

# The influence of liver fluke infection on production in sheep and cattle: a meta-analysis

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1 **ABSTRACT**

2

3 Liver flukes (*Fasciola* spp) are important parasites of sheep and cattle across the world,  
4 causing significant damage to animal health and productivity due to both acute and chronic  
5 infection. Many comprehensive reviews have discussed the results of decades of research  
6 into the impact of fluke infection on livestock performance traits such as weight gain and milk  
7 production. While fluke are considered to be important, there have been no attempts to  
8 collate previous research in a quantitative manner, and nor has there been an attempt to  
9 determine why some studies find substantial effects of fluke while others conclude that  
10 effects of fluke on animal performance are negligible. In this study, we used meta-analysis to  
11 provide quantitative estimates of the impact of liver fluke on animal performance, and to  
12 identify elements of study design that influence the conclusions of such studies. A literature  
13 search provided 233 comparisons of performance in “fluke-infected” and “uninfected”  
14 animals. We standardized these data as log response ratios and calculated effect size  
15 variances in order to weight studies by their sample size and accuracy of their estimates. We  
16 performed multi-level meta-analysis to estimate effects of fluke infection in five traits: daily  
17 weight gain (N = 77); live weight (N = 47); carcass weight (N = 84); total weight gain (N = 18)  
18 and milk production (N = 6). There were significant negative effects of fluke infection on daily  
19 weight gain, live weight and carcass weight (9%, 6% and 0.6% reductions in performance,  
20 respectively), but not total weight gain or milk production. We then used mixed-effects meta-  
21 analysis to estimate the impact of moderator variables, including host, fluke, and study  
22 design factors, on study outcomes. We found that, in general, studies that gave experimental  
23 infections found generally larger effects of fluke than observational or drug studies; younger  
24 animals were more likely to suffer the effects of fluke infection on daily weight gain; and that  
25 effects on live weight increased across the course of an experiment. Our results provide the  
26 first quantitative estimate of the importance of liver fluke on performance across studies and  
27 highlight the elements of study design that can influence conclusions. Furthermore, our

28 literature search revealed areas of research into liver fluke that could be the subject of  
29 greater effort, and types of study that could form the basis of future meta-analyses.

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56 **INTRODUCTION**

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58 Liver flukes (*Fasciola* spp) are amongst the most important helminth parasites of domestic  
59 sheep and cattle worldwide, causing significant financial losses to producers (Schweizer et  
60 al., 2005). They have a typical trematode parasite life-cycle: adults inhabit the host liver and  
61 bile duct system and produce eggs, which are shed in faeces. Miracidia develop within the  
62 eggs and then hatch and search for a mud snail (typically, *Galba trunculata*) intermediate  
63 host, which they penetrate, undergoing multiplication before emerging as cercariae, which  
64 encyst on vegetation as the infectious metacercariae (cysts). These are ingested by the host  
65 while grazing; immature fluke then emerge and migrate through the intestinal wall to the  
66 liver, where they develop into adults around 10-12 weeks after ingestion of cysts (Skuce and  
67 Zadoks, 2013). Liver fluke can cause acute disease associated with migration of immature  
68 fluke, which can lead to death in severe cases, especially in sheep, and chronic disease  
69 caused by the blood-feeding activity of the adults, which can live as long as the host  
70 (Kaplan, 2001). Control of liver fluke remains a challenge in all areas of the world: vaccine  
71 development has been difficult, due in part to the lack of a robust protective host immune  
72 response and a lack of understanding of which antigens to target (Molina-Hernández et al.,  
73 2015; Toet et al., 2014); increasing flukicide resistance (Brockwell et al., 2013; Kamaludeen  
74 et al., 2019; Novobilský and Höglund, 2015); the clonal amplification of the parasite in the  
75 intermediate snail host (Beesley et al., 2018); and the ability of wildlife reservoir hosts to  
76 disseminate the parasite (French et al., 2019).

77

78 A large number of influential reviews have collated decades of research into the effects of  
79 fluke infection on animal performance (Charlier et al., 2013; Dargie, 1980, 1987; Elelu and  
80 Eisler, 2018; Skuce and Zadoks, 2013). Empirical work has demonstrated statistically  
81 significant and sometimes substantial effects of liver fluke infection on traits including  
82 carcass weight (Sanchez-Vazquez and Lewis, 2013), carcass conformation or fatness  
83 (Bellet et al., 2016; Sanchez-Vazquez and Lewis, 2013), age at slaughter (Mazeri et al.,

84 2017), weight gain (Chick et al., 1980; Genicot et al., 1991; Hope Cawdery et al., 1977;  
85 Loyacano et al., 2002; Sykes et al., 1980), milk production (El-Tahawy et al., 2017; May et  
86 al., 2020), as well as the financial costs associated with condemnation of infected livers  
87 (Nyirenda et al., 2019). Other studies, however, have found no support for effects of liver  
88 fluke infection on performance traits including carcass weight (Bellet et al., 2016; Charlier et  
89 al., 2009; Molina et al., 2005), weight gain (Bossaert et al., 2000; Echevarria et al., 1992;  
90 Forbes et al., 2015) and milk production (May et al., 2019; Randall and Bradley, 1980).  
91 These studies vary in the direction and magnitude of effects of fluke, but also in their  
92 characteristics. Firstly, there is biological variation: in parasite species (*F. hepatica* typically  
93 in temperate regions and *F. gigantica* in the tropics) and in animal breed, age and sex. There  
94 is also variation in study design: some studies compare naturally infected with uninfected  
95 animals, some compare control with experimentally-infected animals, and others compare  
96 control with flukicide-treated animals. Finally, effects may vary with location due to climatic  
97 conditions, and with the time since initial infection, as it takes around 8-12 weeks for fluke to  
98 migrate to the liver and mature (Kaplan, 2001). As such, we lack knowledge on (1) the  
99 overall impact of fluke across studies and (2) the effects of study characteristics on outcome.

