

Supplementary figures

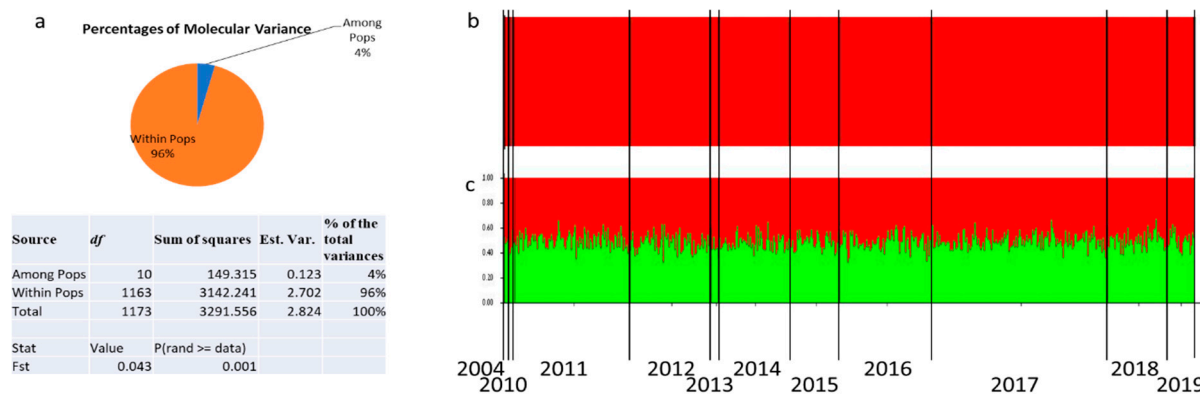


Figure S1: Between years comparisons. a. Hierarchical analysis of molecular variance (AMOVA), summary graph and table. b and c, Population structure analyses, b. Cluster analysis using BAPS for groups of individuals, c. Cluster analysis using 'STRUCTURE' (optimal K=2).

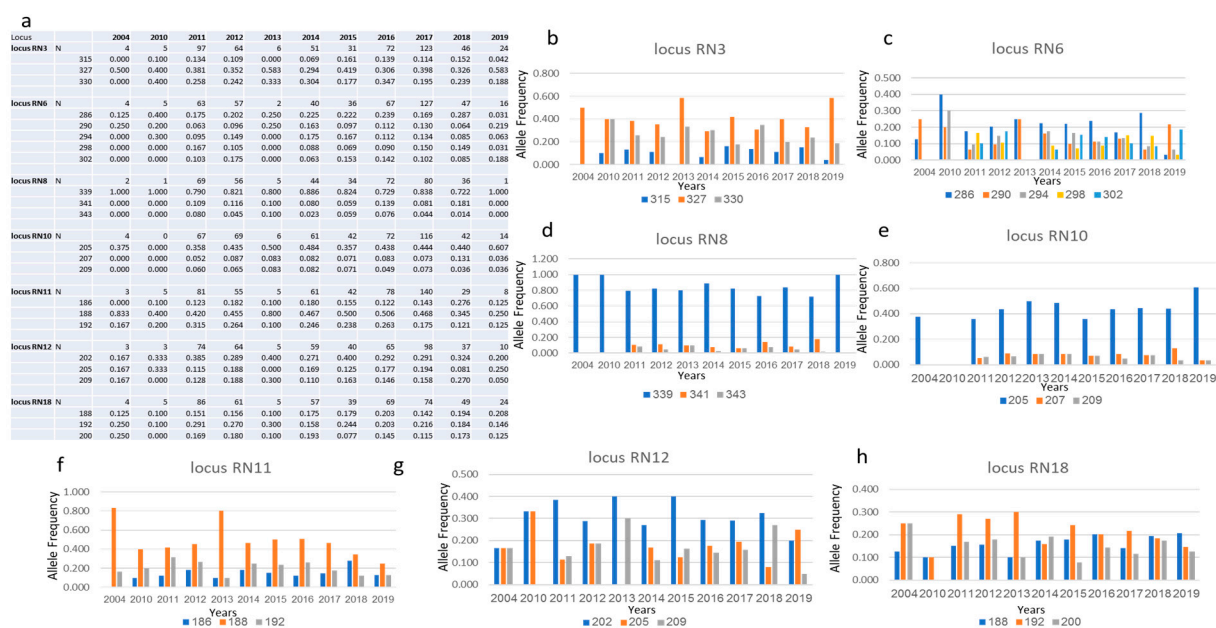


Figure S2: Abundance frequencies for the three most common alleles per locus over the years, a table (a) and graphs (b-h) for each locus (b-h), N=No. of samples.

