Little genetic variability in resilience among cattle exists for a range of performance traits across herds in Ireland differing in *Fasciola hepatica* prevalence[1]

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ABSTRACT: It is anticipated that in the future, livestock will be exposed to a greater risk of infection from parasitic diseases. Therefore, future breeding strategies for livestock, which are generally long-term strategies for change, should target animals adaptable to environments with a high parasitic load. Covariance components were estimated in the present study for a selection of dairy and beef performance traits over herd-years differing in *Fasciola hepatica* load using random regression sire models. Herd-year prevalence of *F. hepatica* was determined by using *F. hepatica*-damaged liver phenotypes which were recorded in abattoirs nationally. The data analyzed consisted up to 83,821 lactation records from dairy cows for a range of milk production and fertility traits, as well as 105,054 young animals with carcass-related information obtained at slaughter. Reaction norms for individual sires were derived from the random regression coefficients. The heritability and additive genetic standard deviations for all traits analyzed remained relatively constant as herd-year *F. hepatica* prevalence gradient increased up to a prevalence level of 0.7; although there was a large increase in heritability and additive genetic standard deviation for milk and fertility traits in the observed *F. hepatica* prevalence levels >0.7, only 5% of the data existed in herd-year prevalence levels >0.7. Very little rescaling, therefore, exists across differing herd-year *F. hepatica* prevalence levels. Within-trait genetic correlations among the performance traits across different herd-year *F. hepatica* prevalence levels were less than unity for all traits. Nevertheless, within-trait genetic correlations for milk production and carcass traits were all >0.8 for *F. hepatica* prevalence levels between 0.2 and 0.8. The lowest estimate of within-trait genetic correlations for the different fertility traits ranged from −0.03 (SE = 1.09) in age of first calving to 0.54 (SE = 0.22) for calving to first service interval. Therefore, there was reranking of sires for fertility traits across different *F. hepatica* prevalence levels. In conclusion, there was little or no genetic variability in sensitivity to *F. hepatica* prevalence levels among cattle for milk production and carcass traits. But, some genetic variability in sensitivity among dairy cows did exist for fertility traits measured across herds differing in *F. hepatica* prevalence.

Key words: carcass, fertility, genotype-by-environment, liver fluke, milk, reaction norm

INTRODUCTION

Interest is intensifying in breeding strategies for animal robustness because of the expected greater frequency and intensity of environmental perturbations in the future (Friggens et al.,

2017). Classical breeding approaches to achieve animal robustness are through crossbreeding complemented with the inclusion of functional traits in multiple-trait breeding objectives (Amer, 2011); these strategies have improved animal fitness and survival in dairy cattle (Berry et al., 2016). However, these strategies do not necessarily consider environmental variability and its impact on the expression of genetic potential. The use of reaction norms across a given (environmental) gradient can be used to depict animal robustness or resilience (Mulder, 2016). A reaction norm, first designated in German as "Reaktionsnorm" (Woltereck, 1909), describes the phenotypic expression of a genotype across a range of environments. A covariance function fitted across a gradient of an environmental condition (e.g., average diet nutrient density) provides estimates of genetic merit for an individual at each point on the continuum; such covariance functions can be readily estimated using random regression methodology (Kolmodin et al., 2002). The estimated animal-specific random regression coefficients can subsequently be used to derive the reaction norm of that individual. In fact, Nguyen et al. (2016) proposed using such random regression methodology to generate estimates of the sensitivity of individual dairy cows to heat tolerance in Australia.

The objective of the present study was to quantify the inter-animal genetic variability in the slope of reaction norms for a selection of performance traits in cattle across environments differing in *Fasciola hepatica* load; this was undertaken in an attempt to quantify the extent of genetic variation in resilience to *F. hepatica*. Results will be useful to determine if breeding programs could be feasibly modified to select for more resilient animals.

MATERIALS AND METHODS

The data used in the present study originated from the Irish national database managed by the Irish Cattle Breeding Federation. Data available from the national database included individual animal pedigree and breed composition, all inter-herd animal movements, 305-d milk production records (dairy cows only), and reproductive records (i.e., service dates, pregnancy diagnoses, and calving dates). Carcass data (i.e., carcass weight, conformation, and fat score) and *F. hepatica*-liver damage data were also available for slaughtered animals.

Data

Milk production. Individual lactation records for 305-d milk yield (kg), fat yield (kg), protein yield (kg), fat content (%), protein content (%), fat-to-protein ratio, and somatic cell count (**SCC**) from 2,194,761 lactations on 1,067,397 dairy cows, calving between the years of 2012 to 2015, inclusive, were available. Somatic cell count was normalized to somatic cell score by taking the natural logarithm of SCC/1,000. Lactation records were discarded if the 305-d milk yield, fat yield, protein yield or SCC was >4 SDs from the respective parity mean.

Fertility data. Data were available, between the years of 2012 and 2016, inclusive, on 3,778,592 artificial and 317,270 natural service records as well as 5,265,360 calving records from 2,447,324 dairy cows. Where the same cow had 2 service records within 5 d of each other, the earlier of the 2 service records was discarded. Service records from herd-years where >80% of cows were recorded as having only 1 service were not considered further, as these herds were likely to have only recorded the last service. Fertility phenotypes were derived similar to outlined in detail by Berry et al. (2013) for dairy cows. Age at first calving was defined as the age, in days, when the heifer calved for the first time; only records between 660 and 1,400 d of age were retained. Calving to first service interval (**CFS**) was defined as the number of days from calving to first service; CFS records were discarded if <20 or >250 d. Calving interval (**CIV**) was defined as the number of days between consecutive calving events. Only CIV records >300 d were retained; CIV records >600 d were discarded unless the CFS record for that lactation was <150 d in which case only CIV records >800 d were discarded (Berry et al., 2013). The binary trait of survival was defined as whether or not a cow successfully reached the next lactation. A cow was deemed to have survived lactation *n* if she had a subsequent calving date for lactation *n* + 1 within 600 d of the cow's calving date for lactation *n*. A cow that did not have a calving date for lactation *n* + 1 and was either slaughtered or there was >200 d between her last milk recording date and the last milk recording date of the herd the cow was residing in, was deemed to not to have survived lactation *n*. Survival was only defined for lactations ≤ 5.

