Supplemental Material

Bioluminescence and environmental light drive the visual evolution of deep-sea shrimp (Oplophoroidea)

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Table S1. Sample metadata

Genus	Species	FICC HBG sample ID's	Depth range (m)	Light environ. coding	Photophores	SWS1 (UV7)	SWS2	SWS/MWS	MWS1	MWS2	LWS
Acanthephyra	*purpurea*	*3480-83*	**300-3292**	**upper meso**	**no**	1	1	0	2	1	3
	stylorostratis	*3475-77*	**750-3548**	**lower meso**	**no**	1	2	0	2	2	3
Notostomus	*elegans*	*7215, 7217, 7227*	**450-5380**	**meso**	**no**	0	2	0	2	1	3
Hymenodora	*gracilis*	*6959, 6964, 7301*	**750-5400**	**lower meso**	**no**	0	1	0	0	0	2
Oplophorus	*gracilirostris*	*7281, 7199, 7201*	**100-2400**	**epi**	**yes**	0	1	0	1	1	3
Janicella	*spinicauda*	*8616–8620** *paper: https://doi.org/10.1038/s41598-020-61284-9* *data*: https://doi.org/10.5061/dryad.2280gb5nt*	**100-1500**	**epi**	**yes**	0	1	0	1	1	2
Meningodora	*mollis*	*7034, 6951, 7291*	**725-5000**	**lower meso**	**no**	0	2	1	3	0	3
Systellaspis	*debilis*	*8390-91, 8395–98, 8465, 8467–69** *paper: DOI: 10.1111/mec.15570* *data*: https://doi.org/10.5061/dryad.rjdfn2z81*	**150-4594**	**epi**	**yes**	0	0	1	1	1	2
	braueri	*8727, 3030*	**1000-3000**	**lower meso**	**no**	0	0	0	1	1	3
	cristata	*8728-29, 8731*	**200-3241**	**upper meso**	**yes, reduced**	0	0	0	1	1	3
Ephyrina	*ombango*	*7044, 7065, 7067*	**670-2500**	**meso**	**no**	0	0	0	1	1	3

epi < 200m, upper meso < 400m, meso 400-700m, lower meso >700m

Depth references

Acanthephyra purpurea	Burghart et al. (2007), Chace (1986), Hopkins et al. (1994), Hopkins et al. (1989), Pequegnat and Wicksten (2006)
Acanthephyra stylorostratis	Burghart et al. (2007), Chace (1986), Hopkins et al. (1994), Hopkins et al. (1989), Judkins (2014), Pequegnat and Wicksten (2006)
Ephyrina ombango	Burghart et al. (2007), Chace (1986), Crosnier and Forest (1973), Pequegnat and Wicksten (2006)
Hymenodora gracilis	Burghart et al. (2007), Chace (1986), Chace et al. (1956), Crosnier and Forest (1973), Judkins (2014), Pequegnat and Wicksten (2006)
Janicella spinicauda	Burghart et al. (2007), Chace (1986), Chace et al. (1956), Crosnier and Forest (1973), Hopkins et al. (1989), Judkins (2014), Pequegnat and Wicksten (2006)
Systellaspis braueri	Burghart et al., 2007
Remaining species	Felder, 2009

Table S2. *De novo* eye transcriptome assembly statistics.

Species	#	Sample ID (HBG FICC #)	Assembly information
Acanthephyra purpurea	3	3480E 3481E 3483E	N50:643 254,135 genes GC = 37.6 C:77.0%[S:60.5%,D:16.5%],F:8.6%,M:14.4%,n:1013
Acanthephyra stylorostratis	3	3475E 3476E 3477E	N50:555 548,411 genes GC = 37.8 C:82.8%[S:56.2%,D:26.6%],F:7.9%,M:9.3%,n:1013
Ephyrina ombango	3	7065E 7067E 7044E	N50:489 484,801 genes GC = 37.6 C:71.9%[S:55.2%,D:16.7%],F:10.5%,M:17.6%,n:1013
Hymenodora gracilis	3	6959E 6964E 7301E	N50:384 484,801 genes GC = 39.0 C:69.4%[S:49.2%,D:20.2%],F:11.7%,M:18.9%,n:1013
Meningodora mollis	3	7034E 6951E 7291E	N50:558 600,623 genes GC = 37.6 C:83.5%[S:54.0%,D:29.5%],F:8.3%,M:8.2%,n:1013
Notostomus elegans	3	7215E 7217E 7227E	N50:564 343,361 genes GC = 37.5 C:74.6%[S:57.1%,D:17.5%],F:10.1%,M:15.3%,n:1013
Oplophorus gracilirostris	3	7281E 7199E 7201E	N50:406 620,518 genes GC = 37.0 C:73.1%[S:60.3%,D:12.8%],F:8.8%,M:18.1%,n:1013
Systellaspis braueri	2	8727E 3030E	N50:461 407,023 genes GC = 39.9 C:73.6%[S:57.7%,D:15.9%],F:9.4%,M:17.0%,n:1013
Systellaspis cristata	3	8731E 8728E 8729E	N50:431 778,714 genes GC = 39.6 C:79.0%[S:54.8%,D:24.2%],F:8.9%,M:12.1%,n:1013
Nematocarcinus ensifer	1	3755	N50:823 103,228genes GC = 38.8 C:55.5%[S:40.5%,D:15.0%],F:17.2%,M:27.3%,n:1013

