Supplementary materials – Lamy et al. Testing metapopulation dynamics using genetic, demographic and ecological data.

Paragraph S1. Types of population structure and associated predictions

Paragraph S2. Different measures and associated equations used in the main text

Table S3. Polymorphism at the ten microsatellite loci studied in *Drepanotrema depressissimum*.

Table S4. Population codes used in Table S5 and S6.

Table S5. Wright's inbreeding coefficient F_{IS}, f, estimated following Weir and Cockerham (1984), per sampling year and locus.

Table S6. Estimates of pairwise F_{ST}, θ, calculated following Weir & Cockerham (1984) for the 25 populations of *Drepanotrema depressissimum* included in the spatial analysis.

Table S7. Estimates of pairwise F_{ST}, θ, calculated following Weir & Cockerham (1984) for the 12 populations (29 samples) of *Drepanotrema depressissimum* included in the temporal analysis.

Paragraph S1. Types of population structure and associated predictions

The metapopulation model is one among several models which have been proposed to describe the structure of natural populations. Historically, the first (and still extremely influential) model of fragmented population was Wright's island model (Wright 1931). In its simplest version, it assumes that all populations have identical and constant size (N) and immigration rate (m), and that immigrants come from independent, randomly drawn populations. This model is both symmetrical (all populations are similar) and spatially-implicit (migration is independent of distance). These two assumptions can be relaxed for the sake of realism. Relaxing the symmetry assumption leads to a model with islands differing with respect to N and / or m (which will be referred to as the asymmetrical island model), while relaxing the assumption of distance-independent migration leads to spatially-explicit models (such as lattice or stepping-stone models; Kimura & Weiss (1964)). These extensions of the island model have metapopulation equivalents when local extinction and colonization events are added. Extinction-colonization cycles introduce a new source of asymmetry among populations, i.e. an age structure determined by the distribution of the time to the last extinction event (Slatkin 1977). These models are of course idealizations, and intermediate models might well be the rule in natural habitats, for example a mix of populations undergoing (or not) extinction / colonization cycles. In practice this means that the question is not to identify which is the "right" model for a given system, but rather which one is the best approximation.

We here assume that several sources of information are available: (i) spatial and temporal data on genetic structure (neutral markers); (ii) ecological information on habitat patch characteristics (e.g., size or connectivity) and history (e.g., perturbation events expected to coincide with population extinction); (iii) demographical information on population

characteristics (e.g., population density or size) and history (e.g., time to the most recent demographic crash).

The spatial distribution of genetic diversity is the first criterion that can be used to contrast models (Table 1). In Wright's symmetric island model, the genetic diversity (H_e), averaged over loci, is expected to be identical in all populations and average F_{ST} should be constant across population pairs (equal to $1 / (1+4Nm)$; where N stand for population size and m stand for immigration rate, Wright (1931)). When the symmetry assumption is not met (i.e. in an asymmetric island model or in a metapopulation), H_e and F_{ST} are expected to differ among populations (Table 1). Average H_e and F_{ST} may also differ from those expected under the symmetric island model, and are sensitive to extinction-colonization cycles (Slatkin 1977). However they depend on parameters which often are beyond our grasp, such as effective sizes, the number of founders during colonization or their relatedness (Wade & McCauley 1988; Whitlock & McCauley 1990). Thus, obtaining precise quantitative expectations is usually impossible. Ecological and demographical information can then be used to qualitatively infer the most important sources of variation, as follows. Under the asymmetric island model, estimates of size of populations and habitat patches, as well as habitat connectivity, should explain a significant part of the variation in H_e and F_{ST}. This may, or not, be true under a metapopulation model, but in addition correlates of extinction rates, such as estimates of habitat / population instability (perturbations and demographic crashes), should also influence H_e and F_{ST} (Table 1). Similarly, estimates of population age (e.g., most recent apparent extinction) or habitat age (most recent perturbation), if available, should correlate positively with diversity and negatively with differentiation in a metapopulation (Whitlock 1992b). This property has been the basis of most genetic tests of the metapopulation concept so far (Whitlock 1992a; McCauley *et al.* 1995; Giles & Goudet 1997; Ingvarsson *et al.* 1997;

Haag *et al.* 2005): younger populations tend to exhibit less diversity and more differentiation than older ones.