Carcass data. Slaughter information consisting of carcass weight (kg), conformation score (1 to 15), fat score (1 to 15) were available from 3,971,427 young animals (i.e., males and females <1,096 d of age that were not a registered sire or had no recorded calving event) between the years of 2012 and 2015. As described by Pabiou et al. (2011), carcass weight was measured, on average, 2 h after slaughter following the removal of the head, legs,

thoracic and abdominal organs, and internal fats and hide. Using video image analysis, carcass conformation and fat scores were graded under the European Union beef carcass classification system (EUROP). Carcass conformation and fat score were both scored on a scale of 1 to 15 as described by Englishby et al. (2016). Records from animals with a carcass weight <180 and >550 kg were not considered further.

F. hepatica Environment

For all cattle slaughtered in Ireland, liver damage caused by *F. hepatica* is diagnosed by veterinarians on the kill-line as either "live *F. hepatica* observed in the liver at the time of slaughter" or the "liver exhibits *F. hepatica* damage without the identifiable presence of live *F. hepatica*" (Twomey et al., 2016). Records of livers deemed unaffected by *F. hepatica* are not recorded in the Irish Cattle Breeding Federation database. Liver damage records were available from 7 abattoirs on 835 dates between the years of 2012 and 2015, inclusive; animals slaughtered in those abattoirs on those dates without any record of liver damage were therefore assumed to have no *F. hepatica*-damaged liver (Twomey et al., 2016). The *F. hepatica*-damaged liver data set contained 121,287 dairy cows (i.e., females that had at least 1 recorded calving event) and 755,294 young animals (i.e., males and females <1,096 d of age that were not a registered sire or had no recorded caving event).

Using the 2 recorded *F. hepatica*-damaged liver phenotypes, 2 separate herd-level environmental phenotypes were derived to reflect the gradient of *F. hepatica* exposure: 1) the herd-year prevalence of live *F. hepatica* in cows, and 2) the herd-year prevalence of *F. hepatica* in young animals. In both instances, only herd-years with ≥12 animals with a *F. hepatica*-damaged liver phenotype (i.e., absent or present) were retained. Following these edits, 1,877 and 12,730 herd-years of cows and young animals remained, respectively. The prevalence of live *F. hepatica* in cows was defined as the number of cows that had a recorded live *F. hepatica* as a proportion of the total number of cows that had a *F. hepatica*-damaged liver phenotype (i.e., absent or present) in that herd in that year. The herd-year prevalence of *F. hepatica* in young animals was defined as the number of young animals that had recorded positive for liver damage caused by *F. hepatica* diagnosed (i.e., either live *F. hepatica* present in the liver or had no live *F. hepatica* present but had damage caused by *F. hepatica*) as a proportion of the total number of young animals that had

recorded positive or negative for *F. hepatica*-damaged liver (i.e., absent or present) in that herd in that year.

Data Edits

Animals that had an inter-herd movement after 90 d of age were not considered further. Only individual animal data from herd-years that had an associated herd-year *F. hepatica* prevalence, as described above, were retained. Animals with an unknown sire were subsequently discarded. General heterosis and recombination loss coefficients for each animal were calculated as $1 - \sum_{i=1}^{n} sire_i \cdot dam_i$ and $1 - \sum_{i=1}^{n} \frac{sire_i^2 + dam_i^2}{2}$, respectively, where $sire_i$ and dam_i are the proportion of breed i in the sire and dam, respectively.

Cow parities >10 were discarded and were categorized as 1, 2, 3, 4, 5, 6, and 7+. Cow age at calving relative to the median age at calving of the respective parity was calculated. For carcass traits, young cattle were partitioned into an age group at slaughter of either between 366 and 730 d, or between 731 and 1,096 d (Twomey et al., 2016); young animals were discarded if they were not assigned either age group. Animal age at slaughter relative to the median age of the age group was also calculated for young cattle.

Contemporary groups for cows were defined as herd-year-season of calving. For young animals, contemporary groups were defined as herd-year-season of birth. All herd-year-season contemporary groups were generated for each trait separately using an algorithm described in detail by Berry and Evans (2014). The algorithm grouped cows, within a given herd, that calved around the same period of the year. For the young cattle, the algorithm clustered animals together that were born in the same herd around the same period of the year. Contemporary groups with <5 animals were discarded from all data sets. Only contemporary groups with >1 sire present in the contemporary group were retained for all data sets in the study. For the final analysis, 82,844 and 83,821 lactation records remained in the milk production data set and fertility data set, respectively, while data from 105,054 young animal records remained in the carcass data set (Fig. 1).

Statistical Analyses

Components of covariances for milk production traits, fertility traits, and carcass traits were
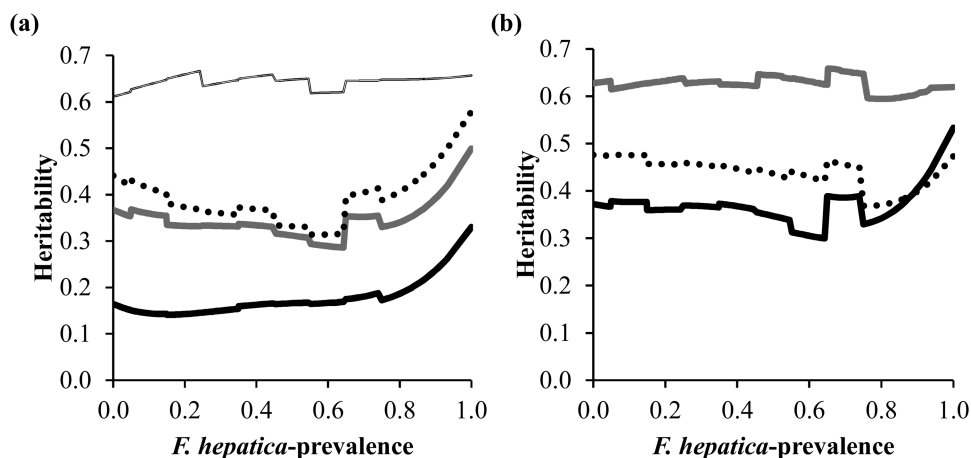
Figure 1. Heritability estimates for 305-d (a) milk yield (dotted line; SE ranged from 0.024 to 0.105), protein yield (solid gray line; SE ranged from 0.022 to 0.102), protein percentage (thin solid black line; SE ranged from 0.029 to 0.086), and somatic cell score (solid black line; SE ranged from 0.014 to 0.101) and (b) fat yield (solid black line; SE ranged from 0.023 to 0.115), fat percentage (solid gray line; SE ranged from 0.028 to 0.098), fat-to-protein ratio (dotted line; SE ranged from 0.025 to 0.104) across herd-year prevalence of live *F. hepatica*.

quantified using random regression sire models fitted across herd-year *F. hepatica* prevalence levels in ASReml (Gilmour et al., 2009). To facilitate the estimation of residual variances for each trait across environments, the herd-year prevalence of live *F. hepatica* in cows was divided into 9 groups as <0.05, ≥0.05 to <0.15, … ≥0.65 to <0.75, and ≥0.75. Since <2% of herd-years had a herd-year prevalence of *F. hepatica* in young animals ≥0.75, the herd-year prevalence of *F. hepatica* in young animals was instead divided into 8 groups as <0.05, ≥0.05 to <0.15, … ≥0.55 to <0.65, and ≥0.65. Residual variances were assumed homogenous within each group but heterogeneous between groups.

