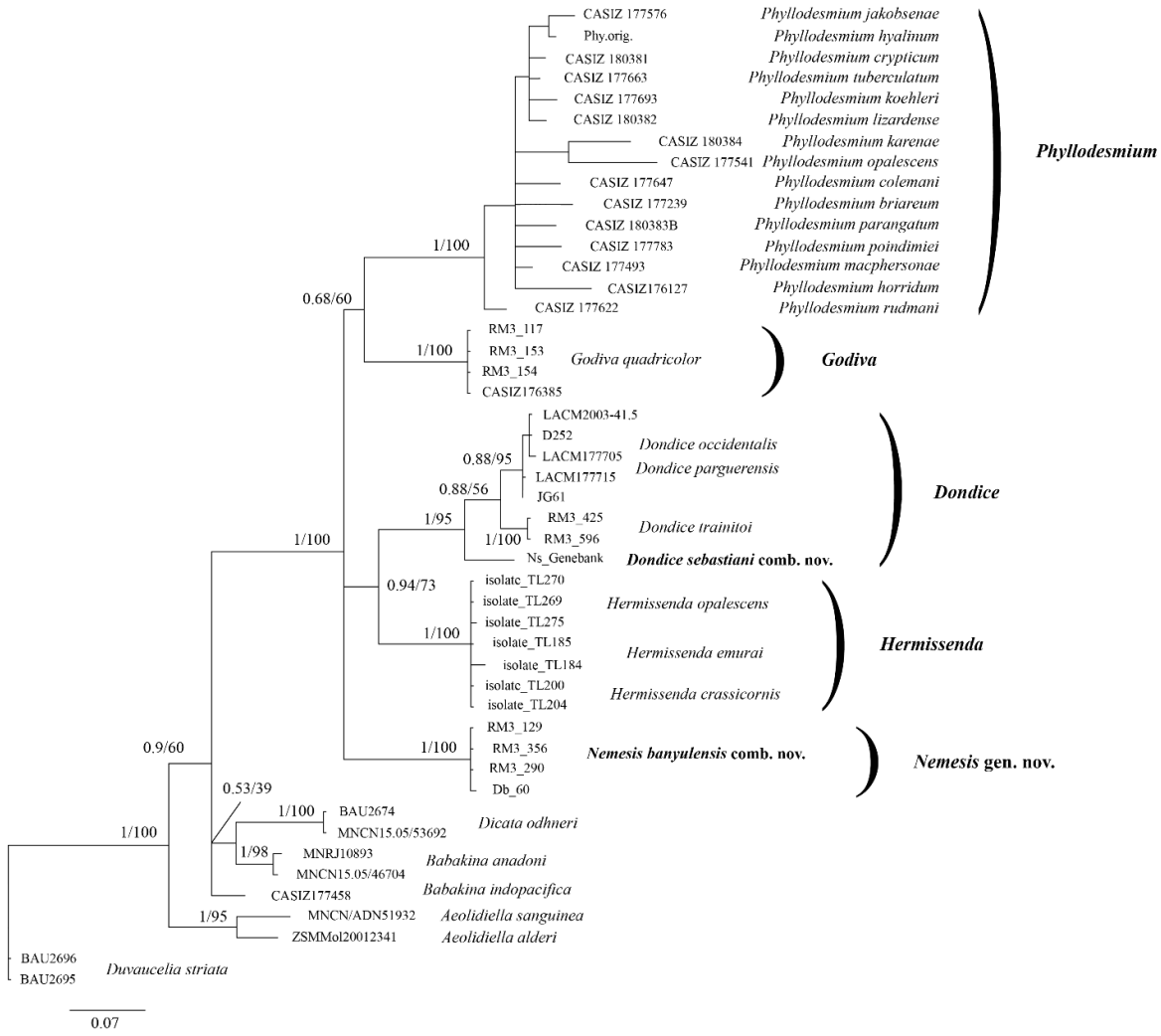
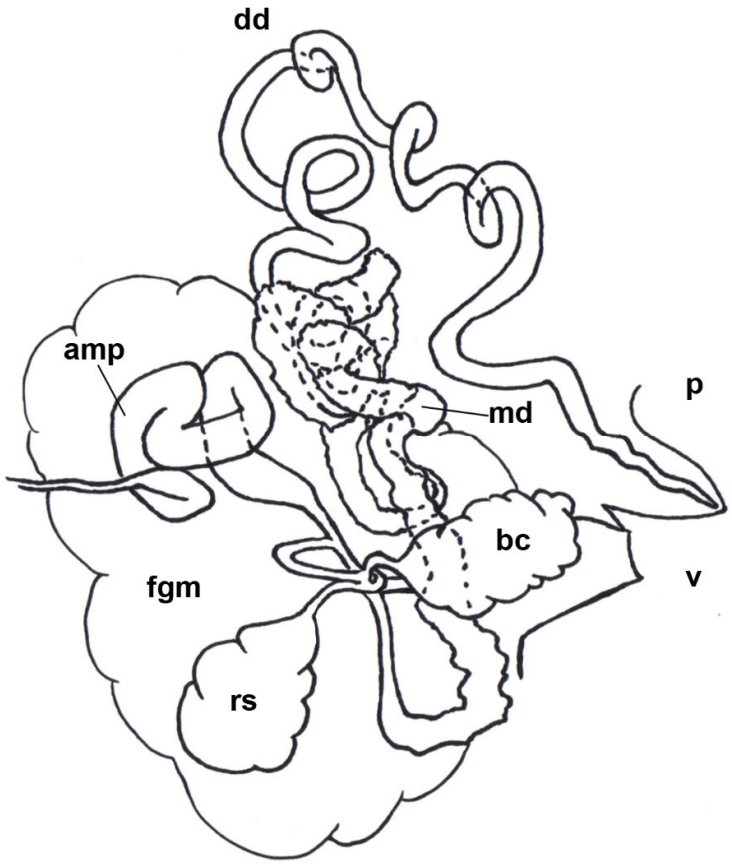



