

Review Article

Rumen Fluke in Cattle and Buffaloes in Asia: A Review

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ABSTRACT

Rumen fluke is a parasitosis that infects ruminant animals across a wide geographical range of countries. It is a severe infection in temperate and tropical climate regions of Asia, Australia, Africa, and Europe, which cause significant economic losses. In this review, the available information to date on rumen fluke species infecting cattle and buffaloes in Asian countries is evaluated. The citation search was performed through specific keywords, literature published from 1964 to 2021, retrieved from electronic databases: Scopus, Web

of Science, Pub Med, Education Resources Information Center (ERIC), Science Direct, Elsevier, and Google Scholar. Twenty-six (26) rumen fluke species belonging to two families: Paramphistomidae 61.5% (16/26) and Gastrothylacidae 38.4% (10/26), were reported in cattle and buffaloes in fourteen Asian countries. *Paramphistomum cervi* and *Cotylophoron cotylophorum* are the most prevalent species with broader distribution in countries than the other genera. The coprological prevalence varies from 0.8% to 98.17% and 0.86% to 78.4% in cattle and

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buffaloes, respectively. The prevalence of rumen fluke by fluke counts method range between 6.45% to 90.6% and 4.29% to 75.07% in cattle and buffaloes, respectively. The sedimentation method and fluke count are reliable tests for detecting rumen fluke in live and slaughtered animals. In conclusion, the rumen fluke should be considered a critical production disease that affects cattle and buffaloes in Asia. Further studies are necessary to determine the rumen fluke-snail associations, develop diagnostic tests to detect prepatent infections in the definitive host, determine the economic importance of rumen fluke, and determine the efficacy of different anthelmintic in the treatment of patent infections in the definitive host.

Keywords: Asian countries, cattle and buffalo, epidemiology, prevalence, rumen fluke

INTRODUCTION

Helminth infections are ubiquitous and seasonal, reside in the digestive tract of ruminants, and are responsible for significant impacts on animal production (Charlier et al., 2014). Bovine is most susceptible to chronic diseases because most bovine production systems are pasture-based (Sargison et al., 2016). Rumen fluke infection is present worldwide in the temperate and tropical climate regions of Asia, Africa, Europe, and Australia (Harizt et al., 2021; Huson et al., 2017; Pfukenyi & Mukaratirwa, 2018) and infects domestic ruminants, such as cattle, buffaloes, sheep, goat and some wild ruminants, which are caused by digenean fluke (Income et al.,

2021; Pfukenyi & Mukaratirwa, 2018). Nowadays, rumen fluke is an emerging parasitic infection in European ruminant animals (Huson et al., 2017). Rumen flukes are responsible for poor feed conversion efficiency leading to weight loss or decreased milk production, which causes significant economic losses (Huson et al., 2017). In tropical and subtropical countries, the prevalence of rumen fluke is high because the climatic condition is suitable for intermediate host mud or freshwater snail to grow and complete the parasite life cycle (Gordon et al., 2013; Hajipour et al., 2021). In Asia, rumen fluke infections due to *Paramphistomum* spp. widespread with high prevalence in South and Southeast Asia (Debbra et al., 2018).

In 1970, the first published information on rumen fluke emerged, reporting the adult fluke in the rumen of European red deer (Sey, 1982). The terminology was changed several times before Fiscoeder created the genus *Paramphistomum* in 1903. They belong to several families such as Paramphistomoidae superfamilies, Paramphistomidae, Gastrothylacidae, Gastrodiscidae, Oliveriidae, Balanorchidae, and Stephanopharyngidae (Taylor et al., 2007). Different paramphistomoid species, particularly those of the Paramphistomidae and Gastrothylacidae families, cause amphistomosis in ruminants (Lotfy et al., 2010). Immature fluke causes severe infection in the small intestine of hosts (Horak, 1971).

Despite being historically viewed as minor importance in ruminants in Asian

countries, recent studies suggest that rumen fluke has increased in Asian countries and is more significant than fascioliasis in the United Kingdom (Huson et al., 2017). However, there is insufficient information about the biology and epidemiology of rumen fluke in Asia. Knowing the basic biology and epidemiology and how it interacts with the ruminant's host is essential. Since there has not been a review on rumen flukes in cattle and buffaloes in Asia, the information that is currently available on the species of rumen flukes that infect large ruminants (cattle and buffaloes) in Asian nations, intermediate snail hosts, and rumen fluke epidemiology has been analysed.

Description

Rumen flukes are small, conical (pear-shaped) maggot-like flukes, and the size is about 3 to 20 mm in length and 1.5 to 7 mm in width in domestic ruminants (Taylor et al., 2007). The larval stages are much smaller, at less than a millimetre in length, and fresh specimens have a pink colour



Figure 1. Adult rumen fluke attached to rumen papillae

(Toolan et al., 2015) (Figure 1). There are two suckers known as an anterior sucker and a posterior sucker (acetabulum). The digestive system of rumen fluke comprises the mouth, pharynx, oesophagus, and two intestinal caeca (Tandon et al., 2014) (Figure 2).

