

Supplementary information – Jarne et al. Connectivity and selfing drives population genetic structure in a patchy landscape: a comparative approach of four co-occurring freshwater snail species.

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Table S1. (provided as a separate Excel table). A (non-exhaustive) list of studies analyzing simultaneously population genetic structure in several species based on neutral genetic markers. These 15 studies were detected through searches using the Web of Science (September 2019) using key-words such as "population genetic structure", "neutral markers", "comparative", and "multispecies". We retained studies conducted at the same (not too large) geographic scale for all species from which population genetic parameters can be inferred (*i.e.* excluding large-scale phylogeographic studies based on DNA sequences). This is probably not an exhaustive list, but it is representative of the kind of studies that have been conducted, and also shows that such comparative approaches are limited to a few examples. Studies were numbered in alphabetical order of first author's name. We return the bibliographic reference, biological group, species name, the geographic area where the study was conducted (* = yes, irr = irrelevant), number of populations and number of individuals per population, sampling scale, the set of comparisons (up to three, sometimes including a large number of variables) that were conducted, environmental variables, genetic markers and number of loci, genetic analyses and variables, main conclusions, and whether interspecific interactions were considered.

Table S2. Variables used to characterize sites (environmental) and population demography of the four species studied based on yearly surveys. For each variable, we return a brief description and the range of observed values. The variable values used in the analyses were averages over the 2001-2007 period. Vegetation cover is the percent of site covered by aquatic vegetation (*i.e.* 30 when 30% of site is covered). Temporal stability is the value on the first axis of a principal component analysis including site hydrological regime (five levels; from frequently dry to fully permanent), percent of years during which the site was found dry, variance of site size over years and variance of vegetation cover over years. Invasion age (*Physa acuta*) and Years since *P. acuta* invasion (other species) was calculated from 2001 until the sampling year of each population and then converted to two classes of sites: not or recently invaded by *P. acuta* vs. invaded for more than two years, coded 1 and 2 respectively, as in Chapuis et al. (2017). Two years corresponds to *ca.* 10-12 generations in these species. Long-term population size was computed as $N_{LT} = \text{Mean}(0.5 d_t + \log_{10}(\text{size}_t))$ averaged over years, where d_t is snail density (semi-log scale: no individuals, < 1 ind. / m², 1 to 5 ind. / m², 5 to 10 ind. / m², ...) and size is defined in the table. Note that this parameter gives more weight to years with very low population size, because of their strong influence on long-term diversity (see Charlesworth & Charlesworth, 2010). Size and vegetation cover were $\text{Log}_{10}(1+X)$ -transformed, after averaging over years, for statistical analyses. See main text and Lamy et al. (2012) for more details.

Variable	Description	Values
Environmental characteristics		
Size	Largest diameter (in meters)	A few to 400
Vegetation cover	Percent of site covered by aquatic vegetation	0 to 100
Connectivity	Connectivity to neighbouring sites	Not to fully connective (four levels)
Stability	Temporal stability	-
Density of favorable habitats	Number of water bodies within a radius of 2 km	0 to 190
Population demography		
Invasion age (<i>Physa acuta</i>)	Number of years since first observation	0 to 7
Years since <i>P. acuta</i> invasion (other species)	Number of years since first <i>P. acuta</i> observation	0 to 7
Long-term population size	Combination of observed densities and site size averaged over years	Obs. density: 1-5 to 1000-5000 ind / m ²

Table S3. Sampled sites per species. Seventy four sites were sampled for the genetic analysis of the four snail species. The number of species sampled per site (N) is returned in the last column (1.57 species / site, s.d. 0.704, range = 1-3) and the number of sites sampled per species on the last row. Acronyms are those used in Figure 1. All sites from Grande-Terre, except two from Marie-Galante (MG) and two from Basse-Terre (BT).

Site	<i>Physa acuta</i>	<i>Aplexa marmorata</i>	<i>Drepanotrema depressissimum</i>	<i>Drepanotrema surinamense</i>	N
Alleaume Nord	Pa1	Am1			2
Balance				Ds2	1
Bamboche			Dd1		1
Bauzon				Ds3	1
Bazin			Dd2		1
Beaufond	Pa2	Am2			2
Beauplan		Am3			1
Bel Etang		Am4		Ds1	2
Belin		Am5		Ds4	2
Blonval Nord			Dd3		1
Caraque Est	Pa3				1
Couronne Conchou		Am6	Dd4		2
Dadoud		Am7			1
David	Pa4	Am8			2
Delisle Sud		Am9	Dd5	Ds5	3
Desbonnes Sud			Dd6		1
Descareaux	Pa5				1
Duteau		Am10			1
Etang Bambou (MG)	Pa6				1
Etang Cocoyer		Am11		Ds6	2
Fauvette Nord		Am12		Ds7	2
Fond Bertrand		Am13		Ds8	2
Fond Rose			Dd7		1
Fond Thézan	Pa7				1
Gaschet	Pa8				1
Geffrier			Dd8		1
Gentilly Nord		Am14			1
Girard		Am15			1
Gorot	Pa9	Am16		Ds9	3
Goudenave	Pa10	Am17			2
Grand Maison		Am18		Ds10	2
Grosse Roche		Am19	Dd9		2
Kancel		Am20	Dd10	Ds11	3
L'Ecluse			Dd11		1
L'Henriette			Dd12		1
Lamarre		Am21		Ds12	2

Laroche Picard		Am22			1
Lebraire		Am23		Ds13	2
Loery Sud				Ds14	1
Lubeth	Pa12	Am24			2
Mahaudiere		Am25	Dd13	Ds15	3
Malakoff		Am26		Ds16	2
Mam'mé		Am27	Dd14	Ds17	3
Dans Fond Prairie		Am28			1
Jacquot Prairie	Pa11				1
Medaille		Am29			1
Montmain		Am30			1
Moulin Belcourt		Am31			1
Neron	Pa13				1
Pavillon		Am32	Dd15	Ds18	3
Pico		Am33	Dd16	Ds19	3
Pistolet			Dd17		1
Pointe des Châteaux			Dd18		1
Port Blanc	Pa14	Am34			2
Porte d'Enfer du Moule	Pa15				1
Porte Enfer Vigie			Dd19		1
Poucet		Am35	Dd20	Ds20	3
Ravine Bellevue				Ds21	1
Ravine Favreau		Am36		Ds22	2
Rav. Grand Bassin (MG)	Pa16				1
Ravine mon Chéri (Pont de Caraque)	Pa17	Am37			2
Ravine Vinty (BT)		Am43			1
Rejoui Nord		Am38	Dd21		2
Saint Jacques	Pa18		Dd22		2
Sainte Marguerite Nord	Pa19	Am39		Ds23	3
Sainte Rose (BT)	Pa20				1
Sainte Rose Ouest		Am40		Ds24	2
Senneville			Dd23		1
Surgy nord				Ds25	1
Terrasson	Pa21	Am41			2
Titon			Dd24		1
Valet Est			Dd25		1
Valet Est Est		Am42		Ds26	2
Zevallos Nord				Ds27	1
		21	43	25	27

Table S4. Characteristics of the populations studied in *Physa acuta* (A), *Aplexa marmorata* (B), *Drepanotrema depressissimum* (C), and *Drepanotrema surinamense* (D). For each population, we give the name, sampling size (n) and year, and mean values among loci of population genetic parameters. All sites are in Grande-Terre, except two from Marie-Galante (MG) and two from Basse-Terre (BT). R_A = allelic richness, H_e = gene diversity, R_G = genotypic richness in the selfers *A. marmorata* and *D. surinamense*, F_{IS} = inbreeding coefficient, $S(F_{IS})$ = selfing rate based on F_{IS} , (- = not calculated because of absence of diversity) and $S(g2)$ = selfing rate returned by RMES (-: not calculated because of too limited heterozygosity). Rarefaction on allelic and genotypic richness based on the smallest sample size per species. F_{IS} and $S(g2)$ values in red, blue and green are significantly different from 0 at the 0.001, 0.01 and 0.05 level respectively.

