

Jacob, S., Laurent, E., Morel-Journel, T. and Schtickzelle, N. 2019. Fragmentation and the context-dependence of dispersal syndromes: matrix harshness modifies resident-disperser phenotypic differences in microcosms. – Oikos doi: 10.1111/oik.06857

Appendix 1

Table A1. Effects of matrix harshness on morphological, mobility and growth dispersal syndromes for each individual genotype. Underlined estimates and statistics in larger front size show overall differences between residents and dispersers (i.e. mean effects over the five genotypes measured separately), and results of contrasts within genotype are also provided. Significant differences are shown in bold.

	Control matrix					Harsh matrix				
	Estimate ± SE		df	T	P	Estimate ± SE		df	T	P
Cell size	-0.08	0.29	48	-0.28	0.784	0.15	0.30	48	0.48	0.633
D3	-0.13	0.32	40	-0.42	0.674	-0.21	0.35	40	-0.61	0.547
D4	-0.50	0.32	40	-1.56	0.125	0.34	0.35	40	0.98	0.331
D6	0.01	0.32	40	0.03	0.977	0.29	0.35	40	0.84	0.404
D13	-0.12	0.32	40	-0.38	0.709	0.38	0.35	40	1.10	0.279
D17	0.34	0.32	40	1.07	0.289	-0.08	0.35	40	-0.22	0.826
Cell elongation	0.72	0.22	48	3.30	0.002	1.31	0.24	48	5.45	<0.001
D3	0.75	0.42	40	1.79	0.081	1.66	0.42	40	3.99	<0.001
D4	0.68	0.42	40	1.63	0.111	1.40	0.42	40	3.38	0.002
D6	1.53	0.42	40	3.63	0.001	2.23	0.42	40	5.37	<0.001
D13	0.60	0.42	40	1.43	0.161	0.20	0.42	40	0.49	0.627
D17	0.06	0.42	40	0.13	0.896	1.04	0.42	40	2.51	0.016
Velocity	0.71	0.21	48	3.38	0.001	1.61	0.27	48	6.01	<0.001
D3	0.72	0.40	40	1.81	0.077	2.13	0.40	40	5.35	<0.001
D4	0.53	0.40	40	1.34	0.187	1.32	0.40	40	3.31	0.002
D6	1.17	0.40	40	2.93	0.006	1.57	0.40	40	3.94	<0.001
D13	0.34	0.40	40	0.85	0.401	2.15	0.40	40	5.41	<0.001
D17	0.78	0.40	40	1.97	0.056	0.88	0.40	40	2.21	0.033
Linearity	0.45	0.28	48	1.60	0.116	0.70	0.28	48	2.52	0.015
D3	0.95	0.43	40	2.20	0.034	2.12	0.44	40	4.79	<0.001
D4	0.05	0.43	40	0.11	0.915	0.24	0.44	40	0.55	0.587
D6	0.51	0.43	40	1.18	0.245	1.25	0.44	40	2.81	0.008
D13	0.21	0.43	40	0.49	0.625	0.20	0.44	40	0.46	0.650
D17	0.52	0.43	40	1.20	0.236	-0.31	0.44	40	-0.69	0.492
Growth rate	0.24	0.29	48	0.83	0.410	-0.03	0.29	48	-0.11	0.913
D3	0.50	0.20	40	2.44	0.019	-0.13	0.25	40	-0.53	0.602
D4	0.53	0.20	40	2.60	0.013	0.18	0.25	40	0.72	0.476
D6	-0.04	0.20	40	-0.20	0.847	0.06	0.25	40	0.25	0.803
D13	0.47	0.20	40	2.31	0.026	-0.10	0.25	40	-0.39	0.699
D17	-0.28	0.20	40	-1.37	0.178	-0.17	0.25	40	-0.70	0.488
Carrying capacity	0.28	0.32	48	0.90	0.375	0.05	0.29	48	0.17	0.867
D3	0.58	0.24	40	2.43	0.020	-0.18	0.26	40	-0.67	0.510
D4	0.53	0.24	40	2.22	0.032	0.39	0.26	40	1.48	0.148
D6	0.16	0.24	40	0.67	0.505	0.17	0.26	40	0.63	0.535
D13	0.48	0.24	40	2.01	0.051	-0.01	0.26	40	-0.01	0.996
D17	-0.31	0.24	40	-1.29	0.206	-0.13	0.26	40	-0.50	0.621