Life Cycle

Rumen flukes need ruminants as definitive hosts and snails as intermediate hosts to complete their life cycle (Taylor et al., 2007). The adult flukes shed eggs in the stomach of infected animals, and eggs are passed to the environment with the faeces. Rumen fluke eggs are large and measure around $160 \times 90 \mu\text{m}$ with a thin or thick eggshell that operculated with a distinct operculum (Figure 3). The eggs hatch under suitable conditions (temperature and humidity), and miracidia are released from

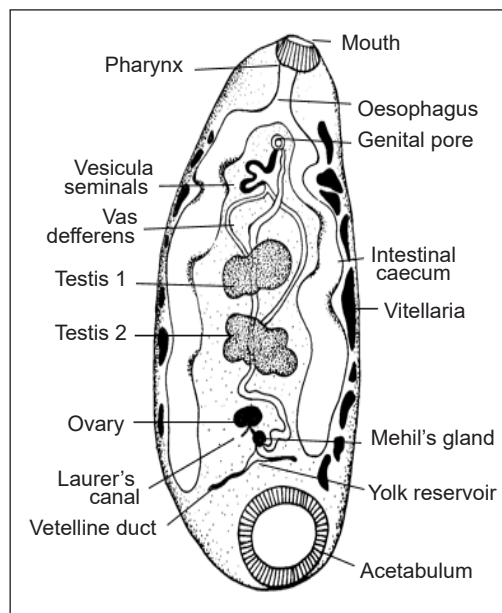


Figure 2. General diagram of a rumen fluke

the eggs (Bhatia et al., 2016; Hajipour et al., 2021). Miracidia searched for a suitable freshwater snail within 24 hours (de Waal, 2010). The miracidium reaches the soft tissues of the molluscan host (snail), either

by innate behaviour, random chance, or chemotaxis (Tandon et al., 2014). Three stages (sporocyst, redia, and cercaria) develop inside the snails from 26 °C to 30 °C. Cercaria is released from the snails and encysts to metacercaria on the plant, which remains viable for up to six months (de Waal, 2010; Horak, 1971; Huson et al., 2017). Finally, the definitive host ingests metacercaria on the plant, excystment occurs in the small intestine, and juvenile fluke hatch and attach to the mucosa, which later (3 to 6 months) migrate to the rumen (de Waal, 2010). In the rumen, the fluke attaches to the ruminal pillar's surface, develops to the adult stage, and sheds the eggs (Taylor et al., 2007) (Figure 4).