We have up to now considered spatially-implicit models, i.e. with no form of isolation by distance. In spatially-explicit models, whatever the underlying dynamics (island or metapopulation), F_{ST} between two sites is also expected to increase with distance (Rousset 1997; Table 1). The extent to which variation in F_{ST} depends on distance *versus* on local diversity (H_e) reflects the relative importance of distance-limited dispersal *versus* asymmetry in patch characteristics (size, connectivity, age) in generating spatial genetic differentiation.

Temporal genetic data can also be used to infer the forces acting on genetic diversity. This approach has been widely taken for inferring population effective size, N_e, in supposedly isolated populations (see review in Luikart *et al.* 2010), more rarely to infer N_e and m in structured populations (Wang & Whitlock 2003). They can also be used to detect signatures of extinction and recolonization (Table 1). If an extinction, followed by immigrant colonization, occurs between two temporal samples at a given site, none of the genes in the second sample (*S2*) comes from the local gene pool (*S1*). This genetic resetting has several consequences: (i) genetic diversity should decrease, as a consequence of the founder effect (Nei *et al.* 1975); (ii) F_{ST} between temporal samples (temporal F_{ST}) should become as high as or even higher than that between two populations; (iii) estimates of N_e and m obtained using Wang and Whitlock's (2003) method, based on the (asymmetrical) island model, should provide very small N_e estimates and / or very high m; (iv) genetic resetting effect should be detectable directly using genetic assignment techniques (Berry *et al.* 2004): the most likely source population for *S2* individuals among sampled populations should not be the *S1* population more often than expected by chance. Alternatively, if *S1* is assigned as the most likely origin of some individuals, extinction has probably not occurred between the two

4

samples. Of course, only a fraction of sites in a metapopulation is expected to undergo extinction and colonisation at a given time. Genetic data could therefore be confronted to demographic and ecological data to evaluate whether apparent population extinctions and / or habitat perturbation indeed result in genetic resetting.

References

Berry O, Tocher MD, Sarre SD (2004). Can assignment tests measure dispersal? *Molecular Ecology*, **13**, 551–561.

Giles BE, Goudet J (1997) Genetic Differentiation in *Silene dioica* Metapopulations: Estimation of Spatiotemporal Effects in a Successional Plant Species. *The American Naturalist*, **149**, 507-526.

Haag CR, Riek M, Hottinger JW, Pajunen VI, Ebert D (2005) Genetic diversity and genetic differentiation in Daphnia metapopulations with subpopulations of known age. *Genetics*, **170**, 1809-1820.

Ingvarsson PK, Olsson K, Ericson L (1997) Extinction-recolonization dynamics in the mycophagous beetle *Phalacrus substriatus. Evolution,* **51**, 187-195.

Kimura M, Weiss G (1964) The stepping-stone model of population structure and the decrease of genetic correlation with distance. *Genetics*, **49**, 561-576.

Luikart G, Ryman N, Tallmon DA, Schwartz MK, Allendorf FW (2010) Estimation of census and effective population sizes: the increasing usefulness of DNA-based approaches. *Conservation Genetics*, **11**, 355-373.

McCauley DE, Raveill J, Antonovics J (1995) Local founding events as determinants of genetic structure in a plant metapopulation. *Heredity*, **75**, 630–636.

Nei M, Maruyama T, Chakraborty R (1975) The bottleneck effect and genetic variability in populations. *Evolution*, **29**, 1–10.

Slatkin M (1977). Gene flow and genetic drift in a species subject to frequent local extinctions. *Theoretical Population Biology*, **12**, 253-262.

Wade MJ, McCauley DE (1988) Extinction and recolonization: their effects on the genetic differentiation of local populations. *Evolution*, **42**, 995–1005.

Wang J, Whitlock MC (2003). Estimating effective population size and migration rates from genetic samples over space and time. *Genetics*, **163**, 429-446.