100

101 In this study, we present a meta-analysis of the impact of liver fluke infection on performance  
102 in sheep and cattle. Meta-analysis aims to collate data from published and unpublished  
103 sources addressing the same question and then puts data from these studies onto a  
104 standardized scale ("effect sizes"), enabling statistical analysis of the overall effect and  
105 causes of variation in outcomes (Gurevitch et al., 2018). The term "meta-analysis" was  
106 coined in 1976 (Glass, 1976) and the techniques were quickly embraced by medical and  
107 social sciences, with studies in ecology and evolution beginning in the early 1990s (Lau et  
108 al., 2013). Only more recently has this approach been applied in veterinary science (Lean et  
109 al., 2009). We followed the PICO (population; intervention; comparator; outcome) approach  
110 to formulate our research questions (Stewart et al., 2013), aiming to compare different  
111 measures of weight and milk production in sheep and cattle infected with fluke against those

112 designated as uninfected. We first estimated an overall effect size using random-effects  
113 meta-analysis and then assessed the impact of biological and study design factors  
114 (“moderators”) on study outcomes. Our results reveal that fluke infection has a particularly  
115 strong influence on weight gain, and that animal age and experimental design are important  
116 factors influencing study outcome.

117

## 118 **METHODS**

119

### 120 **Literature search**

121

122 We searched the scientific literature in order to identify studies that investigated the impact  
123 of liver fluke on performance of sheep and cattle. A *Web of Science* search was conducted  
124 on 18/10/2019 with the search terms (Fasciola OR fluke) AND (Cattle OR cow\* OR calf OR  
125 calves OR sheep) AND (producti\* OR weight OR grow\* OR milk OR performance OR fertility  
126 OR carcas\*) and the search yielded 662 papers. To these, we added all papers cited in a  
127 number of influential reviews on the impacts of fluke on livestock productivity (Charlier et al  
128 2014A; Charlier et al 2014B; Dargie 1987; Elelu & Eiser 2018; Skuce & Zadoks 2013; Dargie  
129 1980). We then added all papers citing these articles using the *Publish or Perish* software  
130 (Harzing 2016). Finally, we added a paper by da Costa et al (2019) that was published in  
131 late October 2019. We also added data provided by Scotbeef Ltd (Hayward et al., in prep)  
132 and McIntosh-Donald Ltd (Skuce et al., in prep). This resulted in a total of 1582 data  
133 sources.

134

135 We reviewed the titles and abstracts of these publications, sifting out publications that were  
136 clearly unsuitable for a variety of reasons (**Figure S1**). Once duplicates were removed, this  
137 initial sift resulted in 106 publications that were fully reviewed. Specifically, we searched for  
138 papers that compared performance in groups of animals that were infected with fluke  
139 (naturally or through experimental infection) versus animals that were uninfected (naturally

140 or through flukicide treatment). We collected data on the mean, standard deviation, standard  
141 error and number of animals with performance measured in each group. Where data were  
142 presented in figures but not in tables or text, we used the R package 'metaDigitise' (Pick et  
143 al 2018) to extract data. Where it seemed that relevant data may have been collected but not  
144 reported in the publication or supporting information, we contacted authors in order to  
145 request data. Once the full review was complete and unsuitable publications removed  
146 (**Figure S2**), our final dataset consisted of 233 effect sizes from 28 sources (**Table 1**).

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## 148 **Data synthesis**

149

150 We analysed the influence of liver fluke infection on five performance traits, as follows:

151

152 *Daily weight gain*: the calculated average increase in body weight per day. In some studies –  
153 mostly experimental – this is live weight gain (weight of the live animal divided by time in  
154 days), but in abattoir studies, this is usually dead weight gain (carcass weight divided by age  
155 in days). These effects are considered the same trait due to (1) the generally close  
156 correlation between live weight and carcass weight and (2) the way in which we tested for  
157 effects of study design in our analysis.

158

159 *Live weight*: the weight of the live animal, generally reported multiple times across the  
160 course of experimental studies.

161

162 *Carcass weight*: the weight of the animal's carcass in abattoir studies.

163

164 *Total weight gain*: the amount of weight gained by the animal from the start of an experiment  
165 to the time of measurement.

166

167 *Milk production*: the weight of milk produced, generally expressed as a daily rate.

168

169 Our included studies reported raw mean performance in animals that were deemed to be  
170 fluke-infected versus animals that were deemed to be uninfected, plus sample sizes for both  
171 groups and standard deviation. Where standard errors were reported, we estimated the  
172 standard deviation as  $SD = SE \times \sqrt{N}$ . We calculated the ratio of means between fluke-  
173 infected and uninfected animals as our standardized measure of effect size and used log-  
174 transformation to normalize the values. Thus, we calculated log response ratio as  $\ln(RR) =$   
175  $\ln(\bar{y}_{inf}) / \ln(\bar{y}_{uninf})$ , where  $\bar{y}_{inf}$  and  $\bar{y}_{uninf}$  are the means of the trait  $y$  in infected and  
176 uninfected animals respectively. We calculated the variance for each effect as  $v_{lnR} =$   
177  $(s_{inf}^2 / (n_{inf} \times \bar{y}_{inf}^2)) + (s_{uninf}^2 / (n_{uninf} \times \bar{y}_{uninf}^2))$  where  $s^2$ ,  $n$ , and  $\bar{y}^2$  are the squared  
178 standard deviation, sample size and squared mean for infected or uninfected individuals  
179 (Koricheva et al 2013).

180

181 The 233 effect sizes were unevenly distributed across our 28 sources, with 4 studies  
182 contributing just one effect size, 5 contributing more than 10 and 3 studies contributing 40  
183 effect sizes each. These last three were abattoir studies where we were provided with raw  
184 data by the authors or the abattoirs themselves and we calculated breed- and sex-specific  
185 statistics for the ten commonest breeds in each data set, in order to better account for these  
186 factors and to maximise our number of effect sizes. Multiple effect sizes were contributed for  
187 a number of reasons including comparisons being made across many weeks of an  
188 experimental study; fluke status being manipulated as well as another experimental  
189 treatment such as diet; data being subdivided by sex and/or breed. We categorized our  
190 effect sizes according to a number of biological and experimental factors, many of which we  
191 included in our meta-regression analyses (see below).

192

193 *Host species*: our data contained more effect sizes from cattle (205, 88%) than sheep (28,  
194 12%).



