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Hidden in plain sight - Multiple resistant species within a strongyle community

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ABSTRACT

Ovine parasitic gastroenteritis is a complex disease routinely treated using anthelmintics. Although many different strongyle species may contribute to parasitic gastroenteritis, not all are equally pathogenic: in temperate regions, the primary pathogen is Teladorsagia circumcincta. In this study we investigated benzimidazole and ivermectin resistance on a commercial sheep farm in southeast Scotland. We assessed the impact of species diversity on the diagnosis of resistance using the faecal egg count reduction test and in vitro bioassays, and correlated the results with the frequency of benzimidazole resistance-associated genotypes measured in the T. circumcincta population by pyrosequencing of the β-tubulin isotype-1 gene.

Faecal egg count reduction test results showed efficacies of 65% for albendazole and 77% for ivermectin, indicating moderate resistance levels on the farm. However, PCR speciation of the same populations pre- and post-treatment revealed that removal of susceptible species had masked the presence of a highly resistant population of T. circumcincta. Less than 25% of individuals in the pre-treatment populations were T. circumcincta, the remainder consisting of Cooperia curticei, Chabertia ovina, Oesophagostomum venulosum and Trichostrongylus spp. In contrast, post-treatment with albendazole or ivermectin, the majority (88% and 100% respectively) of the populations consisted of T. circumcincta. The egg hatch test for benzimidazole resistance and the larval development test for ivermectin resistance were carried out using eggs obtained from the same populations and the results were broadly consistent with the faecal egg count reduction test. Thirty individual T. circumcincta from each sampling time point were assessed for benzimidazole resistance by pyrosequencing, revealing a high frequency and diversity of resistance-associated mutations, including within the population sampled post-ivermectin treatment.

These results highlight the potential diversity of parasite species present on UK farms, and their importance in the diagnosis of anthelmintic resistance. On this particular farm, we demonstrate the presence of a highly dual-resistant population of T. circumcincta, which was strongly selected by treatment with either benzimidazoles or ivermectin, while other potentially less pathogenic species were removed.

1. Introduction

Parasitic gastroenteritis (PGE) is ubiquitous on UK sheep farms and is a significant production limiting disease (Sargison, 2011), resulting in poor weight gain, diarrhoea, dehydration, anaemia and death (Durham and Elliott, 1975). PGE is a complex disease, influenced by many host and management factors and caused by a diverse range of strongyle species (Burgess et al., 2012), of which Teladorsagia circumcincta predominates during the UK summer. The clinical diagnosis in live animals is underpinned by faecal egg counts (FECs) to detect and enumerate strongyle eggs.

Broad-spectrum anthelmintics, including benzimidazoles (BZ) and ivermectin (IVM), are used to treat PGE but resistance is widespread (Kaplan and Vidyashankar, 2012). Two recent studies in Wales and Northern Ireland found between 81 and 94% of farms tested had BZ resistance and 50–51% had IVM resistance (McMahon et al., 2013; Hybu Cig Cymru (HCC), 2015). In practice, anthelmintic efficacy is determined using a faecal egg count reduction test (FECRT). This involves faecal sampling a group of animals pre- and post-treatment (Coles et al., 2006), or comparison of a post-treatment group with a

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control group (Coles et al., 1992). The reduction in strongyle FEC is calculated to determine the anthelmintic efficacy. If the reduction is less than 95%, and the lower 95% confidence interval is less than 90%, anthelmintic resistance is diagnosed (Coles et al., 1992).

The FECRT is a straightforward and useful test, but it has limitations. FECRTs depend on a reduction in strongyle eggs, but these generally consist of a mixed population of strongyle species. Importantly, not all strongyles are considered equally pathogenic in sheep (Crilly and Sargison, 2015), and not all species on a holding are necessarily drug resistant (McKenna, 1997; McMahon et al., 2013; Melville et al., 2016). The FECRT also lacks sensitivity if resistant phenotypes comprise less than 25% of the population (Martin et al., 1989). This phenomenon has been noted in the disparity between BZ resistance genotypes detected by PCR and FECRT results (Kaplan and Vidyashankar, 2012). BZ resistance is associated with non-synonymous single nucleotide polymorphisms (SNPs) within the \( \beta \)-tubulin isotype-1 gene, which appear conserved within and between strongyle species and can be detected by PCR or pyrosequencing (Kwa et al., 1995; Silvestre and Cabaret, 2002; Ghisi et al., 2007; Redman et al., 2015). Molecular tests are highly sensitive and specific, but are only currently available for BZ resistance. While laboratory bioassays for anthelmintic resistance are a possible alternative, they are time consuming and can be technically challenging in mixed species infections.

This study describes a FECRT undertaken on a commercial sheep farm in southeast Scotland to compare BZ and IVM resistance status detected in the field, combined with \textit{in vitro} phenotypic bioassays and pyrosequencing of the \( \beta \)-tubulin isotype-1 gene. The results highlight the importance of parasite species composition in the interpretation of FECRTs and in the design of appropriate and sustainable control strategies.

