

It could be argued that plumbers did more for human health than scientists and doctors. Next time you are in Paris, take a tour of Les Egouts, the sewers. Deep underneath this most wonderful city, you will read that Napoleon considered the establishment of the sewers and the separation of clean and dirty water as his greatest achievement.

We should enter the 21st century with humility. Darwinian evolution will always be with us in a world with over 3000 species of mosquitoes. Nature will always fight back and we will need more than quick technological fixes to deal with this. However, the 20th century taught us that seemingly impossible advances can become obvious and routine with amazing speed. One thing that we can be sure of: there will be more surprises!

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News

New Insights into Platyhelminth Systematics and Evolution

P.D. Olson

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From a systematic perspective, the field of parasitology has been shaped during the 20th century to focus on a diverse, albeit incomplete, assemblage of taxa, loosely united by a 'parasitic' way of life – itself a loose concept. The field, for example, does not typically include the study of viruses, and parasitic insects are generally left to entomology. For a parasitologist, information from such disparate taxonomic groups is of interest because it helps to understand the general nature of parasitism. However, for a phylogeneticist interested in the evolution of a parasitic taxon, more salient information will come from the study of groups sharing a closer phylogenetic affinity, rather than a common ecology or trophic level. A recent symposium, 'Interrelationships of the Platyhelminthes', brought together, for the first time, turbellarian workers and parasitologists in an effort to advance our understanding of platyhelminth evolution, both within and among free-living,

commensal and parasitic forms, and to share new information from morphology, molecular biology, immunocytochemistry and developmental biology of major platyhelminth groups.

On the Acoela

Both the monophyly and phylogenetic position of the Platyhelminthes have been brought into question by recent publications. New molecular findings^{1,2} suggest that the flatworms may be members of either a larger spiralian or lophotrochozoan clade ('coelomates without a coelom'), rather than occupying a pivotal position near the base of a more pectinate phylogeny. More central to the symposium, however, is a recent report³ suggesting that the acoel 'turbellarians' fall outside of the Platyhelminthes as the most basal bilaterian taxon; a position historically attributed to the phylum itself. These and other studies have challenged long-held concepts of platyhelminth evolution, and illustrate the need for new corroborative evidence

and re-examination of traditionally accepted groupings. Such studies, using a disparate array of techniques and data, are under way.

Morphological works^{4,5} usually place the simple acoel flatworms near the base of the Platyhelminthes. However, Ulrich Ehlers (Institute für Zoologie und Anthropologie, Germany), whose classification of the phylum⁴ has been most widely adopted, noted that no unequivocal autapomorphic character unites all platyhelminths, and the inclusion or exclusion of the acoels could not be determined decisively on morphological grounds. Marta Riutort (Universitat de Barcelona, Spain) presented the published study³ based on small subunit ribosomal DNA (ssrDNA) that suggested the exclusion of the acoels from the phylum. In contrast, Cédric Berney's (Université de Genève, Switzerland) analysis of the nuclear protein coding gene *elongation factor 1- α* supported a closer affinity of the acoels to other turbellarians, but was far more limited in taxonomic scope. Olga Raikova (Zoological Institute of the Russian Academy

of Sciences, Russia) examined the monophyly and position of the controversial Acoelomorpha (Acoela + Nemertodermatida) by comparative study of their neural anatomy using immunocytochemical techniques. Her findings supported the uniqueness of the Acoela, but showed conflicting evidence with regard to the putative sister relationship between the Acoela and Nemertodermatida. There is little doubt that this question will continue to receive attention as the phylogenetic affinities impact not only the monophyly of the Platyhelminthes as presently defined, but also potentially the evolution of all bilaterally symmetrical animals.

New Characters

Although a comprehensive understanding of platyhelminth interrelationships cannot be expected for some time, it is encouraging that biologists are seeking new sources of character information, collecting and describing new taxa, and examining this information in a phylogenetic context. For example, Klaus Rohde (University of New England, Australia) examined the ultrastructure of protonephridial flame bulbs and found new synapomorphies uniting the tapeworms and their kin, as well as members of the rhabdocoel turbellarians. Other ultrastructural works focused on spermiogenesis and spermatozoan characters that are now being examined more broadly within the phylum. Jean-Lou Justine (Muséum National d'Histoire Naturelle, France) examined the phylogenetic utility of such characters at the phylum level (for which a number of major synapomorphies were identified), and Nikki Watson (University of New England, Australia) used comparative spermatology to examine relationships within the diverse Rhabdocoela. Matthew Hooe (University of Maine, USA) used fluorescent microscopy to study the body wall musculature of acoels and found new evidence to support a number of higher-level divisions within the group. David Halton (The Queen's University of Belfast, UK) reviewed the phylogenetic utility of neuroactive substances in flatworms; information gathered primarily for chemotherapeutic research. He identified a novel neuropeptide receptor in tapeworms, but noted that the small number of neuropeptides in flatworms in general will limit their utility as phylogenetic markers.

