

Table S2. Simulation parameters. All parameter combinations simulated in the current study to ensure reproducibility of the results. Software code can be downloaded from <https://github.com/kjgilbert/ExpLoad>. Parameters written in italics within parentheses are the exact software input names used by the simulation. 10 replicate simulations were run with data saved every 100 generations.

Parameter	Setting(s) Used
Genome-wide mutation rate (<i>mu</i>)	0.1
Migration rate (<i>m</i>)	0.1
Selection (<i>selectionMode</i>)	Soft (0), Hard (1)
Selection coefficient (<i>s</i>)	+/-0.005, exponential DFE with mean = +/-0.005
Dominance, <i>h</i> (set with line 301 in Individual.cpp)	0.5, 0.3, 0.0, <i>h-s</i> trade-off (see Methods)
Proportion deleterious loci (<i>phi</i>)	0.9
Scenario (<i>expansionMode</i>)	Linear (0)
Demographic scenario (<i>expansionModeKim</i>)	Expansion (0), Shift (2)
<i>T</i> , number of generations between each step of the shift (<i>theta</i>)	NA (free expansion), 5, 10, 15, 20, 25, 30, 40, 50, 60, 84
Generations after burn-in (<i>gens.to.run</i>)	4000
Landscape width (<i>m1</i>)	1, 5
Landscape length (<i>m2</i>)	300
Ancestral population size (for burn-in; <i>anc_pop_size</i>)	10000
Ancestral burn-in generation time (<i>burnin_time</i>)	10
Starting population size (<i>starting_demes</i>)	5
Starting population burn-in on landscape (<i>expansion_start</i>)	5000
Range shift population size (<i>niche_width</i>)	5
Carrying capacity (<i>capacity</i>)	20, 100, 500