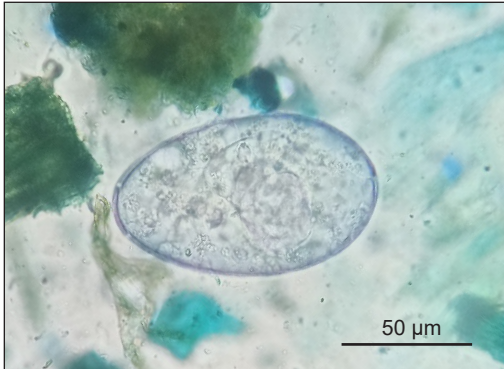


Figure 3. Rumen fluke egg was photographed at 400× by light microscope

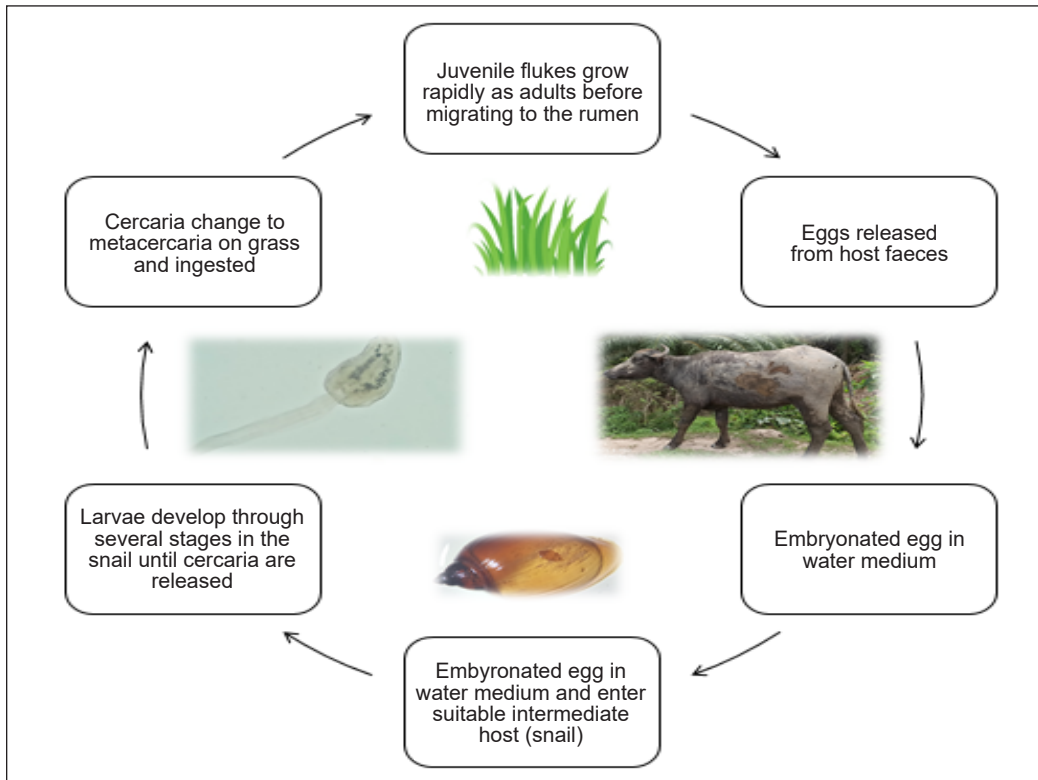


Figure 4. The life cycle of rumen fluke

Rumen Fluke Species Infecting Cattle and Buffaloes in Asian Countries

Rumen fluke species in cattle and buffaloes in Asian countries belong to two families: Paramphistomidae and Gastrothylacidae, and 26 species in cattle and buffaloes are as follows: *Paramphistomum cervi*, *Paramphistomum gotoi*, *Paramphistomum epiclitum*, *Paramphistomum gracile*, *Paramphistomum leydeni*, *Paramphistomum microbothrium*, *Orthocoelium streptocoelium*, *Orthocoelium indonesiense*, *Orthocoelium arambuloi*, *Fischoederius cobboldii*, *Cotylophoron cotylophorum*, *Cotylophoron indicum*, *Calicophoron daubneyi*, *Ceylonocotyle streptocoelium*, *Ceylonocotyle scolicoelium*, *Ceylonocotyle gigantopharynx*, *Gastrothylax compressus*, *Gastrothylax crumenifer*, *Gastrothylax cobboldii*, *Gastrothylax glandiformis*, *Gastrothylax synethes*, *Carmyerius spatiosus*, *Fischoederius elongatus*, *Fischoederius emiljavieri*, *Velasquezotrema tripurensis*, and *Homalogaster poloniae*. The various distribution of rumen fluke species was observed in cattle and buffaloes in different Asian countries (Figure 5).

Table 1 summarises the reported rumen fluke species by different diagnostic methods. It shows that 61.5% (16/26) reported species of rumen flukes to belong to the family Paramphistomidae, and 38.4% (10/26) belong to the family Gastrothylacidae. Out of 61.5% of family Paramphistomidae, 37.5% (6/16) belong to genus *Paramphistomum* followed by 18.75% (3/16) *Orthocoelium*, 18.75% (3/16) *Ceylonocotyle*, 12.5% (2/16) *Cotylophoron*,

6.25% (1/16) *Fischoederius*, and 6.25% (1/16) *Calicophoron*. Out of 38.4% of the family Gastrothylacidae, 50% (5/10) belong to the genus *Gastrothylax*, followed by 20% (2/10) *Fischoederius*, 10% (1/10) *Velasquezotrema*, 10% (1/10) *Carmyerius*, and 10% (1/10) *Homalogaster*.

The present review shows that most *Paramphistomum* and *Cotylophoron* species have wider distribution and higher prevalence for the reported countries than species of the other genera. *Paramphistomum cervi* has the widest distribution, followed by *Cotylophoron cotylophorum* compared with the other species. Sixteen species; *Paramphistomum gotoi*, *Paramphistomum gracile*, *Paramphistomum leydeni*, *Orthocoelium indonesiense*, *Calicophoron daubneyi*, *Ceylonocotyle streptocoelium*, *Ceylonocotyle scolicoelium*, *Ceylonocotyle gigantopharynx*, *Cotylophoron indicum*, *Gastrothylax synethes*, *Gastrothylax compressus*, *Gastrothylax glandiformis*, *Fischoederius elongatus*, *Fischoederius emiljavieri*, *Velasquezotrema tripurensis*, and *Homalogaster poloniae* had the narrowest distribution, being reported only in one country each.

Among the reported species of rumen fluke in Asian countries, *Paramphistomum cervi* and *Paramphistomum epiclitum* are the most common species of rumen fluke and the most significant cause of diseases in cattle and buffaloes (Bhatia et al., 2016; Javed Khan et al., 2006; Rafiq et al., 2020). The present review in Asian countries shows the genus of rumen fluke detected by sedimentation method, fluke count

Table 1
Rumen fluke family, species, and their definitive host in different methods reported in Asian countries

Family	Species	Diagnostic methods	Country	Definitive host	References
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum cervi</i> , <i>Cotylophoron cotylophorum</i> , <i>Gastrothylax crumenifer</i> , and <i>Homalogaster poloniae</i>	Sedimentation and abattoir	Bangladesh	Cattle and buffalo	Alim et al. (2012); Ara et al. (2021); Azam et al. (2012); Mamun et al. (2011); Saha et al. (2013); T. C. Naith et al. (2016)
Paramphistomidae	<i>Paramphistomum</i> spp.	Sedimentation and morphological identification of cercaria	Nepal	Cattle and buffalo	Bista et al. (2018); Regmi et al. (2021)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum</i> spp., <i>Ceylonocotyle streptocoelium</i> , <i>Ceylonocotyle scolicoelium</i> , <i>Ceylonocotyle gigantopharynx</i> , <i>Fischoederius elongatus</i> , <i>Gastrothylax synethes</i> , and <i>Gastrothylax cobboldii</i>	Sedimentation and abattoir	Malaysia	Cattle and buffalo	Debra et al. (2018); Harizt et al. (2021); Khadijah et al. (2017); Schad et al. (1964)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum cervi</i> , <i>Paramphistomum gotoi</i> , <i>Paramphistomum microbothrium</i> , <i>Cotylophoron cotylophorum</i> , <i>Carnyrierius spatiosus</i> , <i>Gastrothylax crumenifer</i> , and <i>Gastrothylax compressus</i>	Molecular methods, sedimentation, and abattoir	Iran	Cattle and buffalo	Hajjipour et al. (2021); Nikpay et al. (2019); Rafiq et al. (2020)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum cervi</i> , <i>Paramphistomum epiclitum</i> , <i>Cotylophoron cotylophorum</i> , and <i>Gastrothylax crumenifer</i>	Molecular methods, sedimentation, and abattoir	Pakistan	Cattle and buffalo	Ali et al. (2018); Iqbal et al. (2013); Javed Khan et al. (2006); Muhammad et al. (2017); Nazar et al. (2019)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum cervi</i> , <i>Paramphistomum epiclitum</i> , <i>Fischoederius cobboldii</i> , <i>Fischoederius elongatus</i> , <i>Cotylophoron cotylophorum</i> , <i>Cotylophoron indicum</i> , <i>Carnyrierius spatiosus</i> , <i>Gastrothylax crumenifer</i> , and <i>Velasquezotrema tripurensis</i>	Molecular methods, sedimentation, serological and abattoir	India	Cattle and buffalo	Ghatani et al. (2014); Maitra et al. (2014); Malathi et al. (2021); Saifullah et al. (2013); Shameem et al. (2018)

