Supplementary Information

Stable Isotope Analysis Challenges Wasp-Waist Food Web Assumptions in an Upwelling Pelagic Ecosystem

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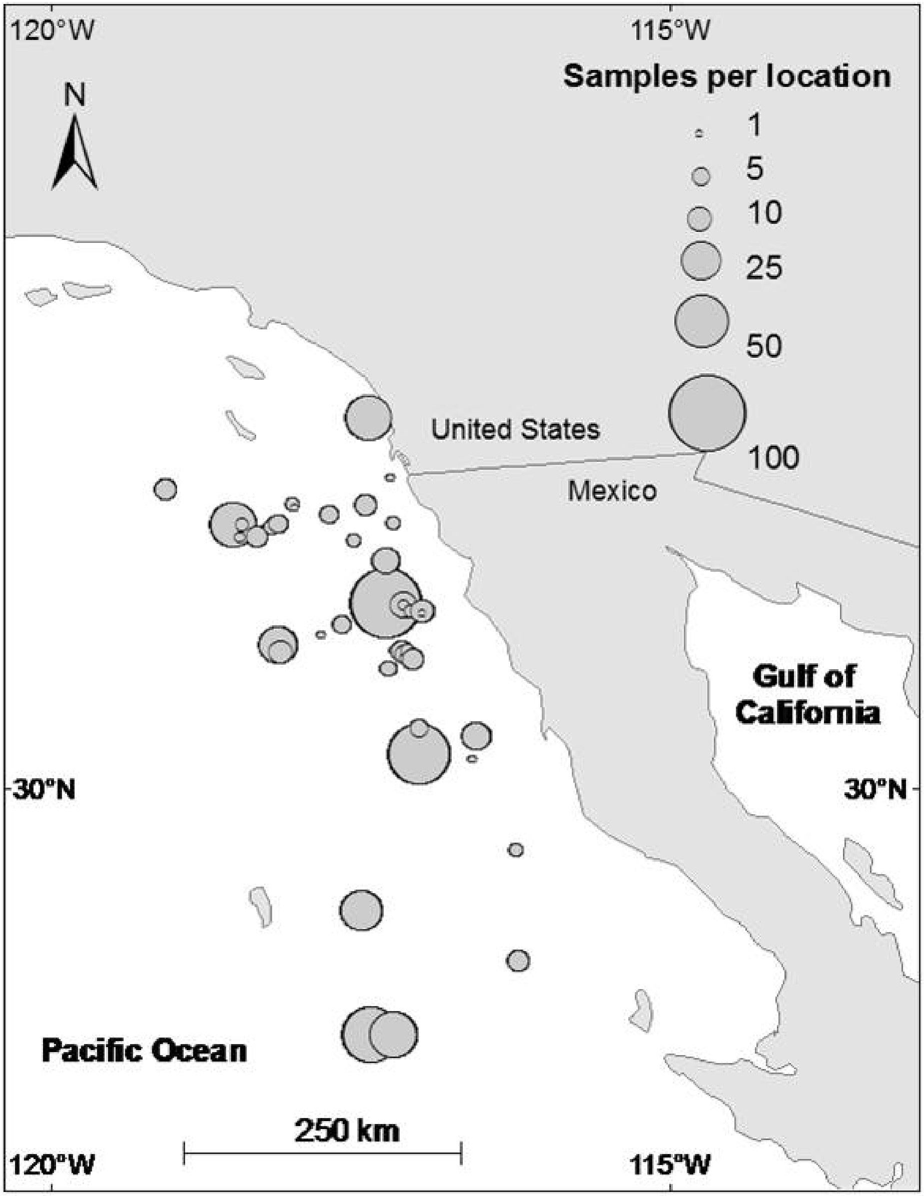
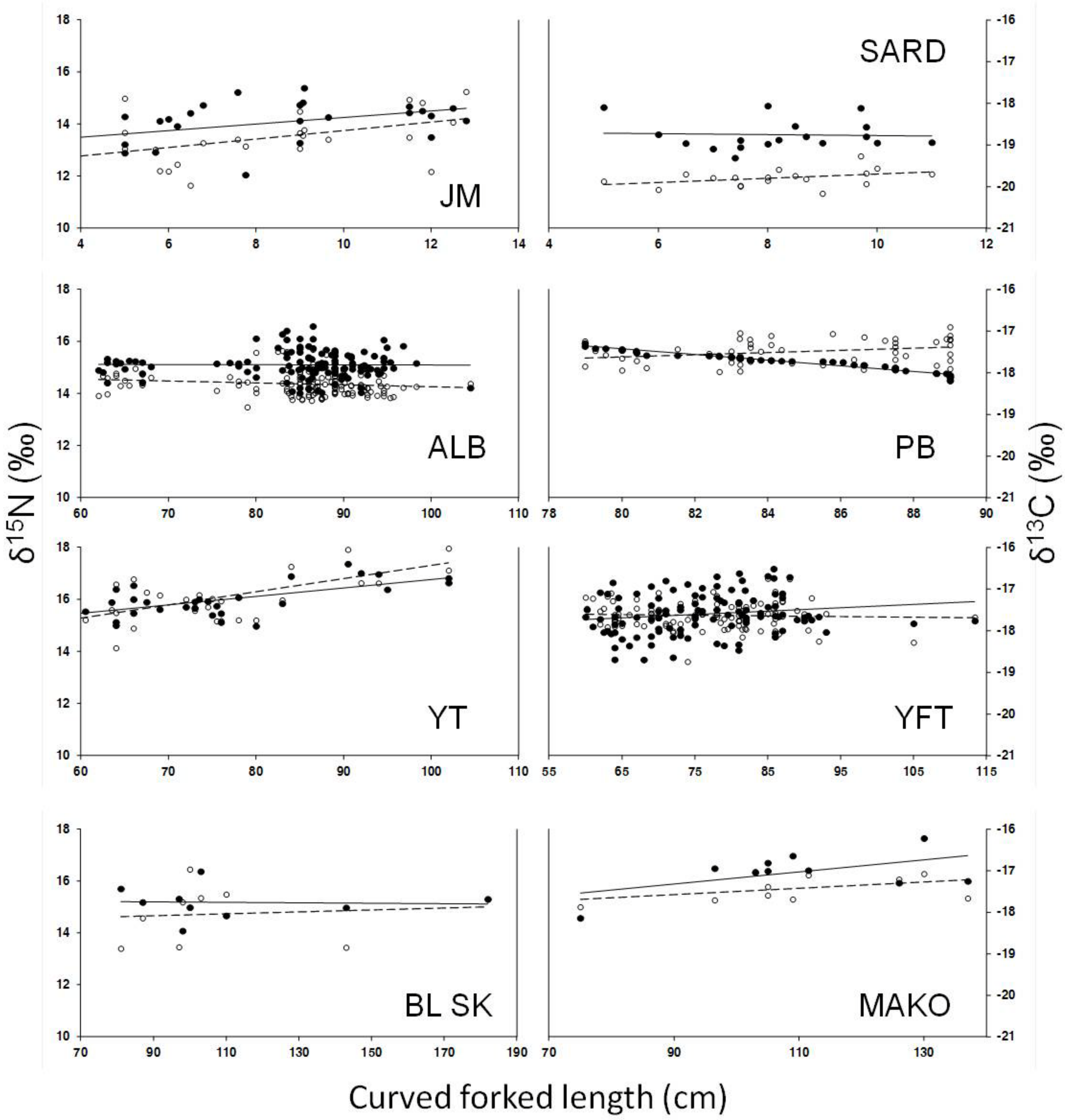