2. Materials and methods

2.1. Study Farm

A lowland sheep farm in southeast Scotland was visited in September 2016, with the agreement of the shepherd and previous knowledge of the presence of anthelmintic resistance (Wilson et al., 2008; Sargison et al., 2012). Each year in the autumn, a proportion of the breeding flock was replaced with bought in ewe lambs. Sheep were able to graze rented pastures, which were also leased to neighbouring sheep farms. In addition, cattle occasionally grazed farm pastures, though had not done so in the last two years. Moxidectin is used routinely at lambing time, with most twin-bearing ewes treated and some triplet- or single-bearing ewes also treated. BZs are used to control \textit{Nematodirus battus} in the lambs, with three treatments used in the year of study. Further anthelmintics are used to control summer PGE in the lambs, and rams are dosed periodically with anthelmintics. Table 1 shows the anthelmintics given during the year of study.

### Table 1

<table>
<thead>
<tr>
<th>Date of treatment</th>
<th>Anthelmintic</th>
<th>Treatment group</th>
</tr>
</thead>
<tbody>
<tr>
<td>1(^{st}) April onwards – at lambing</td>
<td>Moxidectin</td>
<td>Lambed ewes</td>
</tr>
<tr>
<td>23/05/16</td>
<td>Albendazole</td>
<td>Lambs</td>
</tr>
<tr>
<td>14/06/16</td>
<td>Albendazole</td>
<td>Lambs</td>
</tr>
<tr>
<td>01/07/16</td>
<td>Ivermectin</td>
<td>Rams</td>
</tr>
<tr>
<td>06/07/16</td>
<td>Albendazole</td>
<td>Lambs</td>
</tr>
<tr>
<td>20/09/16</td>
<td>Levamisole</td>
<td>Lambs</td>
</tr>
<tr>
<td>20/09/16</td>
<td>FECRT – albendazole or ivermectin</td>
<td>Two groups of lambs</td>
</tr>
</tbody>
</table>

2.2. Faecal egg count reduction test

Thirty-five, five-and-a-half month old lambs were set aside by the farmer and from these, animals were selected randomly for use in the FECRT. Faeces were collected per rectum for FECs pre-treatment, with additional material gathered for further analysis, if voided immediately following treatment. Ten lambs were allocated to the albendazole (BZ) treatment group (5 mg/kg body weight (BW), Albex™ 2.5% w/v SC oral suspension (Chanelle UK)) and twelve lambs to the IVM treatment group (0.2 mg/kg BW, Noromectin® 0.08% w/v Drench Oral Solution (Norbrook)). Lambs were identified to their group but not individually. All were weighed individually, using the shepherd’s weigh scales (EID weigh crate, Shearwell), and dosed \textit{per os} according to their individual weights using a syringe. Repeat faecal samples were collected on days 7 and 14 post-treatment and faeces transferred anaerobically to the laboratory.

A cuvette method, sensitive to 1 egg per gram (epg) (Christie and Jackson, 1982) was used for the FECs. Briefly, faeces were weighed and water was added in a ratio of 10 ml to 1 g, following which 10 ml was strained through a coarse sieve (1 mm aperture). After centrifugation at 234 \( \times \) g for 2 min, the supernatant was aspirated and the egg pellet re-suspended in saturated sodium chloride solution (specific gravity 1.2) with a further centrifugation step (as above). The meniscus was isolated using artery forceps and tipped into a cuvette, which was filled with saturated NaCl solution for counting. Strongyle egg counts were analysed using Minitab (Minitab® 17.1.0, Microsoft). Group arithmetic means were calculated, with 95% confidence intervals (CIs). Differences between medians of sample groups were assessed for significance by a Mann-Whitney test. The FECR percentage and Bayesian CIs were calculated using R Shiny ‘eggCounts’ web interface (Wang and Paul, 2017; Wang et al., 2017).

2.3. Bioassays

Strongyle eggs were harvested for immediate use in bioassays (within three hours of faecal collection) as described in 2.2, but with the following modifications; emulsified faeces were strained through a series of sieves, (215 \( \mu \)m, 125 \( \mu \)m and 63 \( \mu \)m), with eggs collected from a 38 \( \mu \)m sieve. Centrifugation steps were performed as described above, and the meniscus was poured back onto a small, 38 \( \mu \)m sieve. Eggs were washed with tap water to remove salt and collected. A 200 \( \mu \)l aliquot of egg suspension was counted, using the cuvette method, to determine the total number of eggs/ml. The egg concentration was adjusted to 1 egg/\( \mu \)l for the egg hatch test (EHT) and 2 eggs/\( \mu \)l for the larval development test (LDT).