Table 1 (continue)

Family	Species	Diagnostic methods	Country	Definitive host	References
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum gracile</i> , <i>Paramphistomum cervi</i> , <i>Paramphistomum epiclitum</i> and <i>Fischoederius cobboldii</i>	Molecular methods, sedimentation, serological test, and abattoir	Thailand	Cattle and buffalo	Anuehngchai et al. (2017); Japa et al. (2020); Jittapalapong et al. (2011); Sanguankiat et al. (2016)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum cervi</i> and <i>Homalogaster polonae</i>	Molecular methods and abattoir	China	Cattle and buffalo	Liu et al. (2009)
Paramphistomidae and Gastrothylacidae	<i>Cotylophoron cotylophorum</i> , <i>Orthocoelium streptocoelium</i> , and <i>Homalogaster polonae</i>	Molecular method	Japan	Cattle	Itagaki et al. (2003)
Paramphistomidae	<i>Paramphistomum</i> spp.	Sedimentation	Cambodia	Cattle	Dorny et al. (2011)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum cervi</i> , <i>Paramphistomum microbothrium</i> , and <i>Gastrothylax crumenifer</i>	Abattoir	Iraq	Cattle and buffalo	Sadon Al-Biaty et al. (2011)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum</i> spp. <i>Orthocoelium indonesiense</i> , <i>Orthocoelium arambuloi</i> , <i>Fischoederius elongatus</i> , and <i>Gastrothylax glandiformis</i>	Sedimentation and morphological examination	Indonesia	Cattle	Eduardo (2010); Hambal et al. (2020); Rinca et al. (2019)
Paramphistomidae and Gastrothylacidae	<i>Orthocoelium streptocoelium</i> , <i>Orthocoelium arambuloi</i> , and <i>Fischoederius emiljavieri</i>	Abattoir	Philippines	Cattle	Eduardo (2010)
Paramphistomidae and Gastrothylacidae	<i>Orthocoelium streptocoelium</i> , <i>Orthocoelium arambuloi</i> , and <i>Fischoederius emiljavieri</i>	Abattoir	Philippines	Cattle	Eduardo (2010)
Paramphistomidae and Gastrothylacidae	<i>Paramphistomum</i> spp., <i>Gastrothylax crumenifer</i> , <i>Carmyerius</i> spp., and <i>Fischoederius elongatus</i>	Abattoir	Sri Lanka	Cattle and buffalo	Amarasinghe and Kumara (2008)
Paramphistomidae	<i>Paramphistomum leydeni</i> and <i>Calicophoron daubneyi</i>	Molecular methods and abattoir	Turkey	Cattle	Ozdal et al. (2010); Padak and Karakuş (2021)

