

Supplementary Materials for
**DNA metabarcoding highlights cyanobacteria as the main source of primary
production in a pelagic food web model**

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This PDF file includes:

Figs. S1 and S2
Tables S1 to S3
Data S1



Fig. S1: Map of sampling stations. The map is retrieved from the Swedish national archive for oceanographic data: <https://sharkweb.smhi.se/>.

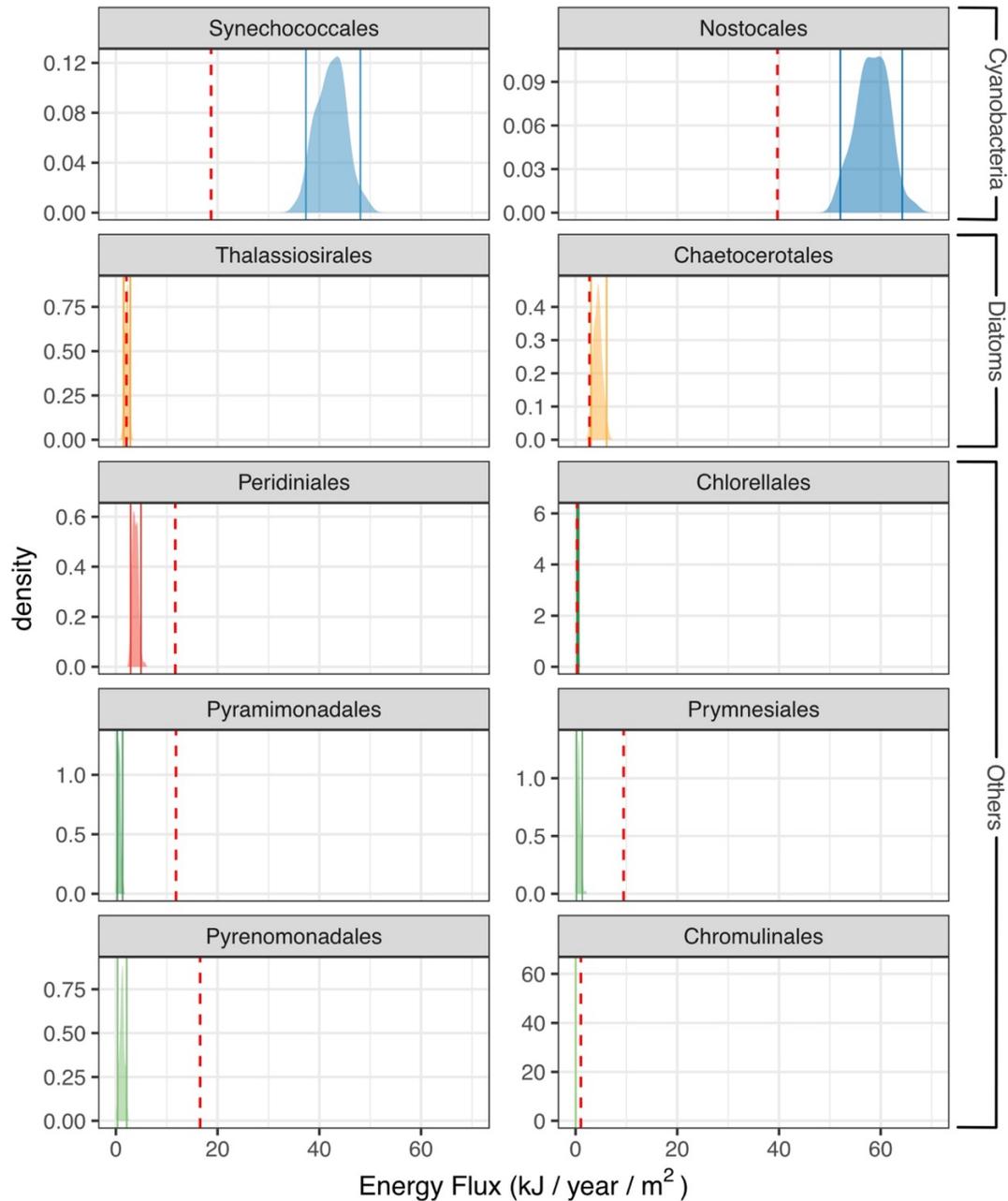


Fig. S2: The influence of uncertainty in prey selectivity on modeled annual secondary production.

To evaluate the influence of uncertainty in prey selectivity on the food web model, we calculated each primary producer's average contribution to secondary production by bootstrapping the selectivity dataset. Density plots show the posterior distribution of average detected energy fluxes over the 100 bootstrap replicates, and solid lines indicates 95% confidence interval of the mean detected energy flux (contribution to primary production). The red dashed lines indicate a null-model scenario that assumes no specific selectivity between predators and prey. The figure indicates that cyanobacteria are the main source of primary production, even when accounting for uncertainty of zooplankton selectivity. The figure also indicates that the model outcome is driven by feeding preferences.