2.3.1. Egg hatch test

An EHT was set up to measure BZ efficacy, essentially as described previously (Coles et al., 2006). Stock solutions of TBZ were prepared by diluting 1 mg/ml of TBZ/DMSO solution into DMSO and were stored in opaque tubes. Briefly, a 24 well plate was set up with a range of final TBZ concentrations as follows: 0.05 \( \mu \)g/ml, 0.1 \( \mu \)g/ml, 0.2 \( \mu \)g/ml, 0.3 \( \mu \)g/ml, 0.4 \( \mu \)g/ml, 0.5 \( \mu \)g/ml and 0.5% DMSO control (Sigma Aldrich). To each well was added: 10 \( \mu \)l of egg suspension, 1890 \( \mu \)l deionised water (Acros Organics) and 100 \( \mu \)l of egg suspension, giving approximately 100 eggs/well.

Four EHTs were performed using pre-treatment samples for each of the BZ and IVM treated lamb groups. For each of the eight tests, all concentrations were repeated in triplicate, when sufficient eggs were available. Plates were incubated in a humid environment at 25 °C for 48 h and the number of unhatched eggs and first stage larvae (L1) recorded at 48 h.

On day 14 post-treatment a reduced EHT was performed for the BZ treated population as follows: all TBZ concentrations were incorporated but a reduced quantity of eggs restricted replicate numbers. Two replicates were carried out for each of 0.05 \( \mu \)g/ml, 0.1 \( \mu \)g/ml and 0.2 \( \mu \)g/
ml. The rest were single wells. Due to a paucity of eggs post-IVM treatment of lambs, it was not possible to perform a full EHT and only two replicates of the ‘definitive dose’ wells (0.1 μg/ml) were included.

The ED50, the effective dose at which 50% of larvae fail to hatch, was calculated using a binomial (probit) general linear model (GLM) in R Studio (version 1.1.383 – © 2009–2017 RStudio, Inc; R version 3.4.3 © 2017). All data were first corrected for the percentage hatch in the DMSO control wells and the TBZ concentrations were log10 transformed. If the ED50 was greater than 0.1 μg/ml TBZ, then the sample population was considered resistant to BZ (Coles et al., 1992; von Samson-Himmelstjerna et al., 2009).

2.3.2. Larval development test

The LDT was performed on strongyle populations obtained pre- and post-IVM treatment (day 0 and day 14) and pre-BZ treatment. Insufficient eggs were recovered post-BZ treatment to allow a LDT to be carried out. A method adapted from Varady et al. (1996) was used to ascertain the ability of larvae to develop in the following concentrations of IVM: 0.57 nM, 1.14 nM, 2.29 nM, 4.54 nM, 9.14 nM, 18.29 nM and 36.58 nM water (control), and 2% DMSO (control). Stock solutions of IVM (Catalogue number 18898, Sigma Aldrich) were prepared by diluting a 0.001 M IVM/DMSO solution into DMSO and were stored in opaque tubes. Briefly, a 48 well plate was set up, each well containing 6 μl of IVM/DMSO solution, 239 μl deionised water and 5 μl of a highly concentrated, reconstituted, lyophilised E. coli OP50 as a food source for the developing larvae (Heim et al., 2015). 50 μl of strongyle eggs were added (concentration of 2 eggs/μl), giving approximately 100 eggs/well. No antimicrobials were used. Wells surrounding those source for the developing larvae (Heim et al., 2015). 50 μl DirectPCR Lysis Reagent (Promega) were used to estimate individual egg counts pre- and post-treatment.

2.4. Molecular biology

2.4.1. Lysates

Lysates were made from individual strongyle eggs, L1 or infective larvae (L3) in 96 well plates from all sampling time points. On day 0, day 7 and day 14 post-treatment, L3 from coproculture were used. On day 14 post-treatment, eggs and L1 from EHTs were used. Briefly, a master mix per 100 wells was prepared as follows: 1000 μl DirectPCR Lysis Reagent (Cell; Viaion Biotech), 50 μl 1 M DTT (Thermo Fisher Scientific) and 10 μl Proteinase K (Fungal; Invitrogen) at 100 mg/ml in DEPC treated water (Ambion). 10 μl was dispensed per well and a single egg or larva lysate was stored at −80 °C.

2.4.2. Speciation of strongyles by PCR

Individual eggs, L1 or L3, harvested as described in 2.4.1, were identified by PCR to species level using the ITS2 region (Wimmer et al., 2004; Redman et al., 2008; Burgess et al., 2012; Bisset et al., 2014). Strongyle numbers speciated were as follows: for the BZ FECRT on day 0, 96 L3, on day 7, 62 L3 and on day 14, 82 eggs or L1. For the IVM FECRT on day 0, 83 L3 were speciated, on day 7, 83 L3 and on day 14, 42 eggs or L1. Two PCR methods were employed. Briefly, single species PCR was performed using GoTaq Flexi polymerase (Promega) according to the manufacturer’s instructions. The total volume of each reaction was 12.5 μl of which 1 μl was 1:20 DNA lysate. Primers designed to amplify the ITS2 region and specific to the species of interest were used. Table 2 shows primer sequences with their original reference, expected amplicon size, and Ta° C. All PCRs were carried out using the following protocol: denaturation at 94 °C for 2 min, then 35 cycles each of 94 °C 30 s, Ta° C 30 s and 72 °C 30 s, with a final extension step of 72 °C 10 min.