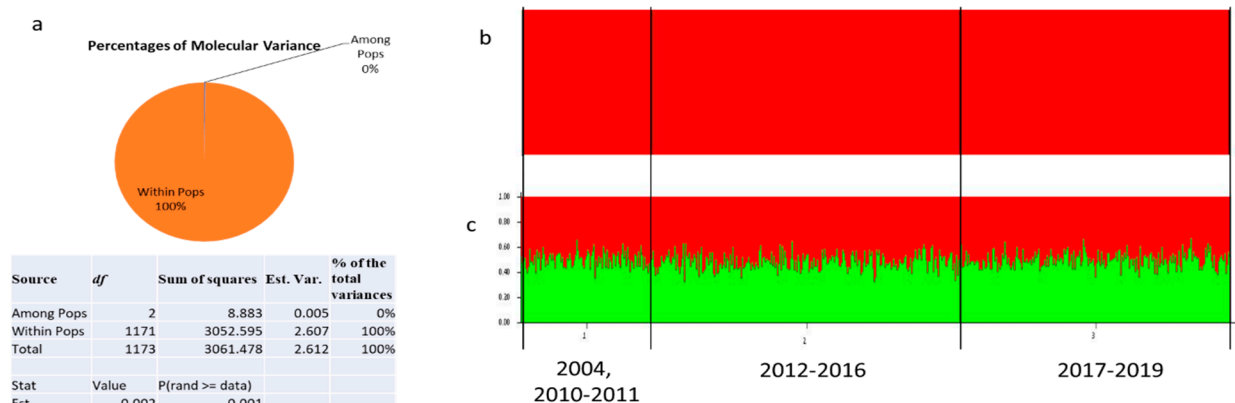


Figure S3: Comparisons between the early collecting period and the late collecting period. a. Hierarchical analysis of molecular variance (AMOVA), a summary graph and table. b and c, Population structure analyses, b. Cluster analysis using BAPS for groups of individuals, c. Cluster analysis using 'STRUCTURE' (optimal K=2).

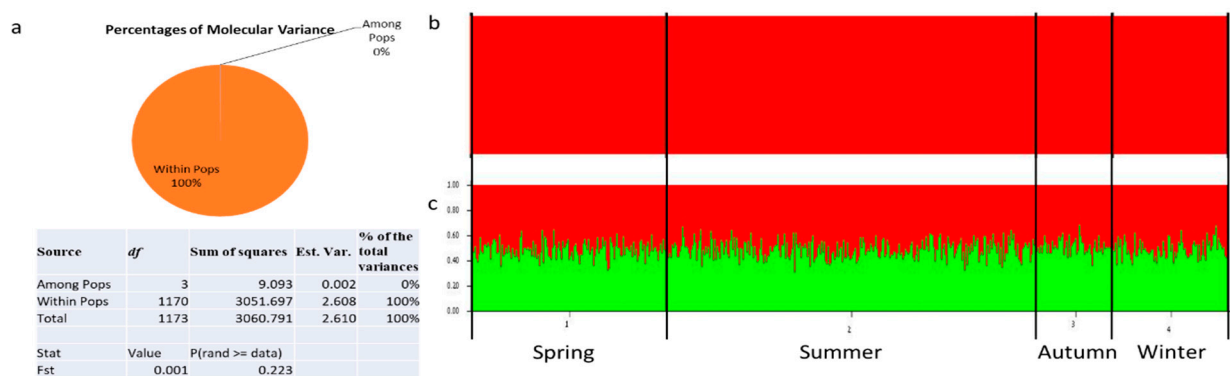


Figure S4: Between seasons comparisons. a. Hierarchical analysis of molecular variance (AMOVA), a summary graph and table. b and c, Population structure analyses, b. Cluster analysis using BAPS for groups of individuals, c. Cluster analysis using 'STRUCTURE' (optimal K=2).

