Supplementary Material

Assessing the Extinction Risk of *Heterocypris incongruens* (Crustacea: Ostracoda) in Climate Change with Sensitivity and Uncertainty Analysis

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Table S1. The life table reported the production of resting eggs obtained by two microcosmos experiments (Rossi et al., 1996; Rossi et al., 2016) for each *H. incongruens* clonal lineages and the number of females (N) that produced resting eggs during the experiments. The microcosmos experiments were carried out under three different environmental conditions: Winter (12° C and 8 light hours / 16 dark hours), Spring/Autumn (24°C and 12 light hours / 12 dark) and Summer (28 °C and 16 light hours / 8 dark hours).

Clonal lineages.	Environmental Conditions					
	Winter		Spring/Autumn		Summer	
	Resting eggs	N	Resting eggs	N	Resting eggs	N
W1	186	1	290	12	590	10
W2	0	0	457	11	146	12
S1	0	0	27	12	69	12
S2	0	0	445	6	112	9
I1	73	2	2	11	3	12
I2	82	3	19	10	3	3
L	67	22	385	21	-	-

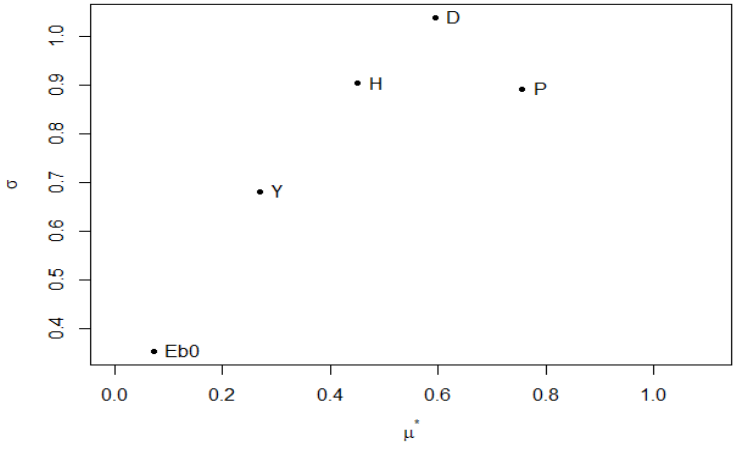

Figure S1. Morris screening on exponential growth model: Eb_0 is the number of resting eggs at time 0, H is the hatching rate, Y is the mean number of resting eggs produced per female, P is the probability that the water balance is positive and D is the deterioration rate. The x-axis represent the mean absolute value for elementary effect (μ), a measure of the importance on dispersion in model output, and the y- axis represent the standard deviation of the elementary effects (σ), a measure of the degree of the interaction effects between factors.

Table S2. For each factor of Cohen equation (Equation (1)) and clonal lineages, distribution and relative parameters were reported for two different climatic conditions: present and climate change. Factors H, D were assumed to be random factors that vary between 0 and 1 in each climatic condition. P and Y distributions were estimated by data (Rossi et al., 1993; Rossi et al., 2016).

Factor	Description	Measure unit	Distribution				
			Clone	Present		Climate change	
H	Hatching rate	n° of eggs that hatch / total n° eggs	W1	uniform	min=0 max =1	uniform	min=0 max =1
			W2	uniform	min=0 max =1	uniform	min=0 max =1
			S2	uniform	min=0 max =1	uniform	min=0 max =1
			L	uniform	min=0 max =1	uniform	min=0 max =1
			S1	uniform	min=0 max =1	uniform	min=0 max =1
			I2	uniform	min=0 max =1	uniform	min=0 max =1
			I1	uniform	min=0 max =1	uniform	min=0 max =1
P	Probability that the water balance is positive	dimensionless	W1	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
			W2	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
			S2	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
			L	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
			S1	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
			I2	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
			I1	beta	α = 0.82 β = 0.47	beta	α = 0.19 β = 0.29
Y	Mean number of resting eggs produced per female	n° of produced eggs / female	W1	poisson	mean=46.30	poisson	mean=46.30
			W2	poisson	mean=25.1	poisson	mean=25.1
			S2	poisson	mean=24	poisson	mean= 24
			L	poisson	mean= 10.5	poisson	mean=10.5
			S1	poisson	mean=4.00	poisson	mean=4 .00
			I2	poisson	mean=3.81	poisson	mean=3.81
			I1	poisson	mean=1.04	poisson	mean= 1.04
D	Egg deterioration rate	n °of decayed eggs / total n° eggs	W1	uniform	min=0 max =1	uniform	min=0 max =1
			W2	uniform	min=0 max =1	uniform	min=0 max =1
			S2	uniform	min=0 max =1	uniform	min=0 max =1
			L	uniform	min=0 max =1	uniform	min=0 max =1
			S1	uniform	min=0 max =1	uniform	min=0 max =1
			I2	uniform	min=0 max =1	uniform	min=0 max =1
			I1	uniform	min=0 max =1	uniform	min=0 max =1

