The following supplements accompany the article

Understanding population dynamics of a numerically dominant species at hydrothermal vents: a matrix modeling approach

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Supplement 1. Estimation of stage survivorship

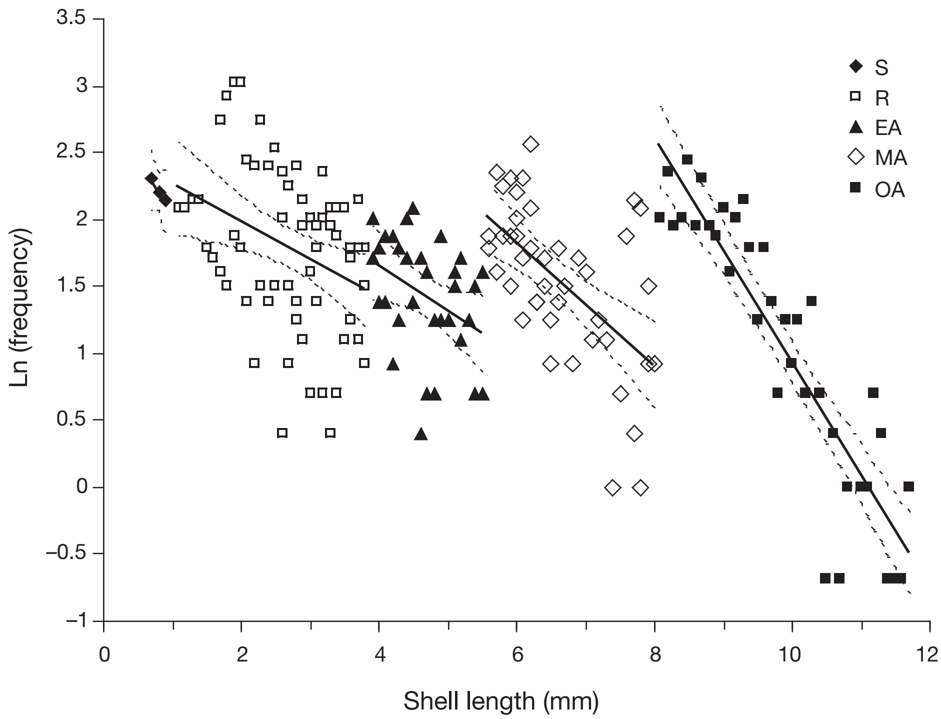

Fig. S1. Linear regressions of ln(N) versus shell length (SL, mm) (±95% CI) for female *Lepetodrilus fucensis* in 5 stage classes: settler (S), ln(N) = −0.810SL + 2.86, r^2 = 0.97, p = 0.108; recruit (R), ln(N) = −0.280SL + 2.54, r^2 = 0.12, p < 0.01; early adult (EA), ln(N) = −0.332SL + 2.97, r^2 = 0.14, p < 0.05; mature adult (MA), ln(N) = −0.455SL + 4.55, r^2 = 0.33, p < 0.001; and old adult (OA), ln(N) = −0.842SL + 9.37, r^2 = 0.81, p < 0.001. N: no. of female L. fucensis. Data are displayed as points rather than bars for clarity. The slope of the regression line for each stage was used as an estimate of mortality over that stage (z_i) (see 'Materials and methods: Matrix model')

Supplement 2. Life-history parameters and population projection matrices for *Lepetodrilus fucensis*

Table S1. *Lepetodrilus fucensis*. Five-stage life-history parameters. Stage duration is given for 3 scenarios of individual growth: slow, intermediate and fast. S: settler: R: recruit: EA: early adult: MA: mature adult: OA: old adult

Stage class		Stage survivorship (σ_i)	Stage duration (mo) (d_i) Slow	Intermediate	Fast	Mean no. of female eggs per adult female (m_i)
1	S	0.4437	3.51	1.75	1.17	0
2	R	0.7555	9.79	4.89	3.26	0
3	EA	0.7175	5.93	2.96	1.98	25.00
4	MA	0.6346	8.74	4.37	2.91	150.4
5	OA	0.4307	13.68	6.84	4.56	998.3

Table S2. *Lepetodrilus fucensis*. Five-stage population projection matrix **A** for 3 individual growth rate scenarios (slow, intermediate and fast) and corresponding population growth rate λ (mo^{-1})

Slow growth (λ = 0.9406)				
0.4054	0	16.64	84.74	475.7
0.03829	0.7310	0	0	0
0	0.02452	0.6615	0	0
0	0	0.05604	0.6245	0
0	0	0	0.01014	0.4307
Intermediate growth (λ = 1.234)				
0.2853	0	19.72	91.67	475.5
0.1584	0.7077	0	0	0
0	0.04780	0.5877	0	0
0	0	0.1298	0.5999	0
0	0	0	0.03470	0.4301
Fast growth (λ = 1.579)				
0.1114	0	23.85	102.1	474.7
0.3323	0.6737	0	0	0
0	0.08180	0.4889	0	0
0	0	0.2286	0.5631	0
0	0	0	0.07150	0.4276

Table S3. Stable stage distribution (**w**) and reproductive value (**v**) for the projection matrices generated under 3 different individual growth rate scenarios (slow, intermediate and fast) shown in Table S2. S: settler: R: recruit: EA: early adult: MA: mature adult: OA: old adult

Stage class		Stable stage distribution (%) Slow	Intermediate	Fast	Reproductive value Slow	Intermediate	Fast
1	S	83.22	75.31	71.39	1	1	1
2	R	15.20	22.66	26.18	14.0	6.0	4.4
3	EA	1.34	1.67	1.96	119.5	66.0	49.0
4	MA	0.24	0.34	0.44	298.0	176.9	129.4
5	OA	<0.01	0.01	0.03	932.9	591.4	411.9