Table S3. Annotated orthologs identified as being under positive selection - using branch-site tests with PAML in Codeml for 1) photophore-bearing species, 2) the family Oplophoridae and 3) strong-migrating species only (<200 m).

Ortholog	Chi-sq	P-value	Annotation	Blast ID
Photophore-bearing species				
OG0013318	38.21	5.05E-09	phosphate carrier protein, mitochondrial-like [*Portunus trituberculatus*]	XP_045109943.1
OG0012454	22.13	1.57E-05	39S ribosomal protein L15, mitochondrial-like [*Penaeus japonicus*]	XP_042874680.1
OG0012886	14.39	7.50E-04	uncharacterized protein LOC113805888 [*Penaeus vannamei*]	XP_027212751.1
OG0012957	13.02	1.49E-03	28S ribosomal protein S28, mitochondrial-like [*Penaeus monodon*]	XP_037781002.1
OG0012971	11.88	2.63E-03	cytochrome b-c1 complex subunit 7-like [*Portunus trituberculatus*]	XP_045119462.1
OG0013122	11.18	3.73E-03	uncharacterized protein LOC123745393 isoform X2 [*Procambarus clarkii*]	XP_045581861.1
OG0012589	10.76	4.61E-03	single insulin-like growth factor-binding domain protein-2 isoform X3 [*Procambarus clarkii*]	XP_045613002.1
OG0012875	10.43	5.44E-03	probable rRNA-processing protein EBP2 homolog [*Procambarus clarkii*]	XP_045586470.1
OG0012661	10.25	5.96E-03	39S ribosomal protein L28, mitochondrial-like [*Penaeus vannamei*]	XP_027233457.1
OG0012848	9.56	8.39E-03	bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]-like [*Penaeus monodon*]	XP_037772368.1
OG0012988	9.30	9.55E-03	28S ribosomal protein S18c, mitochondrial-like [*Penaeus japonicus*]	XP_042880857.1
OG0012485	9.29	9.61E-03	probable 28S ribosomal protein S16, mitochondrial [*Penaeus vannamei*]	XP_027224692.1

Ortholog	Chi-sq	P-value	Annotation	Blast ID
Family Oplophoridae (v. Acanthephyridae)				
OG0013318	36.620512	1.12E-08	phosphate carrier protein, mitochondrial-like [*Portunus trituberculatus*]	XP_045109943.1
OG0012886	34.782148	2.80E-08	uncharacterized protein LOC113805888 [*Penaeus vannamei*]	XP_027212751.1
OG0012483	28.1041	7.89E-07	WD repeat-containing protein 18-like isoform X2 [*Homarus americanus*]	XP_042237295.1
OG0013306	21.515652	2.13E-05	chromatin accessibility complex protein 1-like [*Penaeus vannamei*]	XP_027211292.1
OG0012459	21.14327	2.56E-05	n/a	
OG0012316	19.209748	6.74E-05	uncharacterized protein LOC123764990 [*Procambarus clarkii*]	XP_045609258.1
OG0012661	18.223374	0.00011037	39S ribosomal protein L28, mitochondrial-like [*Penaeus vannamei*]	XP_027233457.1
OG0012388	15.807924	0.00036928	nuclear receptor 2C2-associated protein-like [*Cherax quadricarinatus*]	XP_053643836.1
OG0011969	15.791	0.00037242	39S ribosomal protein L49, mitochondrial-like [*Homarus americanus*]	XP_042235127.1
OG0012183	14.8119	0.00060763	ribosome biogenesis protein BRX1 homolog [*Cherax quadricarinatus*]	XP_053650300.1
OG0012454	11.957556	0.00253192	39S ribosomal protein L15, mitochondrial-like [*Penaeus japonicus*]	XP_042874680.1
OG0012035	10.924744	0.00424348	vitamin K epoxide reductase complex subunit 1-like protein 1 [*Procambarus clarkii*]	XP_045609261.1
OG0012873	10.092526	0.00643333	peptidyl-tRNA hydrolase 2, mitochondrial-like [*Procambarus clarkii*]	XP_045624683.1
OG0012587	9.939018	0.00694656	partner of xrn-2 protein 1-like [*Cherax quadricarinatus*]	XP_053649331.1
OG0013009	9.795778	0.00746232	CD63 antigen-like	XP_047477072.1