R script 1SM. LHS sampling method and extinction rate estimation . We sampling 1000 combinations of factors and we run the simulation for 30 time steps.

```
library(pse)
factors <- c("H", "P", "Y", "D")
q.distribution <- c("qunif", "qbeta","qpois","qunif")
q. sensi <- list(list( min= 0, max=1),list(shape1 = #climatic condition, shape2 =#climatic condition),
                                    list(lambda = #clone's value), list( min=0, max=1))

time <- 30
clone <- function(H,P,Y,D) {
  X <- array()
  extinction <- array()
  X[1] <- 10
  for( i in 1:time){
    l <- ( (1−P) × log((1−H)×(1−D)) ) + P × (log((1−H)×(1-D) + H×Y))
    Xl <- X[length(X)]
    X[i]<- Xl + l ×Xl
  }
  ifelse(X[30] < 1 , extinction[30] <- 1 , extinction[30] <- 0)
  return(extinction[30])
}
Run.clone <- function (my.data) {
  return(mapply(clone, my.data[,1], my.data[,2],my.data[,3],my.data[,4]))
}

myLHS <- LHS(Run.clone, factors, 1000, q.distribution, q.sensi, nboot=1000)
result.clone <- get.results(myLHS)
extinction.rate <- length(which(result.clone == 1)) / 1000
```

Table S3. Correlation coefficients and p values estimated from the correlation analysis. The factor's values were relative to the model output extinction of the egg bank.

			Factor	H	P	Y	D
W1.	Present	rho	H	1	-	-	-
			P	0.24	1	-	-
			Y	−001	−0.070	1	
			D	-0.18	0.41	-0.020	1
		p value	Factor	H	P	Y	D
			H	0	-	-	-
			P	< 0.001	0	-	-
			Y	0.97	0.11	0	-
			D	< 0.0001	< 0.0001	0.62	0
	Climate change	rho	Factor	H	P	Y	D
			H	1	-	-	-
			P	0.24	1	-	-
			Y	−0.043	−0.005	1	-
			D	−0.18	0.43	0.099	1
		p value	Factor	H	P	Y	D
			H	0	-	-	-
			P	< 0.0001	0	-	-
			Y	0.42	0.92	0	-
			D	< 0.0001	< 0.0001	0.06	0
W2	Present	rho	Factor	H	P	Y	D
			H	1	-	-	-
			P	0.14	1	-	-
			Y	0.027	−0.042	1	-
			D	−0.18	0.44	0.019	1
		p value	Factor	H	P	Y	D
			H	0	-	-	-
			P	0.002	0	-	-
			Y	0.57	0.37	0	-
			D	<0.0001	<0.0001	0.68	0
	Climate change	rho	Factor	H	P	Y	D
			H	1	-	-	-
			P	0.086	1	-	-
			Y	0.056	0.032	1	-
			D	−0.21	0.38	0.96	1
		P value	Factor	H	P	Y	D
			H	0	-	-	-
			P	0.08	0	-	-
			Y	0.26	0.52	0	-
			D	<0.0001	<0.0001	0.96	0
S2	Present	rho	Factor	H	P	Y	D
			H	1	-	-	-
			P	0.220	1	-	-
			Y	0.011	−0.0622	1	-
			D	−0.097	0.494	−0.058	1
		p value	Factor	H	P	Y	D
			H	0	-	-	-
			P	< 0.0001	0	-	-
			Y	0.80	0.19	0	-
			D	0.04	<0.0001	0.22	0
	Climate change	rho	Factor	H	P	Y	D
			H	1	-	-	-
			P	0.11	1	-	-