A. Physa acuta

Population	Year	<i>n</i>	<i>R_A</i>	<i>H_e</i>	<i>F_{IS}</i>	<i>S(F_{IS})</i>	<i>S(g₂)</i>
Alleaume Nord	2010	20	2.730	0.391	0.088	0.162	0.206
Beaufond	2010	20	3.574	0.581	0.141	0.247	0.000
Caraque Est	2010	26	3.753	0.593	0.235	0.381	0.227
David	2010	19	3.080	0.546	0.188	0.317	0.000
Descareaux	2007	23	3.625	0.539	0.249	0.398	0.179
Fond Thézan	2010	20	2.685	0.440	0.236	0.382	0.000
Gaschet	2007	31	3.867	0.658	0.120	0.214	0.200
Gorot	2007	8	3.604	0.610	0.253	0.404	0.000
Goudenave	2010	20	4.426	0.657	0.182	0.308	0.238
Lubeth	2010	19	3.724	0.633	0.225	0.367	0.220
Jacquot Prairie	2010	20	3.412	0.603	0.133	0.235	0.000
Neron	2007	32	3.193	0.554	0.089	0.164	0.000
Port Blanc	2010	20	2.102	0.324	0.077	0.143	0.000
Porte d'Enfer du Moule	2007	31	2.833	0.513	0.220	0.360	0.000
Ravine mon Chéri (Pont Caraque)	2010	20	4.291	0.634	0.181	0.307	0.000
Saint Jacques	2010	30	3.545	0.580	0.133	0.235	0.000
Sainte Marguerite Nord	2010	19	3.748	0.570	0.166	0.285	0.000
Terrasson	2010	21	3.768	0.623	0.094	0.172	0.118
Étang Bambou (MG)	2010	20	1.982	0.273	0.241	0.388	0.000
Ravine Grand Bassin (MG)	2010	20	2.106	0.311	0.129	0.229	0.000
Sainte Rose (BT)	2010	20	2.979	0.499	-0.050	-0.105	0.000

B. *Aplexa marmorata*

Population	Year	<i>n</i>	<i>R_A</i>	<i>R_G</i>	<i>H_e</i>	<i>F_{IS}</i>	<i>S(F_{IS})</i>	<i>S(g₂)</i>
Alleaume Nord	2010	20	1.115	1.763	0.024	1.000	1.000	-
Beaufond	2010	19	1.000	1.000	0.000	-	-	-
Beauplan	2009	12	1.737	5.318	0.349	0.910	0.953	0.968
Bel Etang	2009	22	2.044	5.506	0.277	1.000	1.000	-
Belin	2010	20	1.362	4.553	0.124	1.000	1.000	-
Couronne Conchou	2010	12	1.247	2.833	0.072	1.000	1.000	-
Dadoud	2007	31	1.726	3.763	0.273	0.956	0.977	0.977
David	2010	20	1.798	3.957	0.167	0.962	0.981	-
Delisle Sud	2010	12	2.101	6.152	0.232	1.000	1.000	-
Duteau	2009	23	2.073	4.986	0.362	1.000	1.000	-
Etang Cocoyer	2009	10	1.374	5.000	0.115	0.783	0.878	0.999
Fauvette Nord	2009	12	1.236	2.667	0.061	1.000	1.000	-
Fond Bertrand	2010	17	1.124	1.949	0.040	1.000	1.000	-
Gentilly Nord	2010	20	1.494	4.026	0.079	1.000	1.000	-
Girard	2009	12	1.618	4.803	0.178	1.000	1.000	-
Gorot	2009	12	1.250	3.000	0.085	1.000	1.000	-
Goudenave	2010	20	1.687	3.851	0.133	1.000	1.000	-
Grand Maison	2009	12	1.604	5.318	0.114	1.000	1.000	-
Grosse Roche	2007	31	1.625	6.781	0.171	0.976	0.988	-
Kancel	2009	23	1.509	4.682	0.101	0.946	0.972	-
Lamarre	2009	12	1.125	2.000	0.051	1.000	1.000	-
Laroche Picard	2010	20	1.203	2.263	0.035	1.000	1.000	-
Lebraire	2009	12	1.874	4.500	0.378	0.917	0.957	0.968
Lubeth	2010	20	1.327	3.658	0.066	0.905	0.950	-
Mahaudiere	2009	12	1.250	3.818	0.084	0.876	0.934	-
Malakoff	2010	20	1.573	3.763	0.088	0.929	0.963	-
Mam'mé	2009	12	1.848	7.136	0.216	1.000	1.000	-
Dans Fond Prairie	2007	31	2.555	7.573	0.466	0.957	0.978	0.000
Medaille	2009	24	1.154	1.833	0.031	1.000	1.000	-

Montmain	2009	11	1.500	2.000	0.218	1.000	1.000	-
Moulin Belcourt	2009	24	1.860	4.007	0.164	0.905	0.950	0.970
Pavillon	2009	12	1.368	3.818	0.116	1.000	1.000	-
Pico	2010	10	1.997	5.000	0.248	1.000	1.000	-
Port Blanc	2010	20	1.000	1.000	0.000	-	-	-
Poucet	2009	20	2.506	8.816	0.504	0.987	0.994	-
Ravine Favreau	2009	12	1.604	5.470	0.114	1.000	1.000	-
Ravine mon Chéri (Pont de Caraque)	2007	30	1.831	5.616	0.224	0.943	0.971	-
Ravine Vinty (BT)	2010	20	1.864	7.204	0.326	0.904	0.950	0.963
Rejoui Nord	2009	14	1.873	5.999	0.297	0.970	0.985	-
Sainte Marguerite Nord	2010	20	1.830	4.684	0.180	1.000	1.000	-
Sainte Rose Ouest	2009	11	1.493	4.727	0.129	1.000	1.000	-
Terrasson	2007	31	1.497	7.233	0.298	0.959	0.979	0.999
Valet Est Est	2009	22	1.442	2.442	0.091	1.000	1.000	-