195

196 *Host breed*: data came from 4 breeds of sheep and 29 breeds of cattle. Among these were  
197 crosses and cattle denoted simply as “dairy”, “beef” or “mixed”, each of which was included  
198 as a separate breed in our analyses.

199

200 *Host sex*: our data contained 88 effect sizes from females (38%), 106 from males (45%), 30  
201 from mixed-sex groups (13%) and 9 where animal sex was not recorded (4%).

202

203 *Host age group*: animals were divided into three age categories, namely adults (12% of  
204 effect sizes), young (35%) and mixed (53%). For cattle, young animals were  $\leq 12$  months of  
205 age and adults  $\geq 23$  months of age. For sheep, young animals were  $\leq 12$ -13 months of age  
206 and adults were year old (yearlings) or older.

207

208 *Parasite*: the data were dominated by *F. hepatica*, which accounted for 90% of effect sizes,  
209 with 9% contributed by *F. gigantica* and 1% from a single study recording a mixed *Fasciola*  
210 species burden.

211

212 *Experimental design*: 29 effect sizes (12%) came from 6 studies where flukicidal drugs were  
213 used to remove fluke from an experimental group, performance in which was compared with  
214 a control group. In the drug-treated (i.e. “uninfected”) groups, the maximum mean fluke FEC  
215 was 3 eggs/gram and the maximum live fluke burden at post-mortem was 3. While some of  
216 these animals defined as “uninfected” clearly carried fluke, we consider these burdens low  
217 enough as to be negligible. These studies were denoted as “drug”. 56 (24%) effect sizes  
218 were from studies (denoted as “infection”) where animals were experimentally infected with  
219 fluke and compared with uninfected controls. The remaining 148 (64%), denoted “natural”,  
220 were largely from abattoirs and animals that acquired infection (or not) naturally.

221

222 *Week post-infection:* for experimental studies, data were collected from 4-54 weeks post-  
223 infection.

224

225 *Absolute latitude:* our effect sizes were predominantly from studies conducted in the UK  
226 (64%) with others coming from studies conducted in the Americas (12%), Asia (9%), Europe  
227 (8%), Australasia (4%), and Africa (3%). Absolute latitude ranged from 1.25-57.3.

228

### 229 **Multi-level meta-analysis**

230

231 Meta-analyses were performed using the `rma.mv` function of the R package 'metafor'  
232 (Viechtbauer 2010), version 2.1-0. We performed separate random-effects meta-analyses in  
233 order to estimate the mean effect of fluke infection on five traits: daily weight gain, live  
234 weight, carcass weight, total weight gain and milk yield.

235

236 *Global effects:* First, we determined the mean effect of fluke infection on each of the traits.  
237 We used multi-level analyses: in order to account for non-independence of effect sizes  
238 derived from the same studies and from animals of the same breed, we fitted random effects  
239 of study and breed, as well as an observation-level random effect in order to estimate the  
240 residual variance.

241

242 *Meta-regression:* Next, we used a meta-regression approach in order to investigate whether  
243 the effect size depended upon a number of factors related to host and parasite biology or  
244 study design. These included host species (cattle or sheep), host sex, host age group (adult,  
245 young, or mixed), parasite species (*F. hepatica* or *F. gigantica*), study design (observational  
246 study of natural infections, infection experiment, drug treatment experiment), absolute  
247 latitude (continuous), and week post-infection. Each of these moderating variables was  
248 investigated in a separate meta-regression model. In each model, we determined whether  
249 the moderator was supported (i.e. whether the effect size varied according to the moderator)

250 using Wald-type chi-square tests ( $Q_M$ ). We examined whether each level within categorical  
251 moderators was significantly different from zero using z-tests. We did not test all of the  
252 moderators for each of the five traits, since not all traits had variation in all moderators (e.g.  
253 daily weight gain data all came from cattle and so it was not possible to test the 'host  
254 species' moderator).

255

256 Details on the terms fitted for each trait are shown in **Table 2**.

257

### 258 **Analysis of heterogeneity and bias**

259

260 Heterogeneity in effect sizes may be generated through variation between studies and  
261 variation within studies. In order to quantify this, we calculated the proportion of total  
262 variance that was due to variation in effect sizes (the  $I^2$  statistic), where the remainder is  
263 accounted for by sampling error. Since we fitted random effects to account for expected  
264 similarity between effect sizes from the same study and from the same breed of animal, we  
265 calculated modified  $I^2$  (Nakagawa & Santos 2012). Hence, for each meta-analysis, we  
266 calculated  $I^2$  values for the between-study effect and between-breed effect (where these  
267 were fitted (**Table 2**), and the residual effect.

268

269 The causes of bias in meta-analyses can include publication bias (the possibility that studies  
270 finding non-significant effects will not be published) and changes in effect size across time,  
271 e.g. if literature searches are less able to sample early sources. To test for publication bias,  
272 we generated funnel plots and performed regression of meta-analytic model residuals of  
273 each effect size (corrected for random effects and significant moderators) on the variance in  
274 each effect size (Egger, 1997; Nakagawa & Santos 2012). Where the intercept was  
275 significantly different from zero, we concluded that there was significant bias (Nakagawa &  
276 Santos, 2012). Where our data included both published and unpublished studies, we  
277 performed this test on both the full dataset, and then on the published studies only.

278

279 Finally, for each meta-analysis, we tested the effect of year of study as a continuous  
280 moderator in order to determine whether there has been a linear change in effect size across  
281 time, assessing significance using Wald-type chi-square tests ( $Q_M$ ).