Whitlock MC (1992a) Nonequilibrium population-structure in forked fungus beetles: extinction, colonization, and the genetic variance among populations. *The American Naturalist*, **139**, 952-970.

Whitlock MC (1992b) Temporal fluctuations in demographic parameters and the genetic variance among populations. *Evolution*, **46**, 608–615.

Whitlock MC, McCauley DE (1990) Some population genetic consequences of colony formation and extinction: genetic correlations within founding groups. *Evolution*, **44**, 1717–1724.

Wright S (1931) Evolution in Mendelian populations. *Genetics*, **16**, 97-159.

Paragraph S2. Different measures and associated equations used in the main text

Allelic richness (Petit *et al.* 1998)

Allelic richness, R_A, is the number of different alleles found when g genes (the specified sample size) are sampled at a locus. If a total of N ($N > g$) genes are examined at this locus, the expected number of different alleles in a sample of g genes may be obtained by the formula:

$$R_A = \sum_i \left[1 - \binom{N - N_i}{g} \middle/ \binom{N}{g} \right]$$

where N_i represents the number of occurrences of the ith allele among the N sampled genes.

Gene diversity (H_e, corrected for small sample size; Nei 1987)

Gene diversity per locus and population is estimated using an unbiased estimator (Nei 1987):

$$H_{sk} = \frac{n_k}{n_k - 1} \left(1 - \sum_i p_{ik}^2 - \frac{H_{ok}}{2n_k} \right)$$

where n_k is the size of sample k, p_{ik} the frequency of allele A_i in sample k and H_{ok} the observed proportion of heterozygotes in sample k. Mean Gene diversity H_e per population is then computed as the arithmetic mean over all loci.

Weir & Cockerham (1984) estimate θ of Wright's F_{ST}

This parameter is estimated for each locus and overall based on the different variance components, σ_a^2 (the among sample variance component), σ_b^2 (the between individual within sample component) and σ_w^2 (the within individual component). θ is defined as follow:

$$\theta = \frac{\sigma_a^2}{\sigma_a^2 + \sigma_b^2 + \sigma_w^2}$$

where variance components σ_a^2, σ_b^2 and σ_w^2 are estimated for one allele at a locus as:

$$\sigma_a^2 = \frac{\frac{\sum_k n_k (p_k - \bar{p})^2}{np - 1} - \frac{\sum_k n_k \bar{p}(1 - \bar{p}) - 1/4 \sum_k n_k H_{ok} - \sum_k n_k (p_k - \bar{p})^2}{\sum_k n_k - np}}{\frac{1}{np - 1}\left(\sum_k n_k - \frac{\sum_k n_k^2}{\sum_k n_k}\right)}$$

$$\sigma_b^2 = \frac{\sum_k n_k \bar{p}(1 - \bar{p}) - 1/4 \sum_k n_k H_{ok} - \sum_k n_k (p_k - \bar{p})^2}{\sum_k n_k - np} - \frac{1/4 \sum_k n_k H_{ok}}{\sum_k n_k}$$

$$\sigma_w^2 = \frac{1/2 \sum_k n_k H_{ok}}{\sum_k n_k}$$

with n_k is the size of sample k, np the number of samples, H_{ok} the proportion of individuals carrying the allele that are heterozygous, p_k its frequency in sample k and $\bar{p}$ its overall weighted frequency. Expression for each locus and over all loci are obtained by summing over alleles and loci respectively. In this method allele frequencies are weighted according to sample sizes.