C. Drepanotrema depressissimum

Site	Year	<i>n</i>	R_A	H_e	F_{IS}	$S(F_{IS})$	$S(g_2)$
Bamboche	2009	32	9.65	0.83	0.068	0.127	0.000
Bazin	2009	32	12.66	0.892	0.052	0.099	0.025
Blonval Nord	2009	29	10.82	0.887	0.040	0.077	0.043
Couronne Conchou	2009	22	10.74	0.875	0.025	0.049	0.000
Delisle	2010	32	10.49	0.863	0.096	0.175	0.000
Desbonnes Sud	2009	31	6.26	0.736	0.075	0.140	0.000
Fond Rose	2009	32	10.56	0.861	-0.003	-0.006	0.000
Geffrier	2009	30	11.92	0.901	0.012	0.024	0.000
Grosse Roche	2007	32	11.04	0.82	0.018	0.035	0.000
Kancel	2010	32	12.41	0.895	0.030	0.058	0.000
L'Ecluse	2009	30	11.75	0.884	0.064	0.120	0.000
L'Henriette	2009	24	8.01	0.786	0.020	0.039	0.000
Mahaudière	2009	31	11.62	0.878	0.087	0.160	0.000
Mam'mé	2009	31	12.04	0.901	0.021	0.041	0.000
Pavillon	2009	31	14.16	0.921	0.020	0.039	0.000
Pico	2009	32	11.40	0.896	0.024	0.047	0.030
Pistolet	2009	30	10.00	0.82	0.054	0.102	0.000
Pointe des Châteaux	2009	24	6.62	0.761	0.049	0.093	0.168
Porte Enfer Vigie	2009	32	9.84	0.848	0.005	0.010	0.000
Poucet	2009	30	12.21	0.904	0.013	0.026	0.000
Réjoui Nord	2008	31	14.00	0.919	0.017	0.033	0.000
Saint Jacques	2010	30	12.77	0.904	0.041	0.079	0.000
Senneville	2007	30	11.59	0.88	0.046	0.088	0.026
Titon	2009	28	12.57	0.904	0.019	0.037	0.000
Valet Est	2008	31	11.18	0.871	0.014	0.028	0.000

D. *Drepanotrema surinamense*

Population	Year	<i>n</i>	<i>R_A</i>	<i>R_G</i>	<i>H_e</i>	<i>F_{IS}</i>	<i>S(F_{IS})</i>	<i>S(g₂)</i>
Balance	2009	7	2.063	4.000	0.289	1.000	1.000	-
Bauzon	2009	12	1.985	7.000	0.275	1.000	1.000	-
Bel Etang	2009	9	3.194	7.000	0.471	0.705	0.827	0.901
Belin	2009	12	1.509	2.750	0.110	0.906	0.950	0
Delisle Sud	2010	12	1.593	2.750	0.127	1.000	1.000	-
Etang Cocoyer	2009	30	1.000	1.000	0.000	-	-	-
Fauvette Nord	2009	12	1.975	5.082	0.260	0.980	0.990	-
Fond Bertrand	2009	12	1.542	2.432	0.160	1.000	1.000	-
Gorot	2009	30	2.225	5.715	0.361	0.954	0.976	0.999
Grand Maison	2009	12	2.558	5.082	0.354	0.750	0.857	-
Kancel	2010	12	1.931	5.082	0.282	1.000	1.000	-
Lamarre	2009	11	1.000	1.000	0.000	-	-	-
Lebraire	2009	11	1.956	6.067	0.253	0.483	0.651	0.955
Loery Sud	2009	12	1.061	1.848	0.019	1.000	1.000	-
Mahaudière	2009	10	2.902	5.200	0.448	0.872	0.932	0.847
Malakoff	2009	12	2.104	6.045	0.344	0.864	0.927	0.999
Mam'mé	2009	12	2.598	6.682	0.377	0.862	0.926	-
Pavillon	2009	11	2.320	5.452	0.323	0.982	0.991	0.983
Pico	2009	12	2.363	6.682	0.369	0.944	0.971	0.793
Poucet	2009	10	1.413	4.733	0.114	1.000	1.000	-
Ravine Bellevue	2009	12	2.610	5.082	0.375	1.000	1.000	-
Ravine Favreau	2009	12	2.074	5.338	0.322	0.919	0.958	0.984
Sainte Marguerite Nord	2009	12	3.106	5.886	0.453	1.000	1.000	-
Sainte Rose Ouest	2009	12	2.113	6.205	0.308	0.848	0.918	0.992
Surgy nord	2009	32	1.925	3.136	0.321	1.000	1.000	-
Valet Est Est	2010	12	2.061	5.886	0.355	1.000	1.000	-
Zevallos Nord	2009	12	1.863	3.864	0.254	0.979	0.990	-

Table S5. Environmental and demographic variables of the 74 sites sampled in the analysis of genetic variation of the four snail species (see text and Table S2 for explanation of variables and Table S3 for sites). We report the mean values over the 2001-2007 period (year of the first genetic sample) for the size, vegetation cover and connectivity (variables estimated every year). Stability is the value on the first axis of a principal component analysis based on 2001-2007 data. Density of favourable habitats is estimated per site with no temporal variation. Invasion age refers to the time of first report of *P. acuta* per site (2007 situation). Invasion age is coded 1 (not or recently invaded by *P. acuta*) and 2 (invaded for more than two years). Note that long-term size is not reported here, since it is species-specific. Data are not available (-) for the two Basse-Terre (BT) sites (not surveyed) and for the Pointe des Chateaux where regular sampling was initiated in 2009.

Site	Size	Vegetation cover	Connectivity	Stability	Density fav. habitat	Invasion age (2007)
Alleaume Nord	1.374	0.869	0.000	-1.078	39	2
Balance	1.102	1.193	0.750	-1.519	50	2
Bamboche	1.409	0.986	1.250	-1.800	172	2
Bauzon	0.664	0.930	2.000	-0.659	40	2
Bazin	1.516	1.532	0.500	-2.016	75	1
Beaufond	1.151	1.383	0.000	-0.706	45	1
Beauplan	1.160	0.686	0.000	-1.251	34	1
Bel Etang	2.491	1.666	0.000	-1.809	107	1
Belin	1.726	1.229	0.000	-1.529	32	1
Blonval Nord	1.165	0.759	0.250	-0.863	103	2
Caraque Est	1.424	1.244	2.000	-2.022	50	2
Couronne Conchou	1.139	0.980	0.000	-0.461	24	2
Dadoud	1.452	1.798	0.000	-1.631	34	2
David	1.666	1.254	0.000	-1.862	28	1
Delisle Sud	1.546	1.601	0.500	-1.886	86	2
Desbonnes	1.153	0.174	0.000	-1.104	35	1
Descareaux	1.436	0.757	2.000	-1.678	40	2
Duteau	1.448	2.004	0.000	-1.245	58	1

