LifeWatch Data Grant 2014

Filling the gaps in the World Register of Marine species (WoRMS)

[Anisakidae]

Final Report

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1. Data grant background

Taxonomy and systematic of anisakid nematodes have been controversial over the years. Numerous species have been assigned to the family and development of molecular approaches resulted in additional species to be discovered. The WoRMS data base does not contain an updated list of these parasites. At the time of applying for the grant, 147 taxa were classified as Anisakidae in the WoRMS database. This classification was incomplete and included several significant issues such as, neglecting recent changes to the classifications of these parasites particularly after development of molecular approaches for taxonomic purposes.

2. Agreed deliverables (as specified in the Data Grant contract)

The main aim of the LifeWatch project was to make the content of the Anisakidae (Nematoda) within the World Register of Marine Species (WoRMS) more complete by completing the list of anisakid nematodes in WoRMS database (by adding new names, verifying the synonymies and adding information about the type location, distribution and hosts for each species).

- The following results were expected by the end of the contract:
- Addition to the World Register of Marine Species of ca. 100 species.
- Revision of the existing species of anisakids in WoRMS.
- Revision and addition of related information: type location, distribution, hosts.

3. Results of the project:

- List of the concrete completed actions (# added , # revised, # corrected, etc).

In total 166 new taxa (including *Aliascaris indica, Alibagascaris, Anisakis alata, A. alexandri, A. catodontis, A. diomedeae, A. dussumierii, A. insignis, A. ivanizkii, A. kogiae, A. kukenthhalii, A. marina, A. oceanicus, A. patagonica, A. skrjabini, A. tridentate, A. tursiopis, Ascaris aquillae, A. microcephala, A. micropapillata, A. multipapillata, A. ovalis, Brevimulticaecum, B. baylisi, B. heterotis, B. regoi, B. scleropagi, Contracaecum amoyense, C. amoyensis, C. anasi, C. andersoni, C. arii, C. assi, C. australe, C. bancrofti, C. baylisi, C. bioccai, C. bubakii, C. caballeroi, C. ceylanicum, C. chaunaxi, C. chubutensis, C. clelandi, C. coiliae, C. collare, C. cyclopteri, C. diomedeae , C. engonium, C. engraulisi, C. epinepheli, C. equulai, C. erraticum, C. eudyptes, C. eudyptulae, C. fagerholmi, C. fortalezae, C. gibsoni, C. gracile, C. gypsophocae, C. hagedashiae, C. haliaeti, C. hapalogenyos, C. heardi, C.*

histiophori, C. ilishae, C. incurvum, C. legendri, C. longispiculum, C. macquariae, C. magnicollare, C. magnipapillatum, C. magnum, C. margolisi, C. melanogrammi, C. melichthysi, C. microcephalum, C. micropapiltatum, C. milviensis, C. mirounga, C. murrayense, C. nehli, C. nototheniae, C. nycticoracis, C. ogcocephali, C. ogmorhini, C. okadai, C. oschmarini, C. ovale, C. overstreeti, C. pagrosomi, C. paralichthydis, C. pelagicum, C. podicipitis, C. praestriatum, C. punctatum, C. rectum, C. rodhaini, C. rudolphiiD, C. rudolphiiE, C. rudolphiiF, C. saba, C. scomberomori, C. scotti, C. sinulabiatum, C. spasskii, C. tasmaniense, C. tricuspe, C. turkestanicum, C. variegatum, C. yamaguti, Dujardinascaris cenotae, D. helicina, D. malapteruri, Hysterothylacium arii, H. assi, H. baylisi, H. bidentatum, H. carangis, H. chaunaxi, H. coiliae, H. dollfusi, H. epinepheli, H. fortalezae, H. gracile, H. habena, H. hapalogenyos, H. haze, H. histiophori, H. ilishae, H. longispiculum, H. macquariae, H. macrozoarcium, H. magnum, H. melanogrammi, H. melichthysi, H. murrayense, H. naitoi, H. nototheniae, H. ogcocephali, H. okadai, H. otolithii, H. pagrosomi, H. rectum, H. robustum, H. salvelini, H. scomberomori, H. seriolae, H. synpapillus, H. trichiuri, H. tridentatum, H. unidentatum, H. zenis, Kathleena, Pseudoterranova, Pseudoterranova, P. azarasi, P. bulbosa, P. cattani, P. ceticola, P. decipiens, P. krabbei, Stomachus, Terranova antarctica, T. brevicapitata, T. Caballeroi and *T. Pristis)* were added to the database. In addition to the mentioned taxa at least 38 other taxa were significantly revised and at least 51 synonymy, were added.

