



Fasciola and *Paramphistomum* infection in large Ruminants

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Abstract

A study was conducted in six cattle farms and one abattoir located in Kuala Terengganu Malaysia, to determine the occurrence of fluke infection in large ruminants. *Faecal* sample were randomly collected from 60 cattle and sedimentation method were conducted on the samples. Results for the field study revealed that 67% of cattle sampled was found to be positive with only *Fasciola* eggs, 5% was positive with only *Paramphistomum* eggs and 10% was positive for co-infection of both *Fasciola* and *Paramphistomum* eggs. Mean fluke worm egg counts ranged from 2.2 ± 0.77 to 32.1 ± 18.47 e.p.g. Results from abattoir study conducted for three months revealed that 231 cattle and 110 buffaloes were slaughtered and out of this number, 11 livers (3%) were condemned. *Fasciola* (73%) and *Paramphistomum* (18%) were found to be the main result for liver condemnation. Results obtained from this study addressed the problem of fluke infection in cattle and buffaloes. Studies on the intermediate host should be conducted in order to control fluke infection.

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Introduction

In Malaysia, endoparasite infections are the most common type of parasitism among ruminants (Fadzil, 1977). Liver fluke infection is as one of the most important diseases of cattle, buffalo, sheep and goat (Saleha, 1991; Hopkins, 1992). Fluke infection is caused by two *Fasciola* species, *Fasciola hepatica* and *F. gigantica* (Valero *et al.*, 2009; Tolan, 2011). Large ruminants exposed to the liver fluke infection are subjected to liver condemnation, reduction in meat production, reduced growth rate and mortality (Saleha, 1991; Mas-Coma *et al.*, 2005).

The reason in the spread of *Fasciola* infection is the establishment of snail host, *Radix rubiginosa* that is previously known as *Lymnaea rubiginosa* at freshwater habitats (Pullan *et al.*, 1972). Besides that, moisture condition and optimal temperature, is one of the factors for the development of larvae (miracidia), the reproduction of the snails and larval development within the snails (Soulsby, 1982; Mengesha, 1991; Saleha, 1991).

There is lack of information on the current status of fluke infections in cattle and buffaloes in Kuala Terengganu. From a survey in 1972, a few states in Malaysia were found to have fascioliasis in livestock that is in Kedah, Perak, Selangor, Pahang, Negeri Sembilan, Melaka and Johor (Saleha, 1991).

Fascioliasis was found in all states of Peninsular Malaysia (Rajamanickam *et al.*, 1996). Khadijah *et al.* (2015) has reported high prevalence of liver fluke infection in two cattle farms located in Kuala Terengganu. Thus, the objective of this study was to determine the prevalence of fluke infection in cattle and buffaloes located in Kuala Terengganu, Malaysia.

Materials and methods

Sampling site and sampling period

The sampling was conducted at six farms located in Kuala Terengganu that is Kg. Surau Haji Daud (two farms), Kg. Banggol Peradong, Kg Telok Pasu, Kg. Tok Dir and Kg. Bukit Tok Beng (Figure 1).