Etang Bambou (MG)	2.183	1.009	0.250	-1.974	-	1
Etang Cocoyer	2.487	1.372	0.000	-1.748	77	2
Fauvette Nord	1.537	1.335	0.750	-0.778	14	1
Fond Bertrand	1.775	0.961	0.750	-2.110	27	2
Fond Rose	1.006	1.036	0.000	-0.369	36	1
Fond Thézan	1.489	1.101	0.250	-2.254	15	2
Gaschet	1.487	1.263	2.333	-1.041	25	2
Geffrier	0.934	1.221	2.000	-1.060	9	1
Gentilly Nord	1.959	1.393	0.000	-1.726	174	2
Girard	0.955	0.000	1.000	-0.887	50	2
Gorot	0.329	0.000	2.000	-1.265	51	2
Goudenave	1.276	0.572	1.750	-1.656	48	2
Grand Maison	1.554	2.003	1.000	-1.977	36	1
Grosse Roche	1.237	0.725	0.750	-1.337	34	1
Kancel	0.943	1.545	2.000	-0.845	33	2
L'Ecluse	2.196	0.958	0.000	-1.589	56	2
L'Henriette	1.154	1.562	0.000	-2.007	189	1
Lamarre	1.428	1.239	0.250	-1.785	37	2
Laroche Picard	1.290	1.295	0.000	-1.534	53	2
Lebraire	1.073	0.638	0.000	-1.331	25	1
Loery Sud	1.802	1.840	0.000	-1.694	144	2
Lubeth	1.690	1.525	0.500	-1.616	0	1
Mahaudiere	1.759	1.831	0.250	-1.849	27	2
Malakoff	1.433	1.584	0.500	-1.013	40	1
Mam'mé	2.439	1.660	0.000	-1.702	141	1
Dans Fond Prairie	1.404	0.920	2.000	0.004	2	1
Jacquot Prairie	1.794	0.648	2.000	-1.269	65	2
Medaille	0.973	1.379	1.500	-0.925	48	2

Montmain	2.358	1.490	0.250	-1.585	31	2
Moulin Belcourt	0.929	0.213	2.250	-1.463	145	2
Neron	2.109	0.746	0.000	-1.803	39	1
Pavillon	1.862	1.292	1.000	-1.503	82	2
Pico	1.615	1.964	0.750	-1.237	48	1
Pistolet	1.970	1.512	0.500	-1.649	27	1
Pointe des Chateaux	-	-	-	-	-	-
Port Blanc	0.989	0.850	0.000	-1.176	39	1
Porte d'Enfer du Moule	1.407	0.876	0.000	-0.729	37	2
Porte Enfer Vigie	1.138	1.043	0.000	-0.130	14	2
Poucet	0.842	1.488	2.750	-2.017	13	2
Ravine Bellevue	0.806	0.894	2.250	-1.582	37	2
Ravine Favreau	0.690	1.464	2.500	-1.796	99	2
Rav. Grand Bassin (MG)	0.884	0.687	2.000	-1.255	17	2
Ravine mon Chéri (Pont de Caraque)	0.744	1.738	2.500	-2.127	37	2
Ravine Vinty (BT)	-	-	-	-	-	-
Rejoui Nord	1.491	1.291	2.000	-1.838	77	2
Saint Jacques	1.154	1.097	1.000	-1.498	41	1
Sainte Marguerite Nord	1.573	1.609	1.000	-1.763	117	2
Sainte Rose (BT)	-	-	-	-	-	-
Sainte Rose Ouest	2.022	1.234	0.000	-1.637	117	2
Senneville	1.294	1.510	0.000	-1.379	40	1
Surgy nord	2.144	1.503	0.000	-1.884	90	2
Terrasson	1.556	1.442	2.000	-1.484	38	2
Titon	2.005	1.686	2.250	-1.402	13	2
Valet Est	1.328	0.650	1.500	-1.115	36	1
Valet Est Est	1.377	1.529	1.000	-0.917	40	2
Zevallos Nord	1.288	0.238	0.333	-1.170	87	2

Table S6. Effect of environmental parameters on extinction and colonization rates at metapopulation scale in the four species studied. These results were obtained from the same long-term survey than the one used in the present study (Pantel et al. submitted). Dubart et al. (2019), using a slightly different dataset (less sites and more years) conducted analyses in *P. acuta* and *A. marmorata*, and reported the same results, except for the effect of vegetation on extinction (no effect) and on colonization (positive effect) in *P. acuta*. Tests were not performed in cells highlighted in yellow (for example, extinction is not supposed to be affected by connectivity). The effect of long-term size and invasion age were not tested in these studies.

Species	Rate	Size	Vegetation	Connectivity	Stability	DFH
<i>P. acuta</i>	Extinction		<0			
	Colonization	>0	>0	>0		
<i>A. marmorata</i>	Extinction		<0			
	Colonization					
<i>D. depressissimum</i>	Extinction		<0			
	Colonization	>0			<0	
<i>D. surinamense</i>	Extinction		<0			
	Colonization	>0	>0		<0	<0

Table S7. (provided as a separate Excel table) Estimates of pairwise F_{ST} among populations in the four species studied (below the diagonal) and P -values (using Fisher's method for combining single-locus tests) of the associated exact tests on population structure (above the diagonal) returned by GENEPOP. "Highly sign." is returned by GENEPOP when one single-locus test at least has a $P = 0$ probability. Significant F_{ST} values are given in bold italics. Color codes are used for F_{ST} values to facilitate reading (as the range of F_{ST} differs among species, the bound values of each color also differs; see species sheets). Results in *D. depressissimum* are a copy of Table S4 from Lamy et al. (2012). More on populations of the four species in Tables S2 and S3.

Table S8. Comparison of environmental and demographic variables between time periods (central column) and between sites sampled for genetic analysis and all sites (right column). The first comparison is between Period 1 (2001-2007) and Period 2 (2008-2015) and includes the 74 sites in which at least one species was genotyped. Density of favourable habitats is a site-specific variable, and invasion is necessarily related between time periods (a site invaded in the first period is also considered invaded in the second one). We report R^2 between time periods with its 95% confidence interval, and the associate t-value with its degree of freedom and P-value. The second comparison is between these 74 sites and the remaining 170 sites from Grande-Terre. We report R^2 between population groups, and the result of linear models (F -value with its degrees of freedom and P -value). For the only significant difference (stability), the genotyped populations were more stable than the others. Long-term size is not considered at all as it is a species-specific variable.

Variable	Genotyped populations Period 1 vs. period 2	Genotyped populations vs. all other populations
Size	0.818 (0.722 / 0.882) 11.822 / 69 / $2*10^{-16}$	-0.003 0.311, 1 & 242, 0.577
Vegetation cover	0.661 (0.505 / 0.775) 7.314 / 69 / $4*10^{-10}$	0.004 2.109, 1 & 242, 0.147
Connectivity	0.907 (0.854 / 0.941) 17.902 / 69 / $< 2*10^{-16}$	-0.004 0.003, 1 & 242, 0.953
Stability	0.658 (0.501 / 0.772) 7.257 / 69 / $5*10^{-10}$	0.0457 12.64, 1 & 242, $4*10^{-4}$
Density fav. habitats	-	0.009 3.302, 1 & 242, 0.070
Invasion age	-	-0.003 0.314, 1 & 219, 0.575

Table S9. Correlations among environmental and population variables in all genotyped populations (N = 74; in the four species). The variables are size, vegetation cover, connectivity, stability, density of favourable habitats (DFH) and invasion age per site. For each pair of variables, we report the correlation coefficient (1st line), its 95% confidence interval (2nd line), and the *t*-test and *P*-values (3rd line) evaluating whether the correlation coefficient differs from zero. *P*-values below 0.05 are in bold characters. Long-term size is not considered here as it is a species-specific variable. Note that stability (values on the first axis of a principal component analysis) is ranked from very unstable to very stable.