Multiplex PCR was also performed, adapted from a protocol optimised by Bisset et al. (2014). Briefly, each 12.5 μl reaction contained: 2.5 μl SX GoTaq Green buffer, 1.25 μl MgCl2 25 mM, 0.0625 μl GoTaq Flexi polymerase 5 U/μl (Promega), 0.25 μl dNTPs 10 mM each (NEB Inc.), 0.15 μl Generic Forward primer 10 μM, 0.15 μl Generic Reverse primer 10 μM, 0.25 μl Trichostrongylus axei Forward primer 10 μM, 0.35 μl Cooperia curticei Forward 3 primer 10 μM, 0.1 μl Oesophagostomum venulosum Reverse 1 primer 10 μM, 0.15 μl Chabertia ovina Forward 2 primer 10 μM, (Eurofins Genomics) and 6.2875 μl DEPC treated water (Ambion). To this 1 μl of diluted DNA lysate was added. Touchdown PCR conditions were: denaturation at 94 °C for 2 min, then 12 cycles each of 94 °C 15 s, 60 °C, decreasing by 0.5 °C each cycle, to 54.5 °C for 15 s and lastly 72 °C 30 s. Next, 25 cycles each of 94 °C 15 s, 54 °C 15 s, 72 °C 30 s, with a final extension step of 72 °C for 7 min. Products were visualised with SafeView (NBS Biologicals) on 2% agarose gels for single species PCR and 2.5% agarose gels for multiplexed PCR.

Any unidentified strongyles (i.e. positive on the multiplex PCR as a strongylid nematode) were amplified with Phusion High-Fidelity Polymerase (NEB Inc.) using the generic ITS2 primer set (Bisset et al., 2014) and sequenced by Eurofins Genomics. A BLAST search using NCBI was performed for identification. Speciation results were analysed in Microsoft Excel and proportions of each species, determined by PCR, were used to estimate individual T. circumcincta egg counts pre- and post-treatment. A 2-sample proportion test was performed in Minitab to compare speciation results pre- and post-treatment.

2.4.3. Pyrosequencing

Using a method adapted from Skuce et al. (2010), BZ resistance associated SNPs were pyrosequenced in 30 T. circumcincta individuals from each sampling time point (eggs, L1 or L3, as described in 2.4.1), providing a total of 180 individuals for analysis. For the speciation PCRs, on days 0 and 7 of each FECRT, a combination of eggs and L1 were selected, but on day 14 post-treatment for each FECRT, a combination of eggs and L1 was used, totalling 30 individuals. Two regions of the β-tubulin isotype-1 gene (one region including codons 200 and 198, and the other including codon 167) were amplified using the Pyromark PCR kit (Qiagen) according to the manufacturer’s instructions. Briefly, a 25 μl reaction was set up using 12.5 μl 2X Pyromark Master Mix, 0.5 μl of each primer, 10.5 μl DEPC treated water (Ambion) and 1 μl of diluted DNA lysate. PCR conditions were: denaturation at 95 °C for 15 min, then 45 cycles of 94 °C for 30 s, 55 °C for 30 s and 72 °C for 30 s, with a final extension step of 72 °C for 10 min. Pyrosequencing was performed on a Biotage Q96 ID instrument (Qiagen) according to the manufacturer’s protocol’s with pyrograms evaluated manually. The sequences analysed were: 200/198 ‘CAGWAYGTYDRTCGG’ for codons F200Y and E198 A/L, and ‘TCATWCTC’ for codon F167Y. Primers used are shown in Table 2. A 2-sample proportion test was performed in Minitab to compare pyrosequencing results pre- and post-treatments.

3. Results

3.1. FECRT indicates resistance to anthelmintics tested

The FECRTs for both BZ and IVM indicated the presence of anthelmintic resistance (Table 3). The BZ treated lambs showed a reduction of 65% (95% Highest Posterior Density (HPD) Interval: 14.5, 86.2) in their strongyle faecal egg output at day 14 and the IVM group, a 77% (95% HPD Interval: 45.5, 91.6) reduction in faecal egg output.

3.2. Speciation allows interpretation of the FEC by species of interest

Speciation by PCR of ≤ 96 strongyle eggs or larvae was performed
both pre- and post-treatment. Samples analysed from both groups of lambs contained between 20 to 25% \textit{T. circumcincta} pre-treatment with the remaining 75 to 80% composed of a diverse mix of other strongyle species (Figs. 1 and 2). In faecal samples from the BZ treated lambs, both \textit{T. circumcincta} and \textit{C. curticei} were present at 7 days post-treatment, in roughly equal proportions. By day 14 post-treatment, the strongyle population post-BZ was composed of 88% \textit{T. circumcincta} with the remaining 12% comprising a mixture of \textit{C. curticei}, \textit{O. venulosum} and \textit{T. axei} (Fig. 1). In contrast, post-IVM treatment only \textit{T. circumcincta} was present at day 7 and at day 14 (Fig. 2).

