Exploring the genetic background of parasite resistance in selected lines of black and white cattle

K. Brügemann[1], K. May[1,2], C. Scheper[1], C. Strube[2], and S. König[1]

[1]Animal Breeding and Genetics, University of Gießen, Germany
[2]Parasitology, University of Veterinary Medicine Hannover, Germany

Belfast, 30th August 2016

Pasture genetics project

- **about 30 grassland farms in North-west Germany**

- **different Holstein sire origins:**
  - Holstein sires from NZL
  - German “pasture sires”

- **pasture cows should have:**
  - limited body size
  - good fertility and fitness
  - high longevity

Relevant endoparasites in dairy cattle

- **gastrointestinal nematodes (FEC_GI)**
- **bovine lungworm (FLC_DV*)***

} problem in first-season grazing calves, but also in cows

- **liver fluke (FEC_FP)** → mainly subclinical

→ economic losses
(reduced milk production, fertility, …)

weichtiere.at

Aims of the study

- **comparisons of different lines**

German Holstein cow

x NZ sire

HF_NZ

x common sire

HF_DEU

x German pasture sire

HF_DEUp

local black + white dual-purpose cows

DSN

- **estimate genetic (co)variance parameters**

Data

- 17 farms visited twice (June/July 2015 and September/October 2015)
- 1995 faecal samples from 1139 cows
  (HF_NZ: 71 cows, HF_DEU: 636 cows, HF_DEUp: 70 cows, DSN: 362 cows)
- Faecal egg/larvae counts (McMaster, sedimentation, Baermann technique)
- TD traits: milk yield (MY), somatic cell score (SCS), fat-to-protein ratio (FPR)
- Insemination records: success (SFI) and interval from calving to 1st service (CTFS)

Prevalence	June/July	Sept./Oct.
FEC_FP	10 %	9 %
FLC_DV	1 %	3 %
FEC_GI	33 %	23 %

SAS model for line comparison

$$y = Xb + Zu + e$$

y = vector of observations for nematode traits

b = vector of fixed effects including *line* within *sampling period*, *farm*, *lactation stage* (<2, 2-11, 11-20, 20-33, >33 weeks after calving; according to Huth, 1995), and *parity* (1, 2, 3, 4, >4)

u = random *cow* effect accounting for two repeated measurements per cow

e = random *residual* effect

X, Z = incidence matrices

DMU models for genetic analyses (Madsen and Jensen, 2013)

- two components additive-genetic and permanent environment
- same as SAS model, without *line effect*