	Size	Vegetation	Connectivity	Stability	DFH	Invasion age
Size						
Vegetation	0.378 (0.159 / 0.562) 3.400 / 0.001					
Connectivity	-0.445 (-0.614 / -0.236) -4.135 / 9.8 * 10 ⁻⁵	-0.120 (-0.344 / 0.115) -1.012 / 0.315				
Stability	0.336 (-0.146 / -0.552) 3.271 / 0.002	0.309 (-0.081 / -0.506) 2.698 / 0.009	0.003 (-0.230 / 0.236) 0.027 / 0.978			
DFH	0.219 (-0.016 / 0.432) 1.856 / 0.068	0.087 (-0.150 / 0.316) 0.726 / 0.470	-0.157 (-0.378 / 0.080) -1.319 / 0.191	0.330 (-0.103 / -0.524) 2.886 / 0.005		
Invasion age	-0.098 (-0.324 / 0.138) -0.821 / 0.414	-0.103 (-0.328 / 0.133) -0.861 / 0.392	0.341 (0.117 / 0.532) 3.018 / 0.004	0.103 (-0.133 / -0.329) 0.863 / 0.391	0.161 (-0.077 / 0.381) 1.348 / 0.182	

Table S10. Correlations among genetic indicators in the four species studied. The variables describes genetic diversity within populations (R_A , R_G , and H_E ; R_G was estimated in the two selfing species only) and population differentiation (F_{ST}). For each pair of variables, we report the correlation coefficient (1st line), its 95% confidence interval (2nd line), and the t -test, degree of freedom, and P -values (3rd line) evaluating whether the correlation coefficient differs from zero. Note that all P -values lies largely below 0.05.

	F_{ST} vs. R_A	F_{ST} vs. R_G	F_{ST} vs. H_E
<i>Physa acuta</i>	-0.962 (-0.984 / -0.907) -15.381 / 19 / 3×10^{-13}	-	-0.939 (-0.975 / -0.854) -11.94 / 19 / 3×10^{-10}
<i>Aplexa marmorata</i>	-0.916 -0.954 / -0.849 -14.633 / 41 / $< 2.2 \times 10^{-16}$	-0.734 (-0.847 / -0.556) -6.922 / 41 / 2×10^{-8}	-0.721 (-0.839 / -0.536) -6.659 / 41 / 5×10^{-8}
<i>Drepanotrema depressissimum</i>	-0.953 -0.979 / -0.896 -15.244 / 23 / 2×10^{-13}	-	-0.953 -0.979 / -0.895 -15.146 / 23 / 2×10^{-13}
<i>Drepanotrema surinamense</i>	-0.982 -0.992 / -0.961 -26.431 / 25 / $< 2.2 \times 10^{-16}$	-0.825 -0.917 / -0.648 -7.305 / 25 / $< 10^{-7}$	-0.885 -0.946 / -0.762 -9.539 / 25 / 8×10^{-10}

Table S11. Effect of environmental and demographic variables on genetic diversity and differentiation in the four species studied. Results of linear models with **A.** R_A ; **B.** R_G (in selfing species only); **C.** F_{ST} . We proceeded in two steps to avoid a too large number of variables, first considering all five environmental variables (size, vegetation cover, connectivity, stability and density of favourable habitats), and we report the intercept, Akaike information criterion (AIC), adjusted- R^2 and P -value for the best model. For each significant variable, we report the effect size and associated P -value. In a second step long-term population size and invasion age were then evaluated alone, and we indicate the effect size and model AIC for significant effects. The AIC value should be compared to that of the best model mentioned above. In situations in which we found a significant effect on either long-term size or invasion age, we also tested models with all significant variables (results below the Table). - indicates no effect.

A. R_A

Variable	<i>Physa acuta</i>	<i>Aplexa marmorata</i>	<i>Drepanotrema depressissimum</i>	<i>Drepanotrema surinamense</i>
Intercept	3.170	1.168	7.661	1.580
AIC	32.0	42.4	90.9	55.5
adjR ² / P	-0.063 / 0.590	0.025 / 0.320	0.339 / 0.017	-0.082 / 0.729
Size	-	-	-	-
Vegetation cover	-	-	-	-
Connectivity	- ^a	0.173 / 0.029	1.134 / 0.007	-
Stability	-	-	-	-
Density of favorable habitats	-	-	-	-
Long-term population size	-	-	- ^c	-
Invasion age	-	-0.3 / 38.2 ^b	-	-

^a The associated P -value is 0.080

^b The model including connectivity and age (no significant interaction) has an AIC of 31.5

^c The model including connectivity and long-term size (no significant interaction) has an AIC of 86.8

B. R_G (in selfing species only)

Variable	<i>Aplexa marmorata</i>	<i>Drepanotrema surinamense</i>
Intercept	3.701	4.992
AIC	173.5	116.2
adjR ² / P	0.173 / 0.023	0.027 / 0.344
Size	-	-
Vegetation cover	-	-
Connectivity	1.193 / 0.002	-
Stability	-	-
Density of favorable habitats	-	-
Long-term population size	-	-
Invasion age	-1.38 / 168.5 ^a	- ^b

^a The model including connectivity, size and invasion age (no significant interaction) has an AIC of 164.9

^b The model including invasion age has an AIC of 113.2 (the effect is slightly significant and the associated P -value is 0.060)

C. F_{ST}

Variable	<i>Physa acuta</i>	<i>Aplexa marmorata</i>	<i>Drepanotrema depressissimum</i>	<i>Drepanotrema surinamense</i>
Intercept	-0.141	~0	-0.106	~0
AIC	57.8	125.1	57.5	86.5
adjR ² / P	0.049 / 0.049	0.098 / 0.115	0.362 / 0.019	-0.104 / 0.765
Size	-	-	-	-
Vegetation cover	-	-	-0.42 / 0.022	-
Connectivity	-	-0.42 / 0.022	-0.41 / 0.029	-
Stability	-	-	-	-
Density of favorable habitats	-	-	-	-
Long-term population size	-	0.27 / 123.5 ^a	-0.37 / 61.3 ^b	-
Invasion age	-	-	-	-

^a The model including connectivity and size (no significant interaction) has an AIC of 119.1

^b Long-term size is no more significant in a model with vegetation cover and connectivity (both remains significant)

Figure S1. Spatial distribution of environmental factors in Grande-Terre of Guadeloupe. A. Site site (log-transformed). B. Connectivity.

