Spatially explicit genetic structure in the freshwater sponge *Ephydatia fluviatilis* (Linnaeus, 1759) within the framework of the monopolisation hypothesis

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Supplementary Table. Genetic diversity population statistics across loci and populations.
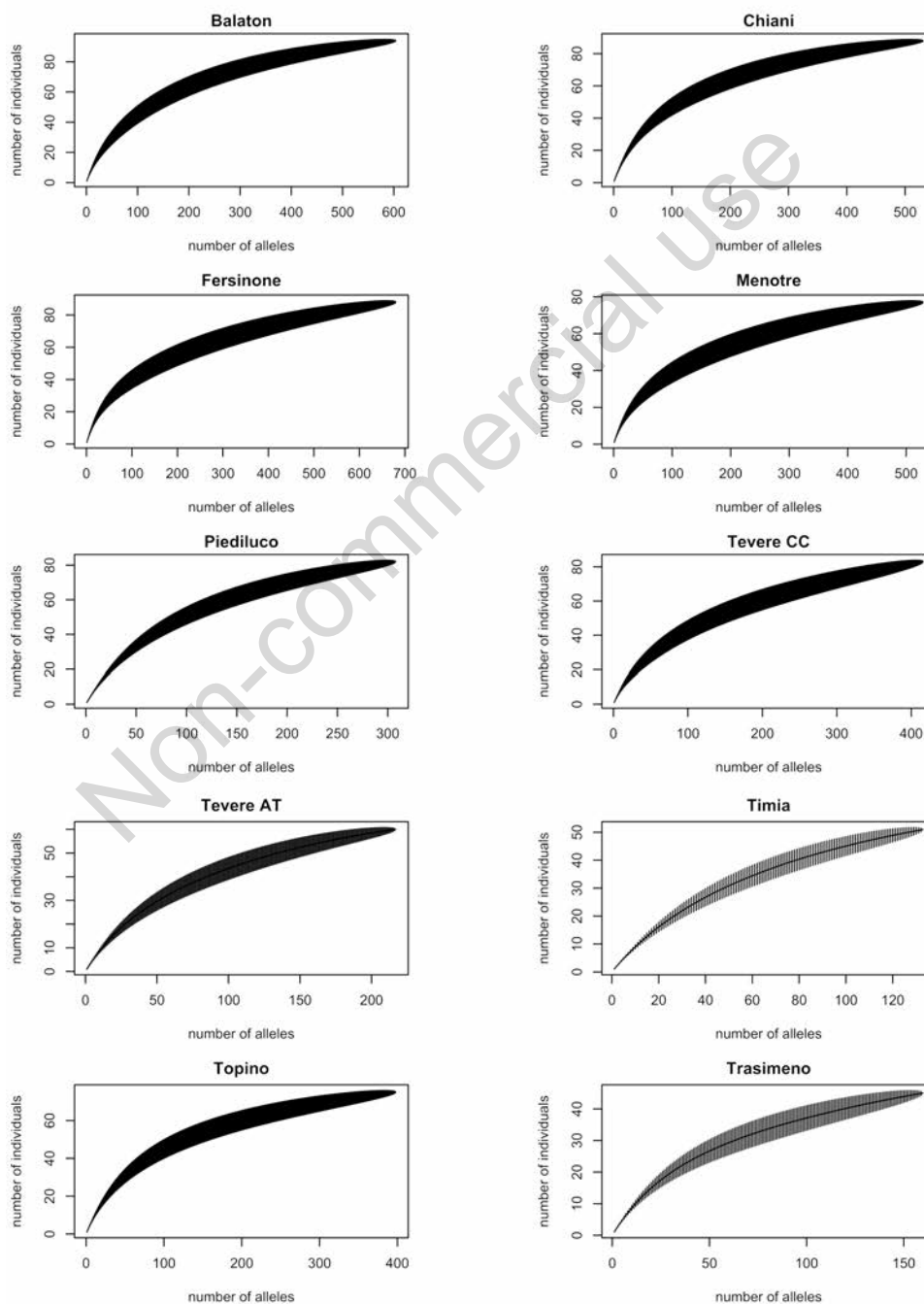
		Efl3	Efl4	Efl5	Efl7	Efl9	Efl10	Efl12	Efl14	Efl17	Efl20	Mean	SD
Piediluco (n=16)	N/null	6/no	7/no	5/no	5/no	5/no	5/yes	9/no	4/yes	6/no	5/no	5.7	1.41
	A	4.77	4.98	5.57	3.43	3.82	4.51	7.34	3.56	5.32	4.11		
	Ho	0.63	0.93	0.81	0.44	0.38	0.21	0.40	0.15	0.75	0.60	0.53	0.24
	He	0.77	0.70	0.79	0.70	0.61	0.76	0.87	0.50	0.80	0.54	0.71	0.11
	P value	0.34	0.45	0.66	0.16	0.01	0.00	0.00	0.00	0.04	0.64		
Trasimeno (n=8) F_{is}: 0.26	N/null	8/no	4/no	7/no	3/no	5/no	4/no	4/yes	5/no	6/no	3/no	4.9	1.66
	A	7.37	4.00	6.50	2.98	4.87	3.88	4.74	4.75	5.73	2.99		
	Ho	0.75	0.86	0.50	0.25	0.63	0.25	0.25	0.50	0.75	0,75	0.55	0.22
	He	0.86	0.78	0.85	0.43	0.81	0.73	0.71	0.77	0.82	0.57	0.73	0.13
	P value	0.07	0.42	0.03	0.14	0.74	0.01	0.00	0.29	0.25	0.70		
Fersinone (n=34) F_{is}: 0.20	N/null	9/no	5/no	19/yes	4/no	6/no	5/no	14/yes	5/no	8/no	9/no	8.4	4.76
	A	5.77	2.91	7.24	2.92	3.53	3.63	2.64	3.70	5.08	3.73		
	Ho	0.59	0.71	0.50	0.47	0.56	0.62	0.13	0.68	0.62	0.26	0.51	0.18
	He	0.76	0.53	0.84	0.62	0.64	0.53	0.43	0.68	0.73	0.67	0.64	0.12
	P value	0.00	0.00	0.00	0.01	0.03	0.07	0.00	0.00	0.05	0.00		
Topino (n=17)	N/null	9/no	4/no	11/no	6/no	6/no	3/no	2/no	9/no	8/no	6/no	6.4	2.87
	A	6.30	3.66	7.59	3.87	5.22	2.66	1.44	6.80	5.81	4.65		
	Ho	0.56	0.53	0.71	0.53	0.88	0.76	0.06	0.76	0.65	0.41	0.59	0.22
	He	0.82	0.68	0.86	0.71	0.77	0.53	0.06	0.87	0.81	0.68	0.68	0.23
	P value	0.05	0.02	0.00	0.27	0.31	0.10	1.00	0.02	0.00	0.00		
Tevere CC (n=20)	N/null	12/no	7/no	9/no	4/no	6/no	4/yes	5/no	7/no	7/no	3/no	6.4	2.67
	A	6.84	4.76	5.89	2.42	4.97	2.64	3.59	5.90	5.26	2.94		
	Ho	0.65	0.70	0.55	0.20	0.70	0.10	0.05	0.70	0.65	0.55	0.48	0.25
	He	0.78	0.72	0.76	0.27	0.80	0.34	0.45	0.84	0.79	0.55	0.63	0.20
	P value	0.08	0.01	0.01	0.05	0.01	0.00	0.00	0.10	0.03	0.05		
Timia (n=7)	N/null	5/no	7/no	8/no	4/no	4/no	4/no	2/no	7/no	5/no	5/no	5.1	1.79
