

# DNA-barcoding Decapoda and Stomatopoda from West-Africa

**ENDRE WILLASSEN**

University Museum of Bergen, Norway

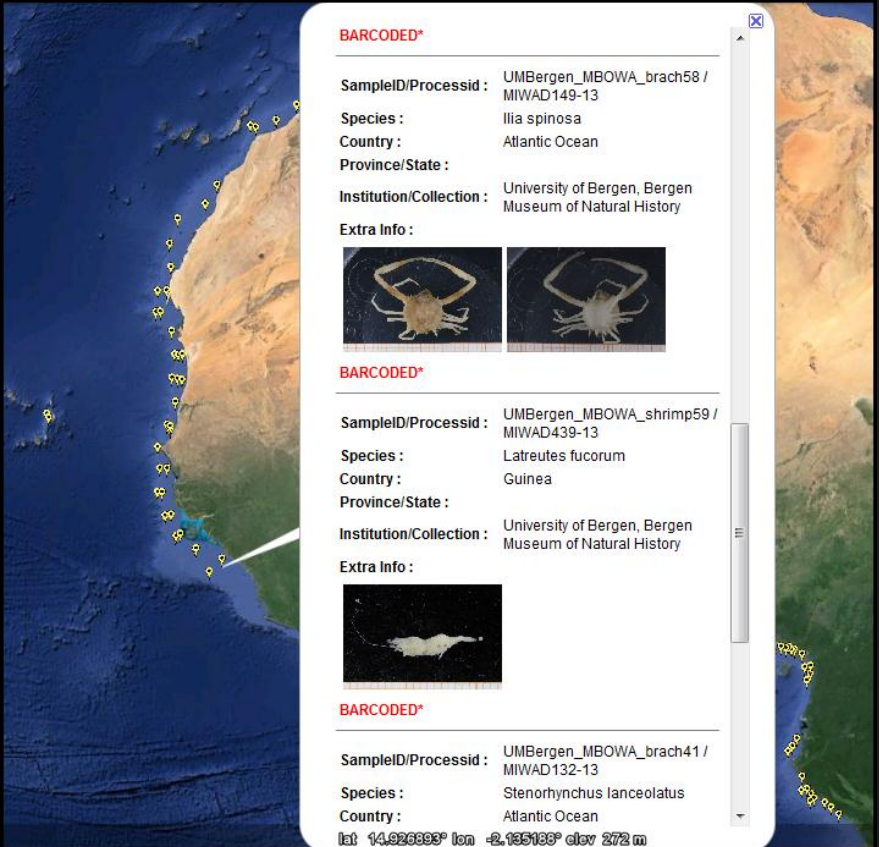
**EVA GARCÍA-ISARCH**

Instituto Español de Oceanografía, Cádiz, Spain


**SUSANA S. DE MATOS-PITA**

Universidade de Vigo, Pontevedra, Spain


Presentation for the  
8th International Crustacean Congress (ICC-8)  
Frankfurt am Main, August 18-23, 2014



**BARCODED\***

SampleID/Processid : UMBergen\_MBOWA\_brach58 / MIWAD149-13  
Species : *Illa spinosa*  
Country : Atlantic Ocean  
Province/State :  
Institution/Collection : University of Bergen, Bergen Museum of Natural History  
Extra Info :  


**BARCODED\***

SampleID/Processid : UMBergen\_MBOWA\_shrimp59 / MIWAD439-13  
Species : *Latreutes fucorum*  
Country : Guinea  
Province/State :  
Institution/Collection : University of Bergen, Bergen Museum of Natural History  
Extra Info :  


**BARCODED\***

SampleID/Processid : UMBergen\_MBOWA\_brach41 / MIWAD132-13  
Species : *Stenorhynchus lanceolatus*  
Country : Atlantic Ocean  
lat: 14.926693° lon: -2.135183° elev: 272 m



Universidade de Vigo



Canary Current  
LIME Project



CCLME



R/V Dr. Fridtjof Nansen

GCLME

Country	Count
Angola	10
Benin	3
Cameroon	52
Cape Verde	13
Gabon	99
Gambia	6
Ghana	21
Guinea	16
Guinea Bissau	26
Guinea Conakry	9
Ivory Coast	7
Liberia	24
Mauritania	33
Morocco	82
Nigeria	77
Republic of Congo	26
Sao Tome & Principe	39
Senegal	22
Sierra Leone	19
Togo	3
Western Sahara	24