The random regression sire models fitted were as follows:

$$V = CG + Het + Rec + age\_calve + parity$$
$$+ \sum_{i=1}^{n} \beta_i P^i fluke + \sum_{i=1}^{n} Sire_i P^i fluke + PE + e$$

$$X = CG + Het + Rec + sex + factory\_date$$
$$+ age\_slaughter + age\_group$$
$$+ \sum_{i=1}^{n} \beta_i P^i fluke + \sum_{i=1}^{n} Sire_i P^i fluke + e$$

where V is the observed milk or fertility trait; X is the observed carcass weight, fat score, and conformation score; CG is the fixed effect of contemporary group; Het is the fixed effect of a general heterosis coefficient (0, >0 to <0.1, ≥0.1 to <0.2 … ≥0.9 to <1, 1); Rec is the fixed effect of a general recombination loss coefficient (0, >0 to <0.05, ≥0.05 to <0.1, … ≥0.45 to <0.5, 0.50, >0.50); age_calve is the fixed effect of age at calving in months relative to the median age of the parity; $parity$ is the fixed effect of parity; sex is the fixed effect of gender; $factory\_date$ is the fixed effect of the date and abattoir of the slaughtered animal; age_group is the fixed effect of age group at slaughter; $age\_slaughter$ is the fixed effect of age at slaughter in months relative to the median age of the age group; β is fixed regression coefficient on *F. hepatica* prevalence; $sire$ is the random regression coefficient on *F. hepatica* prevalence associated with the additive genetic effect of sire; P_n is nth order Legendre polynomial of *F. hepatica* prevalence (including the intercept); $fluke$ is the *F. hepatica* prevalence; PE is the random permanent environmental effect; e is the random residual effect. The pedigree of each animal was traced back to the founder population which was allocated to 11 genetic groups based on breed.

To determine the most parsimonious fixed effect Legendre polynomial regression, a visual comparison of the resulting profile for the different polynomial orders was undertaken. The quadratic fixed effect polynomial was the most appropriate for all traits considered. The most parsimonious order of the random Legendre polynomial regression on sire was determined from the Akaike information criterion and the eigenvalues of the estimated covariance matrix.

The genetic covariance function was estimated as

$$\delta^2 = \Phi' K \Phi$$

where δ^2 is the covariance matrix for *F. hepatica* prevalence, Φ is the matrix of Legendre polynomial *F. hepatica* prevalence regression coefficients, and K is the estimated variance–covariance matrix of the random polynomial coefficients which was

multiplied by 4 to transform from a sire variance to a genetic variance. Using the generated breeding values for all performance traits, reaction norms were also estimated for a random selection of sires that differed in there resilience to *F. hepatica* that had >30 progeny from >5 contemporary groups.

RESULTS

The frequency distribution of the number of records in the different herd-year prevalence levels of *F. hepatica* is in Supplementary Fig. S1. The mean herd-year prevalence level of live *F. hepatica* in dairy cows was 23% to 25% depending on the trait analyzed; 5% of herd-years had a herd-year prevalence >70%. Average herd-year prevalence of *F. hepatica*-damaged livers of young animals was 16%; 3% of herd-years had a herd-year prevalence >70%. The Akaike information criterion improved with each order in the random sire polynomial regression up to at least the third order (i.e., intercept term, linear term, and a quadratic term). However, the fourth eigenvalue of the cubic random regression for each trait only accounted for <1% of the genetic variation. Therefore, a quadratic Legendre polynomial random regression model was chosen as the most parsimonious model for all traits in the present study. Estimated residual variances for all traits were relatively similar across the different strata of herd-year prevalence of *F. hepatica* (Supplementary Figs. S2 and S3). The genetic variance explained by the first eigenvalue of the fitted random regression models ranged from 89% (fat yield) to 99% (protein percentage) for the milk traits, from 65% (age of first calving) to 96% (calving to first service) for the fertility traits, and 89% (carcass fat) to 97% (carcass weight) for the carcass traits.

Resilience in Milk Production

Using a random regression model with just an intercept term on sire, the heritability estimates for the milk yield traits and the ratio traits ranged from 0.27 (protein yield) to 0.30 (milk yield) and from 0.34 (fat-to-protein ratio) to 0.43 (fat percentage), respectively; the heritability estimate of somatic cell score was 0.13 (Supplementary Table S1). Using a quadratic Legendre polynomial random regression model, heritability estimates for the milk production traits, including somatic cell, across *F. hepatica* prevalence levels varied between 0.0 and 0.7 were largely similar to the heritability estimates using the intercept model. However, there was a small increase in heritability estimates for all milk traits once herd-year *F. hepatica* prevalence levels exceeded 0.7 (Fig. 1). The additive genetic standard deviation within each of the milk production yield traits was similar across the *F. hepatica* prevalence levels between 0.0 and 0.7 (milk yield ranged from 503 to 564 kg; Fig. 2). However, the additive genetic standard deviation for the yield traits notably increased once *F. hepatica* prevalence levels exceeded 0.7 (increased up to 650 kg for milk yield; Fig. 2). Similarly, using a quadratic Legendre polynomial random regression model, the additive genetic standard deviation for each of the ratio traits was similar across all herd-year prevalence levels of live *F. hepatica* (protein percentage ranged from 0.15 to 0.16 units; Fig. 2). Nevertheless, the additive genetic standard deviation for somatic cell score did increase gradually with increasing *F. hepatica* prevalence (ranging from 0.271 units at a prevalence level of 0.15, to 0.440 units at a prevalence level of 1.00; Fig. 2).

