



Appendix. Figure 1

Mitochondrial gene orders of *Scutopus ventrolineatus* and *Chaetoderma nitidulum*. Inversions (indicated by the circular arrows) and transpositions of protein coding, tRNA and rRNA genes are depicted among the two taxa. Genes encoded by the opposite strand are underlined. Genes located in apomorphic arrangements are colored. The biggest non coding regions (>300pb) are colored in grey. S1, S2, L1, and L2 designate genes for those tRNAs recognizing the codons AGN, UCN, CUN, and UUR, respectively.

Table 1. Complete mitochondrial genomes used in the phylogenetic analyses.

Taxon	Species	NCBI Accession No.	Reference	
GASTROPODA				
HETEROBRANCHIA				
	Hygrophila: Planorboidea	<i>Biomphalaria glabrata</i> ¹	NC_005439	DeJong et al., 2004
	Nudipleura: Nudibranchia: Doridina	<i>Roboastra europaea</i>	NC_004321	Grande et al., 2002
	Nudipleura: Pleurobranchomorpha	<i>Berthellina</i> sp. ¹	NC_015091	Medina et al. 2011
	Architectibranchia	<i>Micromelo undata</i>	NC_015106	Medina et al., 2011
	Euopisthobranchia: Aplysiomorpha	<i>Aplysia dactylomela</i> ¹	NC_015088	Medina et al., 2011
CAENOGASTROPODA				
	Neogastropoda: Conoidea	<i>Conus borgesii</i>	NC_013243	Cunha et al., 2009
	Neogastropoda: Buccionidea	<i>Ylianassa obsoleta</i> ¹	NC_007781	Simison et al. 2006
	Littorinimorpha: Rissooidea	<i>Oncomelania hupensis</i>	NC_013073	Li and Zhou, 2009*
VETIGASTROPODA				
	Haliotoidea	<i>Haliotis rubra</i>	NC_005940	Maynard et al., 2005
PATELLOGASTROPODA				
	Lottioidea	<i>Lottia digitalis</i> ¹	NC_007782	Simison et al., 2006
NERITIMORPHA				
	Neritidae	<i>Nerita melanotragus</i>	GU810158	Castro and Colgan, 2010
BIVALVIA				
	Unionoidea	<i>Hyriopsis cumingii</i> ¹	NC_011763	Zheng and Li, 2008*
CEPHALOPODA				
	Decapodiformes: Sepiida	<i>Sepia officinalis</i>	NC_007895	Akasaki et al., 2006
	Decapodiformes: Teuthida	<i>Loligo bleekeri</i>	NC_002507	Tomita et al., 2002
	Octopodiformes: Octopoda	<i>Octopus vulgaris</i>	NC_006353	Yokobori et al., 2004
	Nautiloidea	<i>Nautilus macromphalus</i>	NC_007980	Boore, 2006

POLYPLACOPHORA				
	Chitonida	<i>Katharina tunicata</i>	NC_001636	Boore and Brown, 1994
SCAPHOPODA				
	Dentaliidae	<i>Graptacme eborea</i>	NC_006162	Boore et al., 2004
CHAETODERMOMORPHA				
	Chaetodermatida	<i>Chaetoderma nitidulum</i>	NC_013846	Dreyer and Steiner, 2010*
	Limifossorimorpha	<i>Scutopus ventrolineatus</i>	KC_757645	This paper
ANNELIDA				
	Scolecida; Maldanidae	<i>Clymenella torquata</i>	NC_006321	Jennings and Halanych, 2005
	Terebellida; Terebellidae	<i>Pista cristata</i>	NC_011011	Zhong et al., 2008
NEMERTEA				
	Heteronemertea	<i>Lineus viridis</i>	NC_012889	Podsiadlowski et al, 2009
BRACHIOPODA				
	Terebratulida	<i>Terebratulina retusa</i>	NC_000941	Stechmann and Schlegel, 1999
PHORONIDA				
	Phoronidae	<i>Phoronis psammophila</i>	AY368231	Helfenbein and Boore, 2004
ENTOPROCTA				
	Loxosomatidae	<i>Loxosomella aloxiata</i>	NC_010432	Yokobori et al., 2008