282

## 283 **RESULTS**

284

### 285 **Daily weight gain**

286

287 Multi-level meta-analysis of daily weight gain revealed an overall negative effect of fluke  
288 infection ( $\beta_{global} = -0.0981$ , 95%CI = -0.1554 - -0.0408,  $z = -3.36$ ,  $P < 0.001$ ), suggesting that  
289 infected animals gained 9.5% less weight per day than uninfected animals (Figure 1). Meta-  
290 regression analyses revealed that the moderators of parasite species, experimental type,  
291 sex, latitude and week had no influence on the effect size (Table 3), but that there was a  
292 significant effect of the moderator of age ( $Q_M = 5.29$ ,  $P = 0.021$ ), suggesting that young  
293 animals, but not mixed-aged groups, experienced negative effects of fluke. Our results also  
294 revealed that there were negative effects of fluke both in animals infected with *F. gigantica*  
295 and *F. hepatica*, studies that used experimental infections but not drug studies or studies  
296 using natural infections, and in both sexes (Figure 1). Total variation in effect sizes was high  
297 ( $I^2 = 99\%$ ) and largely due to variation between studies ( $I^2 = 91\%$ ), with only a small amount  
298 of residual variation ( $I^2 = 8\%$ ). There was no evidence of changes in effect sizes across time  
299 ( $\beta_{year} = 0.0036$ , 95%CI = -0.0012 – 0.0084,  $z = 1.46$ ,  $P = 0.145$ ). Finally, there was no  
300 evidence of publication bias through inspection of funnel plots (Figure S3) or regression of  
301 model residuals on effect size variances in either the full data set ( $t = -0.30$ ,  $DF = 74$ ,  $P =$   
302  $0.763$ ) or published data ( $t = -0.03$ ,  $DF = 14$ ,  $P = 0.975$ ).

303

### 304 **Live weight**

305

306 Multi-level meta-analysis of live weight revealed a negative effect of fluke infection ( $\beta_{global} =$   
307 0.0611, 95%CI = -0.0877 - -0.0344,  $z = -4.48$ ,  $P < 0.001$ ), suggesting that infected animals  
308 weighed around 6% less than uninfected animals (Figure 2). Meta-regression revealed that  
309 the moderators of parasite species, host species, host age, experimental type, and latitude  
310 had no influence on the effect size (Table 4). There was, however, a significant effect of sex  
311 ( $Q_M = 16.04$ ,  $P < 0.001$ ), with males and especially mixed-sex groups of animals showing a  
312 greater impact of fluke than female only groups (Figure 2). There was also support for week  
313 post-infection ( $Q_M = 7.66$ ,  $P = 0.006$ ), with effects of fluke increasing across time in  
314 experimental fluke challenge studies (Figure S4). Fluke had a negative impact on live weight  
315 in animals infected with *F. hepatica* and *F. gigantica* (although the latter effect was  
316 marginally not supported), in both cattle and sheep, in young animals but not adults, in  
317 studies that administered experimental infections rather than those that cleared infections  
318 with flukicides and in male and mixed-sex groups but not females (Table 4). Total variation in  
319 effect sizes was moderate ( $I^2 = 71\%$ ) and largely due to residual variation ( $I^2 = 50\%$ ), with  
320 smaller variation due to between-study effects ( $I^2 = 22\%$ ). Effect sizes did not change with  
321 time ( $\beta_{year} = -0.0006$ , 95%CI = -0.0023 – 0.0012,  $z = -0.61$ ,  $P = 0.542$ ). Finally, there was no  
322 evidence of publication bias through inspection of funnel plots (Figure S5) or regression of  
323 model residuals on effect size variances ( $t = -0.41$ ,  $P = 0.683$ ).

324

### 325 **Carcass weight**

326

327 Analysis of carcass weight supported a significant negative effect of fluke infection ( $\beta_{global} =$   
328 0.0060, 95%CI = -0.0099 – -0.0021,  $z = -3.00$ ,  $P = 0.003$ ), although the effect size was  
329 negligible, suggesting a 0.6% reduction in carcass weight in infected animals (Figure 3).  
330 Meta-regression revealed that the moderators of age, experimental type, and latitude had no  
331 influence on the effect size (Table 5). There was, however, a significant effect of parasite  
332 species ( $Q_M = 6.44$ ,  $P = 0.011$ ), with animals infected with *F. gigantica* having greater  
333 carcass weight than uninfected animals, and animals infected with *F. hepatica* having

334 marginally lower carcass weight than uninfected animals (Figure 3). Total variation in effect  
335 sizes was high ( $I^2 = 82\%$ ), with a relatively small influence of between-study effects (23%)  
336 and a large contribution of residual variation (59%). Effect sizes increased significantly with  
337 time ( $\beta_{year} = 0.0013$ , 95%CI = 0.0005 – 0.0021,  $z = 3.21$ ,  $P = 0.001$ ). There was no evidence  
338 of publication bias through inspection of funnel plots (Figure S6) or regression analysis in  
339 either the full dataset ( $t = 0.06$ ,  $DF = 82$ ,  $P = 0.951$ ) or the published data ( $t = 0.39$ ,  $DF = 22$ ,  
340  $P = 0.701$ ).

341

### 342 **Total weight gain**

343

344 There was an overall negative influence of fluke infection on total weight gain, and while the  
345 effect did not reach statistical significance, it was of considerable magnitude ( $\beta_{global} = -$   
346  $0.1541$ , 95%CI =  $-0.3258 - 0.0176$ ,  $z = -1.76$ ,  $P = 0.079$ ), with infected animals gaining 14%  
347 less weight than uninfected animals (Figure S7). Meta-regression revealed that the moderators  
348 of parasite species, experimental type, sex, latitude and week had no influence on the effect  
349 size (Table S1). Negative effects of fluke were detected in studies that administered  
350 experimental infections rather than drug treatments, and in males but not mixed-sex groups  
351 (Figure S7). Total variation in effect sizes was high ( $I^2 = 79\%$ ) and largely due to variation  
352 between breeds ( $I^2 = 72\%$ ), with smaller amounts of between-study ( $I^2 = 4\%$ ) and residual  
353 variation ( $I^2 = 2\%$ ). There was no evidence of changes in effect sizes across time ( $\beta_{year} =$   
354  $0.0040$ , 95%CI =  $-0.0086 - 0.0166$ ,  $z = 0.62$ ,  $P = 0.537$ ) and no evidence of publication bias  
355 through funnel plots (Figure S8) or regression analysis ( $t = 0.85$ ,  $P = 0.409$ ).