For the milk production traits, the within-trait genetic correlations among the different *F. hepatica* prevalence levels were less than unity (Supplementary Fig. S4); genetic correlation between fat yield at a prevalence level of 0.33 and fat yield at a prevalence level of 1.00 was as low as 0.49 (SE = 0.066). However, genetic correlations between the same trait at different *F. hepatica* prevalence levels between 0.2 and 0.8 were >0.83 for all of the milk production traits (Table 1). Genetic correlations for somatic cell score at *F. hepatica* prevalence level 0.0, 0.5 and 1.0 with somatic cell score at all other *F. hepatica* prevalence levels were >0.58 (Fig. 3). Although the majority of estimated breeding values of sires for milk yield traits increased as the *F. hepatica* prevalence increased, there were some sires that had a lower estimated breeding value for milk traits as the *F. hepatica* prevalence increased (Fig. 4).

Resilience in Fertility

The heritability estimates for the 4 different fertility traits ranged from 0.01 to 0.03 when estimated just using an intercept random regression model (Supplementary Table S1). Using a quadratic Legendre polynomial random regression model, the heritability estimates across the different *F. hepatica* prevalence levels ranged from 0.01 to 0.06, from 0.01 to 0.60, from 0.026 to 0.19, and from 0.01 to 0.06 for age of first calving, calving to first service interval, calving interval, and survival, respectively (Fig. 5). The additive genetic standard

(a)

(b)
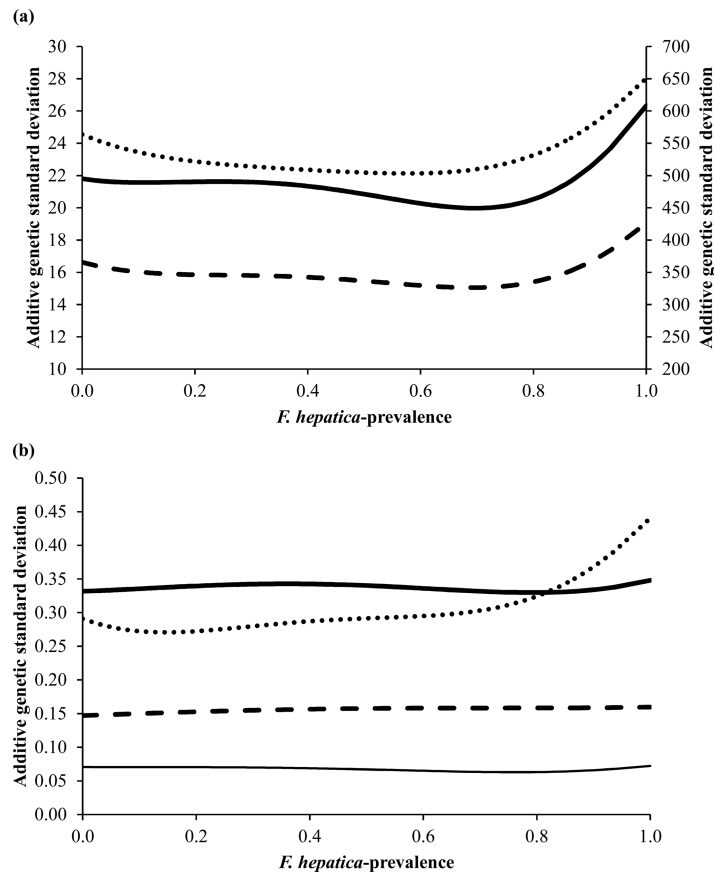
Figure 2. Additive genetic standard deviation estimates for 305-d (a) milk yield (dotted black line; kg; secondary axis), fat yield (thick solid black line; kg; primary axis), protein yield (dashed black line; kg; primary axis) and (b) protein percentage (dashed line; %), fat percentage (thick solid black line; %), fat-to-protein ratio (thin sold black line; %), and somatic cell score (dotted black line; $\log_e$ units) across herd-year prevalence of live *F. hepatica*.

Table 1. The smallest within-trait genetic correlation (SE in parenthesis) for milk production, fertility traits, and carcass traits across herd-year prevalence levels of *F. hepatica,* when the considered range in *F. hepatica* prevalence was 0.3 to 0.7, 0.2 to 0.8, 0.1 to 0.9, or 0.0 to 1.0

	Prevalence range			
Trait	0.3 to 0.7	0.2 to 0.8	0.1 to 0.9	0.0 to 1.0
Milk production traits				
Milk yield	0.97 (0.004)	0.92 (0.010)	0.84 (0.022)	0.73 (0.037)
Fat yield	0.93 (0.008)	0.83 (0.021)	0.67 (0.043)	0.49 (0.066)
Protein yield	0.96 (0.004)	0.90 (0.014)	0.78 (0.031)	0.63 (0.053)
Fat percentage	0.97 (0.002)	0.94 (0.003)	0.88 (0.010)	0.82 (0.020)
Protein percentage	0.99 (0.001)	0.98 (0.001)	0.97 (0.003)	0.95 (0.005)
Fat-to-protein ratio	0.96 (0.004)	0.90 (0.012)	0.78 (0.027)	0.63 (0.048)
Somatic cell score	0.95 (0.008)	0.87 (0.026)	0.74 (0.055)	0.59 (0.086)
Fertility traits				
Age of first calving	0.69 (0.435)	0.40 (0.747)	0.15 (1.010)	−0.03 (1.089)
Calving interval	0.94 (0.026)	0.88 (0.049)	0.83 (0.074)	0.79 (0.099)
Calving to first service	0.76 (0.143)	0.70 (0.173)	0.65 (0.197)	0.54 (0.224)
Survival	0.88 (0.082)	0.73 (0.208)	0.52 (0.365)	0.33 (0.483)
Carcass traits				
Carcass weight	0.99 (0.001)	0.97 (0.003)	0.92 (0.007)	0.83 (0.015)
Carcass conformation	0.97 (0.002)	0.93 (0.006)	0.87 (0.014)	0.77 (0.038)
Carcass fat	0.94 (0.007)	0.85 (0.021)	0.68 (0.051)	0.44 (0.089)
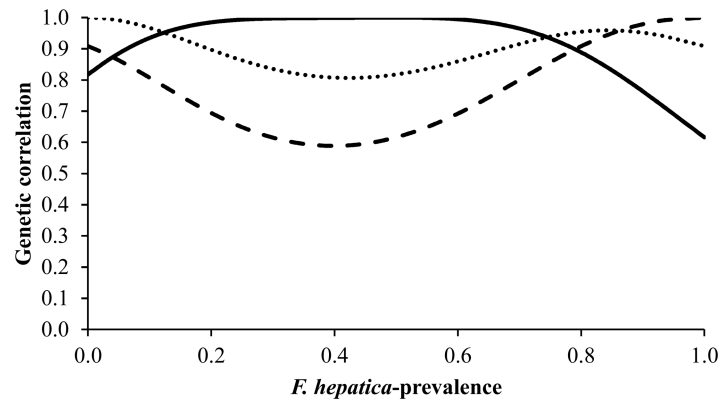
Figure 3. Genetic correlations for somatic cell score at *F. hepatica* prevalence level 0.0 (dotted black line; SE ranged from 0.000 to 0.168), 0.5 (solid black line; SE ranged from 0.000 to 0.143), or 1.0 (dashed black line; SE ranged from 0.000 to 0.114) with somatic cell score at all other *F. hepatica*-prevalence levels.

