## Evidence for cohesive dispersal in the sea

## S1 - Supplementary methods - otolith trace-element sequence similarity analysis

6 The two shoulders (two sides of the core) of the obtained sequence of trace elemental 7 concentrations may differ in the number of pits (ablations) between spikes of high 8 concentrations. For example, the 5 pits of a given element on either side of the core with 9 spikes can be symmetric, like this: 1 0 0 0 1 C 1 0 0 0 1 (C = core); or asymmetric, like 10 this: 1 0 0 0 1 C 1 0 0 1 0. This is due to both natural differences in increment width and 11 to technical difficulties, and thus, obtaining of symmetry in the order of concentrations maxima will be considered as palindrome regardless of asymmetry in the distances of the 12 13 theses concentrations maxima from the core.

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1 2 3

4 5

15 Similarly, differences in the length of the palindrome are expected to be found 16 between otoliths of different fish that have exactly the same palindrome [1]. In addition to 17 the expected differences between the two shoulders of the same otolith, there can be 18 several more causes for potential differences between otoliths: e.g., natural causes, like 19 different qualities of the Aragonite, which can result in differences in the efficiency of the 20 laser; or technical causes, like an otolith mounted with some inclination, resulting in a 21 longer path for the laser through each increment. Even when a good correlation is found 22 between the ablated distance and the number of pits [2], a small change could preclude 23 the possibility to examine similarity based on the raw data (Figure S1).

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In order to simplify the comparison, we compared only one shoulder of the otolith 27 (= one side of the palindrome). After the palindrome is identified and the sequence of reliable spikes determined (Figure S2), each side actually contains the entire chemical 28 29 data. The record of chemical traces starts from the core (which is ideally at the middle of 30 the transect and marked as pit # '0'), and continues towards the edges (the more distant, 31 the later). Since there are natural differences in increment width at different sides of the 32 otolith (which may induce additional differences in spike density), we used only those 33 data obtained from the sulcus side, which was the upper side (ablated first) in our 34 samples.

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36 To generate the sequences used for calculating similarity, the concentration 37 profile of each element was coded according to the presence/absence of concentration 38 maxima [1]. Specifically, a non-zero reading that was higher than the one immediately 39 before and after it was scored as '1', while the other two were scored as '0' (Fig. S1)

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41 Differences in the distances (in pits) between spikes obtained in the sequences of different otoliths also remain when only one side of the palindrome is compared. Some of 42 43 these differences will feature as additional empty pits along the relatively more "spacious" sequence (Figure S1). Such empty pits should be removed in order to 44 eliminate the noise produced by the different transect sizes by frame-shift/s (pit-shift/s) 45 and thus increase the similarity index (J). To achieve this, pair-wise similarities of 46 47 sequences were evaluated using a computerized algorithm designed to maximize J from 48 all the possible frame-shifts of the paired sequences (i.e. all the permutations possible Ben-Tzvi et al. – S1

49 with the removal of 0 to a maximum of 3 empty ablations; Figure S1). In iterations in 50 which the paired, frame-shifted, sequences did not match in length, J was calculated 51 across the length of the shorter sequence.

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53 On average, 0.82 ( $\pm$  0.92) and 1.39 ( $\pm$  1.10) empty pits were removed from the 54 within and between cohort comparisons, respectively. As the same sequence may be 55 frame-shifted differently when paired with different sequences, we estimated the 56 consistency with which a given empty ablation was removed. Specifically, for each fish 57 we calculated the proportion of pair-wise comparisons from which an empty pit was 58 removed. For those pits that were removed at least once, the proportions ranged from 59 0.38 to 1.00 (median: 0.69) and 0.07 to 0.76 (median: 0.39); for within and between 60 cohort comparisons, respectively.

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Expected mean similarities were generated by the random allocation of fish into
the existing cohorts of each species, while preserving the observed cohort size.
Percentiles were calculated across 100 iterations of the randomization process.