Population-specific F_{ST} using GESTE (Foll and Gaggiotti 2006)

The model underlying the estimation of population-specific F_{ST} in GESTE considered a collection of J populations that evolved in isolation after splitting from an ancestral population. The derived populations may have been subject to different amounts of genetic

drift and, therefore, their allele frequencies will show different degrees of differentiation from the ancestral allele frequency. The extent of differentiation between population j and the ancestral population is measured by F_{ST}^j and is the result of its demographic history. A set of I loci is considered and K_i is the number of alleles at the ith locus. $p_i = \{p_{ik}\}$ denote the allele frequencies of the ancestral population at locus i, where p_{ik} is the frequency of the allele k at locus i. $p = \{p_i\}$ denote the entire set of allele frequencies of the ancestral population and $\widetilde{p_{ij}} = \{\widetilde{p_{ijk}}\}$ denote the current allele frequencies at locus i for subpopulation j. Under these assumptions, the allele frequencies at locus i in populations j follow a Dirichlet distribution with parameters $\theta_j p_i$,

$$\widetilde{p_{ij}} \sim Dir(\theta_j p_{i1}, \dots, \theta_j p_{iK_i})$$

Where

$$\theta_j = \frac{1}{F_{ST}^j} - 1$$

F_{ST}^j is very closely related to Wright F_{ST} parameter and can be interpreted as a measure of the shared ancestry within populations.

References

Foll M, Gaggiotti O (2006) Identifying the environmental factors that determine the genetic structure of populations. *Genetics*, **174**, 875-891.

Nei M (1987) *Molecular Evolutionary Genetics*. Columbia University Press.

Petit RJ, El Mousadik A, Pons O (1998). Identifying populations for conservation on the basis of genetic markers. *Conservation Biology*, **12,** 844–855.

Weir B, Cockerham C (1984) Estimating F-statistics for the analysis of population structure. *Evolution*, **38**, 1358–1370.

Wright S (1938). Size of population and breeding structure in relation to evolution. *Science*, **87,** 430-431.

Table S3. Polymorphism at the ten microsatellite loci studied in *Drepanotrema depressissimum*. They were characterized in three PCR multiplex. T is the annealing temperature. Size range gives the size (in base pairs) of the smallest and largest alleles. N is the total number of alleles.

Locus	Multiplex	T	Size range	N
DDE16	1	57	156 - 260	29
DDE04	1	57	215 - 368	44
DDE09	1	57	235 - 395	46
DDE12	2	57	223 - 355	42
DDE22	2	57	215 - 364	49
DDE20	3	60	187 - 284	28
DDE06	3	60	155 - 185	21
DDE14	3	60	253 - 324	18
DDE23	3	60	197 - 492	45
DDE03	3	60	230 - 368	50

Table S4. Population codes used in Table S5 and S6. Year indicates the sampling year.

Site	Year	Code
Pico	2006	PICO2006
	2007	PICO2007
	2009	PICO2009
Grosse Roche	2006	ROC2006
	2007	ROC2007
Senneville	2006	SEN2006
	2007	SEN2007
Valet Est	2006	VEE2006
	2007	VEE2007
	2008	VEE2008
Geffrier	2006	GEF2006
	2007	GEF2007
	2008	GEF2008
	2009	GEF2009
Réjoui Nord	2006	REJ2006
	2007	REJ2007
	2008	REJ2008
L'Ecluse	2006	ECL2006
	2009	ECL2009
Couronne Conchou	2006	COU2006
	2009	COU2009
Fond Rose	2009	FDR09
	2011	FDR11
Mahaudière	2009	MAH09
	2011	MAH11
Pistolet	2009	PIS09
	2011	PIS11
Porte Enfer Vigie	2009	PEV2009
	2011	PEV11
Blonval Nord	2009	BLON2009
Poucet	2009	POU2009
Desbonnes	2009	DESB2009
Bamboche	2009	BAM2009
Bazin	2009	BAZ2009
L'Henriette	2009	HEN2009
Mammé	2009	MAM2009
Titon	2009	TIT2009
Delisle	2010	DEL2010
Pavillon	2009	PAV2009
Saint Jacques	2010	STJ2010

Kancel	2010	KAN2010
Pointe des Châteaux	2009	PTC2009

Table S5. Wright's inbreeding coefficient F_{IS}, *f*, estimated following Weir and Cockerham (1984), per sampling year and locus. Significant values are shown in bold ($P < 0.05$). Significance was assessed using a permutation method.