deviation for age of first calving varied from 6.6 to 8.1 d between *F. hepatica* prevalence levels of 0.0 to 0.7; the additive genetic standard deviation was 16.2 d where the *F. hepatica* prevalence level was 1.0 (Fig. 6). The additive genetic standard deviation for calving to first service interval was lowest (1.88 d) at prevalence level 0.22 but higher at both extreme prevalence levels (Fig. 6). For calving interval, the additive genetic standard deviation increased from 5.75 d at a *F. hepatica* prevalence level of 0.0 to 18.37 at a *F. hepatica* prevalence level of 1.0. For survival, the additive genetic standard deviation increased as *F. hepatica* prevalence increased (ranging from 0.038 units at a prevalence level of 0.0 to 0.082 units at a prevalence level of 1.0; Fig. 6).

Genetic correlations within each fertility trait were weak between extreme *F. hepatica* prevalence levels (Table 1; Fig. 7; Supplementary Fig. S5). Between *F. hepatica* prevalence level of 0.3 and 0.7, genetic correlations within age of first calving, calving to first service, calving interval, and survival were 0.69 (SE = 0.435), 0.76 (0.143), 0.94 (0.026), and 0.88 (0.082), respectively (Table 1). Reaction norms for each fertility trait for a sample of 6 sires with >30 progeny from >5 contemporary groups

are presented in Fig. 8. There is variation in the slopes of the reaction norms for the fertility traits across the *F. hepatica* prevalence levels, with some sires being more resilient to *F. hepatica* prevalence compare to other sires; Fig. 8).

Resilience in Carcass Traits

Using just an intercept sire random regression model, the heritability estimate for carcass weight was 0.59, carcass conformation was 0.86, and carcass fat was 0.44; the respective additive genetic standard deviation estimates were 24.5 kg, 1.14 units, and 0.99 units. The heritability (Fig. 9) and additive genetic standard deviation (Fig. 10) estimates from a quadratic Legendre polynomial random regression model were similar to the estimates from just the intercept model; across the different *F. hepatica* prevalence levels, the additive genetic standard deviation for carcass weight varied from 25.4 to 13.1 kg. The heritability estimates for carcass fat increased with increasing herd-year prevalence of *F. hepatica* (heritability increased from 0.40 to 0.72), but conversely, the heritability of carcass weight (heritability reduced
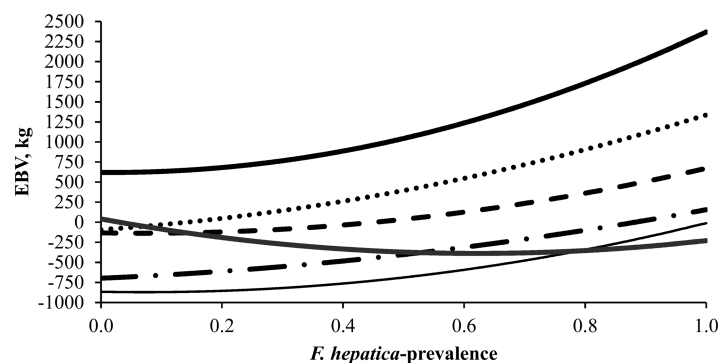
Figure 4. Estimated breeding values (EBV) for milk yield of 6 sires with >30 progeny from >5 contemporary groups, over the range of herd-year prevalence levels of live *F. hepatica* using a quadratic random regression model.
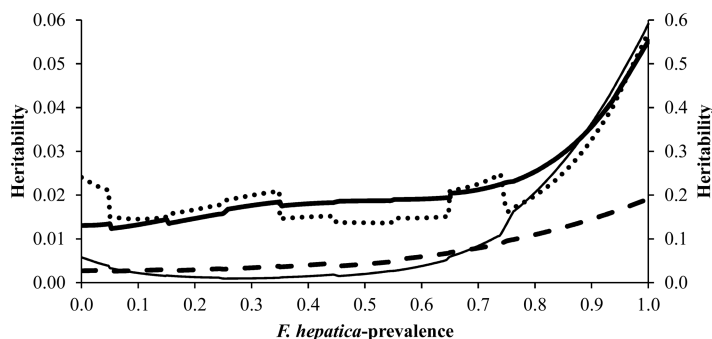
Figure 5. Heritability estimates for age of first calving (dotted black line; SE ranged from 0.008 to 0.178; primary axis), calving to first service (thin solid black line; SE ranged from 0.006 to 0.200; secondary axis), calving interval (dashed black line; SE ranged from 0.007 to 0.096; primary axis), and survival (thick solid black line; SE ranged from 0.006 to 0.200; primary axis) across herd-year prevalence levels of live *F. hepatica*.

from 0.67 to 0.17) and carcass conformation (heritability reduced from 0.98 to 0.44) decreased with increasing prevalence of *F. hepatica* (Fig. 9). The weakest within-trait genetic correlation for carcass weight was 0.83 (SE = 0.015) between prevalence level 0.00 and 0.61, carcass conformation was 0.77 (SE = 0.038) between prevalence level 0.35 and 1.00, and carcass fat was 0.44 (SE = 0.089) between a prevalence level of 0.34 and 1.00, across the herd-year *F. hepatica* prevalence levels (Table 1; Supplementary Fig. S6). Between *F. hepatica* prevalence levels of 0.2 and 0.8, the within-trait genetic correlations were all >0.85.