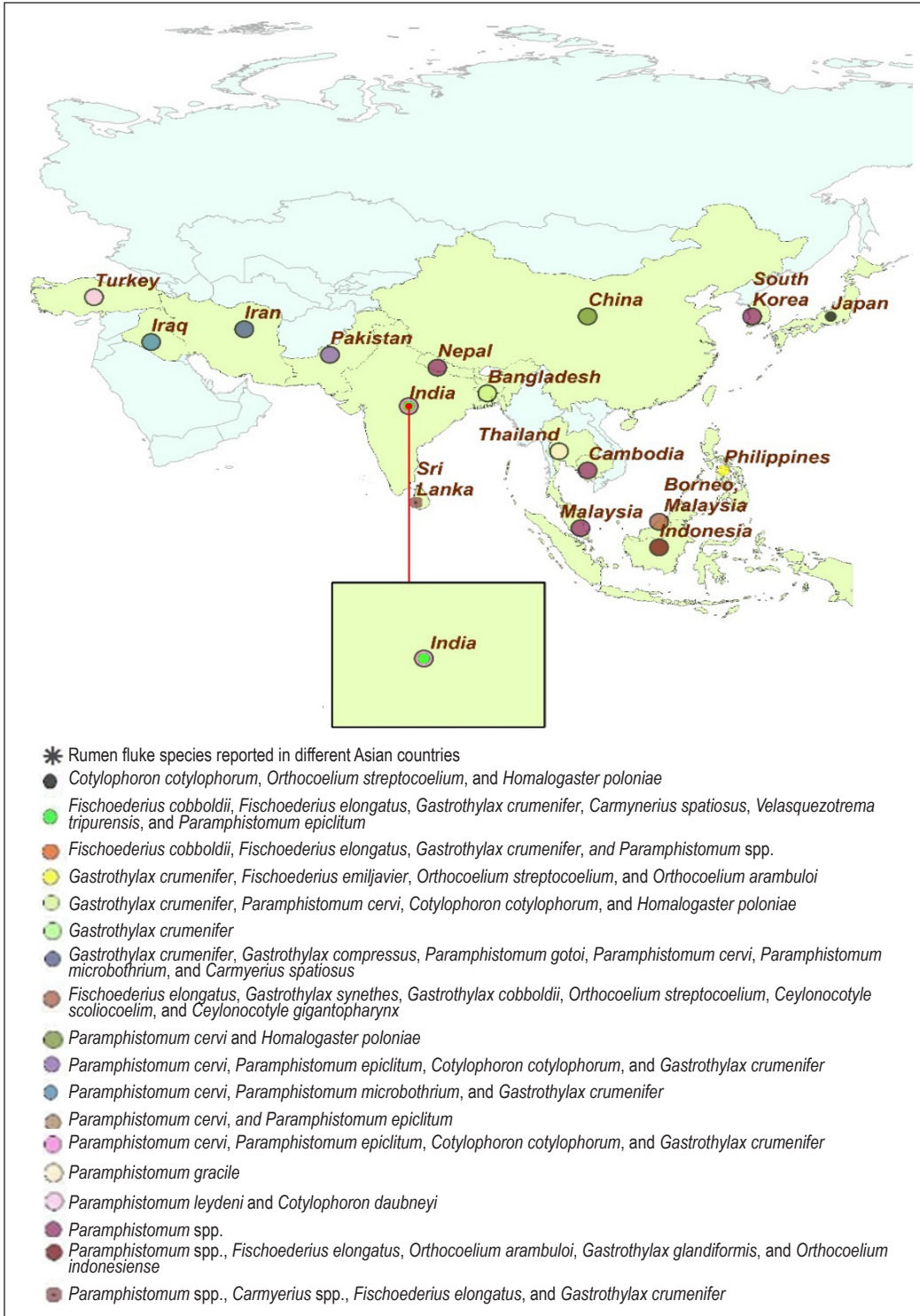


Figure 5. Rumen fluke species reported in cattle and buffaloes of different Asian countries

method from post-mortem examination, and the rumen fluke species detected by serological tests and molecular methods. The sedimentation method may quickly discover eggs in the faeces of an animal carrying an adult fluke. However, this method is of limited value when the disease is in the prepatent period (Taylor et al., 2007), and the eggs cannot be identified up to species level (Mitchell et al., 2021). On the other hand, the filtration method with sieves and sedimentation methods are the most accurate in detecting rumen fluke eggs in faeces (Graham-Brown et al., 2019). Still, it is difficult to identify the rumen fluke species because most have thick-robust bodies and the internal organs are difficult to observe (Lotfy et al., 2010). Molecular methods such as polymerase chain reaction (PCR)-based techniques providing rDNA ITS2 sequence proved to be a good tool for identifying rumen fluke up to species level and determining their phylogenetic relationship (Itagaki et al., 2003; Martinez-Ibeas et al., 2016; Rafiq et al., 2020). The present review in Asian countries shows only *Paramphistomum epiclitum*, *Paramphistomum cervi*, *Paramphistomum leydeni*, *Fischoederius cobboldii*, *Fischoederius elongatus*, *Gastrothylax crumenifer*, *Carmyerius spatiosus*, *Cotylophoron cotylophorum*, *Calicophoron daubneyi*, *Orthocoelium streptocoelium*, *Homalogaster poloniae*, and *Velasquezotrema tripurensis* were detected by molecular and serological methods. However, the rest reported species were detected by sedimentation method and morphological examination of adult flukes.

Epidemiological Factors of Rumen Fluke in Cattle and Buffaloes

The distribution of rumen fluke infecting ruminants has been well documented globally owing to the economic importance from the veterinary standpoint (Huson et al., 2017; Nisar et al., 2021; Pfukenyi & Mukaratirwa, 2018), with a broad geographical spread, particularly in Nigeria, Thailand, and India (Dube, 2010; Kaewnoi et al., 2020; Malathi et al., 2021). Different rumen fluke species predominated in other parts of the world (Rafiq et al., 2020). In areas such as Pakistan and Mexico, *Paramphistomum cervi* is the most frequent species of rumen fluke (Iqbal et al., 2013; Rangel-Ruiz et al., 2003), whereas *Cotylophoron cotylophorum* is the most prevalent species in Australia (Hotessa & Kanko, 2020). *Calicophoron daubneyi* is the most frequent species in the Mediterranean and temperate regions of Algeria, Europe, and the British Isles (Gordon et al., 2013; Huson et al., 2017).