Supplementary Figure S1. Map of the study area showing sampling effort off southern California, USA and northern Baja, Mexico. Sampling occurred from April - October between 2007 and 2010. Markers at each sampling location (●) are scaled according to number of samples taken at that location.



Supplementary Figure S2. Biplots showing relationship between body length and $\delta^{13}C$ (○) and $\delta^{15}N$ (●) values for eight southern California Current residents (SARD (*S. sagax*), JM (*T. symmetricus*), ALB (*T. alalunga*), PB (*T. orientalis*),YFT (*T. albacares*),YT (*S. lalandi*), BLSK (*P. glauca*), SWD (*X. oxyrinchus*)). Scale for *y*-axes ($\delta^{13}C$ and $\delta^{15}N$) is the same for all species. Linear fits shown for body length v. $\delta^{15}N$ (—) and $\delta^{13}C$ (− −) values.

Supplementary Table S1. Linear fits of size versus isotope values in eight species in the CCLME (SARD (*S. sagax*), JM (*T. symmetricus*), ALB (*T. alalunga*), PB (*T. orientalis*),YFT (*T. albacares*),YT (*S. lalandi*), BLSK (*P. glauca*), SWD (*X. oxyrinchus*)). r^2 values for each fit to $\delta^{13}C$ and $\delta^{15}N$ shown for each species. Statistically significant correlations of size and isotope values at the $\alpha = 0.05$ level shown in bold.

	$\delta^{15}N$		$\delta^{13}C$	
Species	**r^2**	**P-value**	**r^2**	**P-value**
JM	0.464	**0.015**	0.514	**0.006**
SARD	0.054	0.830	0.389	0.111
ALB	-0.005	0.961	-0.146	0.110
PB	-0.974	**<0.0001**	0.289	**0.034**
YT	0.670	**<0.0001**	0.708	**<0.0001**
YFT	0.164	0.089	-0.046	0.634
BLSK	-0.044	0.901	-0.295	0.441
MAKO	0.528	0.117	0.131	0.718

Supplementary Table S2. Estimated proportional prey inputs from Bayesian isotope mixing model (MixSir) of trophic groups (TG) to diets of nine predator species and to diets of trophic groups as a whole (TG3-5). Values reported are for 1x10^7 iterations and uninformative priors [1 1 1 1]. Species and TGs marked in bold with an asterisk showed bimodal solutions. TG input estimate values that were bimodal for these species are shown in bold.