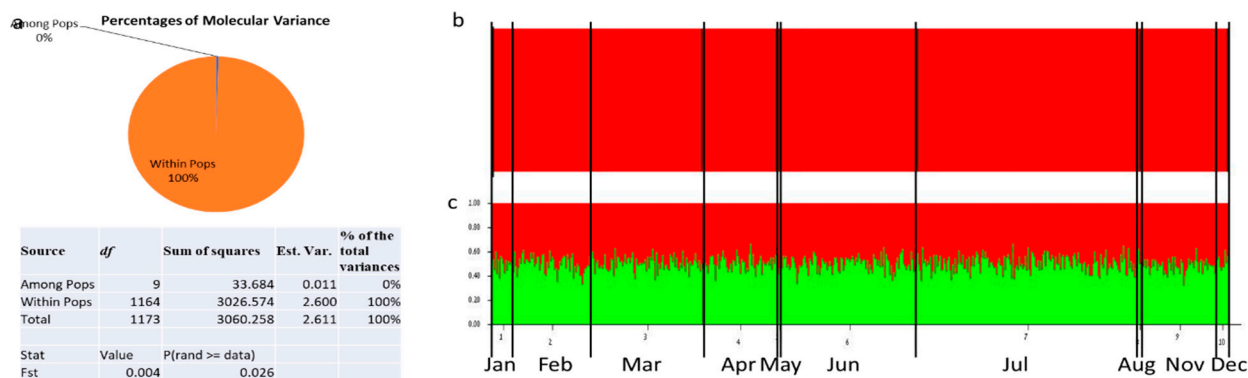


Figure S5 Between months comparisons. a. Hierarchical analysis of molecular variance (AMOVA), a summary graph and table. b and c, Population structure analyses, b. Cluster analysis using BAPS for groups of individuals, c. Cluster analysis using 'STRUCTURE' (optimal K=2).

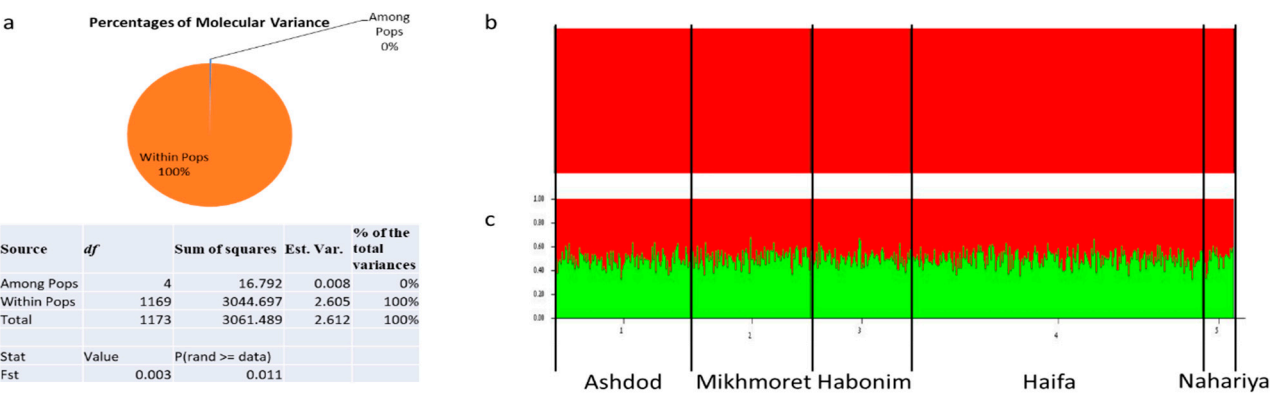


Figure S6: Between collecting regions comparisons. a. Hierarchical analysis of molecular variance (AMOVA), a summary graph and table. b and c, Population structure analyses, b. Cluster analysis using BAPS for groups of individuals, c. Cluster analysis using ‘STRUCTURE’ (optimal K=2).

