An overview of the experimental procedure is shown in figure 1.

Description of it ……

For individuals in the co-infection groups, doses of the parasites were given sequentially…. to best reflect the wild …

Sequential dosing/exposure was used to reflect our knowledge of the pathogens present in the wild in their role as emerging pathogens …. To work out the true dynamics rather than the dose being additive.

Differential number of exposures for the pathogens was used as Rv was considered more pathogenic (able to infect in one dose), were as Bd infection is normally acquired by multiple exposures with infection building over time.

Individuals in the control groups, were handled in the same way as all the treatment groups, receiving a sham (media) exposure/dose in exchange/substitute.

Before the first exposure xxx were euthanised (following HO procedure; buffered % MS222) to check pre-exposure infection….

Water changes….

Food provisioning ….

**(b) endpoint infection**

For both tissue samples, DNA was extracted …..

For the mouthpart, Prepman Ultra was used

For the bodily tissue, DNeasy kit was used to extract ….

We determined the infection burden quantitatively by qPCR ….. using pathogen specific assays.

Bd qPCR [Boyle et al 2004]

Viral loads normalised according to [Leung et al] .. both the extractions and qPCR assays are described in more detail in the supplementary materials (Sxxx).

(c) shedding

(d) viability

﻿(e) Statistical analyses

Sample sizes changed from starting and are documented in the supplementary material (Sxx), which provides a detailed account of sample sizes for each treatment group/species.

Individuals were removed due to ill health, in line with welfare regulations, and tested for both pathogens. All individuals tested returned as negative.

All analyses were conducted in R [ref] with the packages listed in the supplementary material [refs??] (Sxx) and script also provided.

The effect of treatment group on the proportion infected xxxx were assessed in a general linear model (GLM).

Exposure group (Bd, Rv, Bd>Rv and Rv>Bd),

The effect of species

﻿Analyses were conducted in R v. 3.1.2 [38]. The effect of

infection treatment group on the number of adult T. colubriformis worms, the number of adult H. contortus worms and the number of H. contortus arrested larvae were assessed in three general linear models (GLMs). Infection group (mono- or co-infected), days post-initial infection (i.e. cull day; included as a categorical variable) and their interaction were included as independent variables. In addition, the faecal egg count pre-anthelminthic treatment and animals’ total gain in mass were also accounted for by inclusion as independent terms. Following preliminary model assessments, the number of arrested larvae of H. contortus was square root transformed (sqrt(x þ 1)) to normalize the residuals of that GLM. Neither Poisson nor negative binomial error distributions provided better model fits for any model (electronic supplementary material, S2)

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