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Fish that have been together and experienced the same environment are expected to have the same sequence [1] and thus *J* values obtained from these fish after being frame-shifted are expected to be 1 or close to it. However, some of the obtained results within a cohort were below this value (although above the expected random values). We attribute some of these findings to an additional technical issue. The machine we used (Finnigan Element 2 double-focusing sector Inductively Coupled Plasma Mass

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72	Spectrometer) automatically deducts the last blank from each count. Thus, when counts
73	are low and the last blank is high, negative counts may ensue and some of the weaker
74	spikes may disappear. Examining the readings below zero revealed that most of these
75	missing spikes in fact exist (Figure S2). Although we have not considered these spikes in
76	our analysis, this factor explains some of the relatively low $J$ values found within cohorts.
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80	References
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## 90 Figure legend

Α																
Fish	EI	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	Cr	0	1	0	0	0	0	1	0	1	0	1	0	0	0	0
IUI a	Mn Cu	0 1	0	0	0	0	1	0	0 1	0	0 1	1	0 1	1	0	0
3302	Pb	0	0 1	0 0	1 0	0 0	0 1	0 0	1	0 0	0	0 0	0	0 1	0 0	0 0
	Cr	0	0	1	0	0	0	0	1	0	1	0	1	0	0	0
IUI a	Mn	0	0	0	0	0	0	1	0	0	0	0	1	0	1	0
3308	Cu	1	0	0	0	1	0	0	0	1	0	1	0	1	0	0
	Pb	0	0	1	0	0	0	1	0	1	0	0	0	0	1	0
B Fish	-	4	2	3	4	F	c	7	0	9	10	11	12	13	14	15
FISH	EI Cr	1	2	0	4 0	5 0	6 0	7	8 0	9 1	0	1	0	0	0	0
IUI a	Mn	0	0	0	0	0	1	0	Õ	0	0	1	0	1	0	0
3302	Cu	1	0	0	1	0	0	0	1	0	1	0	1	0	0	0
	Pb	0	1	0	0	0	1	0	1	0	0	0	0	1	0	0
IUI a	Cr Mn	0 0	1 0	0 0	0 0	0 0	0 1	1 0	0 0	1	0	1 1	0 0	0 1	0 0	
3308	Cu	1	0	0	1	0	0	0	1	0 0	1	0	1	0	0	
0000	Pb	0	1	0	0	Ő	1	Õ	1	0	0	Õ	0	1	0	
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Fish	EI	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15
	Cr	0	1	0	0	0	0	1	0	1	0	1	0	0	0	0
IUI a 3302	Mn Cu	0 1	0 0	0 0	0 1	0 0	1 0	0 0	0 1	0 0	0 1	1 0	0 1	1 0	0 0	0 0
0002	Pb	0	1	0	0	0	1	Ō	1	0	0	ō	0	1	ō	0
	Cr	0	1	0	0	0	0	1	0	0	0	0	1	0	1	0
IUI b	Mn	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0
3324	Cu	0 0	0	1 0	0	0 0	0 0	1 1	0	0 0	0 0	1 1	0	0 0	0 0	1
	Pb															0
		•	1		1	•	•		0	0	v		0	0	•	
D Fish	EI															
D Fish	<b>El</b> Cr	1	2	3	4	5 0	6 0	7	8 0	9 1	10 0	11 1	12 0	13 0	14 0	15 0
Fish IUI a	Cr Mn	1 0 0	2	3	4 0 0	5	6	7	8 0 0	9	10 0 0	11	12 0 0	13 0 1	14	15
Fish	Cr Mn Cu	1 0 0 1	2 1 0 0	3 0 0 0	4 0 0 1	5 0 0 0	6 0 1 0	7 1 0 0	8 0 0 1	9 1 0 0	10 0 0 1	11 1 1 0	12 0 0 1	13 0 1 0	14 0 0 0	15 0 0
Fish IUI a	Cr Mn Cu Pb	1 0 0 1 0	2 1 0 0 1	3 0 0 0 0	4 0 0 1 0	5 0 0 0 0	6 0 1 0 1	7 1 0 0	8 0 0 1	9 1 0 0	10 0 0 1 0	11 1 1 0 0	12 0 0 1 0	13 0 1 0 1	14 0 0 0 0	15 0 0
Fish IUI a 3302	Cr Mn Cu Pb Cr	1 0 0 1	2 1 0 0	3 0 0 0	4 0 0 1 0 0	5 0 0 0	6 0 1 0	7 1 0 0	8 0 0 1	9 1 0 0	10 0 0 1	11 1 1 0	12 0 0 1	13 0 1 0	14 0 0 0	15 0 0