356

### 357 **Milk production**

358

359 There was no support for a significant overall influence of fluke infection on milk production  
360 ( $\beta_{global} = -0.0500$ , 95%CI =  $-0.1065 - 0.0066$ ,  $z = -1.73$ ,  $P = 0.083$ ; Figure S9). Meta-  
361 regression revealed that the moderators of experimental type and latitude had no influence

362 on the effect size (Table S2). Total variation in effect sizes was high ( $I^2 = 88\%$ ), but we did  
363 not fit random effects of study or breed because they were found to be zero. There was no  
364 evidence of changes in effect sizes across time ( $\beta_{year} = -0.0004$ , 95%CI =  $-0.0040 - 0.0031$ ,  
365  $z = -0.23$ ,  $P = 0.815$ ) and no evidence of publication bias through inspection of a funnel plot  
366 (Figure S10) and regression analysis ( $t = -0.17$ ,  $P = 0.875$ ).

367

## 368 **DISCUSSION**

369

370 In this study, we used a meta-analytic approach in order to estimate the overall influence of  
371 liver fluke infection on performance traits in sheep and cattle. We found large amounts of  
372 variation between studies in the effects they estimated for liver fluke in each trait, and  
373 identified moderator variables that were associated with effect sizes. For each trait, we  
374 initially ran a random-effects meta-analysis in order to estimate an overall effect size. We  
375 found significant and substantial effects of fluke infection on two traits, with a 9% reduction in  
376 daily weight gain (DWG) and a 6% reduction in live weight. Moreover, we found a significant  
377 reduction in carcass weight in fluke-infected animals, although the overall effect was  
378 negligible, with infected animals having 0.6% lower carcass weight than fluke-free animals.  
379 Reductions in total weight gain and milk production in fluke-infected animals were not  
380 statistically supported. We also found that, although moderators were generally not  
381 supported, there was evidence to suggest that studies were more likely to find significant  
382 effects of fluke if they used experimental infection compared to natural infections or infected  
383 versus flukicide-treated animals, and if they studied young animals rather than adults.

384

385 The overall effect of a reduced DWG of 9% is likely to have a significant impact on several  
386 parameters: for the welfare of the animal, experiencing chronic disease (Howell and  
387 Williams, 2020); for the producer, in terms of financial costs (Mehmood et al., 2017;  
388 Schweizer et al., 2005); and for the environment, with the increased greenhouse gas  
389 emissions emitted by less efficient animals (Skuce et al., in prep). There was support for the

390 moderator of age group: the effect of fluke was significantly greater in young animals  
391 compared to mixed-age animals. This is potentially related to the fact that young animals are  
392 likely to be growing, while older animals may be putting on weight rather than growing *per*  
393 *se*; as such, younger animals are more likely to suffer the effects of fluke infection with  
394 regard to their ability to increase in weight. Further, it is possible that this may reflect age-  
395 dependent effects of immunity to the parasite, with younger animals less able to control fluke  
396 infection – although evidence for effective immunity in adults is scant (Hoyle et al., 2003) –  
397 or responding in a way which induces more immunopathology. While the moderator of  
398 experimental design was not supported, infection studies showed an effect of fluke that was  
399 significantly different from zero (Table 3), but this was not the case for drug studies or  
400 studies observing the effects of natural infections. Infection studies may be associated with  
401 larger effect sizes because they tended to involve administration of a single large infective  
402 dose of metacercariae at the start of the experiment; of the 15 experimental infection studies  
403 across our whole dataset, only two used trickle infections. It may well be that a large influx of  
404 immature fluke caused more damage than a natural infection due to the migration of a large  
405 number of larvae simultaneously (Boray, 1967; Ross and Dow, 1966). Another explanation is  
406 that we may have seen smaller effects in drug studies because they may not have fully  
407 cleared fluke infections (even though mean burdens in treated animals were very low), and  
408 in natural infection studies because unlike in experimental challenge studies, there would be  
409 variation in fluke challenge and duration of infection within infected groups resulting in a  
410 more variable response to infection. Finally, we saw significant effects of both *F. hepatica*  
411 and *F. gigantica* on DWG, and very similar effects in both sexes. There was, however, no  
412 variation in effect size with latitude or across time in experimental studies.

413

414 The difference in live weight between infected and uninfected animals of 6% is, as with  
415 DWG, likely to prove relevant to the efficiency of production. Two moderators were  
416 supported. First, there was variation between sex classes, with stronger effects of fluke in  
417 males and mixed-sex groups than in females. This is likely to be due to the fact that all effect



418 sizes of males and mixed-sex groups came from studies on young animals, while most of  
419 those on females (12/14) came from adults, and as with DWG, there were stronger effects of  
420 fluke in young animals. There was also a significant effect of duration of infection, with effect  
421 sizes increasing with week post-infection in experimental infection studies; this result is  
422 consistent with our finding of lower DWG in infected animals, since a difference in DWG  
423 would lead to an increasing divergence in live weight across time. As with DWG, there were  
424 stronger effects of fluke in young animals compared to adults, and in infection experiments  
425 compared to drug experiments, presumably for the same reasons as discussed above for  
426 DWG. A final striking observation was the very similar magnitude of the average effect size  
427 in cattle and sheep, which is potentially surprising given the generally greater capacity for  
428 fluke to cause more severe disease in sheep than cattle (Howell and Williams, 2020).

429

430 While we found a significant impact of fluke infection on carcass weight, the overall effect  
431 was negligible, with infected animals having carcass weights only 0.6% lower than  
432 uninfected animals. The statistical significance of such a small effect size is likely related to  
433 the fact that the majority of the data came from abattoir studies, with very large sample sizes  
434 and very small effect size variances. The utility of carcass weight as a metric for assessing  
435 performance may be questionable, given that most producers will take animals to slaughter  
436 only when they have reached a target weight – and indeed will be penalised for not doing so  
437 – yet carcass weight is still commonly reported as a measure of performance. The only  
438 noteworthy moderator variable was that of fluke species: animals with *F. gigantica* actually  
439 had higher carcass weights than uninfected animals. That said, all of the effect sizes  
440 concerning *F. gigantica* came from a single study (Molina, 2005), in which three groups of  
441 cattle of different ages were heavier when infected with *F. gigantica* compared to their  
442 uninfected counterparts. In the same abattoir study, water buffalo (*Bubalus bubalis*, which  
443 were not included in the meta-analysis) had lighter carcasses when infected with fluke, and  
444 no explanation was apparent or discussed (Molina, 2005). The overall effect size for total  
445 weight gain was substantial, with 14% lower total weight gain in fluke-infected animals,

446 although this was marginally non-significant. Once again, we saw a considerably stronger  
447 effect in infection experiments compared to drug studies.