3.3. Adjustment of the mean FEC by species improves interpretation of the FECRT

An adjustment of the mean FEC by PCR speciation data shows a decrease of approximately 50% in the \textit{T. circumcincta} egg output, and an 82% reduction in \textit{C. curticei} egg output on day 7 following BZ treatment (Fig. 3). No other species were found at day 7 post-BZ treatment. On day 14 post-BZ treatment, \textit{T. circumcincta} egg output had risen considerably relative to day 0, being estimated at 67 epg by speciation. This was not, however, statistically significant. \textit{C. curticei} egg output had fallen to 5 epg from an initial 148 epg on day 0. Overall, there was a significant reduction in egg output from strongyle species other than \textit{T. circumcincta} (\(p = 0.00\)). Following IVM treatment on the same farm there was no change in egg output for \textit{T. circumcincta}, whilst the egg output of all other species was reduced to zero (Fig. 4).

3.4. Phenotyping bioassays (TBZ EHT, IVM LDT)

An EHT (assessing BZ resistance) and a LDT (assessing IVM resistance) were performed on days 0 and 14 to compare FECRT results with \textit{in vitro} phenotype.

### Table 2

<table>
<thead>
<tr>
<th>Species</th>
<th>Primer name (Sequence)</th>
<th>T(_{m}) (°C)</th>
<th>Label</th>
<th>Product size (bp)</th>
<th>Reference</th>
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<tbody>
<tr>
<td>\textit{Teladorsagia circumcincta}</td>
<td>Tc_ITS2 (F: ATACCCGATGGTGTACACGG)</td>
<td>52</td>
<td>421</td>
<td></td>
<td>Burgess 2012</td>
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<tr>
<td></td>
<td>R: CAGGAGAATCAGGGAAGGTAAT</td>
<td></td>
<td></td>
<td></td>
<td>Burgess 2012</td>
</tr>
<tr>
<td>\textit{Trichostrongylus vitrinus}</td>
<td>Tv_ITS2 (F: AGGACATTTAATGGTTAAC)</td>
<td>52</td>
<td>100</td>
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<tr>
<td></td>
<td>R: CGTTACGTGAAGGTTATATA</td>
<td></td>
<td></td>
<td></td>
<td>Wimmer 2004</td>
</tr>
<tr>
<td>\textit{Haemonchus contortus}</td>
<td>Hc_ITS2 (F: TTTAGCTCTGGCGAGGAC)</td>
<td>50</td>
<td>321</td>
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<td></td>
<td>R: TTATACGGTTCAGACCTA</td>
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<td></td>
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<td>\textit{Oesophagostomum venulosum}</td>
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<td>Btub_SK_200_FOR (F: GTTACAATTTCATAACATCACGT)</td>
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<td></td>
<td>Score 2010</td>
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### Table 3

<table>
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<tr>
<th>Sample ID</th>
<th>N(^a)</th>
<th>Mean Strongyle epg(^b)</th>
<th>SD Strongyle epg</th>
<th>Mann-Whitney test Strongyle epg(^c)</th>
<th>Proportional T. circumcincta Mean epg(^d)</th>
<th>SD T. circumcincta epg</th>
<th>Mann-Whitney test T. circumcincta epg(^e)</th>
<th>Strongyle FECR % (Bayesian 95% HPD Interval)(^f)</th>
<th>Teladorsagia circumcincta FECR % (Bayesian 95% HPD Interval)(^g)</th>
<th>Cooperia curtici FECR % (Bayesian 95% HPD Interval)(^h)</th>
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<tr>
<td>BZ D0</td>
<td>10</td>
<td>209</td>
<td>182</td>
<td><strong>p = 0.005</strong></td>
<td><strong>p = 0.005</strong></td>
<td>41.3</td>
<td>36</td>
<td><strong>p = 0.056</strong></td>
<td><strong>p = 0.212</strong></td>
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<tr>
<td>BZ D7</td>
<td>8</td>
<td>47.1</td>
<td>75.4</td>
<td><strong>p = 0.534</strong></td>
<td>21.3</td>
<td>34</td>
<td><strong>p = 0.625</strong></td>
<td><strong>p = 0.625</strong></td>
<td><strong>p = 0.625</strong></td>
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<td>BZ D14</td>
<td>10</td>
<td>77</td>
<td>156</td>
<td><strong>p = 0.534</strong></td>
<td>67</td>
<td>137</td>
<td><strong>p = 0.625</strong></td>
<td><strong>p = 0.625</strong></td>
<td><strong>p = 0.625</strong></td>
<td><strong>p = 0.625</strong></td>
</tr>
<tr>
<td>IVM D0</td>
<td>12</td>
<td>202</td>
<td>186</td>
<td><strong>p = 0.003</strong></td>
<td><strong>p = 0.002</strong></td>
<td>51</td>
<td>47</td>
<td><strong>p = 0.976</strong></td>
<td><strong>p = 0.583</strong></td>
<td><strong>p = 0.583</strong></td>
</tr>
<tr>
<td>IVM D7</td>
<td>11</td>
<td>53.8</td>
<td>53.6</td>
<td><strong>p = 0.666</strong></td>
<td>53.8</td>
<td>53.6</td>
<td><strong>p = 0.666</strong></td>
<td><strong>p = 0.666</strong></td>
<td><strong>p = 0.666</strong></td>
<td><strong>p = 0.666</strong></td>
</tr>
<tr>
<td>IVM D14</td>
<td>12</td>
<td>48.4</td>
<td>57.9</td>
<td><strong>p = 0.666</strong></td>
<td>48.4</td>
<td>57.9</td>
<td><strong>p = 0.666</strong></td>
<td>77.2</td>
<td>9.17</td>
<td>91.8</td>
</tr>
</tbody>
</table>

