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Genetic line comparisons and genetic parameters for endoparasite infections and test-day milk production traits

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ABSTRACT

Keeping dairy cows in grassland systems relies on detailed analyses of genetic resistance against endoparasite infections, including between- and within-breed genetic evaluations. The objectives of this study were (1) to compare different Black and White dairy cattle selection lines for endoparasite infections and (2) the estimation of genetic (co)variance components for endoparasite and test-day milk production traits within the Black and White cattle population. A total of 2,006 fecal samples were taken during 2 farm visits in summer and autumn 2015 from 1,166 cows kept in 17 small- and medium-scale organic and conventional German grassland farms. Fecal egg counts were determined for gastrointestinal nematodes (FEC-GIN) and flukes (FEC-FLU), and fecal larvae counts for the bovine lungworm *Dictyocaulus viviparus* (FLC-DV). The lowest values for gastrointestinal nematode infections were identified for genetic lines adopted to pasture-based production systems, especially selection lines from New Zealand. Heritabilities were low for FEC-GIN ($0.05\text{--}0.06 \pm 0.04$) and FLC-DV (0.05 ± 0.04), but moderate for FEC-FLU (0.33 ± 0.06). Almost identical heritabilities were estimated for different endoparasite trait transformations (log-transformation, square root). The genetic correlation between FEC-GIN and FLC-DV was 1.00 ± 0.60 , slightly negative between FEC-GIN and FEC-FLU (-0.10 ± 0.27), and close to zero between FLC-DV and FEC-FLU (0.03 ± 0.30). Random regression test-day models on a continuous time scale [days in milk (DIM)] were applied to estimate genetic relationships between endoparasite and longitudinal test-day production traits. Genetic correlations were negative between FEC-GIN and milk yield (MY) until DIM 85, and between FEC-FLU and MY until DIM 215. Genetic correlations between FLC-DV and MY were negative throughout lactation, indicating

improved disease resistance for high-productivity cows. Genetic relationships between FEC-GIN and FEC-FLU with milk protein content were negative for all DIM. Apart from the very early and very late lactation stage, genetic correlations between FEC-GIN and milk fat content were negative, whereas they were positive for FEC-FLU. Genetic correlations between FEC-GIN and somatic cell score were positive, indicating similar genetic mechanisms for susceptibility to udder and endoparasite infections. The moderate heritabilities for FEC-FLU suggest inclusion of FEC-FLU into overall organic dairy cattle breeding goals to achieve long-term selection response for disease resistance.

Key words: endoparasite trait, test-day production trait, genetic parameter, random regression model

INTRODUCTION

Endoparasite infections lead to measurable milk production losses in dairy cows, have a detrimental effect on product quality, and cause economic losses in affected herds (Charlier et al., 2005; Holzhauer et al., 2011). Gastrointestinal nematodes (**GIN**), as well as the bovine lungworm (*Dictyocaulus viviparus*), negatively affected growth and health of first-season grazing calves (Ploeger and Kloosterman, 1993; Schnieder et al., 1993). In addition, a significant detrimental effect on productivity of older cattle was observed (Charlier et al., 2009). Schunn et al. (2013) reported seroprevalence rates up to 31.2% for German cattle herds for *D. viviparus*. Infections with the liver fluke *Fasciola hepatica* in adult cattle were mainly subclinical (Kaplan, 2001); nevertheless, substantial economic loss due to reduced milk production has been reported even for subclinical infections (Knubben-Schweizer et al., 2010). For *F. hepatica*, Kuerpick et al. (2013) observed seroprevalence rates up to 38.4% in different German federal states.

In recent years, the percentage of German consumers demanding milk from cows kept in pasture-based production systems is increasing (BÖLW, 2016). As a consequence, and due to other aspects such as high indoor feeding costs and fluctuations of conventional

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milk payment systems, milk from organic or pasture-based production systems is considered as an attractive economic alternative. However, German Holstein cows (**GHC**), in particular, have been selected for modern and large-scale indoor systems for decades, raising questions of possible genotype \times environment interactions and their adaptation capability to harsh environments (König et al., 2005a). In this regard, in grassland systems dairy cows are exposed to higher infection pressure with endoparasites. A challenge for the farm management in organic farming systems is that medical anthelmintic treatments for adult cattle are strongly restricted. Moreover, an increasing resistance of sheep and cattle nematodes against anthelmintics has been observed (Bisset, 1994; Moll et al., 2000; McMahon et al., 2013).