Fish IUI a	Cr Mn Cu Pb	1 0 0 1 0 1	2 1 0 0 1	3 0 0 0 0 0	4 0 0 1 0	5 0 0 0 0	6 0 1 0 1	7 1 0 0 0 0	8 0 1 1 0	9 1 0 0 0	10 0 0 1 0 0	11 1 1 0 0 1	12 0 0 1 0 0	13 0 1 0 1	14 0 0 0 0 0	15 0 0
Fish IUI a 3302 IUI b 3324	Cr Mn Cu Pb Cr Mn	1 0 1 0 1 0	2 1 0 1 1 0 0	3 0 0 0 0 0 0	4 0 0 1 0 0 0	5 0 0 0 0 0	6 0 1 0 1 1	7 1 0 0 0 0 0	8 0 1 1 1 1	9 1 0 0 0 0	10 0 1 0 0 0	11 1 0 0 1 0	12 0 1 0 0 0	13 0 1 0 1 1 0	14 0 0 0 0 0 0	15 0 0
Fish IUI a 3302 IUI b 3324 E	Cr Mn Cu Pb Cr Mn Cu Pb	1 0 1 0 1 0 1 0	2 1 0 1 0 1 0 1 0	3 0 0 0 0 0 0 0 1	4 0 1 0 0 0 0 0	5 0 0 0 0 0 0 0	6 0 1 0 1 1 1 1	7 0 0 0 0 0 0 0 0	8 0 1 1 1 0 1 0 0	9 1 0 0 0 0 0 0 0	10 0 1 0 0 0 1 1 1	11 1 0 0 1 0 0 0	12 0 1 0 0 0 0 0	13 0 1 0 1 0 0 0	14 0 0 0 0 0 1 1 0	15 0 0 0
Fish IUI a 3302 IUI b 3324	Cr Mn Cu Pb Cr Mn Cu Pb	1 0 1 0 1 0 1 1	2 1 0 1 0 1 0 1 0 2	3 0 0 0 0 0 0 1 3	4 0 1 0 0 0 0 0	5 0 0 0 0 0 0 0 5	6 0 1 1 1 1 1 1 6	7 0 0 0 0 0 0 0 0 7	8 0 1 1 0 1 0 8	9 1 0 0 0 0 0 0 0 9	10 0 1 0 0 1 1 1	11 1 0 0 1 0 0 0 0 1 1	12 0 1 0 0 0 0 0	13 0 1 0 1 0 0 0	14 0 0 0 0 0 1 0 1 0	15 0 0 0
Fish IUI a 3302 IUI b 3324 E	Cr Mn Cu Pb Cr Mn Cu Pb	1 0 1 0 1 0 1 0	2 1 0 1 0 1 0 1 0	3 0 0 0 0 0 0 0 1	4 0 1 0 0 0 0 0	5 0 0 0 0 0 0 0	6 0 1 0 1 1 1 1	7 0 0 0 0 0 0 0 0	8 0 1 1 1 0 1 0 0	9 1 0 0 0 0 0 0 0	10 0 1 0 0 0 1 1 1	11 1 0 0 1 0 0 0	12 0 1 0 0 0 0 0	13 0 1 0 1 0 0 0	14 0 0 0 0 0 1 1 0	15 0 0 0
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93 Figure S1: Sequence similarity analysis. The method and logic of similarity analysis are 94 presented as pairs of sequences. The cohort and serial # of the fish are given in the left 95 column. The highest reading for each element at a spike (spike can occupy more than one pit) is marked '1'. All other readings are marked '0'. The number of ablations (from the 96 97 core towards the sulcus) heads each column. Colours are used to track the original pit 98 position after being shifted. Table A: Raw sequence of two fish of the same cohort. 99 Similar spikes are seen in pit 2 of the upper fish and pit 3 of the lower one. There is no 100 similarity between pits along the entire sequence (except for pit # 1) However, deleting 101 pit 2 from the lower sequence will result in a perfect fit, as seen in Table B. Table C: 102 Comparison of two sequences obtained from otoliths of fish from different cohorts. There 103 is no fit between the sequences except for pit # 2 and partial fit in pit # 7. The fit between 104 the sequences is not improved when pit # 1 is deleted from the lower sequence (D) or 105 when pits # 1 & 5 are deleted (E). When a third pit (# 9) is deleted (F) there are two pits 106 which then fit (# 8 & 9 in Table E). To find maximum fit, we allowed removal of pits 107 with no spikes if no similar spike was found on either side. For example pit # 13 in the 108 lower sequence of Table C cannot be deleted since Cr spikes exist on both sides and, 109 thus, by deleting it we would be ignoring one of them and considering only the higher. 110 When two consecutive empty pits exist (e.g. pit # 5 & 6 in the lower sequence of Table 111 C), we allowed the deletion of only one. 112