Where available, other data such as distribution, type locality and host species were added for each taxon. Many new resources including original reports, re-description or major revisions were added as well.

4. (Brief) description of the work/methodology

- The first step was to go through the taxa listed in the WoRMS Database and detect out of date data, such as invalid species that were considered valid or to detect genera that no longer are classified under family Anisakidae.
- Then an updated classification of Anisakidae was employed over all available taxa.
- Missing genera were added to the database
- Species under each genus were reviewed and missing species were added. As mentioned above over 100 species were added to the WoRMS data base for the family Anisakidae either as new additions or synonymies.
- Then the data for each taxon was reviewed and missing data such as synonymy, distribution, host species and type location and accession number were added.
- A large number of resources including original descriptions and also resources including re-descriptions were added to the database.
- Although the aim of the project was to work on family Anisakidae, working and revising some closely related taxa such as members of the family Raphidascarididae

was inevitable as several taxa should have been moved between various families/genera.

5. Problems encountered and how it was solved (or expected solutions).

There were no significant problems during the course of this project; however the database could be more user friendly which would lead to saving a huge amount of time. For example:

1. Adding data in various fields, such as resources, distribution and geo-units should be a straightforward process instead of going through several windows to add a new geo-unit. Linking resources is very difficult also especially when there are so many author names to pick from and no system to sort the author names on more than one field for example by date of publication and initials and co-authors. It especially becomes problematic for common last names such as Johnston.
2. When data is being entered, if any field is not valid the system denies the entry and clears the whole form. It would be more efficient to highlight invalid data in the form without clearing the form.
3. There are several parasitic species, defined based on molecular work that cannot be differentiated morphologically, therefore a new name has not been assigned to these species yet. Instead they have been designated by alphabetical letters after the scientific name. Among family Anisakidae examples are *Controcaecum osculatum sensu lato* that now comprises *Controcaecum osculatum* A to E or *Contracaecum rudolphii sensu lato* that comprises *Contracaecum rudolphii* A to G. I was not able to add these taxa to the database as the system does not accept something like "*Contracaecum rudolphii A*" as a "species".

There were also some issues with the existing information in the database, such as:

1. Previous recent entries which were based on unaccepted old classifications.
2. Some host species did not exist in the database
3. The original description/only data about many taxa that were absent from the data base were in languages other than English making it difficult to add other information such as distribution and location of the type specimens.
4. Lack of data about the location of type specimens in several original descriptions as well as the lack of a consistent format to describe a new species in the earlier descriptions of new species.

6. Other: remarks, suggestions, other information, bibliography, …

1. The majority of the above mentioned issues could have been addressed if there was a template in the form of a spreadsheet available that editors could fill in and then upload to the system. The National Centre for Biotechnology Information (NCBI) has

a similar system in which all data about the gene, primer, organism etc are entered in an Excel spreadsheet and these are uploaded to the system, where later will be assessed by a curator to assign a GenBank accession number.

2. I think if the editor for each group of organisms could be in charge of approving revision or the addition of data for each taxon it would prevent editing by other editors or members who might not be necessarily as familiar with the taxonomy of a specific group.
3. I would like to express my appreciation for supporting this project. Parasites comprise about 75% of the Earth biodiversity and are important part of our ecosystems however despite their important roles and significant impacts, they quite often are neglected across many research studies. Although still there are many parasitic species are yet to be added to the WoRMS database, grant schemes such as LifeWatch WoRMS Data Grant, is a great step toward completion of the database and including parasitic species.