

Table S2. Population genetics analyses of *E. necatrix* sampled at hierarchal spatial scales in Aek Nauli (AEN)

1/ Genetic diversity statistics of *E. necatrix* isolates sampled at multiple hierarchal spatial scales in AEN

Population	N	MLG	eMLG	H	G	G _{max}	λ	E ₅	H _{exp}
One compartment	44	37	30.6±1.10	3.56	33.38	75.86	0.97	0.94	0.35
Different compartments	35	34	34±0.00	3.52	33.11	94.60	0.97	0.98	0.35
AEN total	79	70	33.3±1.11	4.21	64.34	81.44	0.98	0.95	0.35

N = number of individuals; MLG = number of multilocus genotypes observed; eMLG = number of estimated MLG based on smallest sample size calculated using rarefaction; H = Shannon-Wiener index; G = Stoddard and Taylor's index; G_{max} = maximum percentage of genotypic diversity; λ = Simpson's Index; E₅ = Pielou's evenness index; H_{exp} = Nei's unbiased gene diversity

2/ Mating type idiomorph frequencies and linkage disequilibrium tests of *E. necatrix* isolates sampled at multiple hierarchal spatial scales in AEN

Population	MAT1-1:MAT1-2 (p-value χ^2) ^a	Before clone correction		After clone correction	
		rBarD	p-value	rBarD	p-value
One compartment	20:24 (0.55)	0.002	0.295	-9.25E-06	0.496
Different compartments	17:18 (0.87)	0.026	0.029	0.021	0.072
AEN total	37:42(0.57)	-0.010	0.853	-0.010	0.858

^aPearson's chi-square goodness of fit test (χ^2) for the null hypothesis of 1:1 ratio for the occurrence of the two *MAT1* idiomorphs in sexually reproducing populations, with p > 0.05 indicates that null hypothesis was not rejected.

rBarD = the standardised index of association

3/Analysis of molecular variance (AMOVA) of SSR data for *E. necatrix* isolates sampled at multiple hierarchal spatial scales in AEN

	Degrees of freedom	Sum of squares	Mean squares	Estimate of variance	Total variation (%)	Phi	p-value
Between one compartment and different compartments	1	3.13	3.13	-0.05	-1.05	-0.01	0.878
Within hierarchal sampling levels	77	403.88	5.25	5.25	101.05		