# Decapoda & Stomatopoda



Universitetsmuseet i Bergen



# Some ID resources

Capard 1951

Holthuis 1952

Manning & Holthuis 1981

Holthuis 1991

Crosnier & Forest 1973

Miyake & Baba 1970

McLaughlin 2003

Ingle 1993

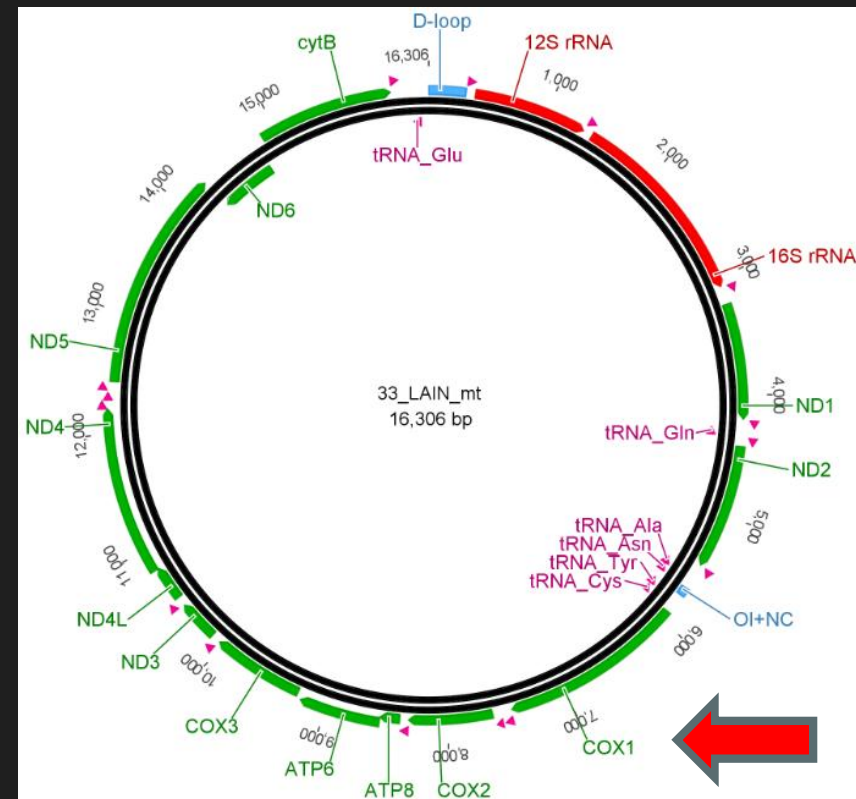
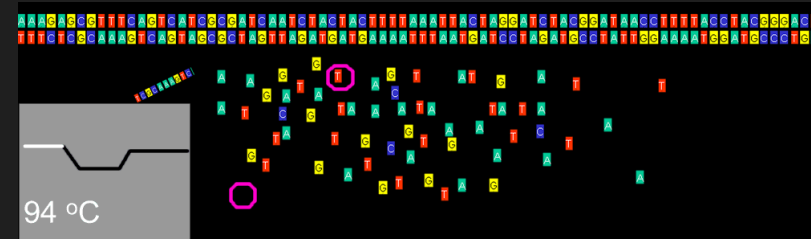
Manning 1977








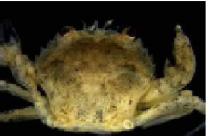



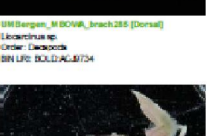








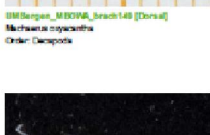
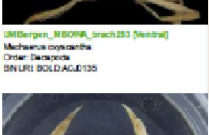


# DNA BARCODING

Ratnasingham, S. & Hebert, P. D. N. (2007). BOLD: The Barcode of Life Data System ([www.barcodinglife.org](http://www.barcodinglife.org)). *Molecular Ecology Notes* 7, 355-364. DOI: [10.1111/j.1471-8286.2006.01678.x](https://doi.org/10.1111/j.1471-8286.2006.01678.x)



Target gene segment:  
mitochondrial cox1

the BOLD system integrates taxonomy and occurrence data with DNA barcodes. <http://www.boldsystems.org/>

Collection Info Metadata									
Collection Date	Country/Ocean	Date/Province	Region	Sector	Latitude	Longitude	Elevation	Depth	
09.06.2005	Nigeria				5.444	4.57		481	
07.06.2005	Nigeria				6.0833	3.9997		281	
27.06.2005	Sao Tome & Principe				1.506	7.186		81	
08.05.2008	Gabon								
29.06.2012	Morocco								
10.06.2012	Cape Verde								
02.06.2012	Mauritania								
03.07.2012	Morocco								
03.07.2012	Morocco								
12.05.2012	Guinea								
14.05.2012	Guinea								
10.05.2008	Gabon								
21.06.2005	Cameroon								
24.06.2006	Cameroon								
20.06.2006	Cameroon								
29.06.2006	Cameroon								
29.06.2005	Sao Tome & Principe								
09.07.2005	Gabon								
10.06.2005	Nigeria								
09.07.2005	Gabon								
09.07.2005	Gabon								
09.07.2005	Gabon								
13.06.2005	Nigeria								