		Estimated proportional prey inputs Uninformative priors [1 1 1 1]							
		Trophic Group 2		**Trophic Group 3**		**Trophic Group 4**		**Trophic Group 5**	
Species	**Code**	**Median**	**95% CI**	**Median**	**95% CI**	**Median**	**95% CI**	**Median**	**95% CI**
S. japonicus	PM	91	84 – 97	3	0 – 11	2	0 – 8	2	0 – 6
P. glauca	BLSK	77	64 – 87	9	1 – 28	6	1 – 19	4	0 – 13
T. alalunga	ALB	77	72 – 80	6	1 – 16	16	8 – 21	1	0 – 4
T. orientalis	PB	44	37 – 51	28	17 – 40	18	7 – 28	10	2 – 18
T. albacares	YFT	54	50 – 58	2	0 – 6	42	31 – 47	2	0 – 9
S. chiliensis*	**BON**	**35**	**6 – 49**	**9**	**0 – 75**	**47**	**6 – 62**	2	0 – 9
S. lalandi*	**YT**	**4**	**0 – 30**	**74**	**3 – 84**	**15**	**2 – 65**	6	0 – 17
X. gladius	SWD	1	0 – 4	96	92 – 99	1	0 – 4	1	0 – 3
I. oxyrinchus	MAKO	5	0 – 16	84	69 – 94	5	0 – 17	4	0 – 13
Trophic Group (TG)									
5*	**MAKO, YT, SWD, BON, YFT, PB, STM, LOL, DG**	**59**	**21 – 62**	**5**	**1 – 66**	4	0 – 12	**31**	**4 – 36**
4	BLSK, ABRL, SLB, ALB, FM, OPA, PM, ONYC	82	76 – 87	11	2 – 21	5	1 – 12	2	0 – 6
3	SARD, EELPT, JM, SEB, ARGO, DBB, SAUR, SEN, MYCT, GON, RC	99	98 – 99	1	0 – 1	0	0 – 1	0	0 – 1

Supplementary Table S3. Estimated proportional prey inputs from Bayesian isotope mixing model (MixSir) of trophic groups (TG) to diets of nine predator species and to diets of trophic groups as a whole (TG3-5). Values reported are for $1\text{x}10^7$ iterations and wasp-waist priors of [1 2 1 1]. Species and TGs marked in bold with an asterisk showed bimodal solutions. TG input estimate values that were bimodal for these species are shown in bold.

		Estimated proportional prey inputs Informed priors [1 2 1 1]							
		Trophic Group 2		**Trophic Group 3**		**Trophic Group 4**		**Trophic Group 5**	
Species	**Code**	**Median**	**95% CI**	**Median**	**95% CI**	**Median**	**95% CI**	**Median**	**95% CI**
S. japonicus	PM	89	82 – 95	6	2 – 14	2	0 – 7	2	0 – 5
P. glauca	BLSK	73	58 – 84	17	4 – 37	5	0 – 15	4	0 – 11
T. alalunga	ALB	75	71 – 79	9	3 – 20	14	6 – 19	1	0 – 4
T. orientalis	PB	43	37 – 50	30	19 – 41	17	6 – 28	10	2 – 18
T. albacares	YFT	53	49 – 58	3	1 – 8	41	31 – 46	2	0 – 9
S. chiliensis*	**BON**	**15**	**2 – 41**	**61**	**6 – 84**	**21**	**2 – 55**	4	0 – 15
S. lalandi	YT	3	0 – 10	75	63 – 85	13	1 – 29	7	1 – 17
X. gladius	SWD	1	0 – 5	96	93 – 99	1	0 – 4	1	0 – 3
I. oxyrinchus	MAKO	5	0 – 14	85	72 – 94	5	0 – 16	4	0 – 12
Trophic Group (TG)									
5*	**MAKO, YT, SWD, BON, YFT, PB, STM, LOL, DG**	**24**	**20 – 59**	**62**	**5 – 68**	4	0 – 14	**9**	**2 – 33**
4	BLSK, ABRL, SLB, ALB, FM, OPA, PM, ONYC	80	75 – 85	14	5 – 22	4	0 – 10	2	0 – 5
3	SARD, EELPT, JM, SEB, ARGO, DBB, SAUR, SEN, MYCT, GON, RC	99	98 – 99	1	0 – 1	0	0 – 1	0	0 – 1