The prevalence and epidemiology of rumen fluke depend on different factors, which include the species of final and intermediate hosts, the fluke potential to infect the hosts, the biological potential of intermediate hosts, and the essential host's management techniques, grazing behaviours, and climate (Horak, 1971; Rangel-Ruiz et al., 2003). Animal grazing area and habitat are significantly associated with the prevalence and intensity of rumen fluke in domestic ruminants (Pfukenyi et al., 2005). Rumen fluke relies on permanent water bodies, such as lakes, rice-growing areas, natural grass pastures with slow-running water, and ponds for their continued

endemicity (Bhatia et al., 2016; Pfukenyi & Mukaratirwa, 2018). In marshy and swampy areas, the rumen fluke outbreak is typical in ruminants and sometimes during the dry season (Pfukenyi & Mukaratirwa, 2018). Cattle develop good immunity, and outbreaks are mainly confined to the animals. However, adults continue to carry low levels of adult parasites and serve as an important reservoir of infection for snails (Taylor et al., 2007).

Snail Intermediate Host

Snail-borne parasite diseases, such as trematodes, pose a serious health risk to humans and animals in many tropical and subtropical areas, as well as causing substantial economic concerns (Lotfy et al., 2010; Lu et al., 2018). Most freshwater/mud snails are the obligatory intermediate host for at least 71 trematode parasites (Bargues & Mas-Coma, 2005). The intermediate host of rumen flukes is freshwater/mud snails such as *Planorbis*, *Lymnaea*, and *Bulinus* (Iqbal et al., 2013; Javed Khan et al., 2006; Taylor et al., 2007). Lymnaeid snails, the intermediate host of rumen fluke, play an essential role in the epidemiology of rumen fluke (Bargues & Mas-Coma, 2005).

The common species of snails that can act as intermediate hosts of rumen fluke reported from different Asian countries include *Radix rubiginosa*, *Radix auricularia*, *Lymnaea truncatula*, *Lymnaea stagnalis*, *Lymnaea natalensis*, *Lymnaea palustris*, *Lymnaea viridis*, *Lymnaea luteola*, *Bulinus truncates*, *Bulinus furskalii*, and *Indoplanorbis exustus* (Dodangeh et al.,

2019; Dung et al., 2013; Martin & Cabrera, 2018; Mohammed et al., 2016). Therefore, rumen fluke is found at high prevalence in most tropical and sub-tropical countries such as Bangladesh, Thailand, Indonesia, and India (Azam et al., 2012; Kaewnoi et al., 2020; Hambal et al., 2020; Malathi et al., 2021), particularly in locations where the climatic and environmental conditions are favourable for the intermediate host snail's survival and multiplications (Gordon et al., 2013; Taylor et al., 2007). Also, these intermediate hosts play an essential role in completing the life cycle of rumen fluke and transmitting the disease (Lotfy et al., 2010; Pfukenyi & Mukaratirwa, 2018).

Furthermore, livestock movement, transport, and export/import have proved their ability to passively proliferate lymnaeid snails (Bargues & Mas-Coma, 2005). The situation is complicated by the ability of the snails to aestivate on dry pastures and become reactivated on the return of rainfall in some areas (Mas-Coma et al., 2009). In addition, moisture and irrigated pastures are often sufficient for the survival of the intermediate host (Bhatia et al., 2016).

Table 2 shows data on the prevalence of rumen fluke infection from 17 countries. The prevalence data of rumen flukes are based on the fluke count and sedimentation method and are primarily conducted in cattle. In Asian countries, species-specific for prevalence data are limited due to problems in identifying rumen fluke species. In the present review, 52 studies used the sedimentation method, 15 fluke count (abattoir inspections), 8 molecular methods, and 2 used serological tests. The fluke

Table 2

Prevalence of rumen fluke in cattle and buffaloes in Asian countries based on faecal examination and fluke count

Host	Country	Total animals	Ranging prevalence (%)	References
Faecal examination				
Cattle	India	12,554	0.8–30.52	A. Gupta et al. (2013); G. Das et al. (2018b); Krishna Murthy and D'Souza (2016); M. Das et al. (2018); Malathi et al. (2021); Maitra et al. (2014); Preethi et al. (2020); S. Nath et al., (2016); Sreedhar (2009); Thakre et al. (2019)
Cattle	Pakistan	1,279	3.65–8.75	Muhammad et al. (2017); Nisar et al. (2021)
Cattle	Iran	1,000	19.5	Hajipour et al. (2021)
Cattle	Thailand	4,402	10.2–97.17	Japa et al. (2020); Jittapalapong et al. (2011); Income et al. (2021); Kaewnoi et al. (2020); Thanasuwan et al. (2021); Yuwajita et al. (2014)
Cattle	Indonesia	303	4–81	Dwinata et al. (2018); Hambal et al. (2020); Rinca et al. (2019)
Cattle	Bangladesh	1,738	18.3–70.8	Akanda et al. (2014); Hassan et al. (2020); Paul et al. (2012); Rashid et al. (2015); Saha et al. (2013)
Cattle	Nepal	165	36.71–39.5	Bista et al. (2018); Regmi et al. (2021)
Cattle	Sri Lanka	147	1.36	Gunathilaka et al. (2018)
Cattle	Malaysia	219	8	Khadijah et al. (2017)
Cattle	Taiwan	310	8.7	Tung et al. (2012)
	Total	22,117	0.8–97.17	
Buffalo	Cambodia	2,391	45	Dorny et al. (2011)
Buffalo	Vietnam	334	78	Geurden et al. (2008)
Buffalo	India	11,943	08.6–46.97	A. Gupta et al. (2018); G. Das et al. (2018a, 2018b); Krishna Murthy and D'Souza (2016); M. Das et al. (2018); Maharana et al. (2016); Malathi et al. (2021); S. Nath et al. (2015, 2016); Swarnakar et al. (2015)
Buffalo	Pakistan	438	12.8–12.9	Muhammad et al. (2017); Nazar et al. (2019)
Buffalo	Nepal	43	21.4	Bista et al. (2018)
Buffalo	Malaysia	129	75.2	Harizt et al. (2021)
Buffalo	Sri Lanka	16	18.75	Gunathilaka et al. (2018)
Buffalo	Bangladesh	1,319	15–78.4	Ara et al. (2021); Mamun et al. (2011); Roy et al. (2016); Saha et al. (2013); T. C. Nath et al. (2016)
	Total	16,613	08.6–78.4	
Fluke count				
Cattle	Iran	2,406	19.7–36.9	Hajipour et al. (2021); Khedri et al. (2015); Nikpay et al. (2019)
Cattle	Bangladesh	612	20.13–90.6	Alim et al. (2012); Azam et al. (2012)