			[*Penaeus chinensis*]	
OG0012056	9.650374	0.00802505	DNA replication complex GINS protein PSF3-like [*Penaeus japonicus*]	XP_042858735.1
OG0012451	9.649668	0.00802789	39S ribosomal protein L38, mitochondrial-like [*Penaeus monodon*]	XP_037795015.1

Ortholog	**Chi-sq**	**P-value**	**Annotation**	**Blast ID**
Strong-migrating species (< 200 meters)				
OG0012454	19.461416	5.94E-05	39S ribosomal protein L15, mitochondrial-like [*Penaeus japonicus*]	XP_042874680.1
OG0012459	13.987534	0.00091758	n/a	
OG0012971	11.649528	0.0029535	cytochrome b-c1 complex subunit 7-like [*Portunus trituberculatus*]	XP_045119462.1
OG0012988	11.437912	0.00328314	28S ribosomal protein S18c, mitochondrial-like [*Penaeus japonicus*]	XP_042880857.1
OG0012316	11.349042	0.00343231	uncharacterized protein LOC123764990 [*Procambarus clarkii*]	XP_045609258.1
OG0012035	11.291978	0.00353165	vitamin K epoxide reductase complex subunit 1-like protein 1 [*Procambarus clarkii*]	XP_045609261.1
OG0012318	10.371386	0.00559606	26S proteasome regulatory subunit 7 [*Penaeus vannamei*]	XP_027209337.1
OG0012875	10.13654	0.0062933	probable rRNA-processing protein EBP2 homolog [*Procambarus clarkii*]	XP_045586470.1
OG0013229	9.47111	0.00877758	macrophage migration inhibitory factor-like [*Penaeus japonicus*]	XP_042875891.1
OG0013318	9.265258	0.00972915	phosphate carrier protein, mitochondrial-like [*Portunus trituberculatus*]	XP_045109943.1
OG0012886	8.913558	0.01159967	uncharacterized protein LOC113805888 [*Penaeus vannamei*]	XP_027212751.1

Table S4- Salmon gene counts for the SWS/MWS opsin recovered in *Systellaspis deblils* and *Meningodora mollis*. Gene counts are given discretely for each biological replicate used to generate the species specific assembly.

	Rep 1	Rep 2	Rep 3	Rep 4	Rep 5	Rep 6	Rep 7	Rep 8	Rep 9	Rep 10
S. debilis SWS/MWS*	6.88	4.77	2.76	4.7	14.71	13	22.16	0	4.22	18.36
M. mollis SWS/MWS	0	5.52	6.94	-	-	-	-	-	-	-

(*Reps 1-5 collected during day/deep water, Reps 6-10 collected during night/shallower waters; see DeLeo and Bracken-Grissom 2020 for additional details.)