pop/year	DDE16	DDE04	DDE09	DDE12	DDE22	DDE20	DDE06	DDE14	DDE23	DDE03
PICO2006	0.097	-0.003	-0.033	0.071	-0.036	0.057	-0.043	0.050	**0.205**	0.024
PICO2007	0.091	-0.029	-0.043	0.069	0.052	-0.085	**0.092**	-	0.065	-0.016
PICO2009	-0.080	0.030	**0.038**	-0.059	0.014	**0.161**	0.018	0.164	-0.019	-0.011
ROC2006	-0.004	0.020	-0.042	0.103	-0.029	-0.022	-0.045	0.030	0.019	-0.011
ROC2007	-0.002	0.031	**-0.031**	-0.041	0.068	0.033	-0.044	-	0.072	0.028
SEN2006	-0.019	-0.034	0.021	0.046	0.043	-0.023	-0.036	-0.078	0.079	-0.060
SEN2007	0.063	0.060	0.011	-0.020	-0.040	-0.050	0.077	**0.104**	**0.114**	0.136
VEE2006	0.036	0.054	0.071	0.038	0.137	-0.001	-0.030	0.003	0.030	**-0.005**
VEE2007	-0.070	**0.104**	**0.150**	0.010	-0.012	0.151	-0.097	-0.090	0.179	0.048
VEE2008	-0.087	-0.031	0.107	0.009	0.097	0.141	-0.021	-0.089	0.041	-0.029
GEF2006	-0.110	0.012	-0.081	-0.086	-0.048	0.084	-0.173	0.073	-0.014	-0.069
GEF2007	0.027	**0.149**	-0.035	0.042	0.010	-0.029	0.055	0.078	0.088	-0.002
GEF2008	-0.123	-0.075	**0.136**	0.004	-0.046	-0.012	-0.033	0.054	0.036	0.036
GEF2009	0.020	-0.030	-0.025	**0.052**	-0.045	-0.036	-0.053	**0.219**	0.062	-0.034
REJ2006	0.097	0.027	-0.055	-0.054	-0.014	0.059	-0.037	0.009	0.108	**0.152**
REJ2007	-0.001	-0.047	0.080	0.044	-0.015	0.012	0.092	0.075	0.121	0.001
REJ2008	**0.197**	0.020	0.034	-0.049	0.009	0.031	0.039	0.004	-0.062	-0.044
ECL2006	-0.030	0.008	0.042	**0.081**	0.013	-0.020	-0.024	-0.004	0.175	-0.019
ECL2009	0.043	0.032	**0.131**	0.043	0.007	0.006	0.100	0.164	0.142	-0.048
COU2006	-0.108	-0.015	-0.046	-0.046	-0.001	0.044	-0.011	-0.105	0.092	-0.016
COU2009	**0.159**	-0.069	-0.054	0.105	0.037	0.035	-0.109	-0.069	0.016	0.182
FDR09	0.110	-0.019	-0.041	0.105	0.078	-0.155	-0.132	-0.047	0.098	-0.058
FDR11	0.041	0.011	-0.035	0.046	**0.035**	0.070	-0.117	0.099	-0.049	0.031
MAH09	-0.068	**0.112**	**0.128**	**0.057**	-0.006	0.077	0.043	**0.169**	**0.384**	-0.030