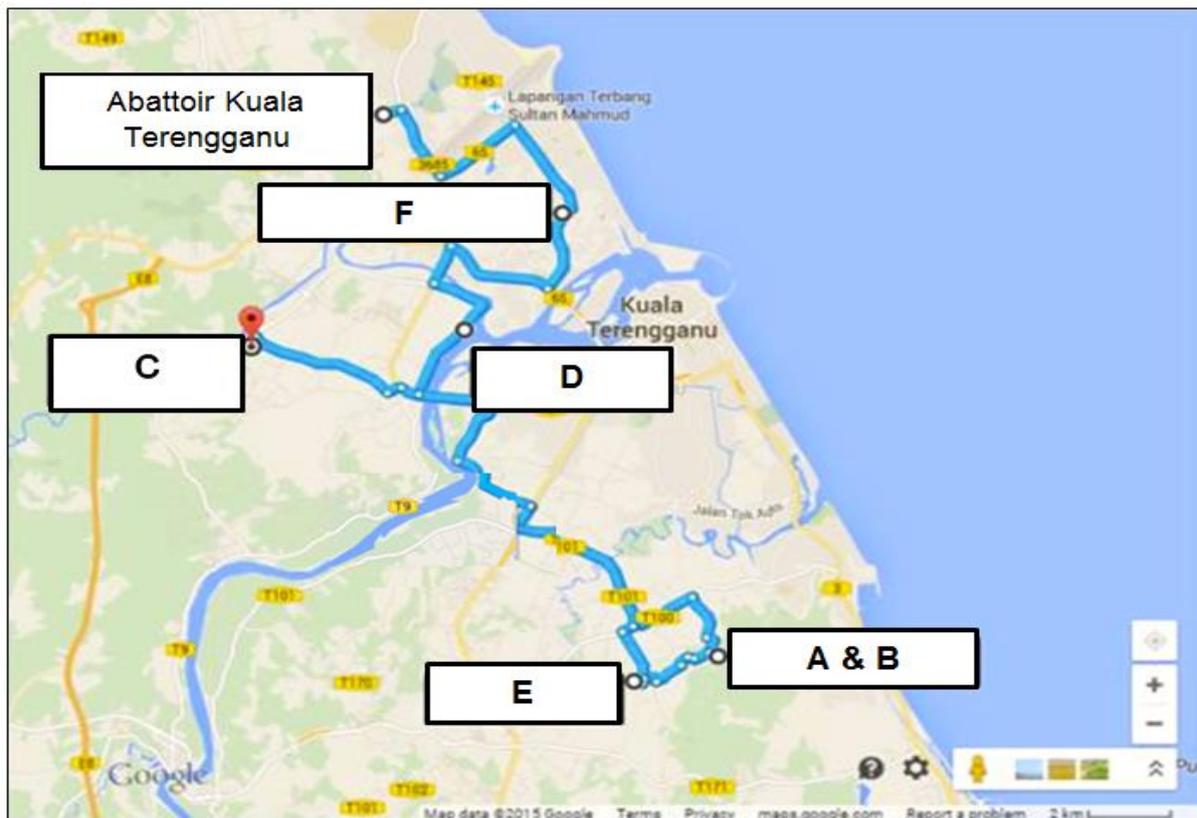


Fig. 1. Location of sampling: Kg. Surau Haji Daud (two farms), Kg. Banggol Peradong, Kg Telok Pasu, Kg. Tok Dir and Kg. Bukit Tok Beng (Google maps, 2016).

Condemned livers were collected from Kompleks Abatoir Kuala Terengganu. This study was conducted from December 2014 until March 2015.

Animals and management information

A total of 59 cattle were randomly chosen for this study. On the sampling day, an information sheet was given to the farmers to obtain information such as deworming history and grazing management. The cattle in were managed in a semi-intensive management, where they were allowed to graze during the day but kept in pen during the night.

A total of eleven condemned livers (cattle and buffaloes) were collected from 348 cattle and buffaloes slaughtered at Kompleks Abatoir Kuala Terengganu.

Sample collection

Sampling on the farms was conducted between 0800–1300h. Rectal faecal samples were collected from each cattle. The faecal samples were processed for fluke egg detection. All the condemned livers were placed in a large plastic bag and brought back to the laboratory. The samples were stored in refrigerator at 4°C until examination to avoid degradation of sample.

Parasitological examination

Sedimentation technique was conducted to detect the presence of fluke eggs from faecal samples. The identification of fluke eggs (liver fluke and stomach fluke) was conducted based on Boray (1982), Mas-

Coma and Bargues (1997) and Mage and Dorchies (1998). Liver fluke eggs appeared in golden shiny colour while stomach fluke eggs appeared bluish-purple in colour. The pathological changes of condemned livers were observed as suggested by Talukder *et al.* (2010) and the identification of matured liver fluke was conducted according to Anderson *et al.* (1999).

Statistical analysis

All statistical analysis was conducted using SPSS Version 20 (IBM Corporation) at confidence level of 95%. Chi-square test was used to compare the frequency of parasitic infections (liver fluke infection, stomach fluke infection and co-infection of liver fluke and stomach fluke) across all farm. Chi Square was also performed to compare respective prevalence of infection (liver fluke infection, stomach fluke infection and co-infection of liver fluke and stomach fluke) between farms. For the liver condemnation, Chi-square test was used to compare between the prevalence and the cause of condemnation.