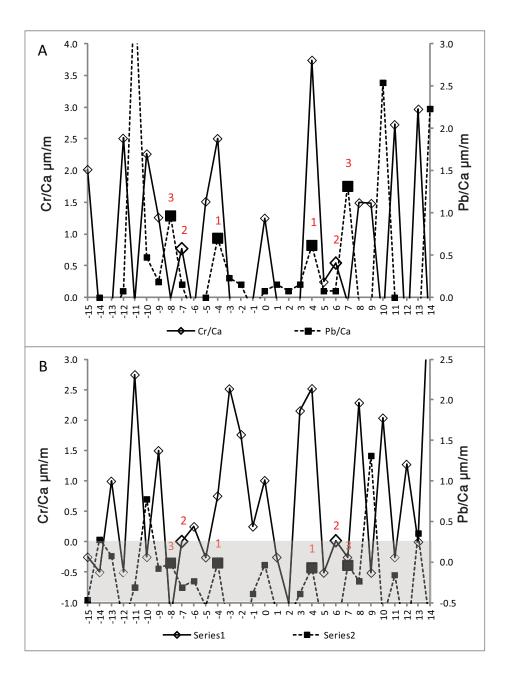




Figure S2: Sample sequence made of two (out of four) elements. Pit # 0 represents the core (which was identified by high concentrations of Mn & Mg2). The distances from the core are given in pits (negative values for pits that were ablated prior to the core). The spikes that are found in the same (mirror) order on both sides of the core form a palindrome. A spike without its pair on the other shoulder is not included in the sequence.

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119	A & B are taken from different N. miryae fish of the same cohort. The sequence is similar
120	except for three spikes (marked with larger symbols and numbered) that were found in
121	the positive zone only in A. The missing spikes, which were found as negative values (the
122	gray area in B; under the last blank which is deleted from each single count by the
123	machine), were not included in the compared sequences and thus explain some of the
124	lower similarities that were obtained from comparisons within the cohort. The method
125	used did not allow the discarding of pits with spikes of more than one element if only one
126	of the elements was missing (e.g. B pits $\#$ -3 & 4) and thus kept the dissimilarity obtained
127	due to the negative result of only one element.
128	