Jaume Baguña (Universitat de Barcelona, Spain) presented two unique types of *ssrDNA* in the Tricladida that

supported a closer affinity of the dugesiid triclads to members of the Terricola than to other members of the Paludicola, the group in which they are currently housed. Similarly, Max Telford (The Natural History Museum, London, UK) presented the evocative finding of novel codon usage in the Neodermata (the parasitic cestodes, digeneans, monogeneans and their kin) that is likely to represent a highly conserved synapomorphy for the clade. His review of the developmental literature pertaining to the phylum showed that exceptionally little is known about the molecular basis of platyhelminth development, except for regeneration studies on planarians⁶. However, what is known about early embryogenesis and *Hox* gene expression^{7,8} shows congruence with molecular results¹⁻³ supporting the position of at least the rhabditophoran flatworms within a derived spiralian clade. We can only hope that this situation will change in the coming years, as there stands the potential to learn a great deal from the developmental genetics of early metazoans.

Tim Littlewood (The Natural History Museum, London, UK) presented the only phylum-wide cladistic analysis based on molecular data. His preliminary analysis of complete 18S *ssrDNA* sequences from more than 280 species stood in stark contrast to the first ever such analysis nine years ago, based on fewer than 20 exemplars⁹. He showed a significant amount of resolution within the phylum and support for the monophyly of many recognized taxonomic groups (eg. Proseriata, Prolecithophora, Tricladida, Neodermata, Cestoda, Digenea, Monogenea). Among the most fundamental phylogenetic questions yet to be firmly resolved is determining the sister group to the strictly parasitic Neodermata, and thus helping to understand the evolution of parasitism within the phylum. Littlewood's analysis showed the sister group to be a large clade that included the triclads and prolecithophorans, as well as a few other aberrant turbellarian taxa. If true, this gives little insight to the condition of the proto-neodermatan, but does dispel some previous hypotheses. For example, the enigmatic *Udonella* sp., once considered a likely candidate¹⁰, is now placed among the monogeneans. Support for a monogenean affinity of *Udonella* sp. was also shown by Walter Boeger (Universidade Federal do Paraná, Brazil) who re-examined their morphology in light of these molecular findings.

Morphology, Molecules and Life History

Morphological study, the underpinning of taxonomy and systematics (and thus evolution) is, in some minds, a dying vocation. However, a majority of new studies suggests this is not so, and perhaps even greater attention is now placed on assessing morphological character homologies. New morphology-based hypotheses for many of the major turbellarian and neodermatan groups included, among others, the Aspidogastrea (K. Rohde), Dugesidae (Ronald Sluys, Institute for Systematics and Population Biology, The Netherlands), Macrostomorpha (Reinhard Rieger, Universität Innsbruck, Austria), Monogonoidea (W. Boeger), and Tetraphyllidea and related cestodes (Janine Caira, University of Connecticut, USA). Combined analyses of morphology and molecules were examined for the two major parasitic groups, Cestoda (Eric Hoberg, Biosystematics and National Parasite Collection, USA) and Digenea (Rod Bray, The Natural History Museum, London, UK), and new molecular based phylogenies are being generated at an ever-increasing rate. Perhaps one of the more interesting examples was a molecular study of generic-level relationships within the Schistosomatidae presented by Scott Snyder (University of Wisconsin Oshkosh, USA). Despite the vast literature on human-infecting *Schistosoma* spp, surprisingly few works have examined the evolution of the entire family. Snyder's work supported an Asian origin of the genus *Schistosoma*, previously thought to have evolved on the African continent.

The complex life cycles of parasitic flatworms are fascinating, and numerous attempts have been made to explain their evolution or to use this information to infer phylogeny. Ian Beveridge (University of Melbourne, Australia) noted that although there are more than 200 known life cycles of tapeworms, the vast majority are members of a single derived order, Cyclophyllidea. Among the digeneans the situation is perhaps slightly better; Thomas Cribb (University of Queensland, Australia) concluded that the three-host life cycle, as seen in the Diplostomoidea, is the basic pattern, two-host life cycles have evolved via abbreviation and forked-tailed cercariae are plesiomorphic. Fortunately, the ever-growing molecular database should be an expedient tool with which to elucidate parasite life cycles by screening larval stages against known adult sequences.