448

449 While traits relating to body weight were well represented, we had a much smaller dataset  
450 for milk yield. Many studies have tested the impact of fluke infection on milk yield and have  
451 found substantial effects (Arenal et al., 2018; Charlier et al., 2007; Howell et al., 2015;  
452 Köstenberger et al., 2017; Mezo et al., 2011), but these have studied effects at the herd level  
453 using bulk tank milk samples and so were not included in our analysis. Other studies of  
454 individual animals did not report the necessary statistics for us to calculate effect size  
455 variance (Khan et al., 2010). Perhaps due to the small number of studies included in our  
456 analyses, we found no overall influence for an effect of fluke on milk yield. A future meta-  
457 analysis of the many bulk tank studies could prove informative in determining overall herd-  
458 level effects.

459

460 The effect of fluke infection has been measured with respect to other performance traits, as  
461 reviewed recently (Charlier et al., 2013; Skuce and Zadoks, 2013), but for these there were  
462 insufficient studies in our initial scoping search for them to be included in the full search and  
463 analysis. For example, there have been many studies of the influence of fluke infection on  
464 wool weight, but during our initial searches, we found that most of these did not report the  
465 standard deviation (or standard errors and sample sizes) that were required to calculate  
466 effect size variance. These older studies did typically report substantial effects of fluke  
467 infection on wool yield: two studies administering a range of infection doses reported lower  
468 yields in infected animals, particularly at higher infectious doses (Edwards et al., 1976;  
469 Hawkins and Morris, 1978) and a study testing the effect of flukicide treatment found that  
470 treatment enhanced wool growth (Hawkins, 1984). Two further studies reported increasing  
471 effects of fluke infection on wool yield over time (Hagh-Nazari and Dalimi, 2000; Roseby,  
472 1970), suggesting that larger effects are seen once adult fluke are established in the liver  
473 from 11-12 weeks post-infection (Kaplan, 2001). In addition, several studies report a

474 negative influence of fluke on reproduction (Marley et al., 1994), including a 39 day delay in  
475 first oestrus in cattle (López-Díaz et al., 1998), a 4.7 day increase in calving interval (Charlier  
476 et al., 2007) and an increase in pregnancy rate from 57% in control ewes to 80% in flukicide-  
477 treated ewes (Hope Cawdery, 1976). Some studies, however, report no significant influence  
478 of fluke infection on reproductive traits (Loyacano et al., 2002; Mezo et al., 2011). Another  
479 performance trait that we did not consider was time to reach slaughter weight, which has  
480 been found to be delayed by 33-93 days in fluke-infected animals, depending on the severity  
481 of infection (Mazeri et al., 2017), but once again, there were too few studies to consider this  
482 as an outcome trait.

483

484 Only a small number of meta-analyses have provided quantitative reviews of the impacts of  
485 disease on performance in livestock and in general have reported stronger effects than we  
486 saw here. A meta-analysis of 75 trials studying the impact of anthelmintic treatment on milk  
487 production in dairy cows reported an increased daily yield of 0.35kg in treated compared to  
488 untreated animals, suggesting a negative influence of helminth infection (almost exclusively  
489 gastrointestinal nematodes based on the studies included) on performance (Sanchez et al.,  
490 2004). A meta-analysis of 18 studies examining the influence of endoparasite – largely  
491 nematode – infection on weight gain in pigs reported a 31% reduction in infected animals,  
492 which was largely due to reduced feed intake in infected animals (Kipper et al., 2011). More  
493 closely related to our study, a meta-analysis of 94 effect sizes examining effects of  
494 nematode infections on sheep performance across Europe found that nematode infection  
495 was associated with a 15% reduction in weight gain, 10% lower wool production and 22%  
496 lower milk yield (Mavrot et al., 2015). While this latter study was unable to estimate the  
497 impact of moderator variables on outcomes, it was able to show that increased parasite  
498 burden, measured as faecal egg count, was associated with a greater negative impact of  
499 infection in “highly parasitized” compared to “low parasitized” individuals (Mavrot et al.,  
500 2015). We were unable to estimate the impact of fluke burden as a moderator in our study  
501 because of the large variation between studies in their design: in most studies, individuals

502 were simply assigned as “infected” or “uninfected”, and in experimental infection studies, a  
503 range of infection doses were given, either as single infections or as trickles across varying  
504 time scales.

505

## 506 **CONCLUSION**

507

508 This meta-analysis has provided quantitative estimates of the impact of liver fluke infection  
509 on the performance of sheep and cattle by collating relevant data from both published and  
510 unpublished sources. We found that effects on live weight gain and live weight were the  
511 most pronounced, while effects on carcass weight and milk production were either negligible  
512 or non-significant. Since we focused on individual-based assessments of infection, there  
513 remains a great deal of data to be exploited for meta-analysis of influences of fluke at the  
514 herd level, particularly regarding bulk-tank milk samples. Our results also reveal that studies  
515 administering experimental infections, and studies of younger animals, are more likely to  
516 reveal effects of fluke that differ from zero, and that detecting effects of natural infection may  
517 be more difficult. Improved diagnostics of fluke infection, particularly those which can  
518 quantify the level of infection, may be required to gain a more accurate estimate of the  
519 impact of subclinical fluke infection on performance in the future, aiding understanding of  
520 between-host variation in resistance and tolerance of infection and aiding the effort to design  
521 improved mitigation strategies for fluke infection.