**Supplementary Figure S1**

Bayesian phylogenetic tree based on the single 16S dataset. Bayesian posterior probability (left) and Bootstrap (right) values are indicated at each node.




**Supplementary Figure S2**

Drawing of the reproductive system of *Nemesis banyulensis* comb. nov. (voucher RM3_290) performed using optical microscope. Legend: amp = ampulla, bc = bursa copulatory, dd = deferent duct, fgm = female gland mass, md = male duct, p = penis, rs = receptaculum seminis, v = vagina.

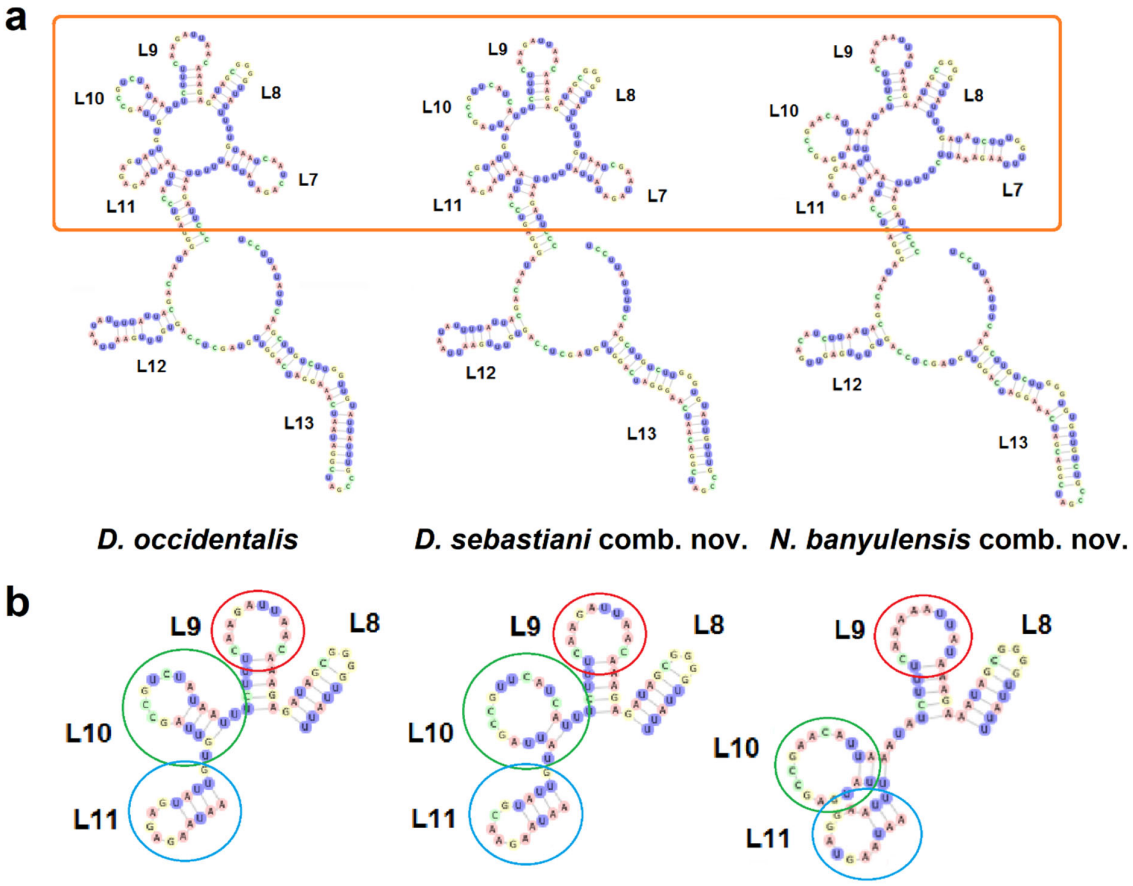