DISCUSSION

Climate change will have a significant effect on future livestock production systems, by increasing societal pressure to adopt agricultural mitigation strategies, particularly in ruminant production systems, as well as by exposure to a greater pathogen load or novel pathogens (Thornton et al., 2009; Rojas-Downing et al., 2017) including parasites (van Dijk et al., 2009). For example, climate change may contribute to an increase in the proportion of European herds exposed to *F. hepatica* (currently

ranging from 6% in Sweden to 86% in Wales; Sekiya et al., 2013). Fox et al. (2011) reported an increase in prevalence and spatiotemporal variation of *F. hepatica* in the United Kingdom over the previous 4 decades, and they attributed that to climate change. Therefore, not only do future livestock breeding programs need to breed animals resistant to both the diversity and pressures of pathogens, but also genetically select animals resilient to environments with high pathogen load (i.e., ability to maintain performance in environments of high pathogen load; Bishop, 2012).

Many studies in cattle have attempted to quantify the extent of genotype × environment (G × E) interactions, but the environmental gradient in these studies have generally been confined to differences in herd nutrition (Pryce et al., 1999; Berry et al., 2003; Ouweltjes et al., 2007), herd mean performance (Kolmodin et al., 2002; Windig et al., 2005; Strandberg et al., 2009), or herd temperature-humidity index (Bryant et al., 2007). There is a dearth of information on the extent of G × E interactions or resilience among cattle across environments differing in disease pathogen load. To our knowledge, herd somatic cell score remains the only health-related trait used in defining the
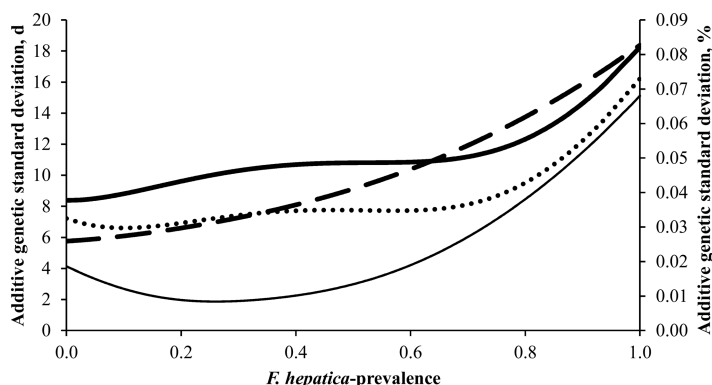

Figure 6. Additive genetic standard deviation estimates for age of first calving (dotted black line; primary axis), calving to first service (thin solid black line; primary axis), calving interval (dashed black line; primary axis), and survival (thick solid black line; secondary axis) across herd-year prevalence levels of live *F. hepatica*.
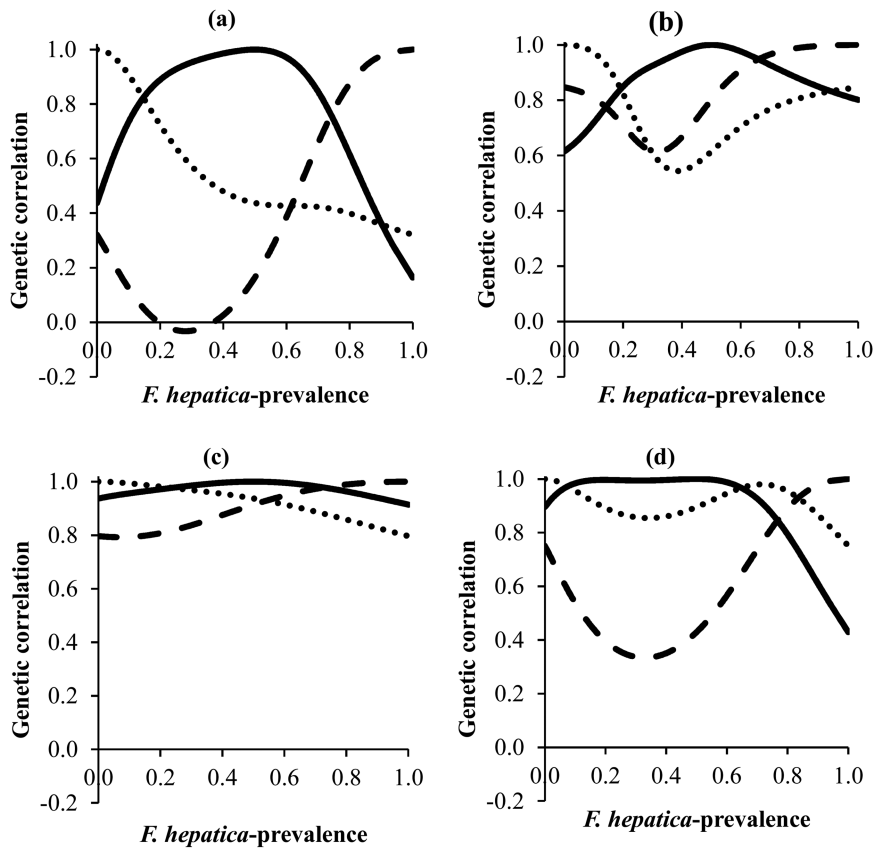
Figure 7. The genetic correlations within trait between *F. hepatica* prevalence level 0.0 (dotted black line), 0.5 (filled solid black line), and 1.0 (dashed black line) and the rest of the *F. hepatica* prevalence levels for (a) age of first calving (not significantly different from one; SE ranged from 0 to 1.21), (b) calving to first service (SE ranged from 0.00 to 0.22), (c) calving interval (SE ranged from 0.00 to 0.13), and (d) survival (SE ranged from 0.00 to 0.57).
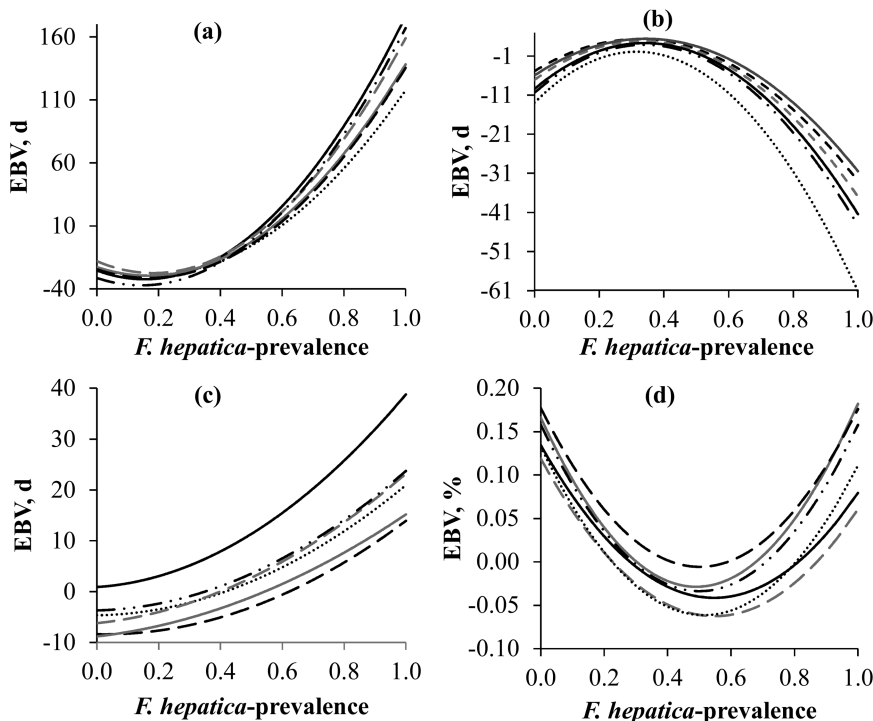
Figure 8. Estimated breeding values (EBV) for 6 sires with >30 progeny from >5 contemporary groups, over the range of herd-year prevalence levels of *F. hepatica* for (a) age of first calving, (b) calving to first service, (c) calving interval, and (d) survival using a quadratic random regression model.
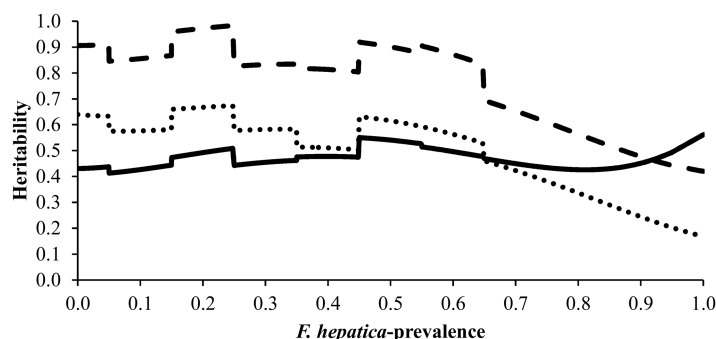
Figure 9. Heritability estimates for carcass weight (dotted black line; SE ranged from 0.023 to 0.171), carcass conformation score (dashed black line; SE ranged from 0.026 to 0.169), and carcass fat score (solid black line; SE ranged from 0.020 to 0.211) across herd-year prevalence levels of *F. hepatica*.