Table 2 (continue)

Host	Country	Total animals	Ranging prevalence (%)	References
Cattle	Iraq	518	6.45–60	Kurtpinar and Latif (1970); Sadoon Al-Biaty et al. (2011)
Cattle	Turkey	447	8.95	Ozdal et al. (2010)
Cattle	Pakistan	34	17.64–50.7	Raza et al. (2009)
Cattle	South Korea	2,124	60	Kang and Kim (1988)
	Total	6,141	6.45–90.6	
Buffalo	India	1,619	4.29–74.7	Patil et al. (2012); Swarnakar et al. (2014)
Buffalo	Pakistan	3,189	17.3–75.07	Asif Raza et al. (2012); Iqbal et al. (2013); Javed Khan et al. (2006)
Buffalo	Iraq	146	40	Kurtpinar and Latif (1970)
	Total	4,954	4.29–75.07	

count method is suitable for detecting rumen fluke in slaughtered animals, but the sedimentation method is the most reliable and cheap method to detect rumen fluke eggs in live animals (Graham-Brown et al., 2019; Taylor et al., 2007).

In Table 2, the coprological prevalence of faecal examination varies from 0.8% to 98.17% and 0.86% to 78.4% in cattle and buffaloes, respectively. The prevalence of rumen fluke by fluke counts method range between 6.45% to 90.6% and 4.29% to 75.07% in cattle and buffaloes, respectively. This prevalence of rumen fluke is variable in different countries, possibly due to climatic conditions of temperature and rainfall, different sample sizes, and livestock management systems (González-Warleta et al., 2013; Pfukenyi et al., 2005). Table 2 also shows that the prevalence of rumen fluke in Asian countries is higher in cattle than in buffaloes. The higher prevalence in cattle contributed to a greater sample size due to the high cattle population compared to buffaloes.

Pathogenesis and Clinical Sign in Cattle and Buffaloes

Pathological changes related to natural paramphistomosis have not been studied (Fuertes et al., 2015). Studies showed that immature rumen fluke is pathogenic and causes catarrhal to necrotic inflammation with thickening and ulceration in the small intestine after nine days of exposure to infected pasture, which cause productivity loss such as decreased in meat and milk, low nutrient conversation, weight loss, and fertility reduction (Chaudhry et al., 2017; Malrait et al., 2015; Mohanta et al., 2017). The frequency and significance of lesions caused by the adult rumen fluke are unclear (Toledo et al., 2006). Most authors suggested that the adult stage of rumen fluke does not produce any pathogenic effect and is harmless, but some experimental studies have shown that in heavy infection, it is associated with ruminal papillae atrophy and ulceration at the site of fluke attachment (Fuertes et al., 2015; Mohanta et al., 2017). The ruminal atrium of cattle

with natural paramphistomosis had the highest parasite burden. According to a post-mortem investigation of the forestomach, the *Calicophoron daubneyi* was the only species of the Paramphistomidae family identified in these animals (González-Warleta et al., 2013). Also, it has been proved that young animals under two years old are the most vulnerable, as adults build immunity more quickly and for more extended periods (Sanabria & Romero, 2008).

Variable mucosal oedema and villous atrophy are seen on histopathological examination of the affected intestine, including concomitant hyperplasia of mucosal crypts and submucosal Brunner's glands and infiltration of the mucosa and submucosa by lymphocyte, eosinophils, mast cells, plasma cells, and globule leucocytes (Fuentes et al., 2015). Mucosa-associated lymphoid follicles can occur on rare occasions (N. K. Gupta, 1993). Submucosal Brunner's glands isolated from the luminal environment may provide an ideal environment for the early growth of immature fluke (Fuentes et al., 2015). The hyperplastic changes persist until the rumen fluke migrates to the rumen, and it is possible to distinguish the microscopic differences from other endoparasites (Fenemore et al., 2021; Huson et al., 2017; N. K. Gupta, 1993).