Figure S3: (a) Folding models of the 16S rRNA domain V of *D. occidentalis, D. sebastiani* comb. nov. and *N. banyulensis* comb. nov. analysed in the present work. The L7-11 stem-loops are boxed. (b) The variable L9-11 stem-loops are encircled to show differences occurring among the three taxa.

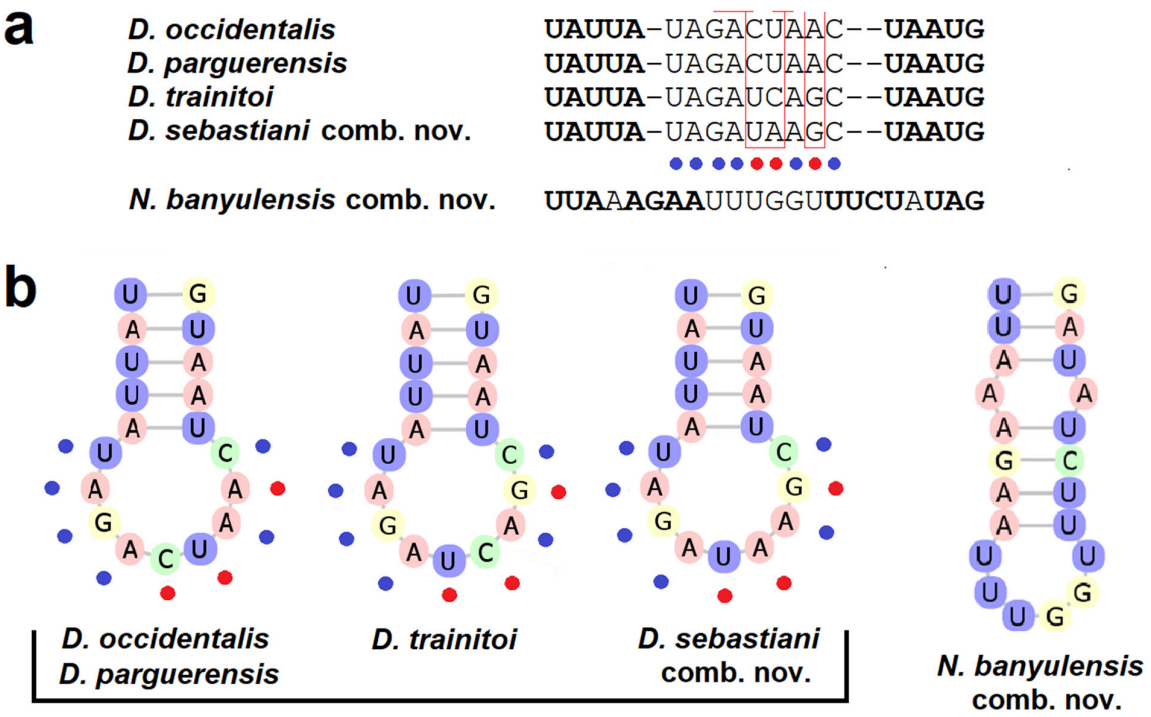



Figure S4: L7 stem-loops of the species here analysed. (a) Primary sequence alignment of the L7 stem-loops among the *Dondice* spp. and *N. banyulensis* comb. nov. (b) Folding models of the L7 stem-loops. Blue circles, conserved nucleotide positions within the *Dondice* clade, red circles diagnostic nucleotides.