Results

Prevalence of liver fluke infection from farms

Mean fluke worm egg counts ranged from 2.2 ± 0.77 to 32.1 ± 18.47 e.p.g for each farm. Among the 59 examined samples, 49 samples were positive for fluke eggs. Out of 49 of the positively infected cattle, 40 (68%) were positively infected by liver fluke and six animals (10%) were infected with both liver fluke and stomach fluke. Only three animals (5%) were infected with stomach fluke (Table 1).

Table 1. The prevalence of liver fluke infection, stomach fluke infection and co-infection of liver fluke and stomach fluke from cattle farms.

Farm ID	Prevalence of liver fluke infection (%)	Prevalence of stomach fluke infection (%)	Prevalence of co-infection (%)
A	100	0	0
B	55	18	0
C	67	11	11
D	63	0	13
E	82	0	0
F	40	0	40
Mean (%)*	67.8 ± 8.56	4.8 ± 3.19	10.7 ± 6.34
Chi-square (χ ²)	32.42	1.69	24.59
P value	<0.05	0.194	<0.05

*Chi square value for the means was 86.36 (p<0.05).

The frequency of liver fluke infection, stomach fluke infection and co-infection of liver fluke and stomach fluke is significantly different across all farm, χ^2 (2, N=84) = 86.36, $p < 0.05$ (Table 1).

Frequency of liver fluke infection was significantly different between the six farms, χ^2 (5, N=407) = 32.42, $p < 0.05$, while frequency of stomach flukes was not significantly different between the two farms, χ^2 (1, N=29) = 1.69, $p = 0.194$ (Table 1).

Frequency of co-infection of liver fluke and stomach fluke was significantly different between three farms, χ^2 (2, N=64) = 24.59, $p < 0.05$ (Table 1).

Liver condemnation at abattoir

The results revealed that 3.2% of the livers were condemned in three month. Table 2 shows the cause of liver condemnation.

The prevalence of liver condemnation caused by liver fluke was high (72.7%) compared to stomach fluke (18%) and liver abscess (9%). Liver fluke is the main cause of liver condemnation, χ^2 (2, N=100) = 72.0, $p < 0.05$ (Table 2). All liver fluke that were found in the condemned liver were measured and identified as *Fasciola gigantica* (Fig. 2). Fig. 3 shows mature *F. gigantica* at hepatic duct of the condemned liver.

Table 2. Causes for liver condemnation and number of liver condemned for each cause.

Causes for liver condemnation	Number of liver condemned (percentage)
Liver fluke	8 (72.7%)
Stomach fluke	2 (18.2%)
Liver abscess	1 (9.1%)
Chi-square (χ^2)	72.02

Discussion

Results from this study suggested that liver fluke infection is prevalent in few large ruminant farms in Kuala Terengganu. The occurrence of the liver fluke infection in this study is an agreement with the findings from Rajamanickam *et al.* (1996) and Khadijah *et al.* (2015) who reported that fasciola could be found in many states in Peninsular Malaysia including Terengganu. However, the prevalence of liver fluke eggs (67%) in the present study is lower than those in previous study (95%) conducted by Khadijah *et al.* (2015) in Kuala Terengganu.

The higher percentage in the previous study may be due to the fact that the study was conducted on only two farms, involving 18 cattle in Kuala Terengganu while the present study involved greater number of cattle. Regardless the different percentages reported in the studies, the results still indicate that liver fluke is a problem in large ruminant farms in Kuala Terengganu. The successful development of liver fluke because of the presence of suitable intermediate host, *Radix rubiginosa*, adequate moisture habitat and optimum temperature (Soulsby, 1982; Mengesha, 1991; Saleha, 1991).

However, the intermediate host *Radix rubiginosa* was not found at the grazing pastures. Future studies should be conducted on the prevalence of intermediate host on these farms.

Besides liver fluke infections, the result shows stomach fluke infection (5%) and co-infection of liver fluke and stomach fluke (11%). This is the first report on co-infection of liver fluke and stomach fluke in Terengganu.

The occurrence of co-infections in this study is parallel to the studies of Abrous *et al.* (2000) and Diaz *et al.* (2006) in which liver fluke and some species of stomach fluke may occur together in ruminants.

It was found that liver condemnation caused by liver fluke infections shows higher prevalence (73%) when compared to other reasons.

This finding is supported by Tham and Sheikh-Omar (1981) who reported 89% condemnation of liver was due to liver fluke infection.