parasite model

simple AM

fertility model

simple AM

→ additional *year-season of calving* effect

→ *(CTFS)*

→ *no permanent environmental effect*

production model

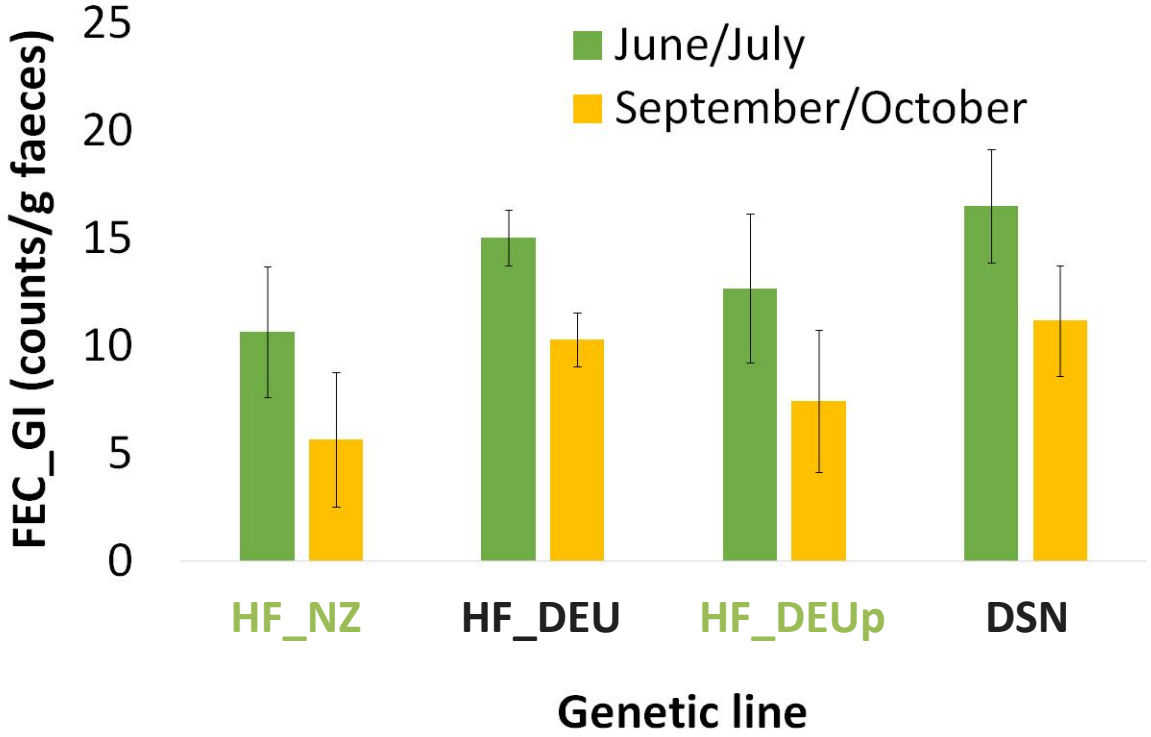
RRM

→ additional *year-season of calving* effect and *HTD*

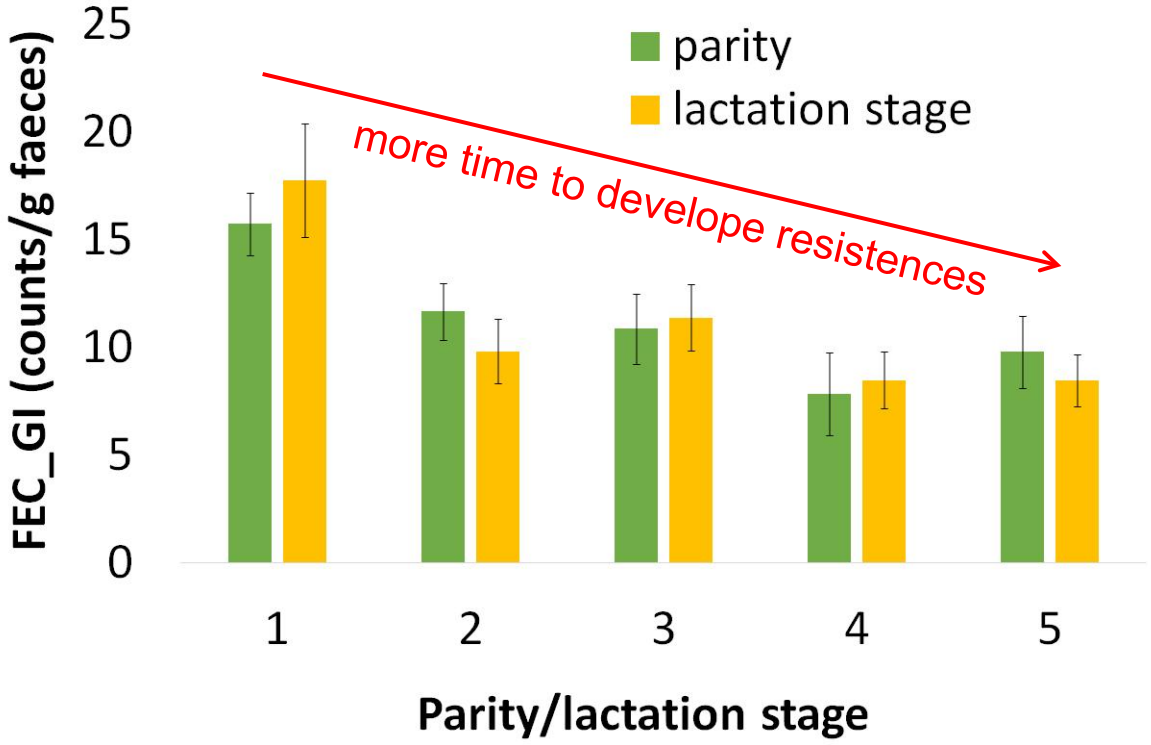
→ *Legendre pol. 2nd order* for DIM instead of *lactation stage*