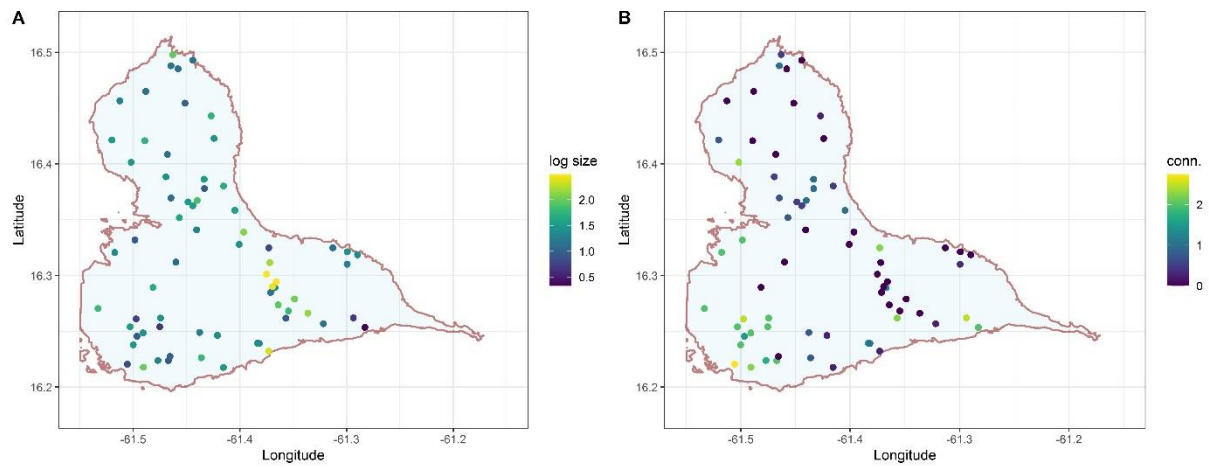
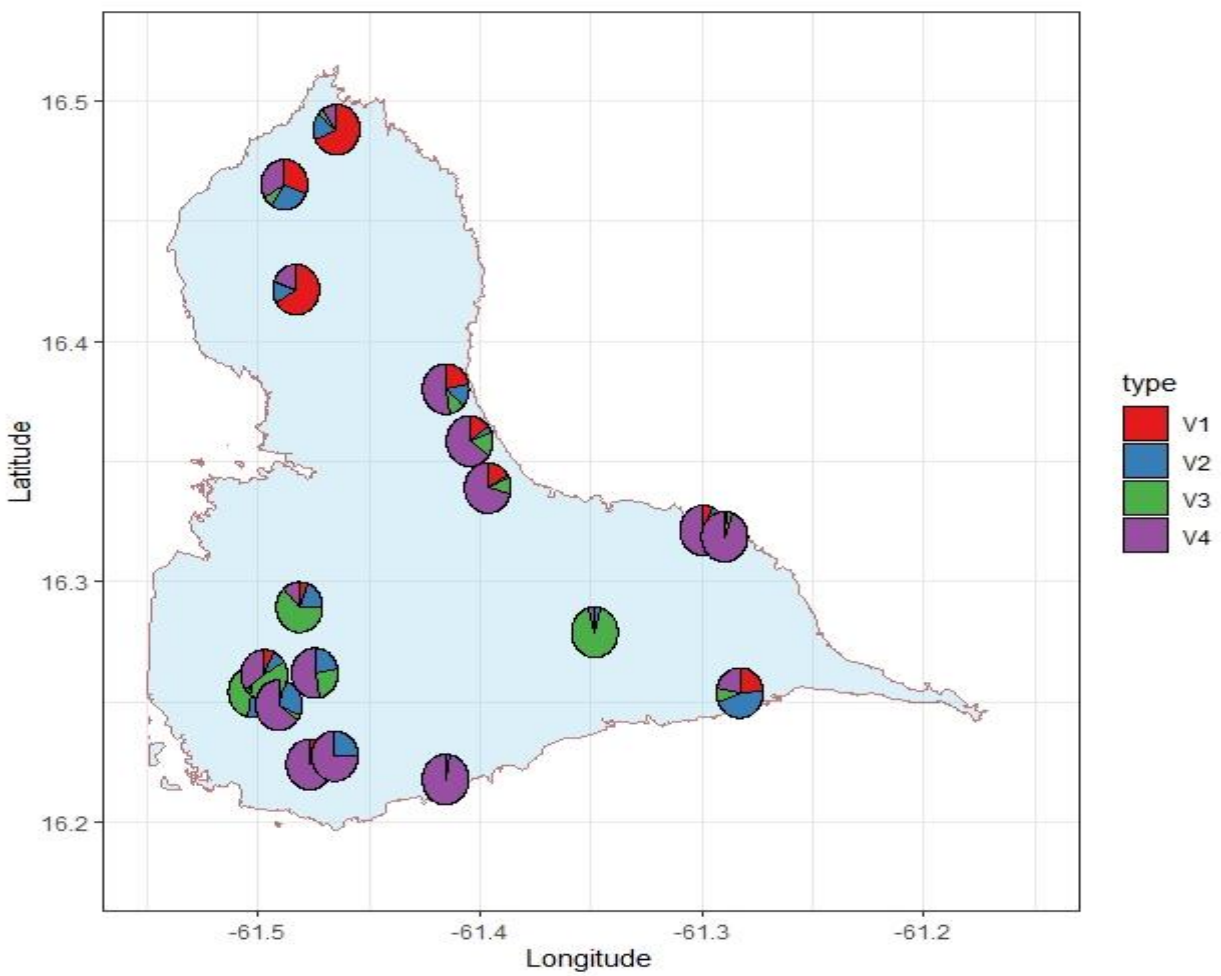
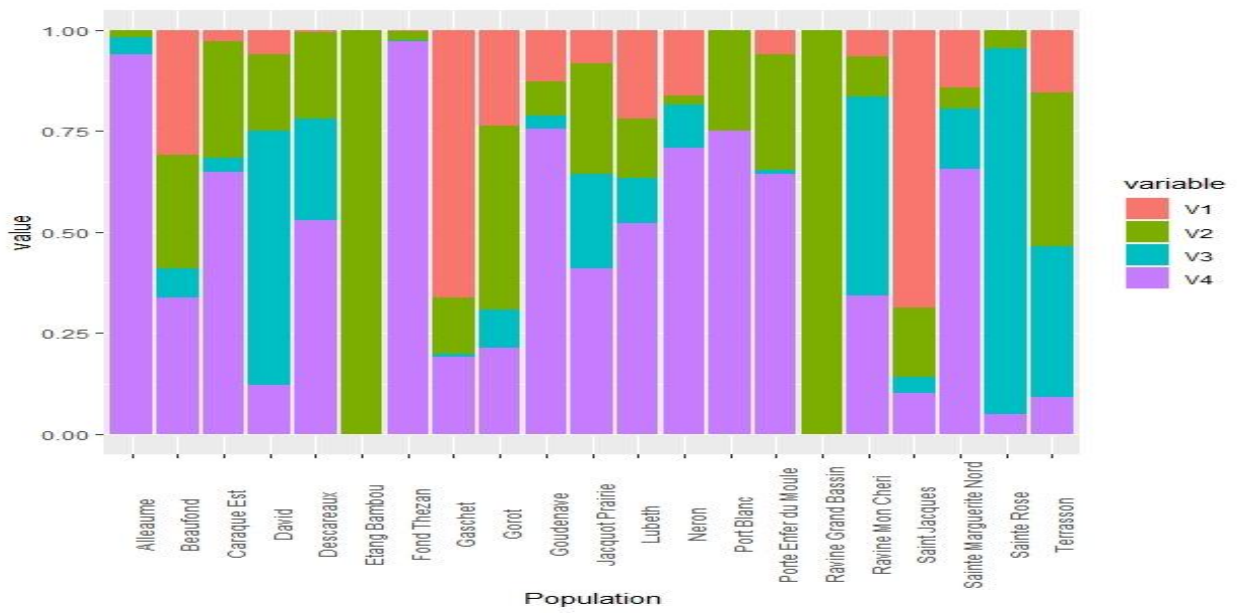