Application of breeding instruments and targeted selection of cattle or of cattle breeds with enhanced resistance against specific pathogens (i.e., gastrointestinal nematodes) was suggested by Morris et al. (1997). Several studies identified phenotypic variations of host resistances among cattle breeds from non-European countries for gastrointestinal nematode infections (Suarez et al., 1990, 1995; Peña et al., 2000; Oliveira et al., 2009); however, those study designs mostly addressed comparisons between *Bos indicus* and *Bos taurus* purebreds or crossbreds under (sub)tropical conditions. Within cattle breeds, endoparasite resistance was compared among specific sire lines (Seifert, 1977; Kloosterman et al., 1978; Barlow and Piper, 1985). Within-breed selection implies availability of genetic parameters for endoparasite resistance, and ongoing genetic evaluations. Heritability estimates in cattle for different gastrointestinal nematode species were low to moderate (reviewed in Table 1), in a range from 0.04 to 0.36 (Barlow and Piper, 1985; Burrow, 2001). For the susceptibility to liver fluke, McClure et al. (2014) reported a heritability of 0.15 for dairy cattle in Ireland. Moreover, infections and reinfections with the bovine lungworm are of economic importance in dairy cattle

herds (Holzhauer et al., 2011; Dank et al., 2015), but not addressed in quantitative-genetic studies.

Genetic correlations between gastrointestinal nematode resistances or fecal egg counts with production parameters (e.g., growth, weight gain) in sheep and beef cattle populations were estimated in various previous studies (Bisset et al., 1992; Gray, 1997; Bouix et al., 1998; Eady et al., 1998; Bishop et al., 2004; Silva et al., 2012). Including milk production traits, genetic correlations were -0.21 between milk yield and fecal nematode egg count, and -0.17 between fat plus protein yield and fecal nematode egg count for Saanen goats in New Zealand (**NZL**; Morris et al., 1997). In contrast, with a focus on gastrointestinal worm egg counts in crossbred ewes, Afolayan et al. (2009) found a slightly positive but unfavorable genetic correlation (0.08) with milk yield and a moderate genetic relationship (0.42) with protein percentage.

To our knowledge, a substantial gap exists addressing (1) genetic associations between endoparasite infections with production traits in dairy and dual-purpose cattle populations and (2) selection strategies for improved endoparasite resistances. Selection and breeding of appropriate genetic lines within the Black and White dairy and dual-purpose cattle population being best adapted to grazing systems might be one possible breeding strategy. During recent decades, breeding organizations in NZL strongly focused on such alternative breeding strategies (i.e., breeding cattle lines for grazing systems by including alternative functional traits into overall breeding goals; Miglior et al., 2005). In terms of economic efficiency, productivity per hectare of grassland and reproduction performance, Holstein Friesian (**HF**) cows from NZL were superior over other cattle breeds or lines in pasture-based production systems in Ireland and Switzerland (McCarthy et al., 2007; Piccand et al., 2013).

The objectives of the present study were 2-fold. First, we used a selection line comparison for endoparasite infections including different Black and White selection

Table 1. Heritability estimates from literature for fecal egg counts of gastrointestinal nematodes (GIN) in cattle

Reference	Country	Breed	h^2
Barlow and Piper, 1985	Australia	Hereford	0.04–0.29
Burrow, 2001	Australia	Australian Belmont Red	0.36
Coppieters et al., 2009	The Netherlands	Dutch Holstein Friesian	0.07–0.21
Gasbarre et al., 1990	United States	Angus	0.08–0.27
Kloosterman et al., 1992	Germany	Dutch Holstein Friesian (pure), Dutch Friesian \times British Friesian, Dutch Friesian \times American Friesian	0.14–0.78
Leighton et al., 1989	United States	Angus	0.29
Mackinnon et al., 1991	Australia	Zebu-cross	0.12–0.25
Morris et al., 2003	New Zealand	Angus	0.32
Morris and Amyes, 2012	New Zealand	Angus and Hereford	0.11–0.28
Passafaro et al., 2015	Brazil	Nellore	0.06–0.33
Zinsstag et al., 2000	Africa	West African N'Dama	0.18

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