vouchers

## A DNA-Based Registry for All Animal Species: The Barcode Index Number (BIN) System

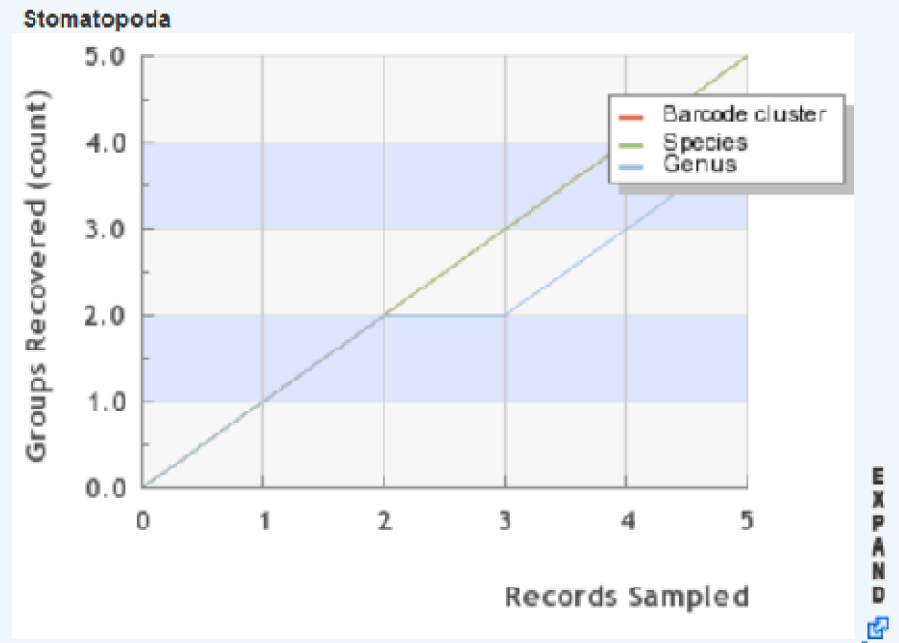
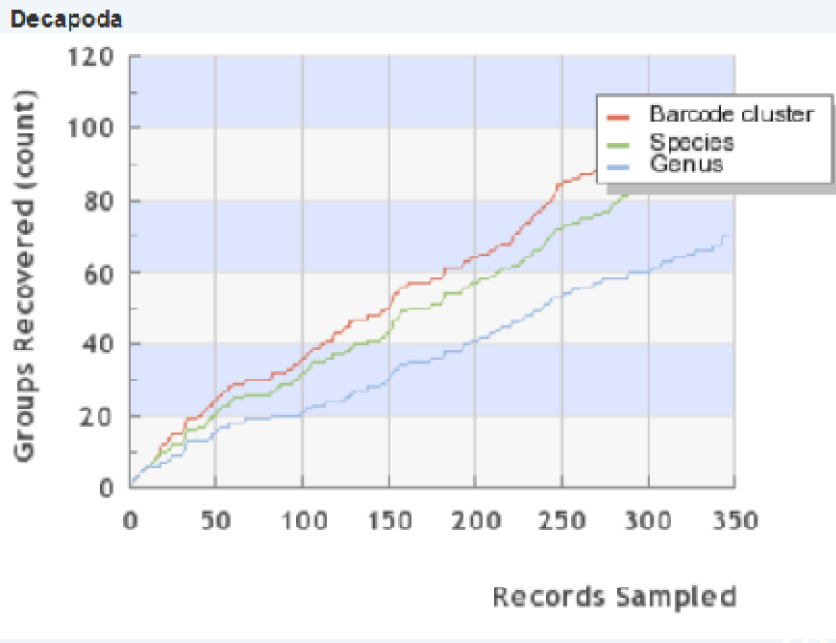
Sujeewan Ratnasingham<sup>1\*</sup>, Paul D. N. Hebert<sup>1,2</sup>

<sup>1</sup>Biodiversity Institute of Ontario, University of Guelph, Guelph, Ontario, Canada, <sup>2</sup>Department of Integrative Biology, University of Guelph, Guelph, Ontario, Canada

“BINs will aid revisionary taxonomy by flagging possible cases of synonymy, and by collating geographical information, descriptive metadata, and images for *specimens that are likely to belong to the same species*, even if it is undescribed”

Ratnasingham & Hebert 2013





**Achelata [2 species]**  
**Anomura [13 species]**  
**Brachyura [54 species]**  
**Caridea [22 species]**  
**Dendrobranchiata [8 species]**