* Unpublished

¹used only the combined data set

References

- Akasaki, T., Nikaido, M., Tsuchiya, K., Segawa, S., Hasegawa, M., Okada, N., 2006. Extensive mitochondrial gene arrangements in coleoid Cephalopoda and their phylogenetic implications. *Mol. Phylogenet. Evol.* 38, 648-658.
- Boore, J., 2006. The complete sequence of the mitochondrial genome of *Nautilus macromphalus* Mollusca: Cephalopoda. *BMC Genomics* 7, 182.
- Boore, J.L., Brown, W.M., 1994. Complete DNA Sequence of the Mitochondrial Genome of the Black Chiton, *Katharina tunicata*. *Genetics* 138, 20.
- Boore, J.L., Medina, M., Rosenberg, L.A., 2004. Complete Sequences of the Highly Rearranged Molluscan Mitochondrial Genomes of the Scaphopod *Graptacme eborea* and the Bivalve *Mytilus edulis*. *Mol. Biol. Evol.* 21.
- Castro, L.R., Colgan, D.J., 2010. The phylogenetic position of Neritimorpha based on the mitochondrial genome of *Nerita melanotragus* Mollusca: Gastropoda. *Mol. Phylogenet. Evol.* 57, 918-923.
- Cunha, R., Grande, C., Zardoya, R., 2009. Neogastropod phylogenetic relationships based on entire mitochondrial genomes. *BMC Evol. Biol.* 9, 210.
- DeJong, R., Emery, A., Adema, C., 2004. The mitochondrial genome of *Biomphalaria glabrata* Gastropoda: Basommatophora, intermediate host of *Schistosoma mansoni*. *J. Parasitol.* 90, 991-997.
- Dreyer, H., Steiner, G., 2004. The complete sequence and gene organization of the mitochondrial genome of the gadilid scaphopod *Siphonondentalium lobatum* Mollusca. *Mol. Phylogenet. Evol.* 31, 605-617.
- Grande, C., Templado, J., Cervera, J.L., Zardoya, R., 2002. The complete mitochondrial genome of the nudibranch *Roboastra europaea* Mollusca: Gastropoda supports the monophyly of opisthobranchs. *Mol. Biol. Evol.* 19, 1672-1685.
- Helfenbein, K. G. and Boore, J. L., 2004. The mitochondrial genome of *Phoronis architecta*. Comparisons demonstrate that phoronids are lophotrochozoan protostomes. *Mol. Biol. Evol.* 21, 153-157.
- Jennings, R.M., Halanych, K.M. 2005. Mitochondrial Genomes of *Clymenella torquata* (Maldanidae) and *Riftia pachyptila* (Siboglinidae): Evidence for conserved gene order in annelida. *Mol. Biol. Evol.* 22, 210-222
- Maynard, B., Kerr, L., McKiernan, J., Jansen, E., Hanna, P., 2005. Mitochondrial DNA sequence and gene organization in Australian backup abalone *Haliotis rubra* leach. *Mar Biotechnol NY* 7, 645 - 658.
- Medina, M., Lal, S., VallÈs, Y., Takaoka, T.L., Dayrat, B.A., Boore, J.L., Gosliner, T., 2011. Crawling through time: Transition of snails to slugs dating back to the Paleozoic, based on mitochondrial phylogenomics. *Mar. Genom.* 4, 51-59.
- Podsiadlowski, L., Braband, A., Struck, T.H., von Dohren, J. And Bartolomaeus, T., 2009. Phylogeny and mitochondrial gene order variation in Lophotrochozoa in the light of new mitogenomic data from Nemertea. *BMC Genomics* 10, 364.
- Simison, W., Lindberg, D., Boore, J., 2006. Rolling circle amplification of metazoan mitochondrial genomes. *Mol. Phylogenet. Evol.* 39, 562-567.
- Stechmann, A. and Schlegel, M., 1999. Analysis of the complete mitochondrial DNA sequence of the brachiopod *Terebratulina retusa* places Brachiopoda within the protostomes. *Proc. R. Soc. Lond., B, Biol. Sci.* 266, 2043-2052.
- Tomita, K., Yokobori, S.-I., Oshima, T., Ueda, T., Watanabe, K., 2002. The Cephalopod *Loligo bleekeri* Mitochondrial Genome: Multiplied Noncoding Regions and Transposition of tRNA Genes. *J. Mol. Evol.* 54, 486-500.
- Yokobori, S.-i., Fukuda, N., Nakamura, M., Aoyama, T., Oshima, T., 2004. Long-Term Conservation of Six Duplicated Structural Genes in Cephalopod Mitochondrial Genomes. *Mol. Biol. Evol.* 21, 2034-2046.
- Yokobori, S., Iseto, T., Asakawa, S., Sasaki, T., Shimizu, N., Yamagishi, A., Oshima, T. and Hirose, E. 2008. Complete nucleotide sequences of mitochondrial genomes of two solitary entoprocts, *Loxocorone allax* and *Loxosomella aloxiata*: implications for lophotrochozoan phylogeny. *Mol. Phylogenet. Evol.* 47, 612-628.
- Zhong, M., Struck, T.H. and Halanych, K.M. 2008. Phylogenetic information from three mitochondrial genomes of Terebelliformia (Annelida) worms and duplication of the methionine tRNA. *Gene* 416, 11-21.