→ *interval* TD - sample date (classes of 100 days)

Line comparisons: lsmeans (with SE) for FEC_GI

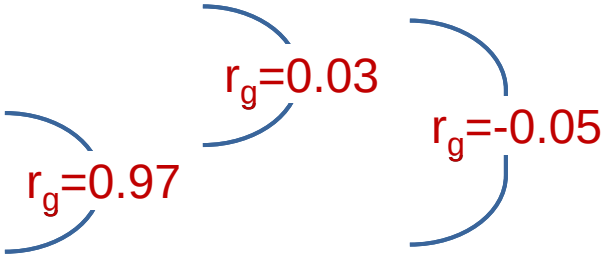


Parity and lactation stage: lsmeans (with SE) for FEC_GI



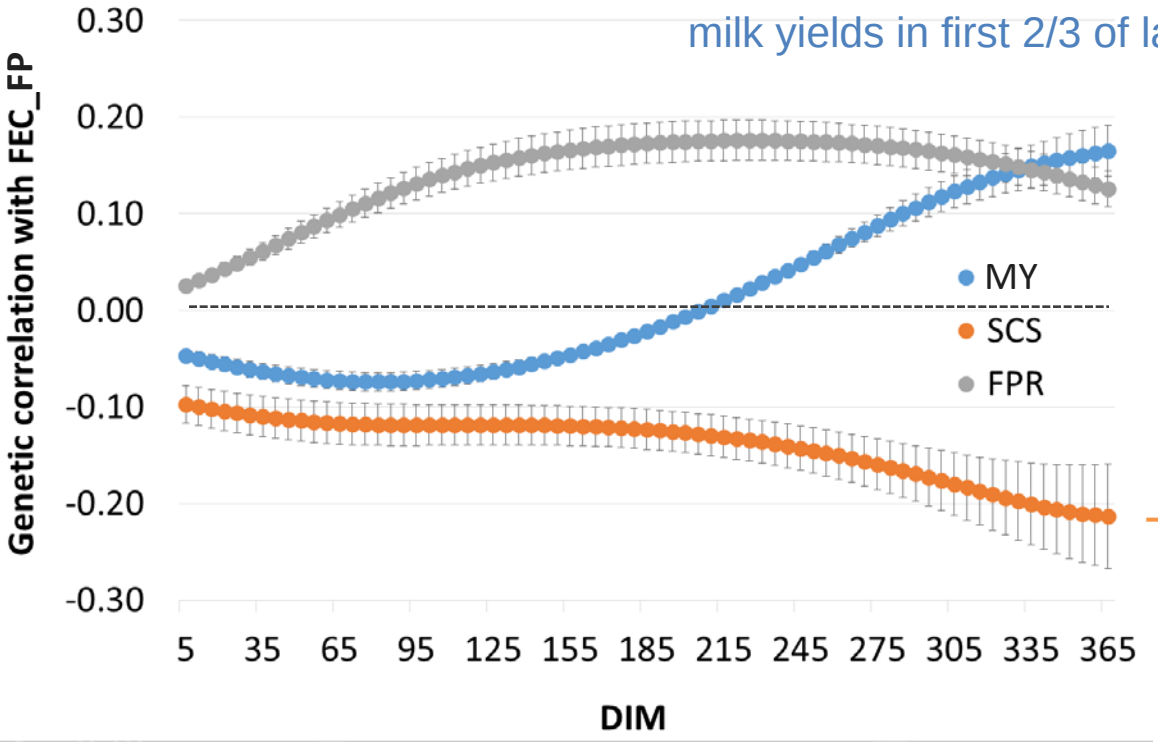
Genetic parameters for endoparasites

	original counts: $h^2 \pm SE$	log-transformed: $h^2 \pm SE$
FEC_FP	0.33 ± 0.06	0.37 ± 0.06
FLC_DV	0.05 ± 0.04	0.05 ± 0.04
FEC_GI	0.05 ± 0.04	0.04 ± 0.04



Genetic correlations for FEC_FP with production traits

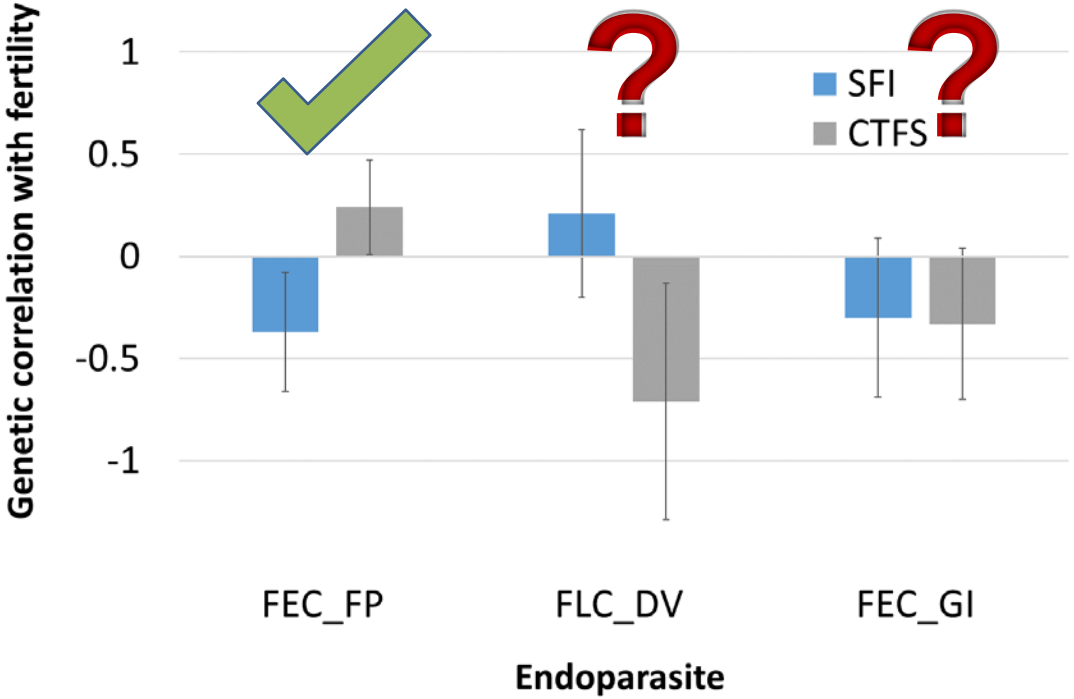
→ fewer infections enable higher milk yields in first 2/3 of lactation



→ no metabolic problems due to parasites in early lactation

→ more egg counts with lower level of somatic cells

Genetic correlations with fertility traits



Conclusions

- NZ bulls + german pasture genetics are less infected
- moderate h^2 for liver fluke (0.33) → consideration in breeding goals for pasture cows
- selection on high milk yields has no negative impact on parasite resistence
- different signs of genetic correlations → challenge for defining overall breeding goals


Thanks for your attention!