Table S1: Average detected energy flux per prey.

Energy Flux (kJ/m²/year)	<i>Temora</i>	<i>Centropages</i>	<i>Pseudocalanus</i>	<i>Acartia</i>	<i>Evadne</i>	<i>Bosmina</i>	<i>Synchaeta</i>	<i>Keratella</i>	Total
Nostocales	10.10	4.18	6.67	17.50	0.58	11.12	2.16	0.21	52.52
Peridinales	4.23	1.12	1.95	1.93	0.00	0.09	2.49	0.00	11.81
Chaetocerotales	1.65	0.91	1.44	2.24	0.08	0.12	0.15	0.00	6.59
Thalassiosirales	1.87	1.35	0.53	1.52	0.01	0.00	0.00	0.00	5.29
Chromulinales	0.11	0.01	0.03	0.02	0.00	0.01	0.00	0.00	0.18
Pyrenomonadales	0.86	1.09	0.00	0.02	0.00	0.15	0.19	0.00	2.32
Prymnesiales	0.00	0.00	0.32	0.07	0.04	0.25	0.37	0.00	1.04
Pyramimonadales	2.63	0.09	0.03	0.40	0.00	0.04	0.00	0.00	3.19
Chlorellales	0.23	0.15	0.03	0.01	0.00	0.01	0.00	0.00	0.43
Synechococcales	20.04	5.76	0.95	2.53	0.12	1.12	0.19	0.01	30.73
Total	41.73	14.66	11.96	26.24	0.83	12.90	5.56	0.22	114.10

Table S2: Stations, dates, and zooplankton species used to calculate the diet preferences (selectivity indices) used in the network model. Prey composition in the water was identified at all sampling events. Each replicate indicates a barcoding library based on 5-12 pooled zooplankton individuals.

Station	Date	Species Sampled	n.	Ref.	
By31 Landsort Deep Lat:58.59367 Lon:18.23640	2017-06-19	<i>Acartia</i> spp.	2	18 and 20	
		<i>Centropages hamatus</i>	4		
		<i>Evadne nordmanni</i>	5		
		<i>Pseudocalanus</i> spp.	5		
		<i>Temora longicornis</i>	6		
		<i>Synchaeta baltica</i>	9		
	2017-08-15	<i>Acartia</i> spp.	8		
		<i>Bosmina</i> spp.	5		
		<i>Centropages hamatus</i> .	5		
<i>Pseudocalanus</i> spp.		5			
<i>Temora longicornis</i>		5			
<i>Synchaeta baltica</i>		4			
2018-03-19	<i>Keratella</i> spp.	5			
	<i>Acartia</i> spp.	4			
	<i>Pseudocalanus</i> spp.	6			
	<i>Temora longicornis</i>	4			
By15 Gotland Deep Lat:57.31222 Lon:20.07620	2019-06-01	<i>Synchaeta baltica</i>	5	This Study	
		<i>Acartia</i> spp.	1		
		<i>Centropages hamatus</i>	4		
		<i>Temora longicornis</i>	2		
		<i>Evadne nordmanni</i>	1		
	2020-09-10	<i>Acartia</i> spp.	3		
		<i>Centropages hamatus</i>	3		
		<i>Temora longicornis</i>	1		
	By5 Bornholm Deep Lat:55.24998 Lon:15.98420	2019-06-15	<i>Acartia</i> spp.		3
			<i>Centropages hamatus</i>		4
<i>Temora longicornis</i>			5		
<i>Evadne nordmanni</i>			3		
2020-09-09		<i>Acartia</i> spp.	2		
		<i>Centropages hamatus</i>	4		
		<i>Temora longicornis</i>	2		

Table S3: Primers and sequences used in this study.

Name	Sequence	Function	Reference
341F	[Adapter1]-CCTACGGGNGGCWGCAG	16S V3-V4 Forward primer	43-44
805R	[Adapter2]-GACTACHVGGGTATCTAATCC	16S V3-V4 Reverse primer	43-44
Adapter1	ACACTCTTCCCTACACGACGCTCTCCGATCT	Linking outer and inner PCR	44
Adapter2	AGACGTGTGCTCTCCGATCT	Linking outer and inner PCR	44
Handle1	AATGATACGGCGACCACCGAGATCTACAC- [IndexF]-[Adapter1]	Forward read Illumina handle	44
Handle2	CAAGCAGAAGACGGCATACGAGAT-[IndexR]- [Adapter2]	Reverse read Illumina handle	44
Index	NNNNNN 16 unique forward sequences and 15 unique reverse sequences	Unique hexamer combination for sample identification.	44

Data S1: All data, code, and a tutorial needed to build the model and reproduce all figures and results from this study are deposited in the Zenodo repository available at <https://doi.org/10.5281/zenodo.7586799>.