after

**Eurysquillidae [3 species]**  
**Squillidae [2 species]**  
**Success:**  
**107 of 133 species**

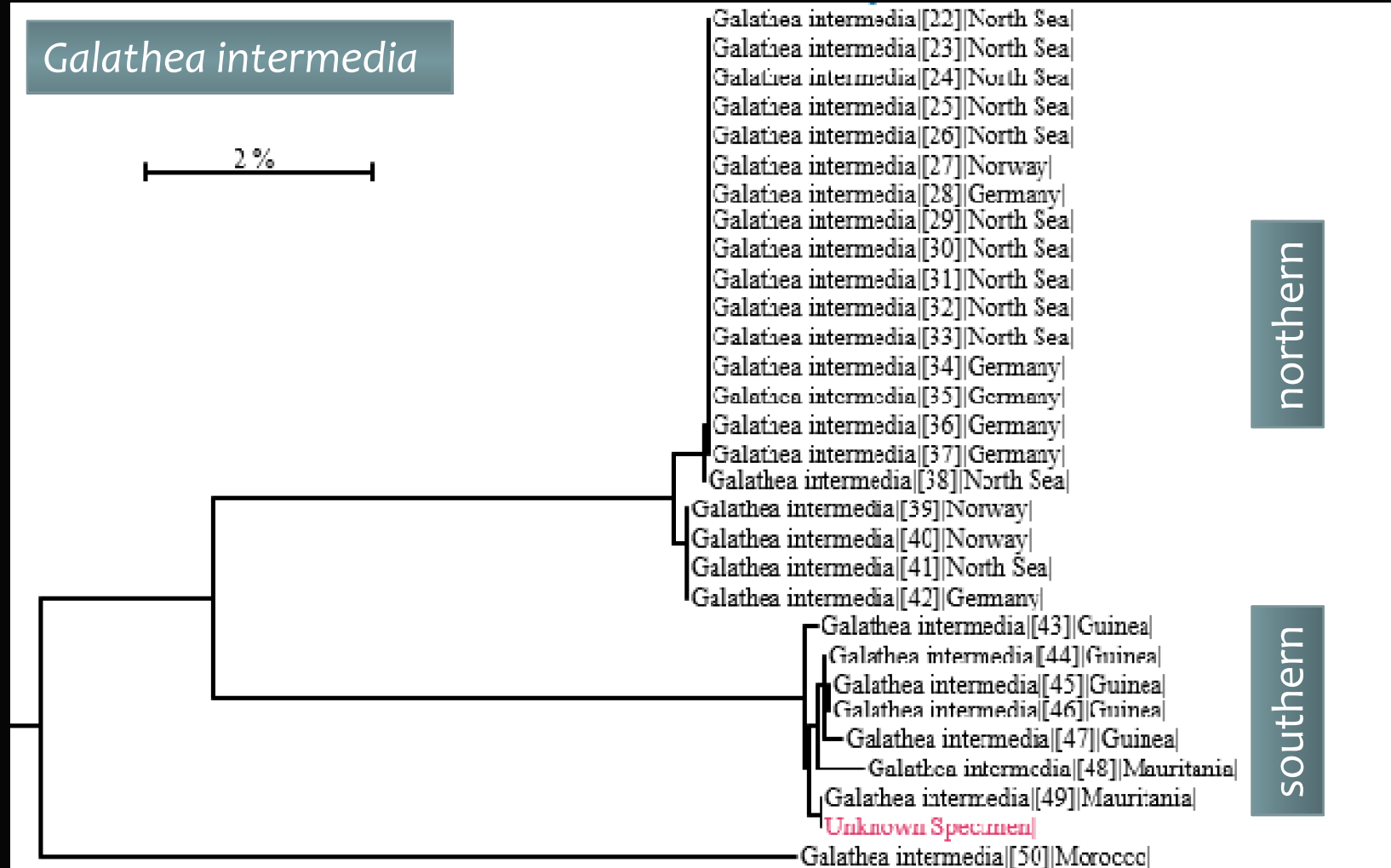


▼ Progress

	Specimens (% complete)	Species (% complete)
COI-5P	364 / 475 (76.6%)	107 / 133 (80.5%)

*Galathea intermedia*

2%



northern

southern



## BIN Discordance Report - MIWAD

### Overview



A searchable database of Barcode Index Numbers (BINs), sequence clusters that closely approximate species. This system allows for rapid validation and use of barcode data where taxonomic data are lacking or unverified.

#### SEQUENCE ANALYSIS

- [Taxon ID Tree](#)
- [Distance Summary](#)
- [Sequence Composition](#)
- [Barcode Gap Analysis](#)
- [Alignment Browser](#)
- [Ancestral State](#)

#### [BIN Discordance Report](#)

[Diagnostic Characters](#)

#### SPECIMEN AGGREGATES

- [Distribution Map](#)
- [Image Library](#)

**Data Selected:** 475 Records 351 Records with BINs Representing 114 BINs

#### Breakdown of Data:

<b>Taxonomically Discordant:</b>	14 BINs	43 Records
<b>Taxonomically Concordant:</b>	68 BINs	276 Records
<b>Singletons:</b>	32 BINs	32 Records

## BINs with Taxonomic Discordance

### Record Search

Process ID	Identification	Conflicting Taxon in BIN	Rank of Conflict	BIN	BIN Total Members	BIN Tax Variation
<input type="checkbox"/> MIWAD439-13	Latreutes fucorum	Hippolytidae	«internal» mismatch			Pandalidae[1], Hippolytidae[1]
<input type="checkbox"/> MIWAD441-13	Pandalina brevisrostris	Pandalidae				
<input type="checkbox"/> MIWAD141-13	Macropodia gilsoni	Inachidae	«external» mismatch		27	Inachidae[26], Polybiidae[1]
<input type="checkbox"/> MIWAD100-13	Macropodia gilsoni	Inachidae				
<input type="checkbox"/> MIWAD138-13	Macropodia gilsoni	Inachidae				
<input type="checkbox"/> MIWAD101-13	Macropodia gilsoni	Inachidae				
<input type="checkbox"/> MIWAD137-13	Macropodia gilsoni	Inachidae				
<input type="checkbox"/> MIWAD139-13	Macropodia gilsoni	Inachidae				
<input type="checkbox"/> MIWAD088-13	Menippe nodifrons	Menippidae				
<input type="checkbox"/> MIWAD076-13	Menippe nodifrons	Menippidae				
<input type="checkbox"/> MIWAD398-13	Alpheus sp.	Alpheus	Genus	BOLD:ACJ9964	2	Synalpheus[1], Alpheus[1]
<input type="checkbox"/> MIWAD473-13	Synalpheus sp.	Synalpheus				



BINs

[XML](#) [TSV](#) [FASTA](#) [TRACE](#) [XML](#) [TSV](#)  
 Specimen Data Sequences Combined

Show Help

Barcode Index Number Registry - for BOLD:AAD5026

Back to [Last Page](#)

Go to public records in this BIN

**BIN DETAILS:**

<b>BIN URI</b>	BOLD:AAD5026	<b>Average Distance:</b>	0.03% (p-dist)
<b>DOI</b>	<a href="http://dx.doi.org/10.5003/OCLD:AAD5026">http://dx.doi.org/10.5003/OCLD:AAD5026</a>	<b>Maximum Distance:</b>	0.16% (p-dist)
<b>Member Count:</b>	27 [27 Public]	<b>Distance to Nearest Neighbor:</b>	0.63% (p-dist)
<b>Barcode Compliant Members:</b>	19		
<b>Founding Record:</b>			

**NEAREST NEIGHBOR (NN) DETAILS:**

<b>Nearest BIN URI:</b>	BOLD:AAF8277	<b>Average Distance:</b>	0.66% (p-dist)
<b>Member Count:</b>	22	<b>Maximum Distance:</b>	1.27% (p-dist)
<b>Nearest Member:</b>	MIWAD099-13	<b>Distance Variance:</b>	0.12% (p-dist)
<b>Nearest Member Taxonomy:</b>	Arthropoda, Malacostraca, Decapoda, Inachidae, Macropodia, Macropodia rostrata		

