

Figure S1. Workflow of the main simulation model.

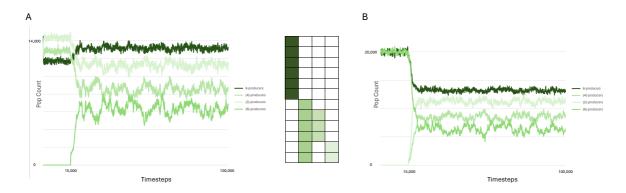


Figure S2. Invasions simulation results with the 6-(6 OR 4-2) system. Simulations were setup with paired grids, one with a 6-6 and another with 6-4-2 at the proportions observed in the "wildtype" equilibrium. Mutation was disabled. After 15,000 timesteps of equilibration the invasion was triggered by swapping parts of the two grids. **A)** 6 into 6-4-2. **B)** 4-2 into 6-6.

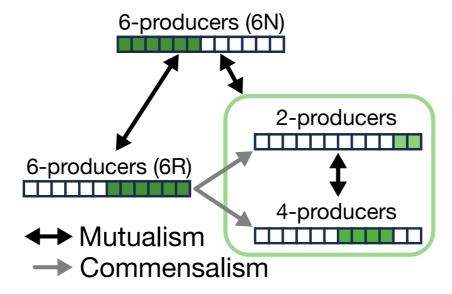


Figure S3. Interactions between the ecotypes in the 6-(6 OR 4-2) system.

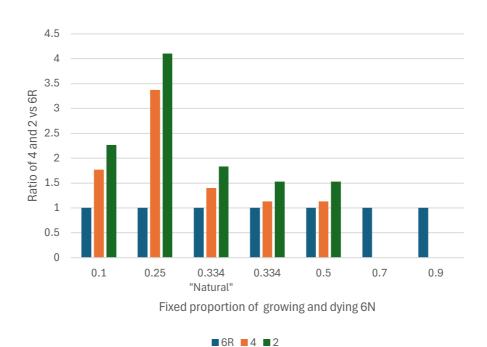


Figure S4. 6N as living blocks. A modification of the 6-(6 OR 4-2) system. 6N is altered to only grow or die when below or above, respectively, to maintain a fixed proportion of 6N cells. 6R, 4, and 2 are initialised at their equilibrium proportions to each other using the amount of free space after initialising 6N. Bars show the ratios of 4 and 2 against 6R, to allow for changing absolute numbers with different numbers of 6N.

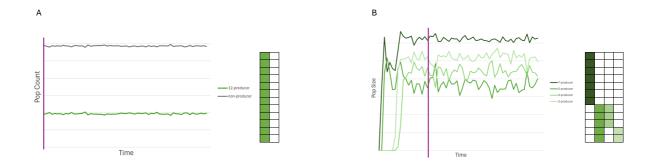


Figure S5. Simulations with super deletions. Simulations started with 12 common goods, a CG cost of 1E-02, default mutation rate and no HGT. A special super deletion parameter was added which allows all production to be converted to non-production in a single event (5.00E-09), i.e., the cell becomes a pure non-producer. **A)** Example of an early superdeletion event. Non-producers rapidly overtake the system, trapping it in a 12-0 configuration. **B)** Example of a late superdeletion event. The system had already formed a quasi-stable 7-(5 OR 3-2) configuration and the non-producer was unable to invade.

Default Parameters	Default values
Grid Size	200x200 cells (40,000 carrying capacity)
Baseline reproduction chance	0.6
Baseline death rate per timestep	0.1
Number of common goods (CGs)	6 or 12
Growth penalty per CG produced (Cost per	1e-04, 1e-03, 1e-02, 1e-01
CG * Baseline reproduction chance)	
Instantaneous chance of reproduction	Baseline reproduction chance (0.6) - (#CGs
	produced * Growth penalty per CG
	produced)
	1 / 2 / 3 / 4 (radius of moore
Interaction range (Moore neighborhood	neighbourhood);
radius)	9 / 25 / 49 / 81 (number of potential
	beneficiaries, producer included)
Mutation rate / per gene / per timestep	5e-06
Horizontal Gene Transfer rate	0

Table S1. Default model parameters.