Previous studies conducted in Vietnam, Philippines and Thailand showed high prevalence in liver condemned due to liver fluke infection, which were 78.3%, 60.8% and 60.19% respectively (Anderson *et al.*, 1999; Molina *et al.*, 2005; Phalee and Wongsawad, 2014).

The result showed 18% of the condemned livers in the current study were positive for mature stomach fluke. While stomach fluke infection is more common in rumen, Khatoun *et al.* (2003) reported that a stomach fluke *Paramphistomum cervi* was found attached to the liver of buffaloes and caused severe damage.



Fig. 2. Adult *Fasciola gigantica* obtained from a condemned liver.

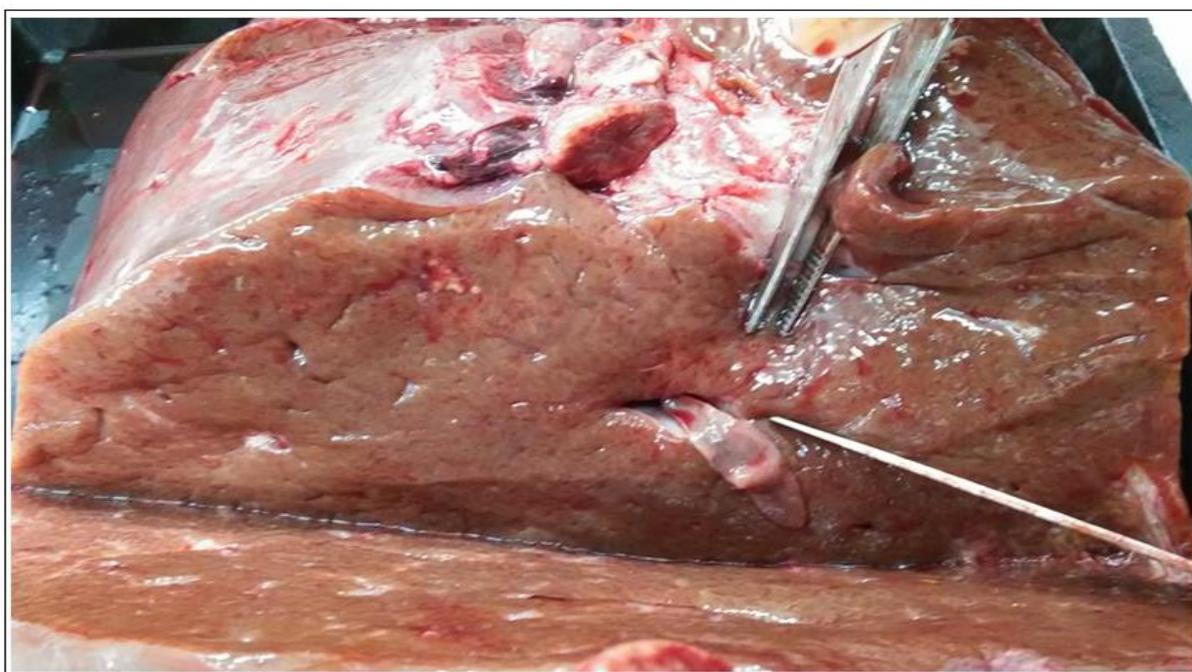


Fig. 3. Adult *Fasciola gigantica* (circle) at hepatic duct of the condemned liver.

The prevalence of liver fluke infection in buffalo was 64% while in cattle only 9%. The nature of buffaloes are always wallowing themselves to the stagnant pools and swampy area that are exposed to metacercaria (infective stage) and the intermediate host, *Radix rubiginosa* that lead to successful infection (Molina *et al.*, 2005; Relf *et al.*, 2011; Fox *et al.*, 2011). From the observation, the condemned liver appeared pale, swollen, enlarged with rounded edges and fibrosis of the bile duct were present, which is an agreement to previous studies (Soesetya, 1975; Molina *et al.*, 2005; Talukder *et al.*, 2010).

Conclusion

Results from this study indicated that liver fluke infection is a problem in farms and abattoir in Terengganu. Liver fluke infection cause production and economic loss because liver condemnation, reduction of animal weights and lead to death. Screening of intermediate host for trematodes infection at the surrounding of farms should be conducted.

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