**TAXONOMY:**

<b>Phylum:</b>	Arthropoda [27]	<input type="checkbox"/>
<b>Class:</b>	Malacostraca [27]	<input type="checkbox"/>
<b>Order:</b>	Decapoda [27]	<input type="checkbox"/>
<b>Family:</b>	Inachidae [20]	<input type="checkbox"/>
	Polybiidae [1]	<input type="checkbox"/>
<b>Subfamily:</b>		
<b>Genus:</b>	Macropodia [26]	<input type="checkbox"/>
	Liocarcinus [1]	<input type="checkbox"/>
<b>Species:</b>	Macropodia tenuirostris [7]	<input type="checkbox"/>
	Macropodia gilsoni [8]	<input type="checkbox"/>
	Macropodia longipes [6]	<input type="checkbox"/>
	Macropodia parva [5]	<input type="checkbox"/>
	Macropodia longirostris [2]	<input type="checkbox"/>
	Liocarcinus holzneri [1]	<input type="checkbox"/>

Add Tags & Comments  0 Associated Tags: No Tags

BIN COMPLIANT WITH METADATA REQUIREMENTS

Specimen Images:









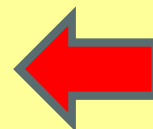
IP D206-11 (Liocarcinus holzneri)  
 License: Unspecified default All Rights Reserved  
 License Holder: Unspecified

### NEAREST NEIGHBOR (NN) DETAILS:

<u>Nearest BIN URI:</u>	BOLD:AAF8277	<u>Average Distance:</u>	0.56% (p-dist)
<u>Member Count:</u>	22	<u>Maximum Distance:</u>	1.27% (p-dist)
<u>Nearest Member:</u>	MIWAD099-13	<u>Distance Variance:</u>	0.12% (p-dist)
<u>Nearest Member Taxonomy:</u>	Arthropoda, Malacostraca, Decapoda, Inachidae, Macropodia, Macropodia rostrata		

### TAXONOMY:

<u>Phylum:</u>	Arthropoda [27]	
<u>Class:</u>	Malacostraca [27]	
<u>Order:</u>	Decapoda [27]	
<u>Family:</u>	Inachidae [26]	
	Polybiidae [1]	
<u>Subfamily:</u>		
<u>Genus:</u>	Macropodia [26]	
	Liocarcinus [1]	
<u>Species:</u>	Macropodia tenuirostris [7]	
	Macropodia gilsoni [6]	
	Macropodia longipes [6]	
	Macropodia parva [5]	
	Macropodia longirostris [2]	
	Liocarcinus holsatus [1]	





*M. gilsoni*? = *M. intermedia*?

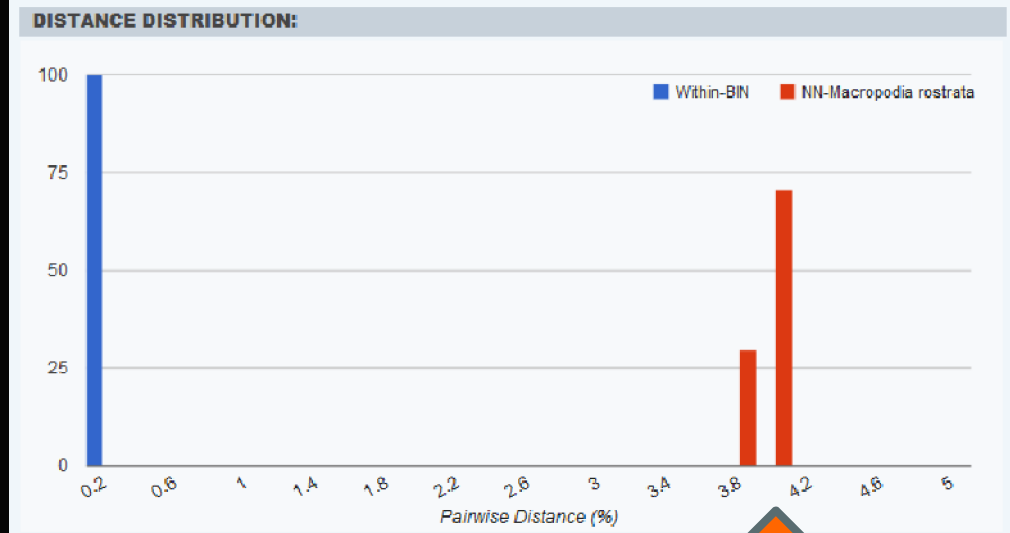
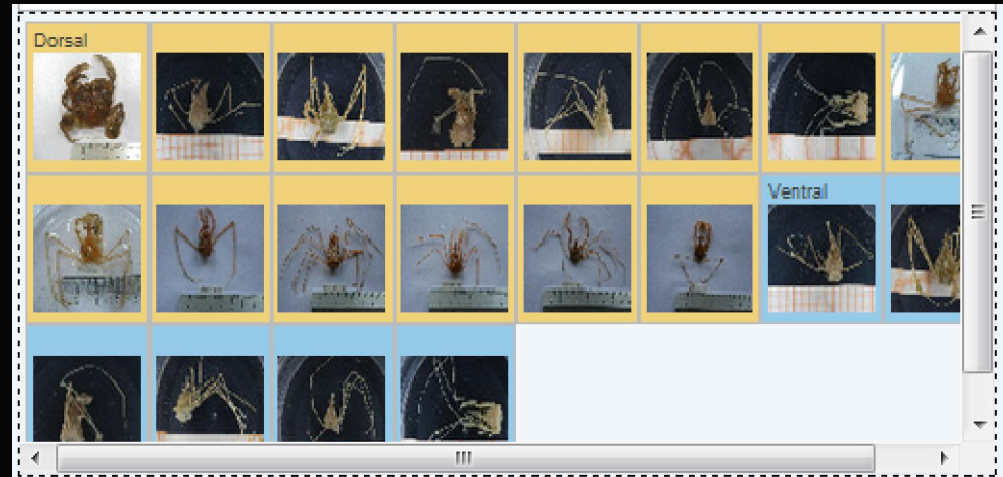
*M. longipes*?