			Y	0.055	−0.08	1	-
			D	−0.14	0.37	-0.0064	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.023	0	-	-
			Y	0.27	0.10	0	-
			D	0.0048	<0.0001	0.89	0
			Factor	H	P	Y	D
			H	1	-	-	-
		Rho	P	0.03	1	-	-
			Y	0.04	−0.06	1	
	Present		D	−0.16	0.48	−0.01	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.49	0	-	-
			Y	0.32	0.18	0	
L			D	<0.003	<0.0001	0.72	0
			Factor	H	P	Y	D
			H	1	-	-	-
		Rho	P	−0.10	1	-	-
			Y	−0.02	−0.17	1	-
	Climate change		D	−0.19	0.48	−0.007	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.03	0	-	-
			Y	0.63	<0.0001	0	-
			D	<0.0001	<0.0001	0.88	0
			Factor	H	P	Y	D
			H	1	-	-	-
		Rho	P	0.0135	1	-	-
			Y	0.038	−0.156	1	-
	Present		D	−0.095	0.344	0.064	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.739	0	-	-
			Y	0.347	<0.0001	0	-
S1			D	0.019	<0.0001	0.11	0
			Factor	H	P	Y	D
			H	1	-	-	-
		Rho	P	−0.073	1	-	-
			Y	−0.04	−0.20	1	-
	Climate change		D	−0.12	0.39	−0.00024	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.86	0	-	-
			Y	0.27	<0.0001	0	-
			D	0.006	<0.0001	0.99	0
			Factor	H	P	Y	D
			H	1	-	-	-
		rho	P	0.09	1	-	-
			Y	−0.037	−0.17	1	-
I2	Present		D	−0.13	0.36	0.10	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.024	0	-	-
			Y	0.35	<0.0001	0	-

			D	0.0006	<0.0001	0.011	0
			Factor	H	P	Y	D
			H	1	-	-	-
		rho	P	−0.031	1	-	-
			Y	−0.026	−0.20	1	-
	Climate change		D	−0.10	0.37	0.01	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.47	0	-	-
			Y	0.54	<0.0001	0	-
			D	0.01	<0.0001	0.67	0
			Factor	H	P	Y	D
			H	1	-	-	-
		Rho	P	0.08	1	-	-
			Y	0.07	−0.012	1	-
	Present		D	−0.10	0.18	0.13	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.036	0	-	-
			Y	0.05	0.74	0	-
			D	0.0064	<0.0001	0.00045	0
1			Factor	H	P	Y	D
			H	1	-	-	-
		Rho	P	0.08	1	-	-
			Y	0.06	−0.11	1	
	Climate change		D	−.12	0.21	0.12	1
			Factor	H	P	Y	D
			H	0	-	-	-
		p value	P	0.033	0	-	-
			Y	0.10	0.003	0	-
			D	0.001	<0.0001	0.0014	0

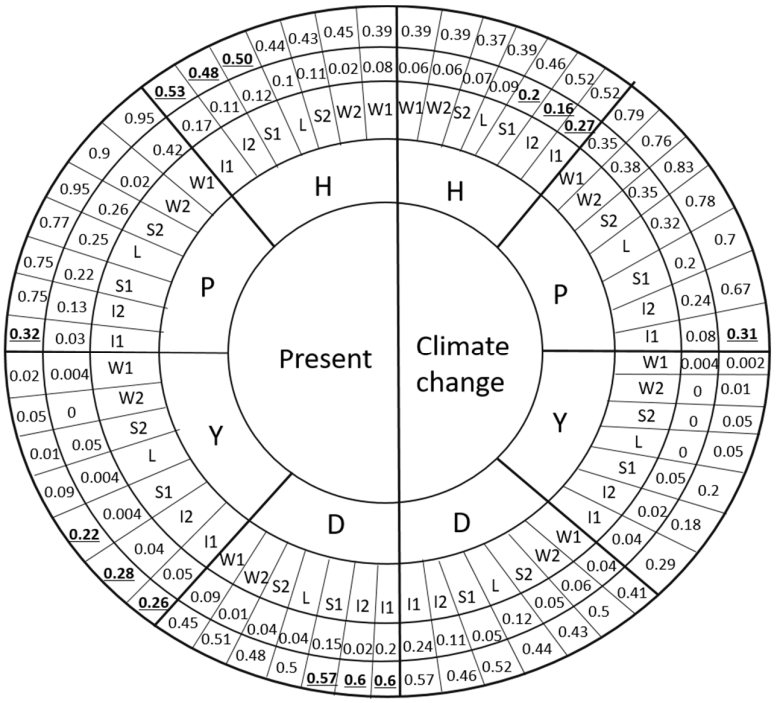

Figure S2. Hierarchical doughnut chart reported from the center to the border: the two climatic conditions: present and climate change; the factors: hatching rate (H), probability that the water balance is positive (P), the mean number of resting eggs produced per female (Y), and the deterioration rate (D); the clonal lineages: W1, W2, S2, Ls, I2, S1, and I1; the Sobol first index; and the Sobol total index. Sobol's indices that differ in importance among clones were reported in the manuscript and they were represented underlined and in bold.