Table 2. Fragments of nuclear ribosomal proteins used in phylogenetic analyses.

Taxon		Nuclear ribosomal proteins ¹												
		40S		60S										
		S8	S15	L3	L4	L5	L6	L8	L10a	L16_L10	L17	L18a	L32	
<i>Pleurobranchaea californica</i>	<i>Gastropoda: Heterobranchia</i>	+	+	+	+	+	+	+	+	+	+	+	+	
<i>Aplysia californica</i>	<i>Gastropoda: Heterobranchia</i>	+	+	+	+	+	+	+	+	+	+	-	+	
<i>Biomphalaria glabrata</i>	<i>Gastropoda: Heterobranchia</i>	+	+	+	+	+	+	+	+	+	-	+	-	
<i>Tritonia diomedea</i>	<i>Gastropoda: Heterobranchia</i>	+	+	-	-	+	+	+	+	+	+	+	+	
<i>Helicoidea</i>	<i>Gastropoda: Heterobranchia</i>	+	-	+	+	-	-	+	+	+	-	+	+	
<i>Ilyanassa obsoleta</i>	<i>Gastropoda: Caenogastropoda</i>	+	-	-	+	+	+	-	+	+	-	+	+	
<i>Theodoxus fluviatilis</i>	<i>Gastropoda: Neritimorpha</i>	+	+	+	+	+	-	+	+	+	+	+	+	
<i>Haliotis</i>	<i>Gastropoda: Vetigastropoda</i>	+	+	+	+	+	+	+	+	+	+	+	-	
<i>Lottia gigantea</i>	<i>Gastropoda: Patellogastropoda</i>	+	+	+	+	+	+	+	+	+	+	+	-	
<i>Dentaliidae</i>	<i>Scaphopoda: Dentaliida</i>	+	+	+	+	+	-	+	+	+	+	-	+	
<i>Hyriopsis cumingii</i>	<i>Bivalvia: Unionoidea</i>	+	+	+	+	+	+	-	-	+	+	+	+	
<i>Loligo</i>	<i>Cephalopoda: Decapodiformes</i>	+	+	+	+	+	+	+	+	+	+	+	+	
<i>Octopus vulgaris</i>	<i>Cephalopoda: Octopodiformes</i>	+	-	+	+	+	+	+	+	+	+	+	+	
<i>Nautilus</i>	<i>Cephalopoda: Nautiloidea</i>	-	+	-	+	+	+	+	+	+	+	+	+	
<i>Chitonida</i>	<i>Polyplacophora</i>	+	-	+	+	-	+	+	+	+	+	+	+	
<i>Scutopus ventrolineatus</i>	<i>Chaetodermomorpha</i>	+	+	+	+	+	+	-	+	+	-	-	+	
<i>Chaetoderma nitidulum</i>	<i>Chaetodermomorpha</i>	+	+	-	-	+	+	+	+	+	+	+	+	
<i>Neomenia</i>	<i>Neomeniomorpha</i>	-	+	-	-	-	+	-	+	+	+	+	-	
<i>Wirenia argentea</i>	<i>Neomeniomorpha</i>	+	+	+	+	+	+	+	+	+	-	+	+	
<i>Capitellidae</i>	<i>Annelida</i>	+	+	+	+	+	+	+	+	+	+	+	-	
<i>Alvinella pompejana</i>	<i>Annelida</i>	+	+	+	+	+	+	+	-	+	+	+	+	
<i>Carinoma</i>	<i>Nemertea</i>	+	+	+	-	-	+	-	+	+	+	+	+	
<i>Terebratalia transversa</i>	<i>Brachiopoda</i>	+	+	+	+	+	+	+	-	-	+	+	+	
<i>Pedicellina</i>	<i>Entoprocta</i>	-	-	-	+	-	-	-	-	+	-	+	-	
No. Amino acids		204	134	244	221	246	151	244	197	203		121	280	117