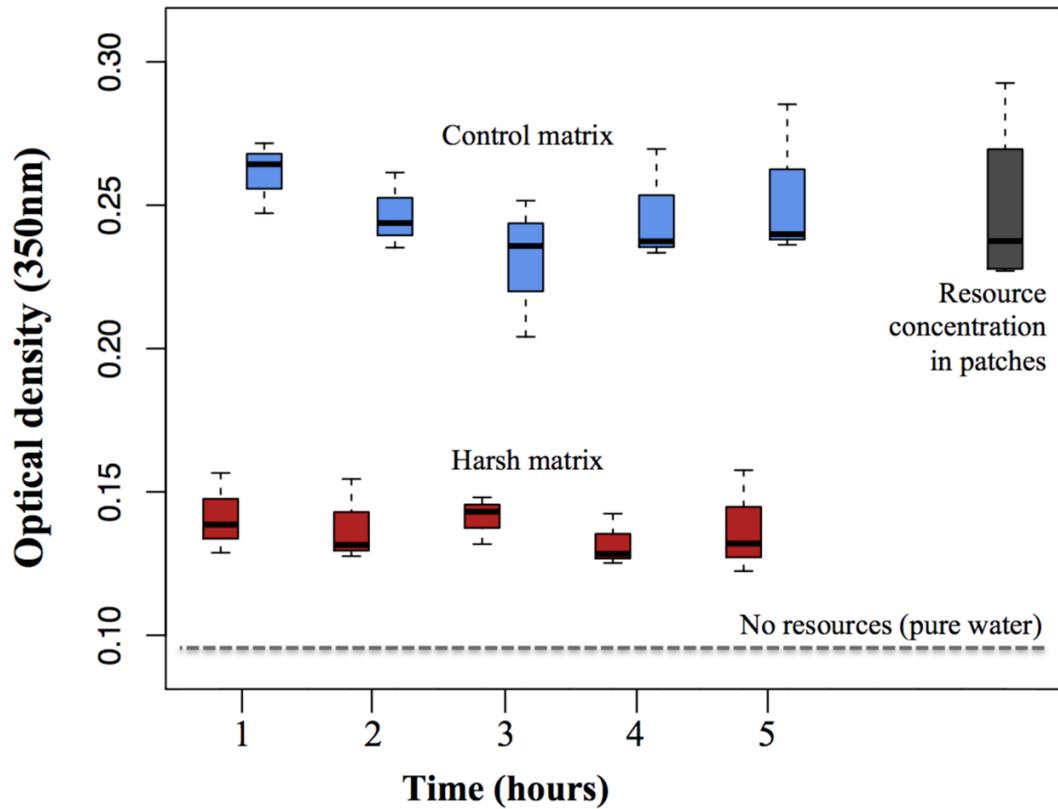


Figure A1. Optical density of liquid growth media in corridors as a function of time in control and harsh matrices in a pilot experiment with 30 dispersal systems (three per matrix treatment and time). Optical density at 350nm is an excellent predictor of resource concentration (Pearson correlation coefficient = 0.999; $t_{58} = 207.1$; $p < 0.001$). Resource concentration in control matrices (*blue*) did not significantly differ from resource concentration in habitat patches (grey; Estimate \pm SE = 0.001 ± 0.013 ; $t = 0.071$; $p = 0.944$). Harsh matrices (red) showed a significantly lower resource concentration compared to patches (0.111 ± 0.009 ; $t = 11.76$; $p < 0.001$) that did not change through time (-0.001 ± 0.002 ; $t = -0.628$; $p = 0.541$). Note that harsh matrices still contained some resources although initially filled only with water ($26.41 \pm 1.85\%$ (mean \pm SE) of resource concentration in patches), resulting from initial diffusion during manipulation.