*M. longirostris*?

*M. parva*?

*M. tenuirostris*?

~~*L. hoisatus*?~~



Nearest neighbour: *M.rostrata*

# Identification Request

Animal Identification  
[COI]

Fungal Identification  
[ITS]

The BOLD Identification System (IDS) for COI accepts sequence identification when one is possible. Further validation with

Historical Databases: [Jul-2013](#) [Jul-2012](#) [Jul-2011](#) [Jul-](#)

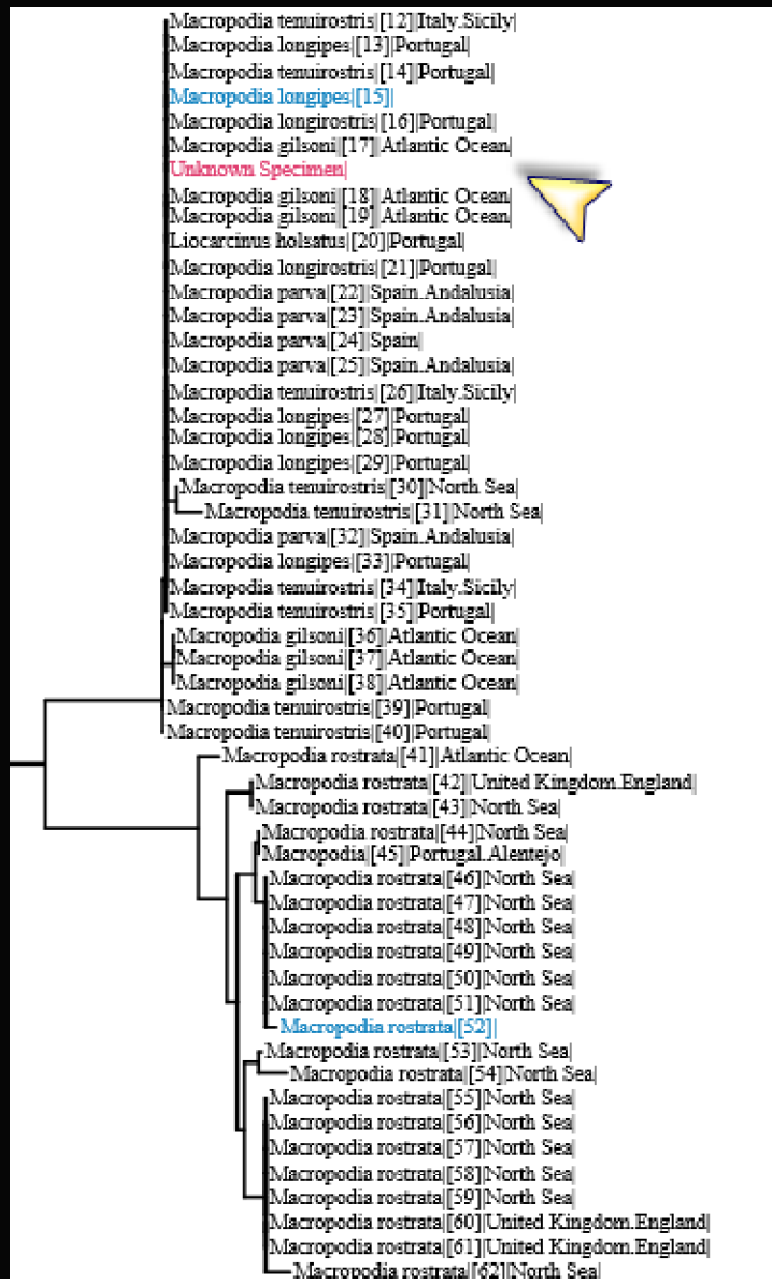
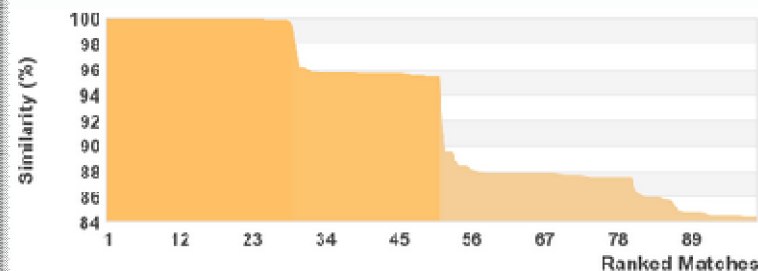
Search Databases:

100%

- All Barcode Records on BOLD (2,843,744 Sequences)
  - Every COI barcode record on BOLD with a minimum of 100% similarity
  - This includes many species represented by only one or two matches and does not provide a probability of placement
- Species Level Barcode Records (1,761,975 Sequences)
  - Every COI barcode record with a species level identification
  - specimens as well as all species with interim taxonomic status
- Public Record Barcode Database (563,322 Sequences)
  - All published COI sequences from BOLD and GenBank

esignation)

Similarity scores of the top 99 matches:





## Sin number two: inadequate a priori identification of specimens

OPINION

### The seven deadly sins of DNA barcoding

R. A. COLLINS\* and R. H. CRUICKSHANK†

*\*Bio-Protection Research Centre, Lincoln University, PO Box 84, Lincoln, 7647, Canterbury, New Zealand, †Department of Ecology, Faculty of Agriculture and Life Sciences, Lincoln University, Lincoln, 7647, Canterbury, New Zealand*

