

## Supplementary material

### **Integrative systematics of clathrinid sponges: morphological, reproductive and phylogenetic characterisation of a new species of *Leucetta* from Antarctica (Porifera, Calcarea, Calcinea) with notes on the occurrence of flagellated sperm**

*Ana Riesgo*<sup>A,D</sup>, *Fernanda F. Cavalcanti*<sup>B</sup>, *Nathan J. Kenny*<sup>A</sup>, *Pilar Ríos*<sup>C</sup>, *Javier Cristobo*<sup>C</sup>  
and *Emilio Lanna*<sup>B</sup>

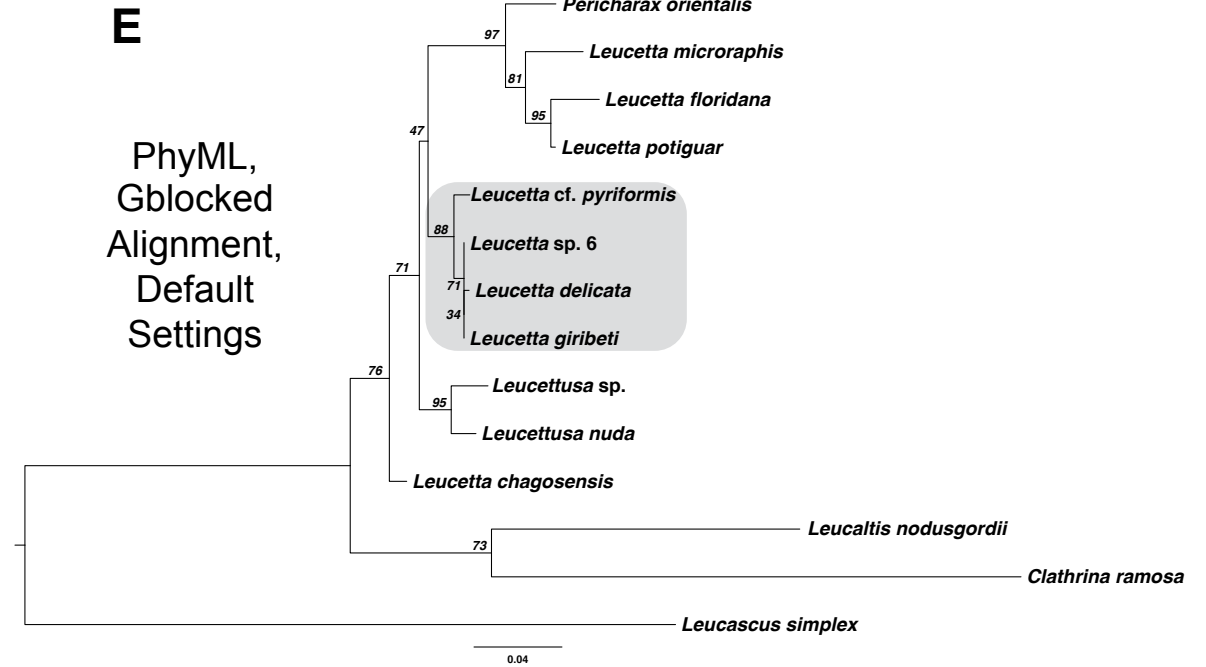
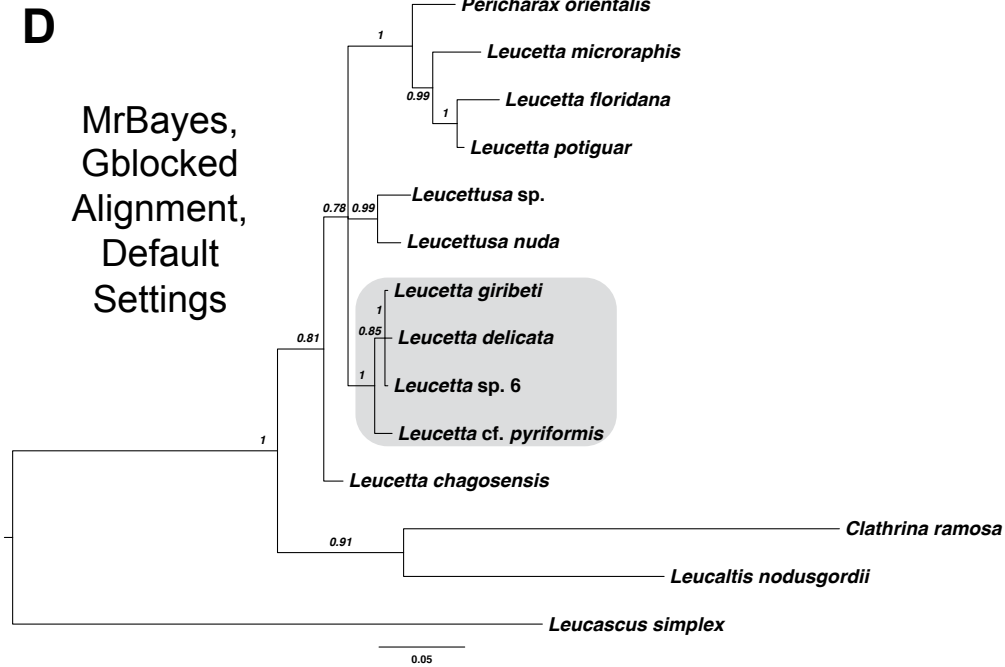
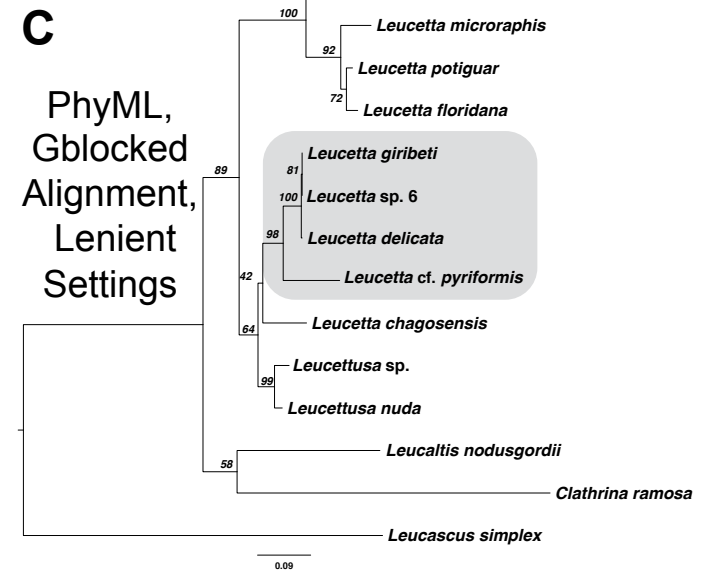
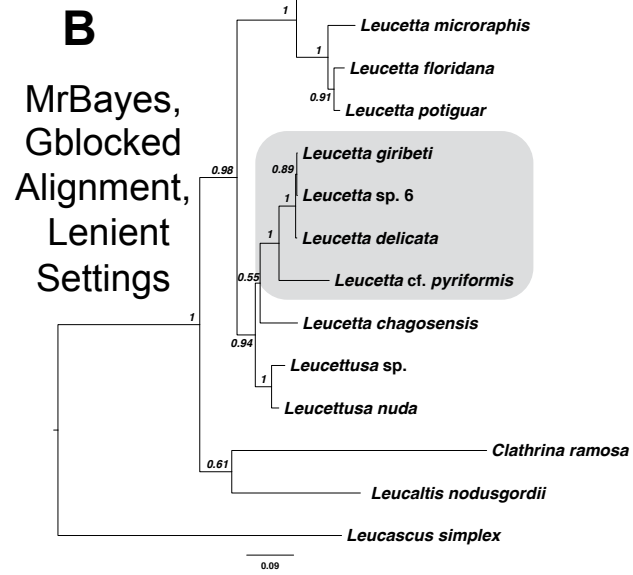
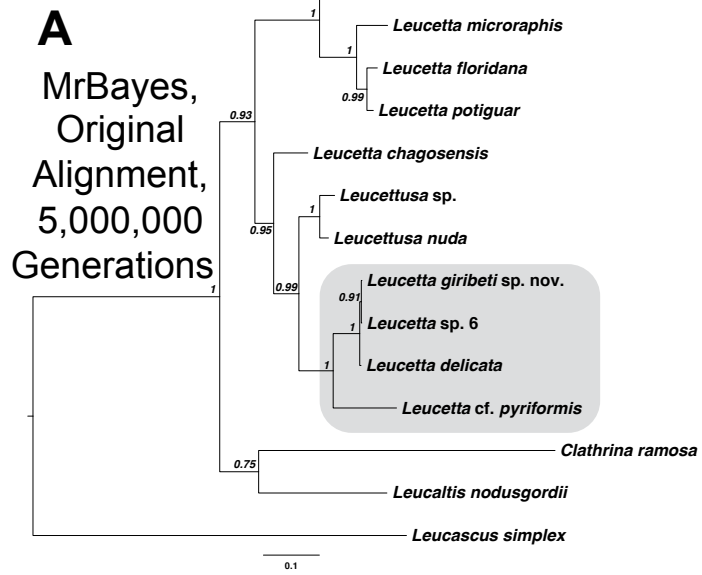
<sup>A</sup>Department of Life Sciences, The Natural History Museum of London, Cromwell Road, London, SW7 5BD, UK.