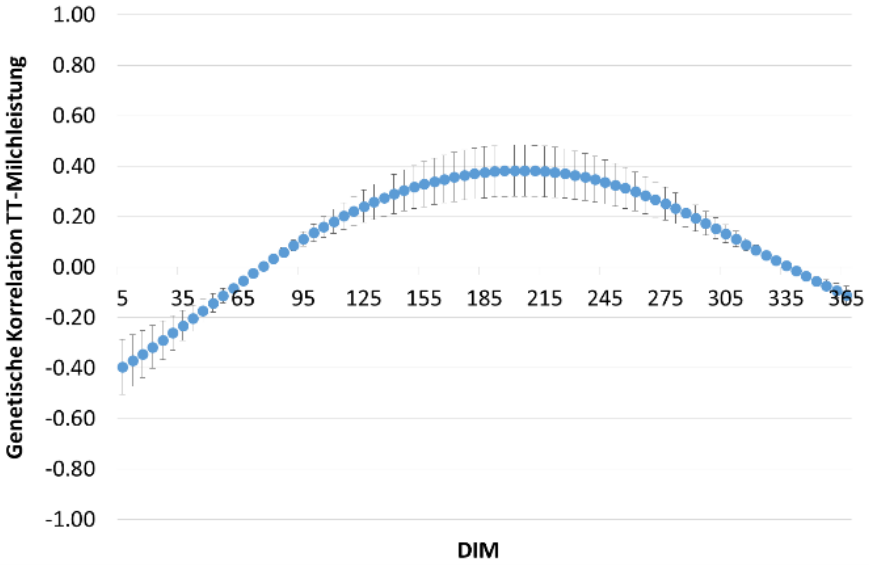
Genetic correlations – production traits (actual TD)

	MY		SCS		FPR	
FEC_FP	-0.52	± 0.20	-0.22	± 0.26	0.07	± 0.21
FLC_DV	-0.49	± 0.40	-0.25	± 0.41	0.61	± 0.38
FEC_GI	-0.05	± 0.39	0.36	± 0.39	0.25	± 0.32

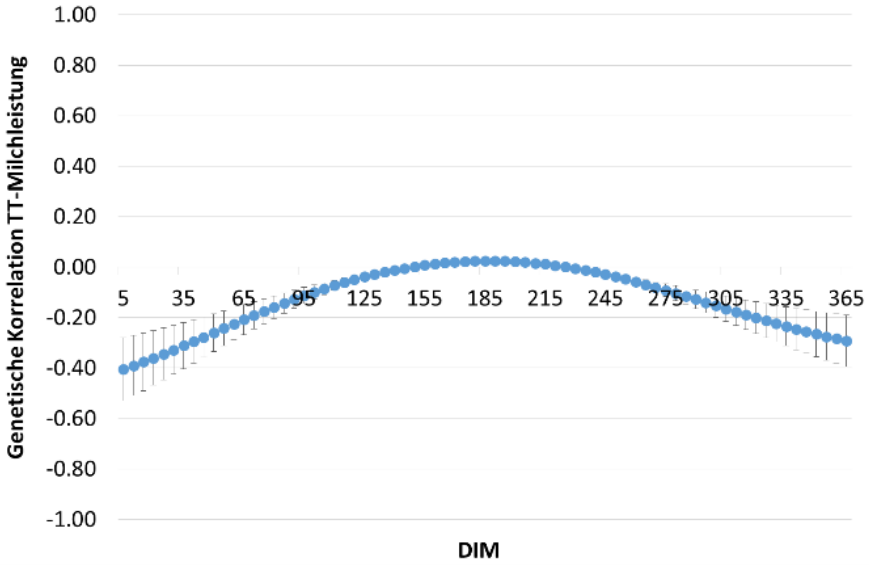
Genetic correlations – production traits (first 2 TD)

	MY		SCS		FPR	
FEC_FP	-0.21	± 0.12	-0.13	± 0.12	0.05	± 0.11
FLC_DV	-0.22	± 0.22	-0.02	± 0.26	0.65	± 0.39
FEC_GI	-0.18	± 0.20	0.15	± 0.24	0.02	± 0.23

RRM - Milk yield



FEC_GI



FLC_DV

Frequencies