Plains)

GLM analysis to test the difference among environments

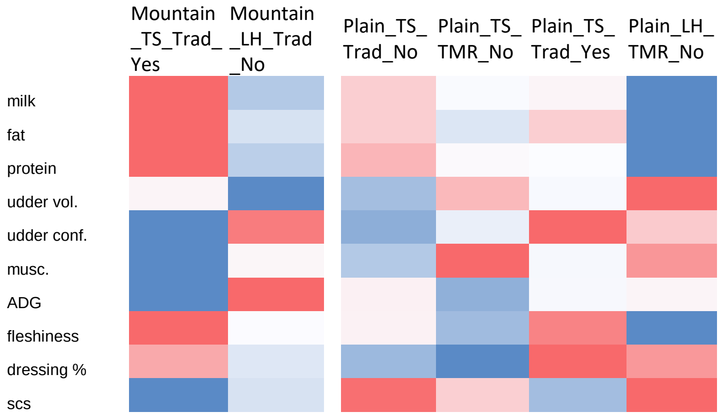
Response to selection R

- *Multivariate R for traits included in Rendena selection index*

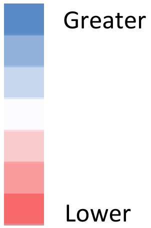




(Sartori et al. 2018)



- Opposite response to selection of traits in different environments & env. groups



- Greater response in modern & efficient environmental conditions (plain, loose housing, TMR, no pasture) in productive traits **BUT NOT** in morphological factors

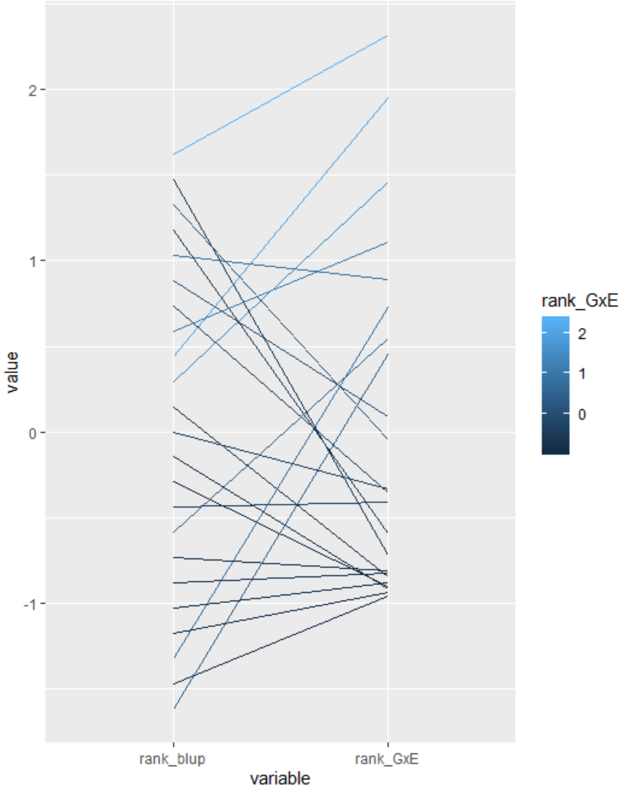
Rank correlation on bulls EBVs

- *Reaction norm model (step2) vs traditional animal model (step1)*

trait	Spearman corr
Muscularity factor	0.873
Udder conformation factor	0.880
Udder volume factor	0.895
Body size	0.860
Fleshiness	0.865
Body shape	0.890
Udder	0.911
Stature	0.852
Body length	0.876
Thorax depth	0.854
Thorax length	0.805
Shoulder, Fore view	0.852
Back, Loins and Rump	0.860
Thigh, Buttocks side	0.862
Thigh, Buttocks rear	0.890
Thinness	0.870
Rump angle	0.902
Rump width	0.833
Rear legs side view	0.869
Feet	0.702
Fore udder attach	0.890
Rear udder attach	0.888
Udder width	0.893
Udder depth	0.861
Suspensory ligament	0.849
Teat placement side	0.859
Teat length	0.869

Corr significantly different from 1

- *Reranking of the first 20 bulls for muscularity factor*



Conclusions

- **GxE term** accounted from 6% to 41% of phenotypic variance in 24 **type traits** + 3 **morphological factors** in Rendena
- **Gradient of heritability** in different environments for all traits
- **Significant differences** of Z’GZ term and h^2 **in different environments** for most of traits

- **Greater selection response for productive traits but not for type traits**
  - in the most efficient environmental contexts (breeding in plains areas, no summer pasture)
  - under improved management conditions (loose housing, total mixed ration)

favourable conditions increase individuals’ genetic response depending on traits and on their genetic correlations

- **Re-ranking** of the bulls comparing the reaction norm model vs. a traditional model

Results suggest to account for GxE for selection in local breeds

THANKS FOR YOUR ATTENTION!!!

QUESTIONS??

Thanks to: Francesco Tiezzi, Nadia Guzzo, Roberto Mantovani (coauthors), Enrico Mancin, Serena Mazza, Gioavnni Bittante and ANARE for data

A.N.A.RE.
ASSOCIAZIONE NAZIONALE ALLEVATORI BOVINI DI RAZZA RENDENA