\(^{a}\)Number of lambs sampled. Lambs were brought in from the field at each sampling time point by the farmer. On day 7 not all lambs were present or contained sufficient material per rectum for an adequate sample to be obtained.

\(^{b}\)Epg per gram.

\(^{c}\)Comparing egg count medians between sampling dates; \(p\) value reported. Risk Difference = \(\eta(D0) – \eta(D14)\), 95% confidence intervals, hypothesis of ‘medians not equal’ using Minitab. Numbers in bold indicate significant differences between sample medians.

\(^{d}\)Mean epg calculated for each individual sample using the strongyle species proportions obtained from PCR of the ITS2 region of L3 (D0, D7) and eggs/L1 (D14).

\(^{e}\)Highest posterior density interval.

\(^{f}\)FECR percentage calculated using R shiny ‘eggCounts’, reported HPD.Low, mode and HPD.High as most accurate estimates. Bayesian CI (HPD.Low and HPD.High) are in brackets.
3.4.1. Egg hatch test

Pre-BZ treatment 79% of eggs hatched in control wells compared to 91% post-BZ treatment (Supplementary Table 1). Just 39% of eggs from the pre-BZ treatment sample hatched in the TBZ EHT at the definitive dose of 0.1 \( \mu \)g/ml (Coles et al., 2006), while post-BZ treatment, 93% hatched (Table 4), giving a resistance ratio of 2.4 (% hatch post-treatment/% hatch pre-treatment). Calculating the ED50 also revealed a difference pre- and post-BZ treatment, with 50% hatching at a higher concentration of TBZ/DMSO post-treatment (0.615 \( \mu \)g/ml) compared with pre-treatment (0.048 \( \mu \)g/ml) (Table 4, Fig. 5), giving a resistance ratio of 12.8 (ED50 post-treatment/ED50 pre-treatment).

While a full EHT was not carried out for pre- and post-IVM samples, 33% of eggs in the pre-IVM treatment population hatched at 0.1 \( \mu \)g/ml TBZ and an ED50 of 0.043 \( \mu \)g/ml was calculated, comparable to the pre-BZ FECRT EHTs (Table 4 and Supplementary Fig. 1). Post-IVM treatment only two replicates of 0.1 \( \mu \)g/ml TBZ were set up, in which 82% eggs hatched, suggesting a resistance ratio of 3.0 at the definitive dose (raw data used, Table 4). This initially surprising result was illuminated by the inclusion of speciation and pyrosequencing data (section 3.5), which revealed that this apparent selection for BZ resistance by IVM instead reflected the presence of a highly dual-resistant *T. circumcincta* population.

3.4.2. Larval development test

Average egg hatch in the 2% DMSO control wells of the LDT was 97%. Pre-treatment 67% of hatched larvae developed to L3 on average (range 53–75%), compared to 86% post-IVM treatment (Supplementary Table 2). No definitive dose has been established for the IVM LDT used in our study, but using a GLM, the ED50 can be determined. Pre-IVM treatment this was 2.43 nM (95% CI: 2.14, 2.81) and post-IVM treatment this rose to 4.07 nM (95% CI: 2.87, 6.36) (Table 5 and Fig. 6), giving a resistance ratio of 1.7. Pre-BZ treatment an ED50 of 2.27 nM was calculated, comparable to that of the pre-IVM group (Table 5 and Supplementary Fig. 2).

3.5. Pyrosequencing of the *T. circumcincta* \( \beta \)-tubulin isotype-1 gene reveals a diverse range of resistance alleles

Previous studies have identified mutations in three codons within the \( \beta \)-tubulin isotype-1 gene that are correlated with BZ resistance...
In total, 180 individual *T. circumcincta* from all FECRT sample populations (30 individuals from each sampling time-point) were pyrosequenced at all three codons (Figs. 7 and 8). Of these, 168 were either homozygous or heterozygous for the resistance mutation at codon 200. In total, seven different allelic sequences were identified in the 123 individuals homozygous for this mutation. Individuals that were heterozygous at one or more resistance-associated codons were also detected at all sampling time points of both the BZ and IVM FECRT. Those with homozygous resistance mutations at codon 198 (P200 F, P198 L, P167 F) were detected on day 0 of the IVM FECRT and on days 7 and 14 of the BZ FECRT. All larvae with resistance-associated polymorphisms at codon 198 encoded leucine rather than alanine. No individuals with homozygous resistance mutations at codon 167 were identified, nor were any individuals identified with mutations at other codons.