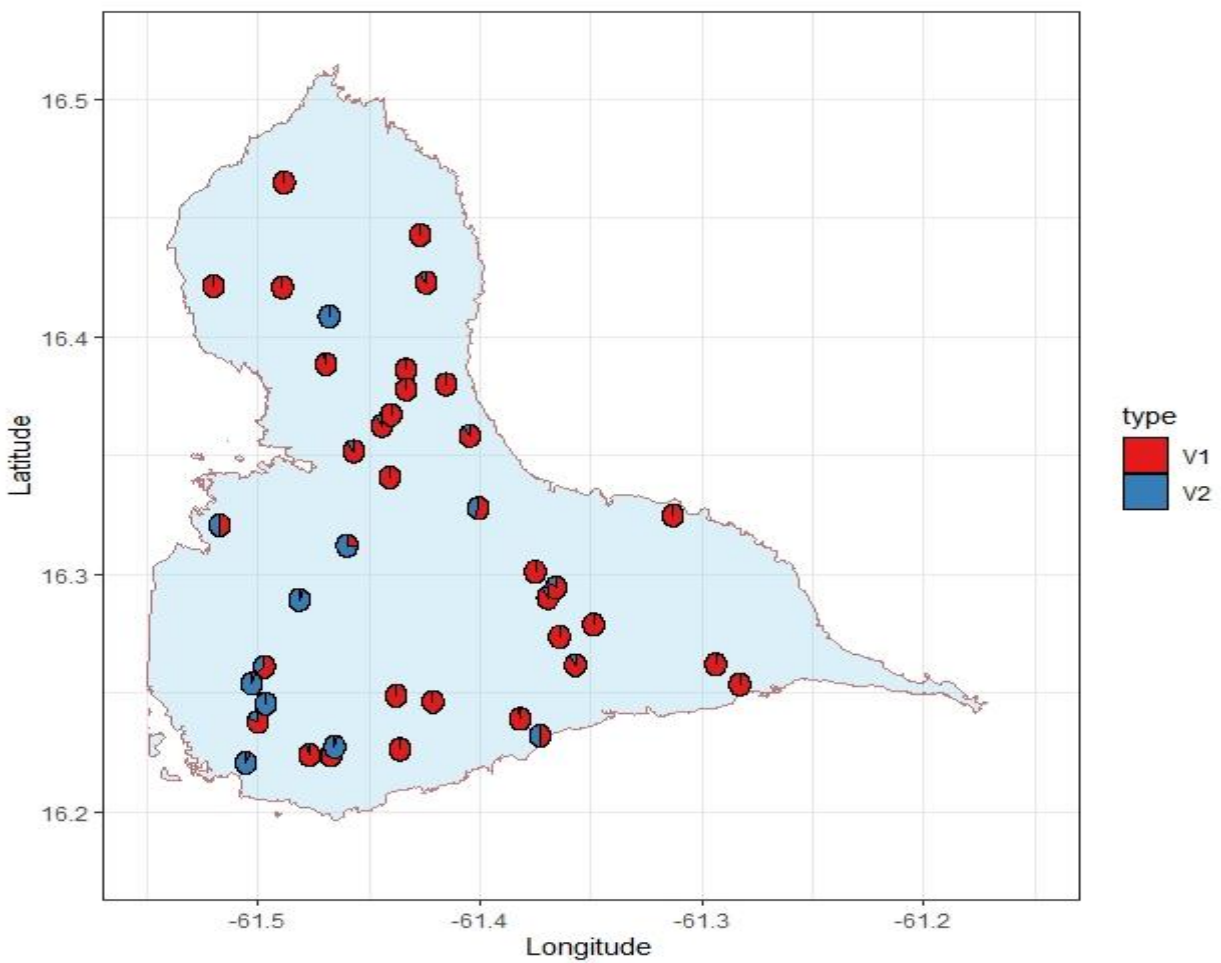
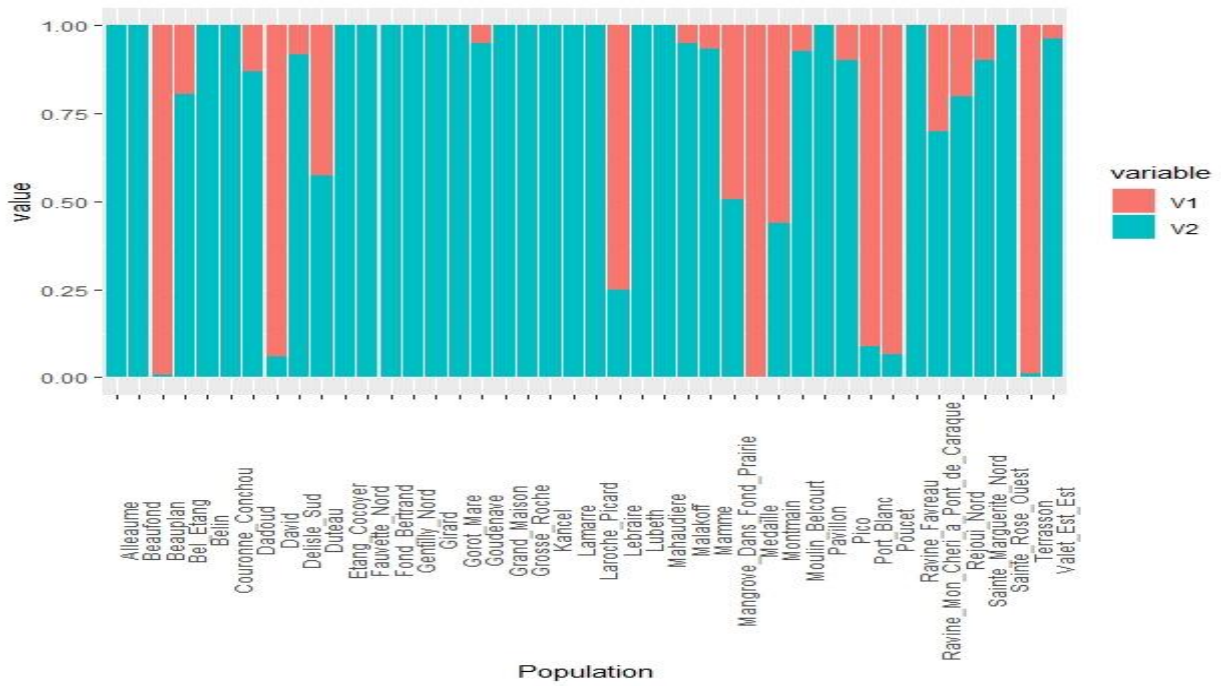


