



HOKKAIDO UNIVERSITY

Title	Discovery, systematics, and taxonomy of new marine Apicomplexa and a myzozoan relative [an abstract of dissertation and a summary of dissertation review]
Author(s)	入谷, 直輝 デーヴィス
Degree Grantor	北海道大学
Degree Name	博士(理学)
Dissertation Number	甲第14197号
Issue Date	2020-09-25
Doc URL	https://hdl.handle.net/2115/79548
Rights(URL)	https://creativecommons.org/licenses/by/4.0/
Type	doctoral thesis
File Information	Iritani_Naoki_Davis_abstract.pdf, 論文内容の要旨



Abstract of Doctoral Dissertation

Degree requested: Doctor of Science Applicant's name: IRITANI, Naoki Davis

Title of Doctoral Dissertation

Discovery, systematics, and taxonomy of new marine Apicomplexa and a myxozoan relative

(アピコンプレックス類および近縁のミゾゾア類における未記載種の発見
およびそれらの系統分類学的研究)

Taxonomy in its essence posits that the entire biosphere is connected by common descent. The binomial system of nomenclature suggested by Carl Linnaeus relies on both similarities and differences among species. Shared traits among species as a result of common ancestry unite organisms into taxonomic units. On the other hand, the different adaptations that make each lineage unique are carefully scrutinized to distinguish related taxa. This seemingly simple and traditional practice has, of course, various challenges that slow the impetus to the classification of life. For example, experts often disagree on what makes two lineages sufficiently different, literature old and new is scattered across obscure journals in various languages, and natural mechanisms such as convergent evolution can confound classification. Taxonomy, despite these complex obstacles, continues to form the foundation of biology by creating an ever-expanding lexicon of nomenclature. Without the proper vocabulary to refer to all life on Earth, interdisciplinary communication and navigating through the disciplinary matrix of biology would be near impossible.

The research included in this dissertation aims to contribute to taxonomy by delving into an enigmatic group of parasitic eukaryotes known as the Apicomplexa and its close relatives. These parasites are speciose and have devastating medical impact to human life and the natural ecosystem. However, there is a noticeably disproportionate depth of knowledge between what is known about a select group of apicomplexan species and what is known about apicomplexan biology as a whole. This dissertation presents descriptions of a new genus, five new species of apicomplexan parasites, and the characterization of an undescribed apicomplexan relative isolated from various animal hosts. These descriptions employ the use of both traditional morphology as well as molecular systematics in an effort to better reconcile morphological data with molecular phylogenetics. At the very core of this work is my attempt at making a humble contribution to the creation of a taxonomy that reflect phylogeny and to help rectify the lack of taxon sampling through species discovery and acquisition of novel data.

The first chapter is a general introduction to apicomplexan biology, taxonomy, and systematics. It aims to provide an overview of the history of apicomplexan biology while highlighting the major lineages within the

group and their main characteristics. The chapter most heavily articulates the Gregarinasina – the main focal taxon of the research included herein. Finally, this review of literature demonstrates that the major obstacles to apicomplexan biology include poor taxon sampling, a lack of research on non-medically significant species, and the dissonance between taxonomy and phylogenetics.

The second chapter describes the discovery of a new species of marine gregarine, *Cuspidella ishkariensis* gen. nov., sp. nov., from a scale worm host found in Hokkaido, Japan. The observation of unusual morphological traits in this new species provided an opportunity to re-evaluate the degree of morphological innovation in marine gregarines. The molecular identity of a previously described scale worm parasite, *Loxomorpha harmothoe* was also recovered and given a phylogenetic position as *Loxomorpha* cf. *harmothoe*. These scale worm parasites form a distinct lineage within the greater marine gregarine phylogeny and a new genus was created to accommodate this discovery.

The third chapter presents four new species of marine gregarines discovered from ascidian hosts from New Zealand: *Lecudina kaiteriteriensis* sp. nov., *L. dolabra* sp. nov., *L. savignyii* sp. nov., and *L. pollywoga* sp. nov. These novel taxa were characterized morphologically using microscopy and phylogenetically using SSU rDNA sequences. The analyses revealed a colourful history of marine gregarines switching hosts between annelid and ascidian hosts. The classification of these new species led to a deep delve into traditional literature whereupon previously undetected taxonomic issues became apparent. To reconcile taxonomy with this improved understanding of evolutionary history, *Lankesteria*, a large, traditional genus of ascidian parasites containing 45 species is combined with *Lecudina*.

The fourth chapter discusses *Platyproteum* sp., a species of parasite found from a sipunculid host in Hokkaido, Japan. This parasite was originally classified as an apicomplexan until a recent phylogenomic analysis showed that it is instead a species situated deep in the myzozoan phylogeny at the base of the Apicomplexa, chromerids, and colpodellids. In corroboration of this idea, *Platyproteum* sp. was shown to be a biflagellate, similar to other non-apicomplexan myzozoans, and the associated flagellar apparatus was characterized using electron microscopy. A phylogenetic analysis of SSU rDNA sequences was also consistent with the identity of *Platyproteum* sp. as a deep branching myzozoan parasite.

In conclusion, through the discoveries and data included in this dissertation, a contribution has been made to address the following: (1) the lack of taxon sampling in apicomplexan biology; (2) improving the understanding of basal apicomplexans and their relatives; and (3) the addition and emendation of names to help taxonomy better reflect a contemporary phylogenetics.