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537

538 **DECLARATION OF INTERESTS**

539

540 The authors have no competing interests to declare.

541

542 **AUTHOR CREDIT STATEMENT**

543

544 **Adam Hayward:** conceptualization, formal analysis, investigation, data curation, writing –  
545 original draft, writing – review and editing, visualization

546 **Philip Skuce:** writing – review and editing; supervision

547 **Tom McNeilly:** writing – review and editing, supervision

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## TABLES

**Table 1.** A summary of the studies from which data was used for the meta-analysis. ‘Experiments’ are as described in the main text, while traits are as follows: CW = carcass weight; DWG = daily weight gain; LW = live weight; milk = milk production; TWG = total weight gain. The data source was either the publication (taken from the text, tables of figures in the publication) or the authors (send upon request by authors). ‘N’ is the number of effect sizes contributed by each study.

Reference	Host	Fluke	Country	Experiment	Traits	Data source	N
(Bellet et al., 2016)	Cattle	<i>F. hepatica</i>	UK	Natural	CW	Authors	4
(Berry, 1977)	Sheep	<i>F. hepatica</i>	UK	Infection	LW	Publication	3
(Bossaert et al., 2000)	Cattle	<i>F. hepatica</i>	Belgium	Infection	DWG	Publication	2
(Chick et al., 1980)	Cattle	<i>F. hepatica</i>	Australia	Infection	LW	Publication	8
(Crossland et al., 1977)	Sheep	<i>F. hepatica</i>	UK	Drug	LW	Publication	12
(da Costa et al., 2019)	Cattle	<i>F. hepatica</i>	Uruguay	Natural	CW	Authors	12
(Echevarria et al., 1992)	Cattle	<i>F. hepatica</i>	Brazil	Drug	CW, DWG, TWG	Publication	9
(El-Tahawy et al., 2017)	Cattle	<i>Fasciola</i> spp.	Egypt	Natural	LW, Milk	Publication	2
(Forbes et al., 2015)	Cattle	<i>F. hepatica</i>	UK	Drug	TWG	Publication	2
(Genicot et al., 1991)	Cattle	<i>F. hepatica</i>	Belgium	Natural, Drug	DWG	Publication	4
(Hope Cawdery et al., 1977)	Cattle	<i>F. hepatica</i>	UK	Infection	LW, TWG	Publication	6
(Jacob et al., 2015)	Cattle	<i>F. gigantica</i>	India	Infection	DWG, LW, TWG	Publication	6
(Jacob et al., 2014)	Cattle	<i>F. gigantica</i>	India	Infection	DWG, LW, TWG	Publication	6
(López-Abán et al., 2007)	Sheep	<i>F. hepatica</i>	Spain	Infection	DWG	Publication	1
(López-Díaz et al., 1998)	Cattle	<i>F. hepatica</i>	Spain	Infection	LW	Publication	1
(Mage et al., 1993)	Cattle	<i>F. hepatica</i>	France	Drug	DWG, TWG	Publication	2
(May et al., 2019)	Cattle	<i>F. hepatica</i>	Germany	Natural	Milk	Publication	1
McIntosh-Donald Ltd	Cattle	<i>F. hepatica</i>	UK	Natural	CW, DWG	Authors	40
(Molina et al., 2005)	Cattle	<i>F. gigantica</i>	Philippines	Natural	CW	Publication	3
(Paczkowski, 2005)	Cattle	<i>F. hepatica</i>	USA	Infection	LW	Publication	1

(Randall and Bradley, 1980)	Cattle	<i>F. hepatica</i>	USA	Drug	Milk	Publication	2
(Reid et al., 1972)	Cattle	<i>F. hepatica</i>	UK	Infection	TWG	Publication	4
(Sanchez-Vazquez and Lewis, 2013)	Cattle	<i>F. hepatica</i>	UK	Natural	CW, DWG	Authors	40
Scotbeef Ltd	Cattle	<i>F. hepatica</i>	UK	Natural	CW, DWG	Authors	40
(Sykes et al., 1980)	Sheep	<i>F. hepatica</i>	UK	Infection	LW	Publication	12
(Twomey et al., 2018)	Cattle	<i>F. hepatica</i>	Ireland	Natural	CW, Milk	Authors	4
(Wamae et al., 1998)	Cattle	<i>F. gigantica</i>	Kenya	Infection	LW, TWG	Publication	4
(Wiedosari et al., 2006)	Cattle	<i>F. gigantica</i>	Indonesia	Infection	DWG	Publication	2
<b>Total</b>							<b>233</b>

**Table 2.** Summary of parameters included in meta-analysis of six production traits. 'N' and 'studies' refers to the maximum number of effect sizes available for each trait, and the number of studies measuring each trait.

<b>Trait</b>	<b>N</b>	<b>Studies</b>	<b>Random effects</b>	<b>Moderators tested in meta-regression</b>
Daily weight gain (DWG)	77	11	Study + Residual	Parasite, Age, Experiment, Sex, Latitude, Week
Live weight	47	11	Study + Residual	Parasite, Host, Age, Experiment, Sex, Latitude, Week
Carcass weight	84	8	Study + Residual	Parasite, Age, Experiment, Sex, Latitude
Total weight gain (TWG)	18	8	Study + Breed + Residual	Parasite, Experiment, Sex, Latitude, Week
Milk production	6	4	Residual	Experiment, Latitude

**Table 3:** Results from meta-analysis of daily weight gain (DWG). 'N' is the number of effects sizes available for analysis. 'Global' indicates the overall effect size from the initial random effects model, while the subsequent moderator effects are from mixed-effects models where each moderator was fitted in turn. 'Effect sizes' and 'Studies' varies because information was not available for some of the effect sizes. 'Q<sub>M</sub>' and the associated 'DF' and 'P' values refer to the Wald-type test for significant differences in effect size due to moderator, while 'z' and 'P' values refer to tests for differences from zero for different levels of each moderator.