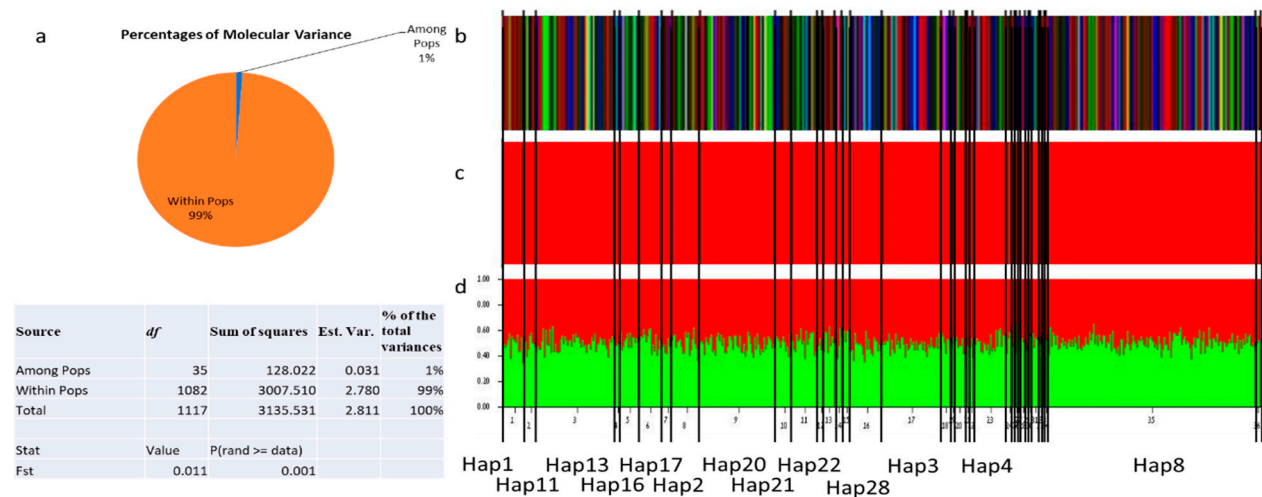


Figure S7: Comparing Between COI haplotypes comparisons. a. Hierarchical analysis of molecular variance (AMOVA), a summary graph and table. b, c and d, Population structure analyses, b. Cluster analysis using BAPS for individuals, c. Cluster analysis using BAPS for groups of individuals. d. Cluster analysis using ‘STRUCTURE’ (optimal K=2). large haplotypes (Hap) are shown.

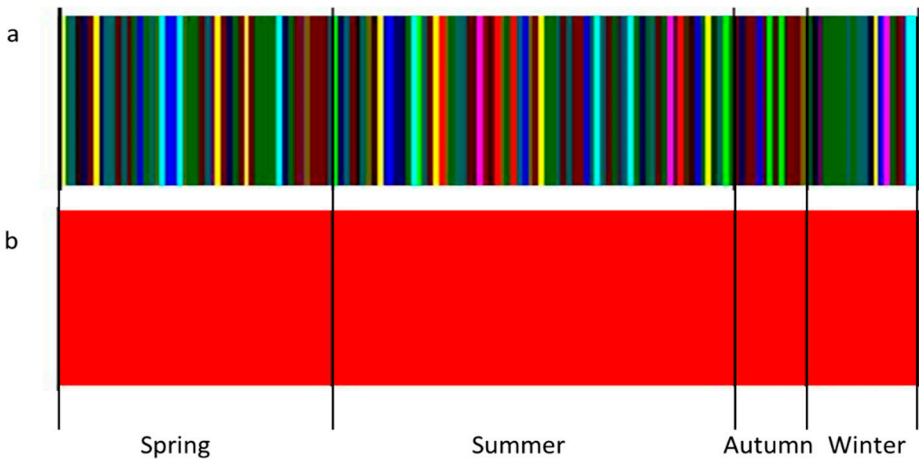


Figure S8: Population structure analyses of samples sharing COI haplotype 8. Between seasons. comparisons a. Cluster analysis of individuals using BAPS, b. Cluster analysis of groups of individuals using BAPS.

Supplementary tables**Table S1:** List of sampling sites, coordinates, years of sampling and number of collected specimens per site.

Sampling Site	Abbr	Coordinates (DD) Long; Lat	Sampling years	No. of specimens
Acre beach	AB	32.925335, 35.066904	2015	2
Ashdod	AS	31.811572, 34.631689	2011, 2015-2019	111
Ashkelon Power-station	APS	31.636630, 34.521274	2012	5
Beit Yanay beach	BY	32.387489, 34.863247	2014	9
Caesarea beach	CB	32.513982, 34.896286	2012	7
Dado beach (Haifa south 1)	DaB	32.793743, 34.955033	2011, 2012, 2015, 2019	34
Dor beach	DoB	32.578905, 34.910757	2012, 2015	16
Habonim beach	HB	32.650581, 34.924477	2011, 2012, 2014, 2015	21
Hadera power station	HPS	32.469408, 34.883947	2011, 2012	36
Haifa Bay	HF	32.862330, 34.997397	2015	4
Tel Shikmona beach	TS	32.826534, 34.957408	2004, 2011-2012, 2014-2018	157
Kiryat Haim beach	KY	32.838781, 35.054534	2011	4
Maayan Tzvi beach	MZ	32.570912, 34.910545	2016, 2017	47
Meridian Beach (Haifa south 2)	MB	32.806889, 34.955312	2011	10
Mikhmoret marina	MM	32.401979, 34.866110	2010-2013, 2014, 2016	53
Nahariya beach	NB	33.009472, 35.086105	2011, 2015	10
Palmahim beach	PB	31.925409, 34.695565	2014	1
Shavei Tzion beach	ST	32.982576, 35.080531	2015-2017	12
Student Beach (Haifa south 3)	SB	32.773316, 34.952649	2016	31
Yotvata Beach	YB	32.832717, 34.972731	2011, 2012	17

