

Human Intestinal Flukes

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From Discovery to Treatment and Control

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Preface

Digenetic trematodes are an important group of parasites infecting humans and animals. They are morphologically characterized by dorsoventrally flat body and the presence of at least two suckers, oral and ventral suckers, and, in some cases, another sucker, i.e., the genital sucker. They are exclusively parasitic and, in most cases, hermaphroditic, with the exception of schistosomes, which have separate sex. Trematodes can be classified into two large categories, namely, contact (water)-borne and foodborne species. The former is a highly important group, i.e., schistosomes (family Schistosomatidae), which can cause infections in mesenteric and vesical blood vessels of animals and humans. The latter is another important group causing infections in the alimentary tract, including the bile duct, intestine, esophageal wall, pancreatic duct, or the lung parenchyma and extrapulmonary locations.

More than one billion people are estimated to be at risk of infection with foodborne trematodes, and about 56 million were infected as of 2005 (Fürst et al. 2012). These foodborne trematodes are largely classified into liver, lung, and intestinal flukes. Among them, intestinal flukes are the largest group in which at least 74 species are involved in causing zoonotic infections in humans (Yu and Mott 1994; Chai 2007). The number of people infected with these flukes is estimated to be about seven million people worldwide (Toledo et al. 2014). However, this may be a far underestimate of the actual number.

The zoonotic intestinal flukes are morphologically diverse and comprise of a total of 38 genera belonging to 16 families: the Heterophyidae (*Metagonimus*, *Heterophyes*, *Haplorchis*, *Acanthotrema*, *Apophallus*, *Ascocotyle*, *Centrocestus*, *Cryptocotyle*, *Heterophyopsis*, *Procerovum*, *Pygidiopsis*, *Stellantchasmus*, and *Stictodora*), Echinostomatidae (*Echinostoma*, *Isthmiophora*, *Echinochasmus*, *Acanthoparyphium*, *Artyfechinostomum*, *Echinoparyphium*, *Himasthla*, and *Hypoderaeum*), amphistomes (*Fischoederius*, *Gastrodiscoides*, and *Watsonius*), Diplostomidae (*Neodiplostomum* and *Fibricola*), Fasciolidae (*Fasciolopsis*), Gymnophallidae (*Gymnophalloides*), Lecithodendriid-like flukes (*Caprimolgorchis* and *Phaneropsolus*), Plagiorchiidae (*Plagiorchis*), Brachylaimidae (*Brachylaima*), Strigeidae (*Cotylurus*), Microphallidae (*Gynaecotyla* and *Microphallus*), Isoparorchiiidae (*Isoparorchis*), Troglotrematidae (*Nanophyetus*), and

Cyathocotylidae (*Prohemistomum*) (Yu and Mott 1994; Chai and Lee 2002; Fried et al. 2004; Chai 2007; Chai et al. 2009). Life cycles and geographical distributions are diverse and characteristic for each species.

Intestinal fluke infections are commonly considered as tropical endemic diseases in Asian countries where six million people are infected (Fürst et al. 2012). However, the geographical limits and the population at risk are currently expanding and changing in relation to factors such as growing international markets, improved transportation systems, changes in eating habits in western countries, and demographic changes (Toledo et al. 2014). Global warming and environmental changes may be another important factor for the endemicity changes. The pathogenicity of intestinal flukes is generally mild, but investigation is needed to see how it is in immunocompromised individuals. There are problems to be solved for specific diagnosis of intestinal fluke infections (Chai et al. 2005). In this book, characteristics of each species of intestinal fluke, in terms of biology, epidemiology, host-parasite relationships, pathogenicity, clinical aspects, diagnosis, and treatment, are reviewed in detail.

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Contents

1	Heterophyids.....	1
2	Echinostomes	169
3	Amphistomes	345
4	Diplostomes.....	369
5	Fasciolids.....	397
6	Gymnophallids	417
7	Lecithodendriid-Like Flukes.....	443
8	Plagiorchiids	463
9	Miscellaneous Zoonotic Species	491
	Index.....	521

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