

Can we predict human cases from livestock cases? Understanding the link between livestock and human cryptosporidiosis

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Body of the Abstract

Cryptosporidium is an important gastrointestinal protozoan parasite that infects many animal species, including humans. Transmission routes vary by host and species with zoonotic transmission of *Cryptosporidium parvum* between livestock and humans, and human-to-human transmission of the host adapted species *Cryptosporidium hominis*. Our aim was to explore the relationship between confirmed human and livestock cases.

We explored the seasonal patterns of monthly confirmed human and livestock (sheep and cattle) Scottish cases of cryptosporidiosis, between 2007 and 2017 and examined statistical relationships between different partitions of the datasets informed by the seasonal patterns. We then developed dynamic regression models with autoregressive integrated moving average (ARIMA) errors using lagged livestock cases as predictors of the number of human cases in (i) first seven months (ii) any single month. Data were divided into sub-sets to train and validate the models. The best models were selected based on some information criteria and measures of predictive accuracy.

There are bimodal cattle and human seasonal peaks in the spring and autumn/winter. Sheep cases have a single spring seasonal peak. Positive correlations found between human cases and one-step-lagged livestock cases were stronger when based on the first seven months of the year. The final model fitted to this period showed that current month and previous month's livestock cases jointly accounted for over 80% variations in the number of human cases, compared to 73% when fitted to the entire dataset.

The positive association and the lag between diagnoses in animals and humans suggests potential zoonotic transmission of *Cryptosporidium parvum* in the winter/spring. This enabled the development of models with high predictive accuracy that predict the expected number of human diagnoses for a given number of diagnoses in cattle and sheep.

This work demonstrates the utility of using livestock disease information to optimally predict associated human disease cases.