In ornamental cyprinid fishes:

- ” 35 % of the BINS contained more than one species name.
- ” The number rose to 53 % in 5-6 months

# Our sequencing of *Ethusa* failed



<input checked="" type="checkbox"/>	<a href="#">Ethusa rugulosa</a>	<a href="#">UMBergen MBOWA brach210</a>	<a href="#">MIWAD210-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusa rugulosa</a>	<a href="#">UMBergen MBOWA brach261</a>	<a href="#">MIWAD261-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusa rugulosa</a>	<a href="#">UMBergen MBOWA brach239</a>	<a href="#">MIWAD239-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusa rugulosa</a>	<a href="#">UMBergen MBOWA brach240</a>	<a href="#">MIWAD240-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusa sp.</a>	<a href="#">UMBergen MBOWA brach187</a>	<a href="#">MIWAD106-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusa vossi</a>	<a href="#">UMBergen MBOWA brach216</a>	<a href="#">MIWAD216-13</a>	336 [0n]			
<input checked="" type="checkbox"/>	<a href="#">Ethusa vossi</a>	<a href="#">UMBergen MBOWA brach217</a>	<a href="#">MIWAD217-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusa vossi</a>	<a href="#">UMBergen MBOWA brach215</a>	<a href="#">MIWAD215-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusina beninia</a>	<a href="#">UMBergen MBOWA brach186</a>	<a href="#">MIWAD105-13</a>	0			
<input checked="" type="checkbox"/>	<a href="#">Ethusina beninia</a>	<a href="#">UMBergen MBOWA brach185</a>	<a href="#">MIWAD104-13</a>	0			



## Brachyura cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial.

PopSet: 197260937

[GenBank](#) [FASTA](#)

### Study Details

Phylogeny of Dorippoidea (Crustacea, Decapoda, Brachyura) inferred from three mitochondrial genes

Sin, Y.W., Lai, J.C.Y., Ng, P.K.L. and Chu, K.H.

(2009) Invertebr. Syst. 23:(3)223-230

Go to:

### Sequences in this data set

[EU636987.1](#) Ranina ranina cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636986.1](#) Lauridromia dehaani cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636985.1](#) Parethusa sp. YWS-2008 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636984.1](#) Ethusa sexdentata isolate 6 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636983.1](#) Ethusa sexdentata isolate 5 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636982.1](#) Ethusa sexdentata isolate 4 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636981.1](#) Medorippe lanata isolate 25 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636980.1](#) Dorippoides nudipes isolate 16 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636979.1](#) Dorippe quadridens isolate 9 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636978.1](#) Dorippe quadridens isolate 1 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636977.1](#) Philippidorippe philippinensis isolate 2 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636976.1](#) Heikeopsis arachnoides isolate 27 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636975.1](#) Neodorippe simplex isolate 20 cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial  
[EU636974.1](#) Paradorippe granulata cytochrome oxidase subunit I (COI) gene, partial cds; mitochondrial

Palinurus elephas|GBCMD7107-13||Palinuridae|BOLD:AAA9098

Palinurus elephas|GBCMD7103-13||Palinuridae|BOLD:AAA9098

Palinurus elephas|GBCMD7117-13||Palinuridae|BOLD:AAA9098

# Species data are fuzzy products of human minds

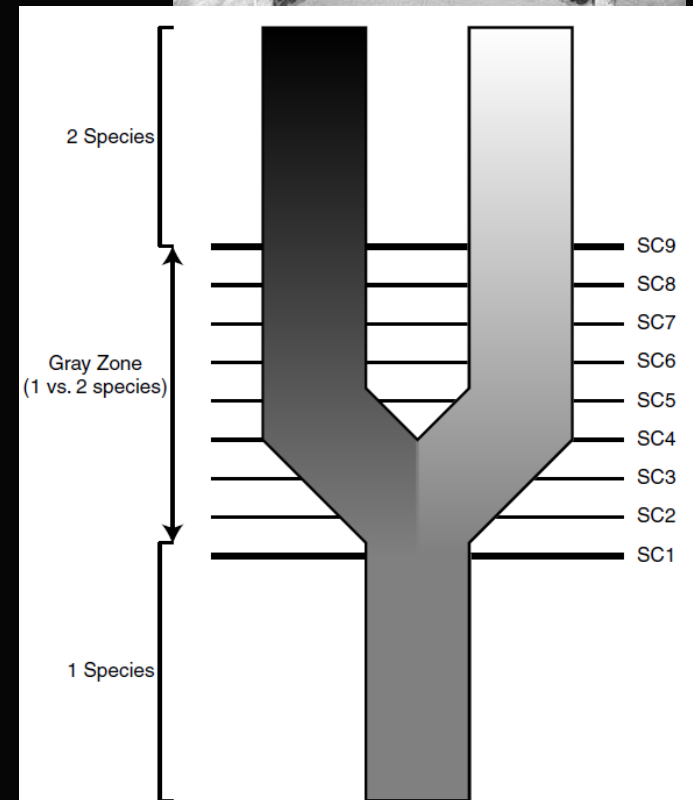
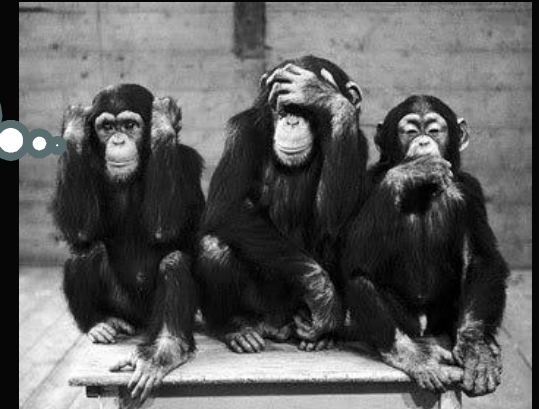
## Taxonomy users:

local vs global perspectives  
regional knowledge cultures  
litterature language / access  
fidelity to «authoritative specialists»

## Taxonomy producers:

different species concepts  
author idiosyncrasies (split / lump)  
slow turnover rates of revisions

Don't want to hear!