MAH11	**0.288**	-0.062	0.027	0.029	0.065	0.073	-0.087	**0.150**	0.198	**0.194**
PIS09	0.011	**0.063**	-0.071	0.012	-0.006	0.022	**0.246**	0.049	**0.319**	0.008
PIS11	0.143	0.086	0.099	-0.038	-0.016	0.025	0.118	0.032	0.163	-0.011
PEV2009	0.054	0.005	-0.038	0.020	0.032	0.056	-0.123	-0.070	0.152	-0.054
PEV11	0.021	0.066	-0.118	-0.017	-0.034	-0.049	-0.011	0.054	-0.064	0.008
BLON2009	-0.050	0.130	0.038	0.002	0.021	0.056	0.038	0.071	0.121	-0.015
POU2009	-0.054	0.029	0.083	-0.014	0.054	0.020	-0.082	0.012	0.134	-0.067
DESB2009	0.072	0.075	0.068	0.018	-0.050	**0.254**	**0.241**	-0.101	**0.268**	0.073
BAM2009	-0.002	0.024	**0.075**	0.018	-0.041	-0.034	0.009	0.040	**0.558**	0.049
BAZ2009	0.058	0.047	0.074	0.066	0.163	0.049	-0.050	**0.045**	0.015	0.045
HEN2009	0.034	-0.021	0.028	-0.081	-0.084	0.138	**0.406**	-0.099	0.025	-0.040
MAM2009	-0.073	-0.035	-0.021	0.020	**0.024**	0.028	-0.056	0.072	**0.251**	0.009
TIT2009	0.006	0.005	-0.013	0.050	0.018	-0.002	0.196	-0.092	0.045	0.003
DEL2010	0.112	0.069	0.040	0.074	0.134	-0.041	0.059	**0.407**	-0.015	0.098
PAV2009	0.051	-0.043	-0.016	0.026	-0.038	0.002	0.041	0.121	**0.021**	0.045
STJ2010	0.091	-0.064	0.059	-0.024	0.018	**0.098**	0.173	0.042	0.067	-0.018
KAN2010	-0.094	0.091	**0.017**	-0.037	0.015	-0.003	0.058	0.136	0.050	0.071
PTC2009	**-0.065**	**0.047**	0.119	**0.081**	-0.132	**0.064**	0.094	0.070	0.066	0.165

Table S6. Estimates of pairwise F_{ST}, θ, calculated following Weir & Cockerham (1984) for the 25 populations of *Drepanotrema depressissimum* included in the spatial analysis. All values are significant ($P < 0.001$). Significance was assessed using exact tests (Raymond & Rousset 1995).

	PICO2009	ROC2007	SEN2007	VEE2008	GEF2009	REJ2008	ECL2009	COU2009	FDR09	MAH09	PIS09	PEV2009	BLON2009	POU2009
ROC2007	0.073													
SEN2007	0.047	0.054												
VEE2008	0.051	0.067	0.041											
GEF2009	0.041	0.08	0.049	0.059										
REJ2008	0.028	0.043	0.021	0.024	0.031									
ECL2009	0.047	0.07	0.034	0.043	0.052	0.025								
COU2009	0.05	0.071	0.049	0.055	0.051	0.028	0.051							
FDR09	0.057	0.076	0.043	0.053	0.053	0.033	0.052	0.066						
MAH09	0.054	0.065	0.04	0.052	0.044	0.028	0.034	0.054	0.056					
PIS09	0.081	0.08	0.044	0.069	0.081	0.046	0.056	0.083	0.056	0.06				
PEV2009	0.06	0.101	0.067	0.088	0.05	0.053	0.065	0.074	0.078	0.056	0.107			
BLON2009	0.048	0.066	0.054	0.045	0.052	0.027	0.045	0.045	0.066	0.042	0.08	0.068		
POU2009	0.039	0.063	0.03	0.045	0.033	0.015	0.028	0.044	0.048	0.035	0.065	0.051	0.038	
DESB2009	0.117	0.135	0.098	0.115	0.125	0.089	0.115	0.132	0.091	0.093	0.102	0.139	0.124	0.101
BAM2009	0.075	0.073	0.041	0.065	0.065	0.04	0.056	0.07	0.059	0.06	0.069	0.098	0.075	0.058
BAZ2009	0.031	0.048	0.035	0.044	0.038	0.017	0.036	0.046	0.043	0.043	0.059	0.065	0.045	0.029
HEN2009	0.095	0.106	0.077	0.092	0.093	0.074	0.077	0.094	0.095	0.075	0.11	0.111	0.079	0.08
MAM2009	0.03	0.067	0.04	0.048	0.033	0.024	0.039	0.04	0.053	0.046	0.073	0.055	0.042	0.03
TIT2009	0.035	0.051	0.036	0.04	0.031	0.019	0.04	0.041	0.044	0.046	0.066	0.063	0.045	0.025
DEL2010	0.059	0.077	0.059	0.053	0.06	0.032	0.058	0.064	0.064	0.065	0.081	0.09	0.065	0.048
PAV2009	0.03	0.051	0.025	0.031	0.029	0.006	0.028	0.033	0.034	0.029	0.044	0.058	0.035	0.018