Figure S2. Mean ancestry per population derived from the sNMF approach. The upper figure indicates mean ancestry per cluster inferred by sNMF (V_i) and per population and the lower figure gives the same information in a geographical perspective (pie-chart plotted on the Grande-Terre map). A. *Physa acuta*. B. *Aplexa marmorata*. C. *Drepanotrema surinamense*. No results are reported in *Drepanotrema depressissimum*, since we failed to detect any clustering. The populations from Marie-Galante and Basse-Terre are not represented.

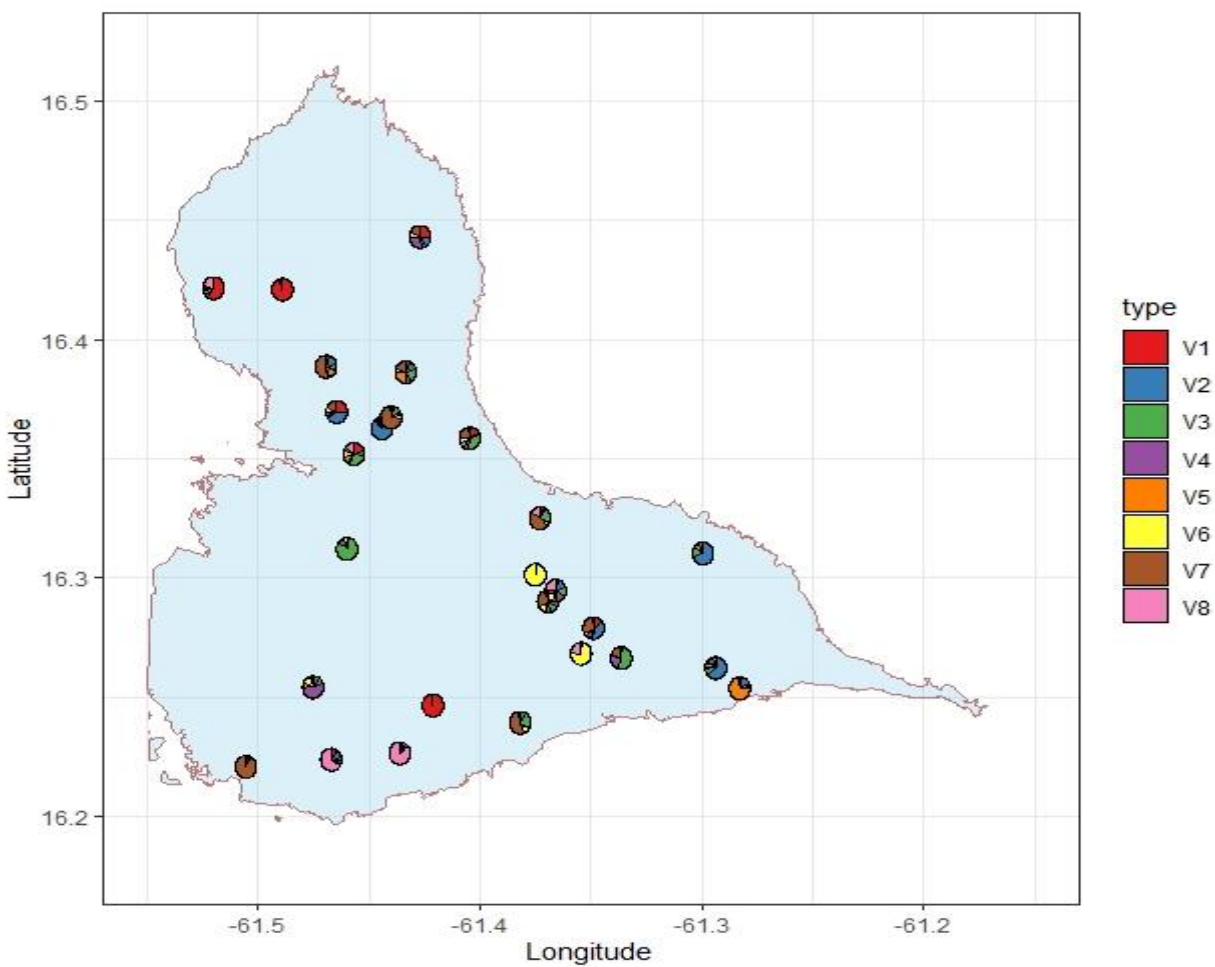
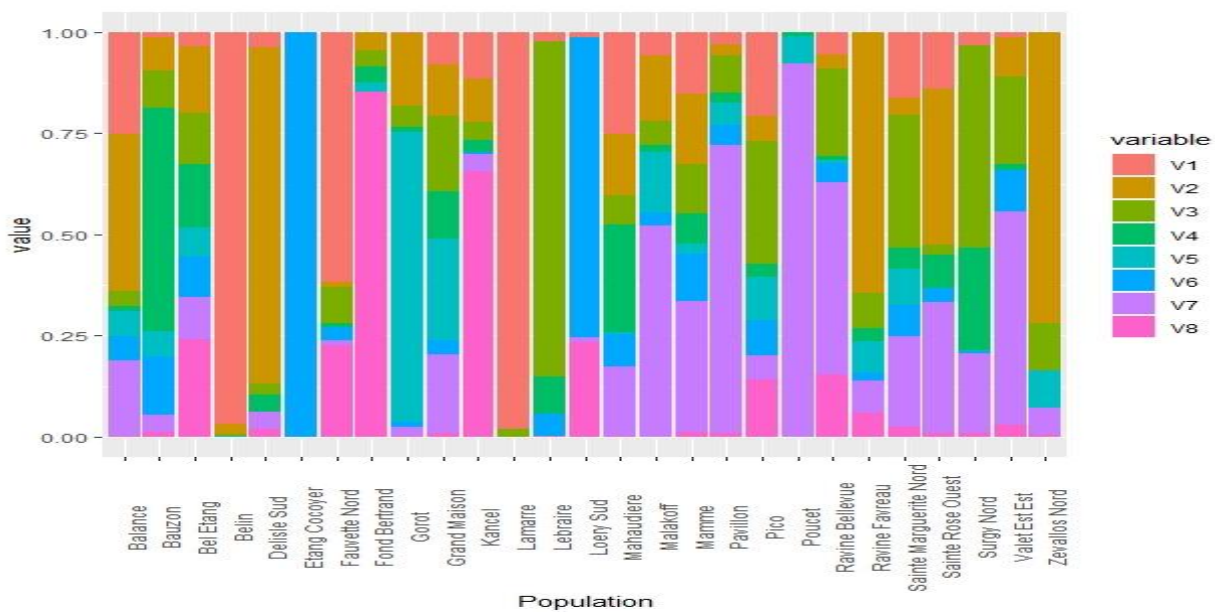
A. (*Physa acuta*)



B. (*Aplexa marmorata*)



C. (Drepanotrema surinamense)



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