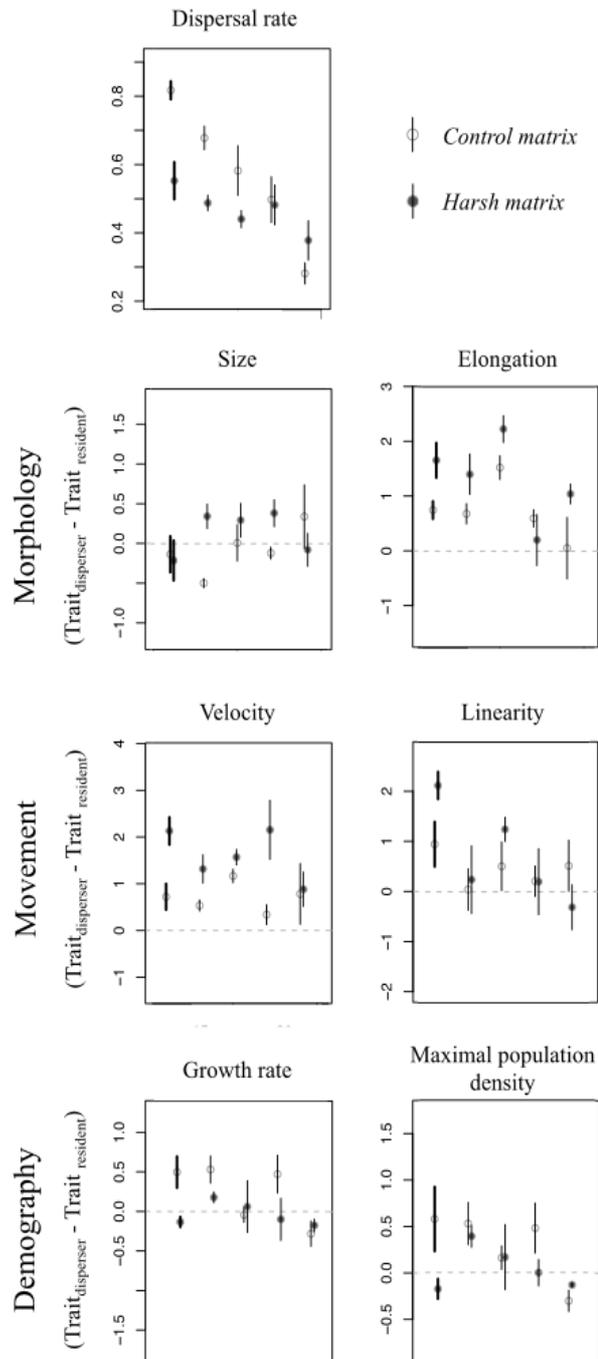


Figure A2. Effects of matrix harshness on dispersal rate and morphological, movement and demographic dispersal syndromes for each genotype in isogenic cultures (control matrix = grey dots; harsh matrix = black dots). Dispersal syndromes were computed as the difference of scaled trait values between dispersers and residents ($\text{Trait}_{\text{disperser}} - \text{Trait}_{\text{resident}}$). Mean \pm SE are shown.

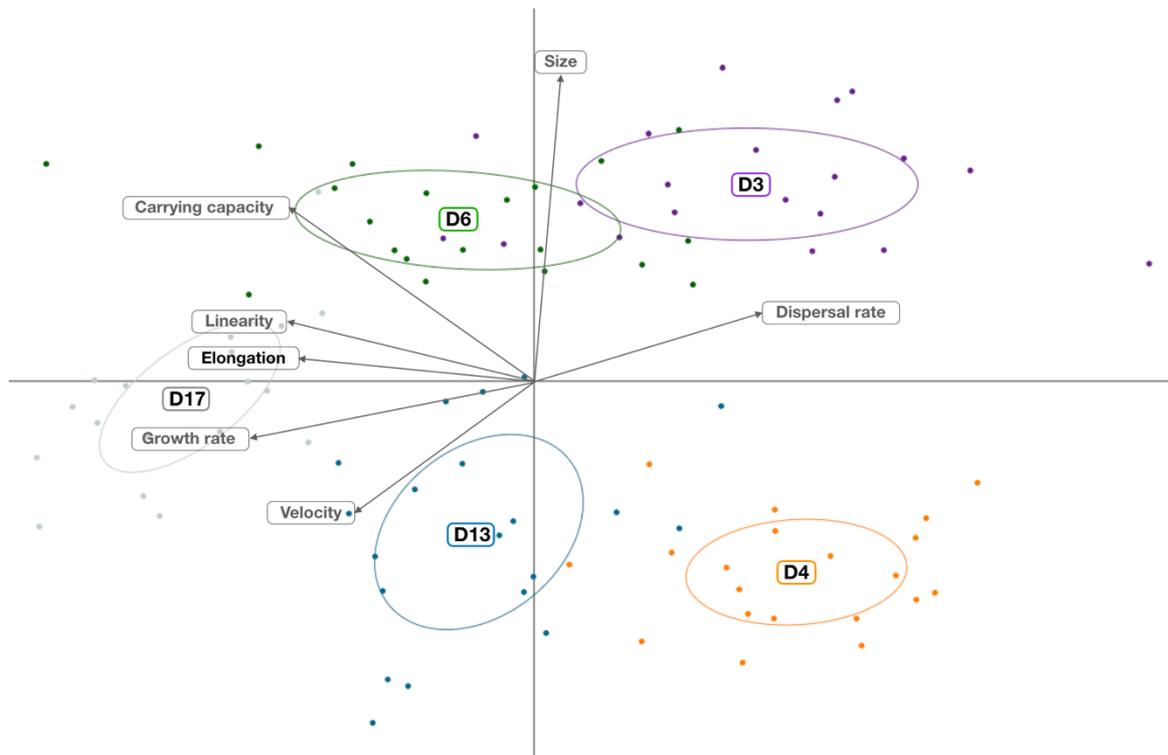


Figure A3. Illustration through a principal component analysis of differences among genotypes in the multiple dispersal-related traits quantified. Grey arrows show the contribution of traits to each axis of the principal component analysis. Genotypes are represented by differently coloured points and ellipses. Note that contrary to Fig. 1b, the present PCA include dispersal rate.