environmental gradient when investigating G × E interactions or resilience for performance traits in dairy cattle, and even at that, the number of studies are few (Calus and Veerkamp, 2003; Streit et al., 2012). The present study, therefore, attempted to quantify the impact of increasing environmental parasitic load (*F. hepatica*) on individual animal performance for a range of different performance traits.

Resilience to Parasite Diseases

In the present study, resilience was defined as the productivity of an animal in the face of infection similar to that proposed by Bishop (2012). Resilience to parasite diseases has previously been documented in sheep by Albers et al. (1987) who compared the phenotype of resilience by measuring the growth rate of individual sheep in a controlled experimental model of *Haemonchus contortus* infection. Alternatively, Morris et al. (2010) used age of first anthelmintic treatment or the number of anthelmintic treatments required when lambs were selectively treated based on weight and dag score (measure of fecal soiling around the tail) to measure resilience. Morris et al. (2010) reported a heritability estimate for the age of first treatment (i.e., anthelminthic) of 0.13 (SE = 0.02) and a close to zero genetic correlation (−0.1; SE = 0.02) between

resistance (i.e., fecal egg count) and resilience (i.e., age at first treatment). However, these phenotypes of resilience are not suitable for genetic selection as the underlying genetic variation is confounded with genetic variation for growth (Bisset and Morris, 1996). Mulder (2016) suggested that G × E interactions using environmental pathogen (i.e., parasite) load as the environmental gradient would in fact be a better indication of the extent of genetic variability of resilience to diseases. The existence of G × E interactions (and resilience) is determined by 1) the change in genetic variation across the environmental gradient (i.e., scaling effect) and 2) the genetic correlation between the same trait in different environments being less than unity (i.e., reranking; Falconer, 1952; Falconer and Mackay, 1996).

Scaling Effect

Results from the present study indicate little or no genetic variability in resilience among cattle to *F. hepatica* for a wide range of performance indicators. The within-trait estimated genetic variances for milk and fertility traits were similar across the majority of *F. hepatica* prevalence levels with the exception of prevalence levels >0.7 (i.e., 305-d milk yield ranged from 503 to 564 kg). However, the increase in genetic variance in prevalence levels >0.7 for some traits could simply be a function of
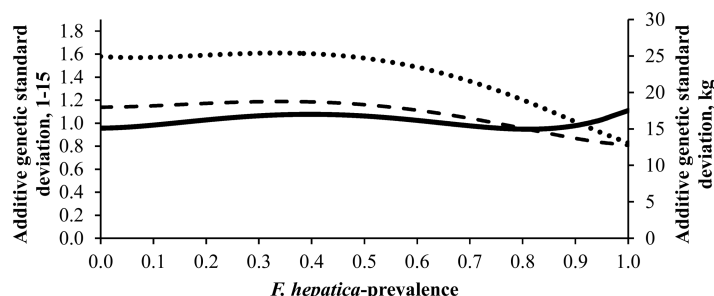
Figure 10. Additive genetic standard deviation estimates for carcass weight (dotted black line; secondary axis), carcass confirmation score (dashed black line; primary axis), and carcass fat score (solid black line; primary axis) across herd-year prevalence levels of *F. hepatica*.