¹ Kocot, K.M., Cannon, J.T., Todt, C., Citarella, M.R., Kohn, A.B., Meyer, A., Santos, S.R., Schander, C., Moroz, L.L., Lieb, B., Halanych, K.M., (2011) Phylogenomics reveals deep molluscan relationships. *Nature* 477: 452-456.

Table 3. Output of the Protein Partition Finder

Data set	Best Model	alpha	pinvar
MITO amino acids	best partition: per group (<i>atp</i>, <i>cox</i>, <i>cob</i>, <i>nad</i>); -lnL= 67264.29		
<i>atp</i>	mART	0.87281	
<i>cox</i>	LG	0.434848	
<i>cob</i>	mART	0.642182	
<i>nad</i>	mART	0.655589	
NUC amino acids	best partition: all genes separated; -lnL= 36866.21		
40S_S8	LG	0.81703	
40S_S15	JTT	0.675925	
60S_L3	LG	0.593494	
60S_L4	LG	0.705006	
60S_L5	LG	1.253	0.268898
60S_L6	LG	0.514199	
60S_L8	LG	0.530343	
60S_L10a	LG	1.154	0.265532
60S_L16_L10	LG	0.615296	0.241674
60S_L17	JTT	0.843745	0.157126
60S_L18a	Blosum62	1.049	
60S_L32	LG	0.864881	0.225493
Combined (MITO+NUC)	best partition: <i>atp</i>6/8 and <i>nad</i>4/4L, remaining separated; -lnL= 178340.19		
<i>atp</i> 6/8	mART	0.747941	
<i>cox</i> 1	LG	0.473613	
<i>cox</i> 2	mART	0.675584	
<i>cox</i> 3	mART	0.577307	
<i>cob</i>	mART	0.588785	
<i>nad</i> 1	mART	0.586762	

<i>nad2</i>	mART	0.63904
<i>nad3</i>	mART	0.960463
<i>nad4/4L</i>	LG	0.631425
<i>nad5</i>	LG	0.487988
<i>nad6</i>	mART	0.764513
40S_S8	LG	0.752367
40S_S15	JTT	0.521373
60S_L3	LG	0.555502
60S_L4	LG	0.761228
60S_L5	LG	0.610006
60S_L6	LG	0.60341
60S_L8	LG	0.462332
60S_L10a	LG	0.504528
60S_L16_L10	LG	0.372527
60S_L17	LG	0.440494
60S_L18a	Blosum62	0.959612
60S_L32	LG	0.41837