Table S4. Changes to the stable stage distribution (**w**) (%), generated under 3 different individual growth rate scenarios (slow, intermediate and fast), due to a decrease in larval survival probability ($\sigma_1{}^{1/2}$) by 50 and 99.5%. Stable stage distribution for basic population projection matrices are given in Table S3. S: settler: R: recruit: EA: early adult: MA: mature adult: OA: old adult

Stage class		–50%			–99.5%		
		Slow	Intermediate	Fast	Slow	Intermediate	Fast
1	S	79.65	71.37	67.39	35.26	31.85	29.80
2	R	17.77	25.47	28.94	29.93	34.81	35.86
3	EA	2.11	2.50	2.84	18.60	16.20	15.56
4	MA	0.46	0.62	0.77	14.48	13.66	13.75
5	OA	0.01	0.03	0.06	1.73	3.48	5.03

Supplement 3. Uncertainty analysis

An uncertainty analysis was conducted to assess the amount of variation in the model predictions of λ, given the sampling variation observed in the parameters (stage survivorship, stage duration, and mean no. of female eggs per adult female, σ_i, d_i, and m_i respectively), by running 2000 Monte Carlo simulations of the model for each individual growth rate (slow, intermediate and fast). At the beginning of each simulation, a value for each parameter was randomly selected from its corresponding distribution. For σ_i and d_i, we used a normal distribution generated from the mean and standard error of each parameter estimate. For m_i, we used a uniform distribution between upper and lower values, which were generated from the 95% confidence interval limits in the actual fecundity–shell length relationship (see 'Materials and methods: Matrix model') at the mid-point shell length of each stage. We used the percentile method of Manly (1997) to calculate the 95% confidence interval of the output of the Monte Carlo simulation.

The broad and overlapping 95% confidence intervals around the predictions of λ for all 3 individual growth rates (slow: λ = 0.94, 95% CI = 0.75 to 1.73; intermediate: λ = 1.23, 95% CI = 0.72 to 1.60; fast: λ = 1.58, 95% CI = 0.72 to 1.72) are a result of the uncertainty associated with the parameter estimates, particularly for d_i. This relatively high level of uncertainty in the basic model predictions of λ suggests caution in interpreting the longer term predictions of our model.

LITERATURE CITED

Manly BFJ (1997) Randomization, bootstrap and Monte Carlo methods in biology, 2nd edn. Chapman & Hall/CRC, New York, NY, p 39–44

Supplement 4. Length-frequency distributions for established *Lepetodrilus fucensis* populations

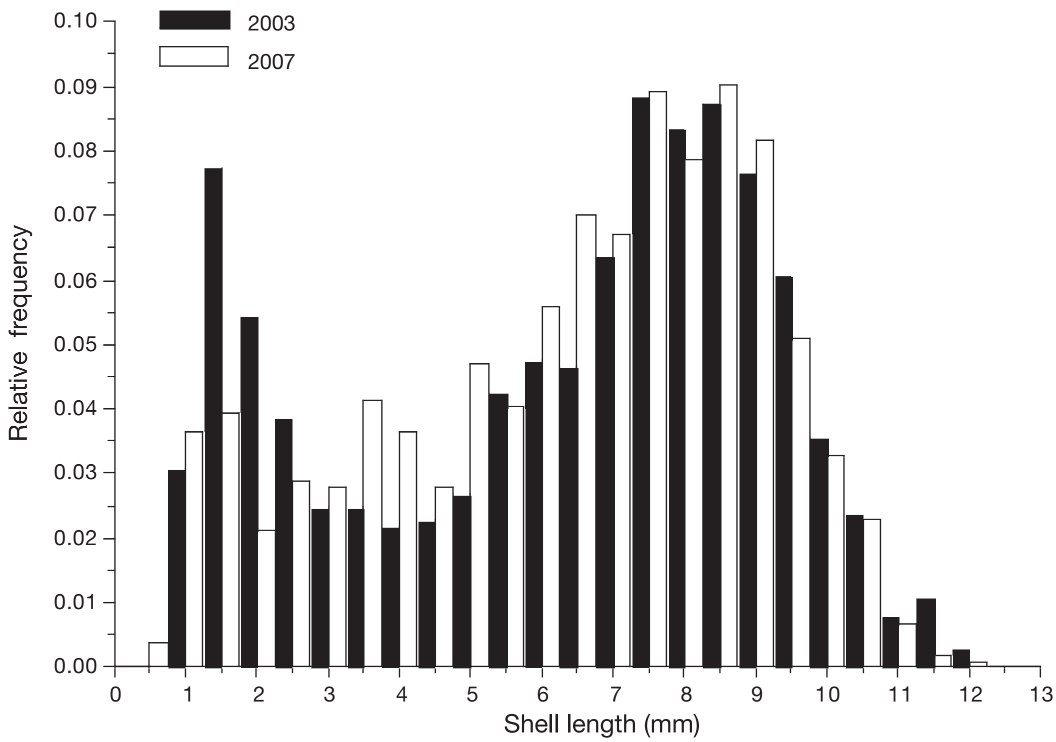

Fig. S2. *Lepetodrilus fucensis*. Length-frequency distributions of established populations collected at the ROPOS vent site, Axial Volcano, in 2003 and 2007. The 2 distributions do not differ significantly from one another (Kolmogorov-Smirnov 2-sample test, α = 0.01, D = 0.072, p > 0.01)