<sup>B</sup>Universidade Federal da Bahia, Instituto de Biologia, Rua Barão de Jeremoabo s/n, Ondina, Salvador/Bahia, 40170-115, Brazil.

<sup>C</sup>Instituto Español de Oceanografía, Avenuenida Príncipe de Asturias, 70 bis, E-33212, Gijón, Asturias, Spain.

<sup>D</sup>Corresponding author. Email: a.riesgo@nhm.ac.uk

**Fig. S1.** Phylogenetic trees generated for the ITS dataset. A. Bayesian inference (MrBayes) analysis with the original dataset. B. Bayesian inference (MrBayes) analysis with a subset of nucleotides selected from the original dataset using lenient settings in Gblocks. C. Maximum likelihood analysis (PhyML) with a subset of nucleotides selected from the original dataset using lenient settings in Gblocks. D. Bayesian inference (MrBayes) analysis with a subset of nucleotides selected from the original dataset using default (strict) settings in Gblocks. E. Maximum likelihood analysis (PhyML) with a subset of nucleotides selected from the original dataset using default (strict) settings in Gblocks. (*See next page.*)



NB for both C and E, numbers at base of nodes are bootstrap support, expressed /100 replicates but run for 1000

**Table S1. Inter-specific (left corner) and intra-specific (right corner, in grey) genetic distances (K2P) among all species of *Leucetta*, *Leucettusa* and *Leucaltis* for the ITS dataset**

NA refers to the fact that only a single sequence was included. In blue (left) the distances among *Leucetta giribeti*, *L. delicata* and *Leucetta* sp. 6 and intra-specific distances (right) of *L. potiguar* and *L. floridana*

	<i>Leucetta floridana</i>	<i>Leucetta giribeti</i>	<i>Leucetta delicata</i>	<i>Leucetta chagosensis</i>	<i>Leucetta microraphis</i>	<i>Leucetta potiguar</i>	<i>Leucetta</i> cf. <i>pyriformis</i>	<i>Leucetta</i> sp. 6	<i>Leucettusa</i> sp.	<i>Leucaltis nodusgordii</i>	<i>Leucettusa nuda</i>
<i>Leucetta floridana</i>	<b>0.002</b>	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Leucetta giribeti</i>	0.232	NA	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Leucetta delicata</i>	0.235	<b>0.003</b>	NA	NA	NA	NA	NA	NA	NA	NA	NA
<i>Leucetta chagosensis</i>	0.201	0.112	0.114	NA	NA	NA	NA	NA	NA	NA	NA
<i>Leucetta microraphis</i>	0.062	0.231	0.234	0.213	NA	NA	NA	NA	NA	NA	NA
<i>Leucetta potiguar</i>	0.031	0.224	0.227	0.198	0.053	<b>0.002</b>	NA	NA	NA	NA	NA
<i>Leucetta</i> cf. <i>pyriformis</i>	0.221	0.092	0.092	0.147	0.22	0.218	NA	NA	NA	NA	NA
<i>Leucetta</i> sp. 6	0.232	<b>0.000</b>	<b>0.003</b>	0.112	0.231	0.224	0.092	NA	NA	NA	NA
<i>Leucettusa</i> sp.	0.212	0.104	0.104	0.1	0.227	0.21	0.141	0.104	NA	NA	NA
<i>Leucaltis nodusgordii</i>	0.322	0.309	0.307	0.271	0.326	0.314	0.314	0.309	0.279	NA	NA
<i>Leucettusa nuda</i>	0.208	0.094	0.094	0.096	0.22	0.204	0.141	0.094	0.036	0.279	NA