Moderator	N	Studies	Q <sub>M</sub>	DF	P	Level	Estimate (logRR)	Lower 95%CI	Upper 95%CI	z	P
Global	77	11					-0.0981	-0.1554	-0.0408	-3.36	<0.001
Parasite	77	11	1.27	1	0.259	<i>F. gigantica</i>	-0.1622	-0.2859	-0.0384	-2.57	0.010
						<i>F. hepatica</i>	-0.0800	-0.1511	-0.0089	-2.21	0.027
Age	76	10	5.29	1	0.021	Juvenile	-0.1512	-0.2177	-0.0846	-4.45	<0.001
						Mixed	-0.0404	-0.1073	0.0264	-1.19	0.236
Experiment	77	11	1.61	2	0.446	Drug	-0.0818	-0.2147	0.0512	-1.21	0.228
						Infection	-0.1516	-0.2527	-0.0505	-2.94	0.003
						Natural	-0.0658	-0.1531	0.0215	-1.48	0.139
Sex	74	10	2.77	1	0.096	Female	-0.0933	-0.1541	-0.0324	-3.01	0.003
						Male	-0.1039	-0.1641	-0.0437	-3.38	<0.001
Latitude	77	11	2.22	1	0.149	Continuous	0.0043	-0.0003	0.0090	1.82	0.149
Week	13	6	2.09	1	0.148	Continuous	0.0061	-0.0022	0.0144	1.45	0.148

**Table 4.** Results from meta-analysis of live weight. 'N' is the number of effects sizes available for analysis. 'Global' indicates the overall effect size from the initial random effects model, while the subsequent moderator effects are from mixed-effects models where each moderator was fitted in turn. 'Effect sizes' and 'Studies' varies because information was not available for some of the effect sizes. 'Q<sub>M</sub>' and the associated 'DF' and 'P' values refer to the Wald-type test for significant differences in effect size due to moderator, while 'z' and 'P' values refer to tests for differences from zero for different levels of each moderator.

Moderator	N	Studies	Q <sub>M</sub>	DF	P	Level	Estimate (logRR)	Lower 95%CI	Upper 95%CI	z	P
Global	47	11					-0.0611	-0.0877	-0.0344	-4.48	<0.001
Parasite	46	10	0.01	1	0.913	<i>F. gigantica</i>	-0.0519	-0.1109	0.0070	-1.73	0.084
						<i>F. hepatica</i>	-0.0556	-0.0860	-0.0253	-3.59	0.003
Host	47	11	0.01	1	0.910	Cattle	-0.0598	-0.0960	-0.0236	-3.24	0.001
						Sheep	-0.0631	-0.1076	-0.0186	-2.78	0.005
Age	47	11	2.38	1	0.123	Adult	-0.0222	-0.0757	0.0312	-0.81	0.415
						Juvenile	-0.0704	-0.0973	-0.0435	-5.12	<0.001
Experiment	46	10	1.84	1	0.174	Drug	-0.0225	-0.0743	0.0293	-0.85	0.395
						Infection	-0.0642	-0.0915	-0.0368	-4.60	<0.001
Sex	47	11	16.04	2	<0.001	Female	-0.0234	-0.0518	0.0050	-1.62	0.106
						Male	-0.0478	-0.0785	-0.0172	-3.06	0.002
						Mixed	-0.1042	-0.1330	-0.0755	-7.10	<0.001
Latitude	47	11	0.15	1	0.696	Continuous	-0.0003	-0.0021	0.0014	-0.39	0.696
Week	33	8	7.66	1	0.006	Continuous	-0.0023	-0.0039	-0.0007	-2.77	0.006

**Table 5.** Results from meta-analysis of carcass weight. 'N' is the number of effects sizes available for analysis. 'Global' indicates the overall effect size from the initial random effects model, while the subsequent moderator effects are from mixed-effects models where each moderator was fitted in turn. 'Effect sizes' and 'Studies' varies because information was not available for some of the effect sizes. 'Q<sub>M</sub>' and the associated 'DF' and 'P' values refer to the Wald-type test for significant differences in effect size due to moderator, while 'z' and 'P' values refer to tests for differences from zero for different levels of each moderator.

Moderator	N	Studies	Q <sub>M</sub>	DF	P	Level	Estimate (logRR)	Lower 95%CI	Upper 95%CI	z	P
Global	84	8					-0.0060	-0.0099	-0.0021	-3.00	0.003
Parasite	84	8	6.44	1	0.011	<i>F. gigantica</i>	0.1497	0.0294	0.2700	2.44	0.015
						<i>F. hepatica</i>	-0.0062	-0.0101	0.0023	-3.10	0.002
Age	84	8	0.37	2	0.831	Adult	-0.0042	-0.0127	0.0044	-0.96	0.340
						Juvenile	-0.0081	-0.0209	0.0048	-1.23	0.219
						Mixed	-0.0063	-0.0114	-0.0011	-2.40	0.017
Experiment	84	8	0.01	1	0.914	Drug	-0.0178	-0.2332	0.1975	-0.16	0.871
						Natural	-0.0060	-0.0099	-0.0021	-2.99	0.003
Sex	81	7	0.32	2	0.851	Female	-0.0056	-0.0102	-0.0009	-2.34	0.019
						Male	-0.0066	-0.0113	-0.0019	-2.78	0.006
						Mixed	-0.0043	-0.0170	0.0084	-0.67	0.506
Latitude	84	8	1.30	1	0.254	Continuous	-0.0003	-0.0008	0.0002	-1.13	0.257

## FIGURE LEGENDS

**Figure 1.** Estimated response ratio (RR) from meta-regression analysis of fluke-infected and uninfected animals for daily weight gain (DWG). A response ratio of 1 indicates equal performance in infected and uninfected animals; values <1 indicate poorer performance in infected animals. Plots show estimated mean effect of the global effect on infection (Intercept), plus the effect of infection in different moderators, with 95%CI.

**Figure 2.** Estimated response ratio (RR) from meta-regression analysis of fluke-infected and uninfected animals for live weight. A response ratio of 1 indicates equal performance in infected and uninfected animals; values <1 indicate poorer performance in infected animals. Plots show estimated mean effect of the global effect on infection (Intercept), plus the effect of infection in different moderators, with 95%CI.

**Figure 3.** Estimated response ratio (RR) from meta-regression analysis of fluke-infected and uninfected animals for carcass weight. A response ratio of 1 indicates equal performance in infected and uninfected animals; values <1 indicate poorer performance in infected animals. Plots show estimated mean effect of the global effect on infection (Intercept), plus the effect of infection in different moderators, with 95%CI.