### Table 4

<table>
<thead>
<tr>
<th>Assay</th>
<th>EHT ED$_{50}$ (μg/ml)</th>
<th>Percentage hatch in 0.1 μg/ml</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pre-BZ FECRT (four plates combined analysis)</td>
<td>0.048 (0.045, 0.052)</td>
<td>39.1% (8.58)</td>
</tr>
<tr>
<td>Post-BZ FECRT</td>
<td>0.615 (0.538, 0.730)</td>
<td>93.1% (0.23)</td>
</tr>
<tr>
<td>Pre-IVM FECRT (four plates combined analysis)</td>
<td>0.043 (0.040, 0.046)</td>
<td>32.6% (6.06)</td>
</tr>
<tr>
<td>Post-IVM FECRT</td>
<td>–</td>
<td>82.4% (3.43)</td>
</tr>
</tbody>
</table>

*Raw data was adjusted for response in 0.5% DMSO control wells. 95% confidence intervals reported in brackets.

*Adjusted for response in 0.5% DMSO control wells. Standard deviation reported in brackets.

*No DMSO well was included post-IVM treatment and only two replicate wells for 0.1 μg/ml were included. This therefore is the uncorrected percentage hatch. The uncorrected percentage hatch in the 0.1 μg/ml wells pre-IVM treatment was 27.52% (5.0 standard deviation).*

### Table 5

<table>
<thead>
<tr>
<th>Assay</th>
<th>IVM LDT ED$_{50}$ (nM)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pre-BZ FECRT (two plates combined analysis)</td>
<td>2.27 (2.05, 2.56)</td>
</tr>
<tr>
<td>Pre-IVM FECRT (two plates combined analysis)</td>
<td>2.43 (2.14, 2.81)</td>
</tr>
<tr>
<td>Post-IVM FECRT</td>
<td>4.07 (2.87, 6.36)</td>
</tr>
</tbody>
</table>

*Raw data was adjusted for response in 2% DMSO control wells. 95% confidence intervals reported in brackets.

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**Fig. 5.** Egg hatch test: pre- and post-benzimidazole faecal egg count reduction test. The corrected EHT data is shown, with log$_{10}$(thiabendazole concentration) plotted against the proportion hatching. The data was modelled in R using a binomial GLM (probit), and the regression line is plotted here.

**Fig. 6.** Larval development test: pre- and post-ivermectin faecal egg count reduction test. The corrected LDT data is shown, with log$_{10}$(ivermectin concentration) plotted against the proportion developing to L3. The data was modelled in R using a binomial GLM (probit), and the regression line is plotted here.

**Fig. 7.** Benzimidazole faecal egg count reduction test: pyrosequenced genotypes of β-tubulin isotype-1. Thirty *T. circumcincta* individuals were sequenced at each sampling time point at codons 167, 198 and 200 of the β-tubulin isotype-1 gene.

(F200Y, E198 A/L, F167Y) (Kwa et al., 1995; Barrère et al., 2012; Kotze et al., 2012). In total, 180 individual *T. circumcincta* from all FECRT sample populations (30 individuals from each sampling time-point) were pyrosequenced at all three codons (Figs. 7 and 8). Of these, 168 were either homozygous or heterozygous for the resistance mutation at codon 200. In total, seven different allelic sequences were identified in the 123 individuals homozygous for this mutation. Individuals that were heterozygous at one or more resistance-associated codons were also detected at all sampling time points of both the BZ and IVM FECRT. Those with homozygous resistance mutations at codon 198 (P200 F, P198 L, P167 F) were detected on day 0 of the IVM FECRT and on days 7 and 14 of the BZ FECRT. All larvae with resistance-associated polymorphisms at codon 198 encoded leucine rather than alanine. No individuals with homozygous resistance mutations at codon 167 were identified, nor were any individuals identified with mutations at other codons.
The farm is moderate in area, being only about 60 ha, enabling frequent grazing of all pastures, which has been linked in other studies with increased species diversity, due in part to the ability of rarer species with longer pre-patent periods and shorter pasture survival times to be effectively maintained within the flock (Silvestre et al., 2000).