	A	5.00	8.00	7.00	3.00	4.00	4.00	2.00	7.00	5.00	5.00		
	Ho	0.29	1.00	0.57	0.71	0.57	0.43	0.00	0.57	0.57	0.86	0.56	0.27
	He	0.67	0.91	0.90	0.63	0.67	0.63	0.26	0.89	0.79	0.76	0.71	0.18
	P value	0.03	0.68	0.00	1.00	0.68	0.11	0.08	0.08	0.07	0.77		
Tevere AT (n=11)	N/null	6/no	5/no	7/no	7/no	5/no	6/no	1/no	11/no	4/no	4/no	5.6	2.59
	A	5.24	4.81	5.99	4.76	4.03	5.15	1.00	7.69	3.40	3.87		
	Ho	0.55	0.82	0.73	0.45	0.55	0.45	-	0.73	0.90	0.91	0.61	0.26
	He	0.69	0.78	0.82	0.79	0.47	0.80	-	0.79	0.62	0.69	0.65	0.24
	P value	0.01	0.11	0.04	0.04	1.00	0.00	-	0.17	0.10	0.40		
Chiani (n=27)	N/null	8/no	9/no	12/no	5/no	6/yes	3/no	14/no	6/no	5/no	4/no	7.2	3.55
	A	5.97	5.22	7.87	3.84	4.82	2.80	8.52	4.62	3.11	3.05		
	Ho	0.41	0.77	0.56	0.46	0.35	0.15	0.48	0.67	0.22	0.30	0.44	0.18
	He	0.82	0.72	0.89	0.66	0.70	0.44	0.90	0.71	0.36	0.60	0.68	0.17
	P value	0.00	0.16	0.00	0.03	0.00	0.00	0.00	0.11	0.01	0.00		
Menotre 2.91(n=28)	N/null	10/yes	9/no	13/yes	5/no	6/no	3/no	7/no	9/yes	7/no	5/no	7.4	
	A	6.48	6.32	7.43	2.58	4.50	2.55	3.71	5.39	4.79	3.96		
	Ho	0.46	0.54	0.43	0.17	0.54	0.39	0.07	0.38	0.46	0.37	0.38	0.14
	He	0.85	0.84	0.87	0.49	0.72	0.38	0.38	0.68	0.67	0.67	0.66	0.17
	P value	0.00	0.00	0.00	0.00	0.04	0.06	0.00	0.00	0.00	0.00		

Supplementary Table. Continued from previous page.

		Efl3	Efl4	Efl5	Efl7	Efl9	Efl10	Efl12	Efl14	Efl17	Efl20	Mean	SD
Balaton (n=31)	N/null	8/no	8/no	10/no	5/no	11/no	6/no	12/yes	14/no	6/no	8/yes	8.7	2.94
	A	5.25	4.52	4.75	2.59	6.63	4.32	7.65	7.82	3.57	3.98		
	Ho	0.74	0.74	0.47	0.28	0.74	0.55	0.52	0.65	0.65	0.20	0.55	0.18
	He	0.77	0.65	0.69	0.35	0.84	0.66	0.89	0.89	0.57	0.55	0.69	0.16
	P value	0.27	0.19	0.03	0.11	0.22	0.00	0.00	0.00	0.56	0.00		
Total alleles		19	18	31	8	13	9	24	23	13	16		

SD, standard deviation; N, number of alleles per population; null, null presence of alleles at each locus; n, number of genotyped individuals; A, allelic richness; Ho, observed heterozygosity; He, expected heterozygosity; -, value not calculated by software.

Supplementary Figure 1. Cumulative curves and 95% confidence intervals of the number of alleles for each population.