STJ2010	0.031	0.063	0.029	0.041	0.023	0.017	0.037	0.044	0.038	0.027	0.047	0.045	0.039	0.025
KAN2010	0.041	0.08	0.042	0.043	0.042	0.028	0.038	0.047	0.05	0.044	0.064	0.06	0.044	0.031
PTC2009	0.102	0.12	0.108	0.123	0.116	0.094	0.1	0.115	0.131	0.119	0.121	0.14	0.119	0.1

	DESB2009	BAM2009	BAZ2009	HEN2009	MAM2009	TIT2009	DEL2010	PAV2009	STJ2010	KAN2010
BAM2009	0.119									
BAZ2009	0.097	0.059								
HEN2009	0.149	0.09	0.087							
MAM2009	0.102	0.06	0.031	0.086						
TIT2009	0.117	0.054	0.034	0.082	0.03					
DEL2010	0.109	0.076	0.041	0.103	0.05	0.057				
PAV2009	0.094	0.043	0.019	0.078	0.023	0.023	0.038			
STJ2010	0.098	0.054	0.028	0.076	0.028	0.029	0.049	0.019		
KAN2010	0.11	0.063	0.037	0.082	0.032	0.037	0.053	0.028	0.035	
PTC2009	0.191	0.127	0.106	0.162	0.105	0.1	0.114	0.097	0.103	0.113

References: Raymond M, Rousset F (1995) An exact test for population differentiation. *Evolution*, **49**, 1280-1283.

Table S7. Estimates of pairwise F_{ST}, θ, calculated following Weir & Cockerham (1984) for the 12 populations (29 samples) of *Drepanotrema depressissimum* included in the temporal analysis. Bold values indicate estimates that are not significant ($P > 0.05$; all other values had $P < 0.001$). Significance was assessed using exact tests (Raymond & Rousset 1995).

		Pico			Grosse Roche		Senneville		Valet Est			Geffrier			
		2006	2007	2009	2006	2007	2006	2007	2006	2007	2008	2006	2007	2008	2009
Pico	2006	0,000													
	2007	**-0.003**	0,000												
	2009	0.011	0.01	0,000											
Grosse Roche	2006	0.069	0.075	0.073	0,000										
	2007	0.073	0.077	0.073	**-0.005**	0,000									
Senneville	2006	0.052	0.05	0.047	0.053	0.055	0,000								
	2007	0.051	0.045	0.047	0.05	0.054	**0.002**	0,000							
Valet Est	2006	0.056	0.057	0.053	0.08	0.078	0.05	0.048	0,000						
	2007	0.063	0.065	0.059	0.073	0.07	0.05	0.049	**0,000**	0,000					
	2008	0.052	0.053	0.051	0.067	0.067	0.05	0.041	**-0.001**	**0.001**	0,000				
Geffrier	2006	0.044	0.04	0.042	0.067	0.071	0.04	0.042	0.048	0.048	0.048	0,000			
	2007	0.035	0.028	0.036	0.076	0.079	0.041	0.043	0.046	0.048	0.049	**0.001**	0,000		
	2008	0.039	0.035	0.036	0.06	0.064	0.036	0.034	0.042	0.044	0.044	**-0.002**	**0.002**	0,000	
	2009	0.041	0.038	0.041	0.077	0.08	0.048	0.049	0.053	0.057	0.059	0.011	**0.006**	0.008	0,000
Rejoui	2006	0.036	0.037	0.035	0.035	0.04	0.024	0.023	0.037	0.033	0.034	0.03	0.029	0.022	0.038
	2007	0.033	0.035	0.032	0.04	0.045	0.026	0.019	0.033	0.03	0.025	0.029	0.024	0.021	0.033
	2008	0.028	0.029	0.028	0.039	0.043	0.023	0.021	0.028	0.03	0.024	0.025	0.023	0.019	0.031