The clinical signs of rumen fluke which have been reported from different countries include dullness, diarrhoea, which is accompanied by anorexia and intense thirst, weight loss, depression, severe water scour, anaemia, hypoproteinaemia,

hypalbuminaemia, sub-mandibular oedema, and rectal haemorrhage (Fenemore et al., 2021; Lotfy et al., 2010; Rangel-Ruiz et al., 2003). Mortality in an acute outbreak can be as high as 90% (Dube, 2010; Taylor et al., 2007).

Diagnosis

Rumen fluke diagnosis includes clinical signs, egg detection in the faecal sample, post-mortem examination, and molecular methods (Malrait et al., 2015; Rieu et al., 2007). Commercial tests like Flukefinder and FLOTAC are also available (Cringoli et al., 2010). Commercial tests are more sensitive than sedimentation methods (Duthaler et al., 2010). Unlike liver fluke, no commercial immunological diagnostic test is available for rumen fluke. Clinical signs can diagnose diseases in live animals (Taylor et al., 2007). Laboratory testing may quickly discover eggs in the faeces of an animal carrying an adult fluke. Still, this method is of little value since the disease occurs during the prepatent period, and the eggs could not be identified up to species level (Fenemore et al., 2021). Among the coprological tests, the filtration method with sieves and sedimentation methods are the most accurate for detecting rumen fluke eggs in faeces (Horak, 1971).

In post-mortem examination, adult fluke can be detected easily. Still, it is difficult to identify at the species level because challenging to observe the thick, robust bodies, and internal organs (Lotfy et al., 2010). A faecal examination is the best method for detecting the parasite in

live animals and determining the burden of fluke in the forestomach of live animals (Sargison et al., 2016). The fluke count method is a reliable method with good sensitivity and specificity compared to faecal egg count, and it has been proven that more than 100 eggs per gram indicate the presence of more than 100 adult rumen flukes in the rumen or reticulum (Rieu et al., 2007; Sargison et al., 2016). On the other hand, immunological diagnosis is still early for diagnosing rumen fluke (Tandon et al., 2014). However, a few studies proved that coproantigen detection provides an excellent alternative to the conventional method for diagnosing rumen fluke in livestock (Anuracpreeda et al., 2017; Saifullah et al., 2013). Finally, understanding the rumen fluke life cycle and control options requires accurate species identification for rumen fluke (Gordon et al., 2013). Because of all these problems, a molecular method such as PCR-based techniques providing rDNA ITS2 sequence proved to be good tools for identifying rumen fluke up to species level and determining their phylogenetic relationship (Chamuah et al., 2016; Itagaki et al., 2003; Martinez-Ibeas et al., 2016).

Treatment and Control of Rumen Fluke

The typical flukicides used in cattle and sheep do not kill rumen fluke (Animal Health and Veterinary Laboratories Agency [AHVLA], 2013). Among antihelmintic drugs, oxclozanide and closantel with faecal egg count reduction (FECR) values of 97% to 99% were found to be the drug of choice for the treatment of rumen fluke

(Arias et al., 2013; Fenemore et al., 2021). Mild infections do not affect animal health or productivity (Fenemore et al., 2021). According to Animal Health Ireland (AHI) (2011), detecting rumen fluke eggs in faecal samples or detecting adults in small numbers in the rumen is not a reason to carry out specific control measures (AHI, 2011). Current veterinary advice is necessary to avoid the overuse of any flukicide to reduce resistance. Roughly treating rumen fluke is rarely justified, except on farms where severe disease and economic losses are confirmed (AHI, 2011).

The disease incidence is closely linked to environmental conditions, ecology, and the infection of intermediate snail hosts in a given location (Tariq et al., 2008). High rainfall areas and areas where animals have access to streams, ditches, ponds, wetlands, and marshy regions have a greater prevalence of rumen fluke (Fenemore et al., 2021). Keeping domestic ruminants away from infected pastures is the way to avoid rumen fluke infections (Pfukenyi et al., 2005). The most effective strategy for controlling rumen fluke is to remove the snail intermediate host from the rumen fluke life cycle (N. K. Gupta, 1993). It is recommended that wetlands or marshy/swampy areas be fenced off or drained and ensure that clean pastures and cercaria-free troughs are provided to the livestock (Taylor et al., 2007).

CONCLUSION

In the present review, 26 rumen fluke species belonging to two families

occurred in cattle and buffaloes in Asian countries. The prevalence of rumen fluke is high in some Asian countries. Genus *Paramphistomum* and *Cotylophoron* in the family of Paramphistomidae have a wider distribution and higher prevalence than the species of other genera. The prevalence data show that the fluke count method is reliable for determining the prevalence of rumen fluke in slaughtered cattle and buffaloes. In contrast, the sedimentation method is highly suitable for detecting rumen fluke infection in live animals. Molecular methods proved good tools for identifying rumen fluke up to species level. Based on recent studies, rumen fluke should now be considered a vital production disease of ruminant livestock in Asia. It is necessary to comprehend and manage all aspects of epidemiological factors that may impact cattle and buffaloes' productivity and farming efficiency to control the rumen fluke infections. Therefore, more studies are needed to identify the species of rumen fluke in most Asian countries, explore the economic impact of rumen fluke, detect a specific type of snail that acts as an intermediate host for rumen fluke, the anthelmintic efficacy, and develop the diagnostic techniques that can detect the prepatent infections of rumen fluke in livestock.

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