Table S2: Statistical analysis for the sampled jellyfish populations, organized based on their collecting year. a. Mean and SE over Loci for each population. N= No. of samples, Na = No. of Different Alleles, Ne = No. of Effective Alleles, HO=observed heterozygotes, HE= expected heterozygotes, F=fixation index. b. Pairwise Population Fst Values for between years analyses

a.

Population (Years)		N	Na	Ne	Ho	He	F
2004	Mean	3.429	4.000	3.474	0.690	0.579	-0.208
	SE	0.297	0.756	0.718	0.146	0.120	0.093
2010	Mean	3.429	3.571	2.897	0.686	0.520	-0.326
	SE	0.812	0.896	0.701	0.179	0.136	0.066
2011	Mean	76.714	16.000	5.236	0.651	0.745	0.130
	SE	4.539	3.388	0.972	0.077	0.069	0.057
2012	Mean	60.857	13.143	4.897	0.666	0.731	0.090
	SE	1.945	3.232	0.803	0.095	0.074	0.084
2013	Mean	4.857	4.286	2.775	0.552	0.579	0.015
	SE	0.508	0.644	0.429	0.055	0.068	0.065
2014	Mean	53.286	12.714	4.935	0.625	0.716	0.154
	SE	3.212	2.876	0.868	0.092	0.088	0.048
2015	Mean	37.714	11.714	4.781	0.708	0.725	0.031
	SE	1.584	2.697	0.806	0.084	0.073	0.038
2016	Mean	70.714	15.143	4.985	0.683	0.745	0.081
	SE	1.599	3.807	0.845	0.053	0.058	0.026
2017	Mean	108.286	19.429	5.329	0.673	0.740	0.080
	SE	9.403	3.287	0.965	0.068	0.078	0.025
2018	Mean	40.857	12.857	5.073	0.648	0.761	0.142
	SE	2.721	2.132	0.722	0.064	0.055	0.064
2019	Mean	13.857	8.857	5.139	0.505	0.670	0.250
	SE	3.181	1.438	1.118	0.109	0.120	0.074
Grand Mean and SE over Loci and Pops							
Total		N	Na	Ne	Ho	He	F
	Mean	43.091	11.065	4.502	0.644	0.683	0.050
	SE	3.934	0.919	0.256	0.029	0.027	0.024

b.

Year	2004	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019
2004	0.000										
2010	0.173	0.000									
2011	0.051	0.114	0.000								
2012	0.049	0.113	0.004	0.000							
2013	0.061	0.152	0.037	0.037	0.000						
2014	0.045	0.109	0.008	0.005	0.039	0.000					
2015	0.045	0.108	0.005	0.004	0.031	0.008	0.000				

2016	0.053	0.115	0.005	0.004	0.035	0.006	0.007	0.000			
2017	0.042	0.111	0.005	0.003	0.033	0.005	0.004	0.006	0.000		
2018	0.066	0.125	0.010	0.008	0.043	0.012	0.012	0.008	0.009	0.000	
2019	0.061	0.144	0.032	0.028	0.059	0.025	0.029	0.035	0.023	0.038	0.000

Table S3: Pairwise population Fst values between collecting periods (representing three groups of years)

	2004, 2010-2011	2012-2016	2017 - 2019
2004 2010-2011	0.000		
2012-2016	0.002	0.000	
2017- 2019	0.004	0.002	0.000

Table S4: Summary of statistical analyses for the jellyfish populations, organized based on their collecting seasons. a. Mean and SE over Loci for each season. N= No. of samples, Na = No. of Different Alleles, Ne = No. of Effective Alleles, HO=observed heterozygotes, HE= expected heterozygotes, F=fixation index. b. Pairwise population Fst values between the seasons

a.