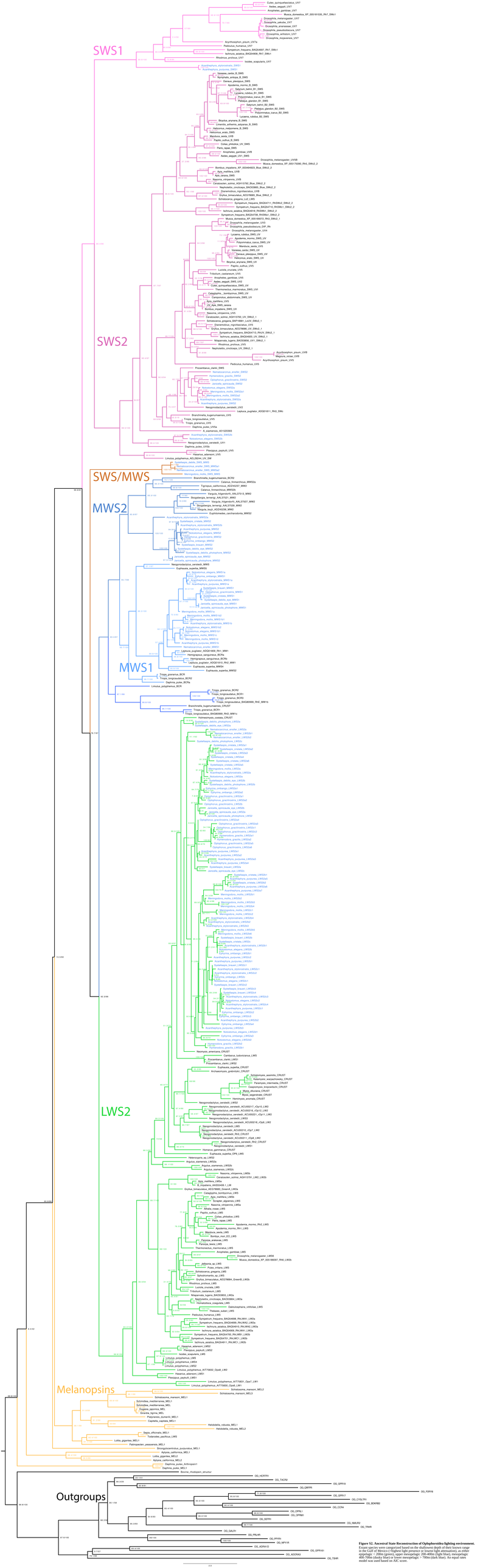


Figure S2. Ancestral State Reconstruction of Ophophoroidea lighting environment. Estimated light environment based on the shallowest depth of their known range in the ocean: shallow (>200m) (green), upper mesopelagic (200-400m) (light blue), mesopelagic (400-700m (dark blue) or lower mesopelagic > 700m (dark blue). Arc equal rates model was used based on AIC score.

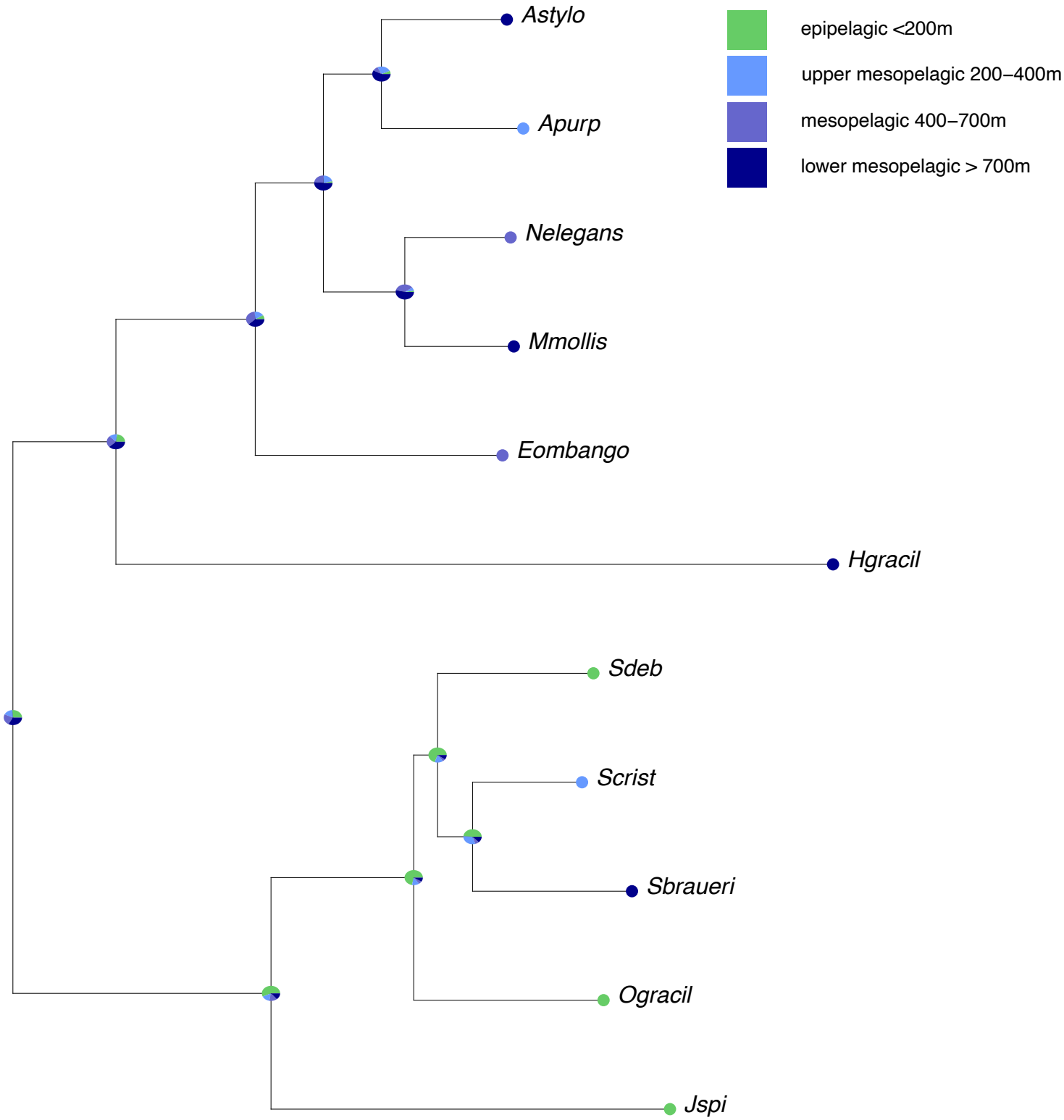
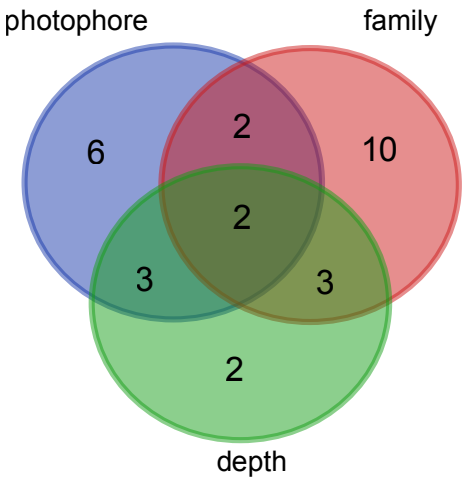