the mathematical properties of random regressions, which are heavily levered by data at the boundaries of the parametric space (Meyer, 1998). This may have been a contributing factor in the present study since only 5% of the fertility and milk data were represented in the prevalence levels >0.7. Higher estimates for genetic variance at the extremities of the parameter space have also been documented in other studies that used random regression models (Berry et al., 2003; Hurley et al., 2017; Visentin et al., 2017). Furthermore, in a supplementary analysis, the genetic variation for each performance trait in each of the 9 F. hepatica prevalence strata (used to estimate the residual variance components) was estimated using traditional univariate models with just a random sire effect; no large increase in genetic variation was detected for any trait in the high prevalence category. This further supports the view that the observed exaggerated increase in genetic variation in F. hepatica prevalence levels >0.7 in the present study when estimated using the random regression model, is due to the mathematical properties of the random regressions themselves. Additionally, the eigenfunction associated with the largest eigenvalue of the estimated covariance matrix for each trait did not fluctuate across the F. hepatica prevalence levels, and the largest eigenvalue accounted for >89% of the genetic variation for all the traits, with the exception of age of first calving and survival; the largest eigenvalue for age at first calving and survival explained 65% and 83% of the respective genetic variance. Therefore, ignoring F. hepatica prevalence levels >0.7 (i.e., 5% of the data), only a biologically small scaling effect was detected for any trait. In other words, most sires are expected to have similar breeding values in the low F. hepatica environments as in high F. hepatica environments. Although only 6% of the carcass data was in F. hepatica prevalence levels >0.5, the within-trait estimated genetic variances for carcass traits were similar for all F. hepatica prevalence levels, Corroborating the lack of a change in genetic variance over an environmental trajectory as observed in the present study, Streit et al. (2012) also documented a relatively constant genetic variation for milk traits across a herd mean somatic cell score trajectory in German Holstein cows. Based on an analysis on 151,696 first lactation dairy cows, Calus and Veerkamp (2003) reported that the additive genetic standard deviations for somatic cell score only slightly increased from 0.94 (herd-year somatic cell score in the 10th percentile) to 1.07 (herd-year somatic cell score in the 90th percentile) $\log_{10}$ units when using herd-year somatic cell score as the environmental descriptor. Furthermore, genetic parameter estimates for carcass weight in 16,867 Scottish Blackface lambs were similar in 2 different similarly managed research flocks managed similarly yet significantly different in mean temperature and rainfall (rainfall differed by 1,500 mm annually between the 2 flocks; McLaren et al., 2012). Although F. hepatica environmental load was not recorded by McLaren et al. (2012), it was likely that a difference in F. hepatica (and possibly other parasites) environmental load existed between the 2 farms, since areas with higher temperature and/or rainfall have more F. hepatica present (Selemetas and de Waal, 2015). In conclusion, within the ranges of environments commonly observed on farms in Ireland, there appears to be little evidence of genetic variation in reaction norms for traditional performance traits across herd-years differing in F. hepatica prevalence.

Reranking

Although some genetic correlations estimated in the present study within the same trait in different F. hepatica prevalence levels were as low as −0.03 (age of first calving) for F. hepatica prevalence levels between 0 and 0.8, little existence of reranking for milk production and carcass traits were evident; all genetic correlations were in fact >0.8. Robertson (1959) suggested that traits with a genetic correlation >0.8 should be treated as being the same trait. Thus, there is no need for genetic evaluations to consider milk and carcass performance in environments differing in F. hepatica prevalence to be different traits. The same is true for consideration of separate breeding programs depending on the environment in which the animals will be producing. This conclusion is substantiated by a simulation described by Mulder et al. (2006) who reported that maximum genetic gain can be achieved by using only 1 breeding program if genetic correlations between environments were >0.6. The minimal extent of reranking in the present study for milk production and carcass traits in environments differing in F. hepatica prevalence was somewhat expected as milk production and carcass traits are only weakly genetically (May et al., 2017; Twomey et al., 2018) and phenotypically (Mezo et al., 2011; Sanchez-Vazquez and Lewis, 2013) associated with phenotypes reflecting F. hepatica infection. Nonetheless, a noticeable weakening of the within-trait genetic correlations between milk productions traits in F. hepatica prevalence levels >0.8 and the rest of the F. hepatica prevalence levels, however,

these were associated to larger standard errors. For example, the genetic correlation between milk yield at *F. hepatica* prevalence level 0.1 and 0.5 was 0.97, whereas the genetic correlation between milk yield at *F. hepatica* prevalence level 0.5 and 0.9 was 0.87, and the respective standard errors were 0.003 and 0.019. Although no previous study has attempted to quantify the extent of G × E interaction in dairy cows across environments differing in parasitic load, little reranking for milk production traits has been documented when comparing the contrasting milk production systems of grazing and confinement environments (genetic correlations ranged from 0.89 to 0.91; Kearney et al., 2004). Streit et al. (2012) also concluded that there was almost no reranking for milk traits in German Friesian cows across environments differing in herd mean somatic cell score (genetic correlations were >0.90).

Despite the lack of widespread reranking for milk production and carcass traits in the present study, considerable reranking of sires was expected for the fertility traits across the different *F. hepatica* prevalence levels; nonetheless, the estimated genetic correlations were associated with large sampling variability attributable mainly to the low heritability of the fertility traits and also a paucity of data at the extremes. The presence of the G × E interaction for fertility traits in environments differing in *F. hepatica* prevalence was not unexpected given the known genetic association that exists between fertility traits and *F. hepatica*-phenotypes (Twomey et al., 2018). The larger extent of reranking for fertility traits in the present study suggests that sires that descended in rank as *F. hepatica* prevalence increased were not resilient to the environmental load of *F. hepatica*.

CONCLUSION

The lack of any major change in genetic variance of the performance traits across the majority of *F. hepatica* prevalence levels suggests minimal rescaling. More importantly, however the strong positive genetic correlations within all traits across the different environments for *F. hepatica* prevalence in the present study, suggests that there is minimal reranking of sires for milk production and carcass traits. Therefore, little or no genetic variation for resilience to *F. hepatica* was observed in the present study when milk production and carcass traits were used as performance indicators. Considerable reranking was evident, however, for fertility in environments differing in *F. hepatica* prevalence, although the estimated genetic correlations were associated with relatively large standard

errors. Thus, genetic evaluations for fertility traits should ideally take cognizant of the *F. hepatica* environmental load; moreover, further quantification of the extent of G × E for fertility traits across herds differing in mean health status is warranted. Nonetheless, as the majority of herds in the present study currently do not have an extremely high environmental load for *F. hepatica*, it would not probably be economically feasible to implement a national breeding goal which considers resilience to *F. hepatica*. However, the impact of climate change on forecasted *F. hepatica* prevalence may suggest consideration may be merited in the future.

SUPPLEMENTARY DATA

Supplementary data are available at *Journal of Animal Science* online.

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