

ZOOTAXA

1218

**An exceptionally rich complex of Sanguinicolidae von Graff, 1907
(Platyhelminthes: Trematoda)
from Siganidae, Labridae and Mullidae (Teleostei: Perciformes)
from the Indo-west Pacific Region**

MATTHEW J. NOLAN & THOMAS H. CRIBB



Magnolia Press
Auckland, New Zealand

MATTHEW J. NOLAN & THOMAS H. CRIBB

An exceptionally rich complex of Sanguinicolidae von Graff, 1907 (Platyhelminthes: Trematoda) from Siganidae, Labridae and Mullidae (Teleostei: Perciformes) from the Indo-west Pacific Region
(*Zootaxa* 1218)

80 pp.; 30 cm.

26 May 2006

ISBN 1-877407-66-6 (paperback)

ISBN 1-877407-67-4 (Online edition)

FIRST PUBLISHED IN 2006 BY

Magnolia Press

P.O. Box 41383

Auckland 1030

New Zealand

e-mail: zootaxa@mapress.com

<http://www.mapress.com/zootaxa/>

© 2006 Magnolia Press

All rights reserved.

No part of this publication may be reproduced, stored, transmitted or disseminated, in any form, or by any means, without prior written permission from the publisher, to whom all requests to reproduce copyright material should be directed in writing.

This authorization does not extend to any other kind of copying, by any means, in any form, and for any purpose other than private research use.

ISSN 1175-5326 (Print edition)

ISSN 1175-5334 (Online edition)

An exceptionally rich complex of Sanguinicolidae von Graff, 1907 (Platyhelminthes: Trematoda) from Siganidae, Labridae and Mullidae (Teleostei: Perciformes) from the Indo-West Pacific Region

MATTHEW J. NOLAN¹ & THOMAS H. CRIBB²

The Department of Microbiology and Parasitology and Centre for Marine Studies, the University of Queensland, Brisbane, Queensland 4072, Australia

E-mail: ¹ m.nolan1@uq.edu.au; ² t.cribb@uq.edu.au

Talbe of contents

Abstract	4
Introduction	5
Material and methods	6
Results	13
“Thread-like” sanguinicolids	13
Overview and approach	14
Molecular results	14
Morphological results	23
Sanguinicolidae von Graff, 1907	24
<i>Ankistromeces</i> Nolan & Cribb, 2004	24
<i>Ankistromeces dunwichensis</i> n. sp. (Figs. 9–11)	24
<i>Ankistromeces olsoni</i> n. sp. (Figs. 12–14)	30
Sanguinicolidae von Graff, 1907	32
<i>Phthinomita</i> n. g.	32
Genus level taxonomy	33
<i>Phthinomita symplocos</i> n. sp. (Figs. 8, 15–22)	35
<i>Phthinomita adlardi</i> n. sp. (Figs. 23–25)	38
<i>Phthinomita brooksi</i> n. sp. (Figs. 26–28)	40
<i>Phthinomita hallae</i> n. sp. (Figs. 29–31)	43
<i>Phthinomita ingramae</i> n. sp. (Figs. 32–34)	46
<i>Phthinomita jonesi</i> n. sp. (Figs. 35–37)	48
<i>Phthinomita littlewoodi</i> n. sp. (Figs. 38–40)	50
<i>Phthinomita robertsthomsoni</i> n. sp. (Figs. 41–43)	52
<i>Phthinomita sasali</i> n. sp. (Figs. 44–46)	55
Sanguinicolid prevalence in the Labridae	57

<i>Phthinomita munozae</i> n. sp. (Figs. 47–49)	57
Sanguinicolid prevalence in the Mullidae	61
<i>Phthinomita poulini</i> n. sp. (Figs. 50–62)	61
Discussion	64
Acknowledgements	75
References	75

Abstract

We describe an unprecedented radiation of sanguinicolid blood flukes (Digenea: Sanguinicolidae) from two species of Labridae (*Choerodon venustus* and *C. cauteroma*), seven species of Mullidae (*Mulloidichthys vanicolensis*, *Parupeneus barberinoides*, *P. barberinus*, *P. bifasciatus*, *P. cyclostomus*, *P. indicus* and *P. multifasciatus*) and ten species of Siganidae (*Siganus argenteus*, *S. corallinus*, *S. doliatus*, *S. fuscescens*, *S. lineatus*, *S. margaritiferus*, *S. puellus*, *S. punctatus*, *S. virgatus* and *S. vulpinus*) from sites off Australia and Palau. The flukes were morphologically similar in having the combination of a long thread-like body, tegumental spines in lateral transverse rows, a vestigial oral sucker bearing concentric rows of fine spines, an H-shaped intestine, a cirrus-sac, a notch level with the male genital pore, a lateral or post-ovarian uterus, a uterine chamber and separate genital pores. These species are divided into two genera on the basis of testis number. Sanguinicolids from *Siganus fuscescens* have a single large testis between the intestinal bifurcation and the ovary and are placed in *Ankistromeces* Nolan & Cribb, 2004. Species from the remaining nine species of Siganidae, Labridae and Mullidae are placed in *Phthinomita* n. g.; these species have two testes, the anterior testis being large and between the intestinal bifurcation and the ovary whereas the small posterior testis is at the posterior end of the body and appears rudimentary or degenerate and probably non-functional. The second internal transcribed spacer (ITS2) of ribosomal DNA (rDNA) from 29 host/parasite/location combinations (h/p/l) was sequenced together with that of *Ankistromeces mariae* Nolan & Cribb, 2004 for comparison. From 135 samples we found 19 distinct genotypes which were interpreted as representing at least that many species. Replicate sequences were obtained for 25 of 30 h/p/l combinations (including *A. mariae*); there was no intraspecific variation between replicates sequences for any of these. Interspecific variation ranged from 1–41 base differences (0.3–12.7% sequence divergence). The 19 putative species were difficult to recognise by morphological examination. We describe 13 new species; we do not describe (=name) six species characterised solely by molecular sequences and three putative species for which morphological data is available but for which molecular data is not. We have neither morphological nor molecular data for sanguinicolids harboured in five hosts species (*Siganus margaritiferus*, *S. puellus*, *Choerodon cauteroma*, *Parupeneus indicus* and *P. multifasciatus*) in which we have seen infections. Where host species were infected in different localities they almost always harboured distinct species. Some host species (for example, *S. argenteus* and *S. lineatus* from Lizard Island) harboured two or three species in a single geographical location. This suggests that, for parts of this system, parasite speciation has outstripped host speciation. Distance analysis of ITS2 showed species from each host family (Siganidae, Mullidae and Labridae) did not form monophyletic clades to the exclusion of species from other host families. However, a host defined clade was formed by the sequences from sanguinicolids from *S. fuscescens*.