Seasons		N	Na	Ne	Ho	He	F
Spring (Mar, Apr and May)	Mean	126.429	18.429	5.077	0.674	0.736	0.090
	SE	2.951	4.309	0.856	0.078	0.075	0.030
Summer (Jun, Jul and Aug)	Mean	236.857	21.143	5.144	0.658	0.742	0.116
	SE	8.351	4.527	0.933	0.071	0.068	0.036
Autumn (Sept, Oct and Nov)	Mean	39.000	14.429	5.332	0.703	0.753	0.049
	SE	7.293	2.080	0.892	0.059	0.067	0.052
Winter (Dec, Jan and Feb)	Mean	71.714	16.000	5.115	0.659	0.743	0.103
	SE	1.809	2.610	0.871	0.058	0.070	0.026
Grand Mean and SE over Loci and Seasons							
Total		N	Na	Ne	Ho	He	F
	Mean	118.500	17.500	5.167	0.674	0.743	0.090
	SE	14.716	1.740	0.419	0.032	0.033	0.018

b.

seasons	Spring	Summer	Autumn	Winter
Spring	0.000			
Summer	0.001	0.000		
Autumn	0.007	0.007	0.000	
Winter	0.002	0.002	0.007	0.000

Table S5: Summary of the statistical analysis conducted on the jellyfish samples categorized by the month of collection. a. Mean and SE over loci for each month. N= No. of samples, Na = No. of different alleles, Ne = No. of effective alleles, HO=observed heterozygotes, HE= expected heterozygotes, F=fixation index. b. Pairwise population Fst values between months

a.

Month		N	Na	Ne	Ho	He	F
Jan	Mean	13.857	8.429	5.040	0.669	0.675	-0.004
	SE	0.459	1.525	1.080	0.110	0.113	0.028
Feb	Mean	52.000	14.286	5.047	0.668	0.749	0.094
	SE	1.732	2.168	0.835	0.050	0.062	0.043
Mar	Mean	74.000	15.429	5.033	0.646	0.724	0.110
	SE	3.532	3.228	0.824	0.091	0.089	0.045
Apr	Mean	49.714	12.857	4.779	0.709	0.732	0.037
	SE	2.784	3.391	0.836	0.069	0.063	0.022
May	Mean	2.714	3.000	2.406	0.571	0.536	-0.084
	SE	0.184	0.378	0.380	0.088	0.054	0.128
Jun	Mean	80.000	17.571	5.089	0.666	0.744	0.098
	SE	4.515	3.436	0.899	0.065	0.065	0.045
Jul	Mean	154.429	17.857	5.128	0.656	0.740	0.122
	SE	5.177	4.032	0.928	0.076	0.069	0.041
Aug	Mean	2.429	2.857	2.524	0.571	0.512	-0.155
	SE	0.202	0.459	0.416	0.135	0.100	0.161
Nov	Mean	39.000	14.429	5.332	0.703	0.753	0.049
	SE	7.293	2.080	0.892	0.059	0.067	0.052
Dec	Mean	5.857	4.429	3.117	0.581	0.625	0.069
	SE	1.204	0.782	0.512	0.133	0.061	0.210
Grand Mean and SE over Loci and months							
		N	Na	Ne	Ho	He	F
Total	Mean	47.400	11.114	4.349	0.644	0.679	0.036
	SE	5.510	1.000	0.269	0.028	0.025	0.030

b.

Month	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Nov	Dec
Jan	0.000									
Feb	0.022	0.000								
Mar	0.015	0.007	0.000							
Apr	0.018	0.005	0.008	0.000						
May	0.091	0.077	0.073	0.083	0.000					
Jun	0.019	0.004	0.006	0.004	0.071	0.000				
Jul	0.018	0.003	0.004	0.003	0.073	0.002	0.000			
Aug	0.061	0.073	0.055	0.064	0.123	0.064	0.063	0.000		
Nov	0.018	0.009	0.011	0.007	0.077	0.007	0.007	0.062	0.000	
Dec	0.088	0.054	0.061	0.061	0.108	0.057	0.055	0.127	0.059	0.000

Table S6: Summary of statistical analyses for jellyfish populations, organized based on their collecting regions. a. Mean and SE over Loci for each collecting region. N= No. of samples, Na = No. of Different Alleles, Ne = No. of Effective Alleles, HO=observed heterozygotes, HE= expected heterozygotes, F=fixation index. b. Pairwise population Fst values between the collecting regions

a.