Several species, namely *C. curticei*, *O. venulosum* and *T. axei*, were also found to be present post-BZ treatment in addition to *T. circumcincta*. This suggests some level of resistance within these populations, consistent with previous studies (Hunt et al., 1992; Moreno et al., 2004; Palcy et al., 2010; Keegan et al., 2017). In contrast to the BZ FECRT, only *T. circumcincta* was detected post-IVM treatment, suggesting that other strongyle species present on the farm are susceptible to IVM, despite apparent resistance to BZ. The pattern of anthelmintic usage on the farm over the year may impact resistance development following treatment with BZ or IVM. BZ anthelmintics were routinely used several times in the spring to control *N. battus*, at a time point when pasture larvae are predominantly present from overwintered survival (Gibson and Everett, 1972), lamb strongyle FECs were minimal and species prevalence diversity was low within the lambs (being principally *T. circumcincta*, data not shown). At this time, and with monthly dosing treatment, BZ resistance may be more efficiently selected within the different species populations due to the smaller pasture population in refugia (Martin et al., 1981). In comparison, IVM is used for the most part in late summer, when pasture larval levels are higher and egg counts greater. Any resistant species surviving at this time would need to be present in sufficient numbers within the host, to prevent dilution of resistant alleles by susceptible larvae ingested from pasture. Perhaps more importantly for IVM resistance development, routine use of oral moxidectin on this farm at lambing time may have influenced the IVM phenotype of the *T. circumcincta* population. The persistent effect of moxidectin prevents establishment by *H. contortus* and *T. circumcincta* larvae for up to five weeks post-treatment (Kerboeuf et al., 1995), but it does not target immature larvae of other species (Zoetis product datasheet, Cydectin® 0.1% w/v oral solution), decreasing the macrocyclic lactone selection pressure on the wider strongyle community.

The FECRT was followed up using two additional tests of phenotypic resistance: an EHT for BZ resistance and a LDT for IVM. The EHT has been studied extensively using laboratory isolates of various species, and has also been utilised in some field studies (Calvete et al., 2014). An EHT differentiates between resistant and susceptible populations by the known ability of TBZ to prevent hatching of BZ susceptible eggs (Le Jambre, 1976). The EHT results reported in this study were consistent with the FECRT data. By comparing the ED₅₀ of the pre- and post-BZ treatment assays, a considerable increase was noted in the concentration at which 50% of the eggs failed to hatch, from 0.048 μg/ml to 0.615 μg/ml TBZ. Although a full EHT was not carried out post-IVM, a three-fold increase was observed in the percentage hatch in the wells containing 0.1 μg/ml TBZ, following in vivo IVM treatment, suggesting a dual-resistant population. Following ring testing of the EHT, von Samson-Himmelstjerna et al. (2009) suggested that the presence of a resistant sub-population might be detected by recording the percentage hatch in the 0.2 and 0.3 μg/ml wells. Interestingly, in our pre-treatment EHTs we noted 31% and 24% egg hatch at these concentrations respectively, similar percentages to the proportion of *T. circumcincta* represented.

In contrast, the LDT was less informative, possibly related to the small number of replicates used in the post-IVM test. Although each of the pre-FECRT LDTs were comparable with each other, suggesting the LDT was repeatable, the fold-change post-IVM treatment was small (RR: 1.7). Two controls were used in the LDT; 2% DMSO and deionised water. Despite hatching of almost all eggs, development to L3 in the 2% DMSO control wells could be as low as 53%, with higher levels of development recorded in the water wells. However, these results are similar to others reported in the literature: rates of larval development varied from 64 to 86% for the L3 of *Oesophagostomum* species in 6%
Currently, molecular markers are available for IBZ resistance (Kwa et al., 1995; Silvestre and Cabaret, 2002; Ghisi et al., 2007; Redman et al., 2015), and markers are being further characterised for levamisole resistance (Boulin et al., 2011; Barrère et al., 2012). It is possible to use the IBZ resistance genetic markers to assess the presence and origin of resistance in field populations (Redman et al., 2015), but little is known about IVM resistance, which is thought to be polygenic (Kotze et al., 2014). Modern methods of parasite speciation such as the nemabiome (Avramenko et al., 2017) and multiplex tandem PCR (Roebel et al., 2017) offer promise for the future diagnosis of anthelmintic resistant worms. However, until the use of such molecular tools becomes widespread, FECRT will continue to provide a useful measure of drug efficacy, but in the absence of species prevalence data, must be interpreted with care. The presence of a dual-resistant *T. circumcincta* population in this farm indicates that the use of either anthelmintic will preferentially select for this pathogenic species, and that combination treatments of IBZ and IVM, or rotation of anthelmintic classes may not be beneficial for this flock.

5. Conclusion

This study clearly demonstrates the complicating factors of stronglye diversity in field populations when interpreting a FECRT. We would therefore encourage the routine speciation of strongyles obtained during both pre- and post-treatment FEC samples, for optimal interpretation of the results, with the additional testing of a combination of products for each group of lambs used in the FECRT to enable detection of dual-resistant species. Pyrosequencing gave additional information but would be unlikely to provide significant insight to a farmer in practice except in the early stages of IBZ resistance (e.g. for *N. battus* (Morrison et al., 2014)); however, pyrosequencing would be useful for monitoring management strategies in the research setting, or if a IBZ drench was not used during the FECRT.

Acknowledgements

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Appendix A. Supplementary data

Supplementary material related to this article can be found in the online version, at doi:https://doi.org/10.1016/j.vetpar.2018.06.012.

References


