

## Supplementary Material

### Molecular phylogenetic analyses reveal a new southern hemisphere oniscidean family (Crustacea: Isopoda) with a unique water transport system

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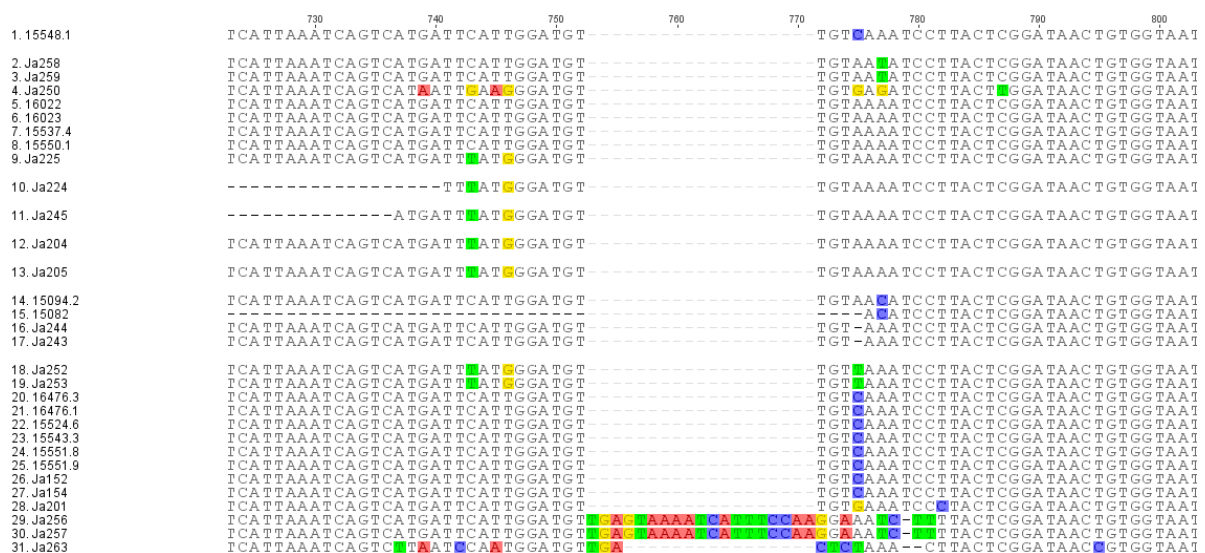
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**Fig. S1.** Part of the alignment of 18S core element (1) showing a ~21-bp gap in all examined Crinocheta and Synocheta species. In *Diplocheta* (*Ligia* sp., *L. oceanica*) this gap is covered by 19–21 nucleotides.



**Fig. S2.** The 50% majority rule Bayesian inference (BI) tree from the 28S dataset belonging to nine known oniscidean families. The numbers adjacent to nodes are BI posterior probabilities. Abbreviations for generic names are given in Appendix 1.



**Table S1. Garli partitioning schemes, lnL, number of parameters and AIC values**

The numbers in the partitioning scheme column denote: 1, 2 and 3 for the *COI* first, second and third codon positions, respectively; 4 and 5 for the core and variable regions of the *18S* gene, respectively; 6 for the *28S* gene

Partitioning scheme	lnL	Parameters (#free parameters + (subsets-1))	AIC
P1: (1,2,3,4,5,6)	-19325.64397	10	38671.28794
P2: (1,2,3)(4,5)(6)	-18753.05649	$10+7+9+(3-1)=28$	37562.11298
P3: (1,2)(3)(4,5)(6)	-18380.06583	$10+5+7+9+(4-1)=34$	36828.13166
P4: (1)(2)(3)(4,5)(6)	-18296.9014	$10+10+5+7+9+(5-1)=45$	36683.8028
P5: (1,2,3)(4,5,6)	-18901.43427	$10+9+(2-1)=20$	37842.86854
P6: (1,2)(3)(4,5,6)	-18527.9075	$10+5+9+(3-1)=26$	37107.815
P7: (1)(2)(3)(4,5,6)	-18432.12293	$10+10+5+9+(4-1)=37$	36938.24586
P8: (1,2,3)(4,5,6)	-18901.43314	$10+9+(2-1)=20$	37842.86628
P9: (1,2,3)(4)(5)(6)	-18597.46653	$10+6+9+9+(4-1)=37$	37268.93306
P10: (1,2)(3)(4)(5)(6)	-18224.22739	$10+5+6+9+9+(5-1)=43$	36534.45478
P11: (1)(2)(3)(4)(5)(6)	-18128.45071	$10+10+5+6+9+9+(6-1)=54$	36364.90142