Collecting regions		N	Na	Ne	Ho	He	F
Ashdod	Mean	74.714	18.714	5.325	0.652	0.751	0.137
	SE	11.600	3.021	0.965	0.066	0.066	0.026
Mikhmoret	Mean	87.286	15.429	4.880	0.652	0.727	0.119
	SE	4.893	3.206	0.843	0.089	0.074	0.055
Habonim	Mean	72.571	15.143	4.780	0.676	0.729	0.064
	SE	2.716	3.210	0.800	0.062	0.071	0.022
Haifa	Mean	216.286	21.571	5.293	0.675	0.745	0.095
	SE	1.569	5.195	0.921	0.073	0.073	0.030
Nahariya	Mean	23.143	9.429	4.436	0.645	0.733	0.112
	SE	1.056	1.556	0.719	0.032	0.046	0.035
Grand Mean and SE over Loci and regions							
		N	Na	Ne	Ho	He	F
Total	Mean	94.800	16.057	4.943	0.660	0.737	0.105
	SE	11.341	1.604	0.363	0.028	0.028	0.016

b.

Collecting regions	Ashdod	Mikhmoret	Habonim	Haifa	Nahariya
Ashdod	0.000				
Mikhmoret	0.006	0.000			
Habonim	0.006	0.003	0.000		
Haifa	0.004	0.002	0.003	0.000	
Nahariya	0.010	0.011	0.013	0.010	0.000

Table S7: Pairwise population Fst values between haplotypes (for >5 samples in each haplotype)

Haplotypes	Hp1	Hp11	Hp13	Hp16	Hp17	Hp19	Hp2	Hp20	Hp21	Hp22	Hp24	Hp25	Hp26	Hp28	Hp3	Hp30	Hp33	Hp4	Hp6	Hp8
Hp1	0.000																			
Hp11	0.032	0.000																		
Hp13	0.011	0.019	0.000																	
Hp16	0.030	0.030	0.017	0.000																
Hp17	0.034	0.036	0.015	0.023	0.000															
Hp19	0.029	0.045	0.027	0.040	0.046	0.000														
Hp2	0.022	0.023	0.009	0.016	0.020	0.030	0.000													
Hp20	0.011	0.020	0.005	0.017	0.024	0.024	0.014	0.000												
Hp21	0.018	0.029	0.010	0.018	0.024	0.024	0.013	0.010	0.000											
Hp22	0.021	0.031	0.012	0.022	0.024	0.028	0.017	0.011	0.013	0.000										
Hp24	0.037	0.028	0.020	0.031	0.023	0.046	0.025	0.023	0.029	0.026	0.000									
Hp25	0.052	0.041	0.036	0.049	0.044	0.065	0.038	0.039	0.043	0.052	0.035	0.000								
Hp26	0.091	0.075	0.059	0.074	0.045	0.094	0.059	0.072	0.074	0.074	0.061	0.080	0.000							
Hp28	0.023	0.027	0.014	0.015	0.028	0.029	0.016	0.011	0.016	0.018	0.030	0.045	0.081	0.000						
Hp3	0.011	0.019	0.006	0.024	0.023	0.025	0.016	0.006	0.015	0.018	0.026	0.040	0.072	0.013	0.000					
Hp30	0.027	0.033	0.017	0.030	0.026	0.050	0.029	0.020	0.029	0.031	0.020	0.046	0.073	0.028	0.021	0.000				
Hp33	0.037	0.057	0.029	0.043	0.046	0.043	0.035	0.029	0.037	0.036	0.044	0.075	0.094	0.043	0.036	0.051	0.000			
Hp4	0.017	0.033	0.014	0.022	0.026	0.023	0.019	0.010	0.013	0.016	0.038	0.055	0.076	0.017	0.016	0.031	0.034	0.000		
Hp6	0.049	0.038	0.031	0.035	0.041	0.072	0.031	0.036	0.042	0.038	0.052	0.058	0.080	0.042	0.041	0.052	0.068	0.045	0.000	
Hp8	0.014	0.022	0.004	0.014	0.014	0.023	0.008	0.005	0.009	0.010	0.018	0.035	0.054	0.009	0.008	0.017	0.029	0.010	0.034	0.000