		0.045	0.046	0.038	0.072	0.076	0.049	0.041	0.055	0.057	0.047	0.039	0.035	0.034	0.042
Ecluse	*2006*	0.045	0.046	0.038	0.072	0.076	0.049	0.041	0.055	0.057	0.047	0.039	0.035	0.034	0.042
	2009	0.052	0.052	0.047	0.064	0.07	0.042	0.034	0.051	0.051	0.043	0.046	0.045	0.04	0.052
Couronne	*2006*	0.054	0.054	0.05	0.084	0.082	0.053	0.046	0.06	0.06	0.058	0.054	0.051	0.048	0.051
Conchou	*2009*	0.046	0.057	0.05	0.07	0.071	0.049	0.049	0.062	0.056	0.055	0.052	0.051	0.045	0.051
Fond Rose	*2009*	0.061	0.053	0.057	0.077	0.076	0.04	0.043	0.055	0.053	0.053	0.041	0.044	0.037	0.053
	2011	0.045	0.049	0.046	0.064	0.063	0.038	0.039	0.043	0.042	0.042	0.039	0.033	0.033	0.043
Mahaudière	*2009*	0.054	0.055	0.054	0.066	0.065	0.037	0.04	0.057	0.059	0.052	0.049	0.044	0.044	0.044
	2011	0.077	0.082	0.081	0.086	0.087	0.066	0.061	0.089	0.087	0.082	0.084	0.076	0.075	0.075
Pistolet	*2009*	0.079	0.086	0.081	0.076	0.08	0.049	0.044	0.075	0.066	0.069	0.063	0.071	0.062	0.081
	2011	0.069	0.078	0.071	0.059	0.063	0.044	0.039	0.063	0.052	0.057	0.055	0.063	0.051	0.072
Porte Enfer Vigie	*2009*	0.071	0.075	0.06	0.094	0.101	0.063	0.067	0.096	0.093	0.088	0.057	0.051	0.054	0.05
	2011	0.068	0.069	0.057	0.079	0.083	0.052	0.055	0.087	0.083	0.078	0.055	0.051	0.051	0.056

		Rejoui			*Ecluse*		*Couronne Conchou*		*Fond Rose*		*Mahaudière*		*Pistolet*		*Porte Enfer Vigie*	
		2006	*2007*	*2008*	*2006*	*2009*	*2006*	*2009*	*2009*	*2011*	*2009*	*2011*	*2009*	*2011*	*2009*	*2011*
Rejoui	*2006*	0,000														

	2007	**0.002**	0,000													
	2008	**0.002**	**-0.001**	0,000												
Ecluse	2006	0.031	0.03	0.029	0,000											
	2009	0.025	0.027	0.025	**0.001**	0,000										
Couronne Conchou	2006	0.044	0.042	0.035	0.039	0.05	0,000									
	2009	0.037	0.029	0.028	0.048	0.051	0.049	0,000								
Fond Rose	2009	0.031	0.033	0.033	0.054	0.052	0.063	0.066	0,000							
	2011	0.025	0.026	0.023	0.043	0.045	0.049	0.049	0.042	0,000						
Mahaudière	2009	0.025	0.024	0.028	0.039	0.034	0.064	0.054	0.056	0.044	0,000					
	2011	0.054	0.052	0.058	0.058	0.058	0.082	0.076	0.082	0.061	0.042	0,000				
Pistolet	2009	0.038	0.048	0.046	0.068	0.056	0.089	0.083	0.056	0.062	0.06	0.086	0,000			
	2011	0.026	0.035	0.035	0.058	0.048	0.076	0.069	0.048	0.05	0.053	0.074	**-0.001**	0,000		
Porte Enfer Vigie	2009	0.056	0.054	0.053	0.063	0.065	0.078	0.074	0.078	0.059	0.056	0.088	0.107	0.092	0,000	
	2011	0.048	0.047	0.047	0.06	0.057	0.078	0.068	0.07	0.063	0.054	0.085	0.086	0.074	0.012	0,000

References

Raymond M, Rousset F (1995) An exact test for population differentiation. *Evolution*, **49**, 1280-1283.