# Taxonomic feed-back loops\* (integrative)

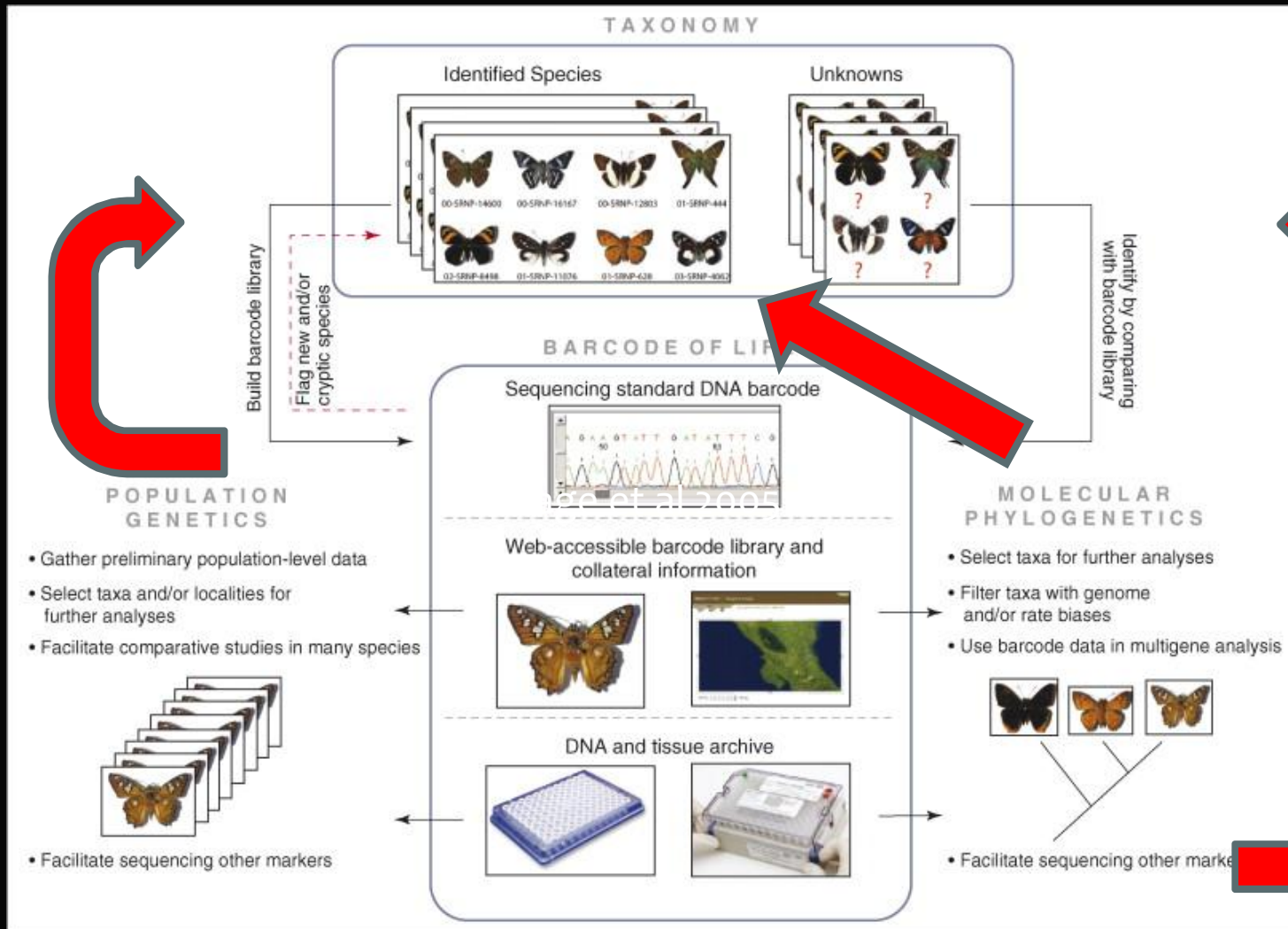


Figure from: Mehrdad Hajibabaei et al 2007

\*Page et al 2005



## Acknowledgements

Many thanks to:

Christoffer Schander, Univ. Bergen (deceased)

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Katrine Kongshavn, Univ. Bergen

Jon A. Kongsrud, Univ. Bergen

Cathrine Henriksen, Univ. Bergen

Christoph Noever, Univ. Bergen

Dirk Steinke and helpful staff at BIO, Guelph

Financial support:

JRS Biodiversity Foundation

Norwegian Environment Agency



## Downloads

**WEB page: [MIWA.b.uib.no](http://MIWA.b.uib.no)**



Access list of sampling stations with [map](#) in Google.

Click the link and select "Map of Latitude" to view map.  
Select "Satellite" for satellite image.

Use "Filter" to include / exclude data.

### RECENT POSTS

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[Opportunities for master studies](#)

[Slipper lobster](#)

[Thank you to all our workshop participants!](#)

[Workshop summary of Crustacea](#)

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