Perspective

Considerable effort is being made to resolve long-standing problems in the systematics and evolution of the Platyhelminthes. Molecular data provide valuable new information and a means of evaluating putative morphological homologies and life history strategies. Progress indicates that understanding platyhelminth interrelationships at all taxonomic levels is achievable, and will come from studies utilising the wide array of techniques now available. It is hoped that continued solidarity between parasitologists and turbellarian workers will help realise this common goal.

Acknowledgements

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Systematics Association and the British Society for Parasitology. Participants from over 24 countries convened, appropriately, at the site where the theory of evolution by natural selection was first presented in 1858. Much of the work presented will form the basis of a peer-reviewed, edited volume of the same title scheduled to appear in early 2000, published by Taylor & Francis. The author gratefully acknowledges the support of a Marshall-Sherfield Fellowship (Marshall Aid Commemoration Commission, UK) during the writing of this report.

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Peter D. Olson is at The Natural History Museum, Department of Zoology, Division of Parasitic Worms, Cromwell Road, London, UK SW7 5BD. **Tel: +44 207 942 5568, Fax: +44 207 942 5151, e-mail: P.Olson@nhm.ac.uk**

Molecular Helminthology Moves Forward

M. Blaxter, R. Maizels and M. Kennedy

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At the beginning of July, Edinburgh was the place to be for molecular, biochemical or immunological helminthologists. The field of molecular helminthology has been spurred on in recent years by the completion of the *Caenorhabditis elegans* genome^{1,2}. For nematode parasitologists in particular, this free-living model has become a useful and rewarding testbed for understanding the biology of parasites.

Let Me Count the Ways...

Patty Kuwabara (Sanger Centre, Cambridge, UK) gave an overview of the post-sequencing functional genomics initiatives on 'the worm', particularly the use of reverse genetics, RNA interference (RNAi) phenocopying of null mutants and microarray technology. Transgenic *C. elegans* can be constructed to carry parasite genes, and Collette Britton (University of Glasgow, UK) presented an analysis of promoter segments of *Haemonchus* protease genes that gave specific expression in the *C. elegans* gut. Many researchers are using analysis of *C. elegans* orthologues of their favourite parasite genes to understand structure–function relationships. For example, a *Trichinella* muscle-stage larva transcription factor

has its closest known homologue in *C. elegans* (Bernadette Connolly, University of Bern, Switzerland), a homologue of the *Brugia* cytidine deaminase was shown to be upregulated at the moults in *C. elegans* (Fiona Thompson, University of Glasgow, UK), alternately spliced avermectin receptors from *Haemonchus* were compared and contrasted to those in *C. elegans* (Adrian Wolstenholme, University of Bath, UK), while the *C. elegans* homeobox gene cluster is being compared with that found in *Brugia* (Aziz Aboobaker, University of Edinburgh, UK).

Novel Vaccine and Drug Targets

One of the exciting rediscoveries of recent years has been the endosymbiotic bacteria (*Wolbachia*) of many filarial nematodes (*Brugia*, *Wuchereria*, *Onchocerca*, but not *Acanthocephalonema*). Achim Hoerauf (Bernhard-Nocht-Institute, Hamburg, Germany) presented preliminary, positive results of tetracycline therapy (directed against the bacterial endosymbionts) of onchocerciasis in Ghana. Potential drug targets were discussed by Tony Page (University of Glasgow, UK), who is analysing the structure–function relationships of novel cuticle biosynthesis enzymes (proline isomerases, prolyl hydroxylase and protein disulphide isomerase) of *C. elegans* and parasitic nematodes. Helminth

proteases and the possibilities for developing novel antiparasite agents were discussed by John Dalton (Dublin City University, Ireland) and those from *Schistosoma* by Jason Salter and Conor Caffrey (University of San Francisco, USA).

The nematode surface and secretions, and the *Schistosoma* tegument, were topics of studies on plant-parasitic-nematode secretions and their roles in establishing feeding sites in the host (John Jones, Scottish Crop Research Institute, Dundee, UK; David Bird, North Carolina State University, USA), on the biology and molecular biology of secreted and surface acetylcholinesterases of *Nippostrongylus* (Murray Selkirk, Imperial College, London, UK) and *Schistosoma* (Alison Agnew, University of Leeds, UK), and on the definition of an unprecedented protein phosphorylation system present extracellularly on the surface of *Trichinella* (Kleoniki Gounaris, Imperial College, London, UK). The interaction between the genomes of the parasites and their hosts was emphasized by Al Scott (John Hopkins School of Hygiene, Baltimore, USA), who described the biological effects of a macrophage migration factor homologue secreted by mammalian-stage *Brugia*, while Xingxing Zang (University of Edinburgh, UK) described *Brugia* homologues of serpin that may also interfere with the immune system.