Figure S2. Ancestral State Reconstruction of Oplophoroidea lighting environment.

Figure S3. Overlap among orthologs under positive selection.



Selection (foreground) test	# significant orthologs	Ortholog (annotation) under positive selection
photophore	6	uncharacterized protein LOC123745393 isoform X2 [Procambarus clarkii]
		venom protein 302-like isoform X2 [Procambarus clarkii]
		probable 28S ribosomal protein S16, mitochondrial [Penaeus vannamei]
		28S ribosomal protein S28, mitochondrial-like [Penaeus monodon]
		bis(5'-nucleosyl)-tetraphosphatase [asymmetrical]-like [Penaeus monodon]
		single insulin-like growth factor-binding domain protein-2 isoform X3 [Procambarus
family	10	DNA replication complex GINS protein PSF3-like [Penaeus japonicus]
		partner of xrn-2 protein 1-like [Cherax quadricarinatus]
		peptidyl-tRNA hydrolase 2, mitochondrial-like [Procambarus clarkii]
		ribosome biogenesis protein BRX1 homolog [Cherax quadricarinatus]
		nuclear receptor 2C2-associated protein-like [Cherax quadricarinatus]
		39S ribosomal protein L49, mitochondrial-like [Homarus americanus]
		WD repeat-containing protein 18-like isoform X2 [Homarus americanus]
		39S ribosomal protein L38, mitochondrial-like [Penaeus monodon]
		CD63 antigen-like [Penaeus chinensis]
		chromatin accessibility complex protein 1-like [Penaeus vannamei]
depth	2	macrophage migration inhibitory factor-like [Penaeus japonicus]
		26S proteasome regulatory subunit 7 [Penaeus vannamei]
photophore, depth, family	2	39S ribosomal protein L15, mitochondrial-like [Penaeus japonicus]
		phosphate carrier protein, mitochondrial-like [Portunus trituberculatus]
photophore, family	2	uncharacterized protein LOC113805888 [Penaeus vannamei]
		39S ribosomal protein L28, mitochondrial-like [Penaeus vannamei]
photophore,depth	3	28S ribosomal protein S18c, mitochondrial-like [Penaeus japonicus]
		cytochrome b-c1 complex subunit 7-like [Portunus trituberculatus]
		probable rRNA-processing protein EBP2 homolog [Procambarus clarkii]
family, depth	3	vitamin K epoxide reductase complex subunit 1-like protein 1 [Procambarus clarkii
		uncharacterized protein LOC123764990 [Procambarus clarkii]
		n/a; OG0012459