

Supplementary materials for “On the Origin of Phenotypic Plasticity”

T. Sakamoto and H. Innan

April 26, 2022

1 Details of the simulation model

In each generation in a simulation run, the life cycle is assumed to be in the order of development, reproduction (selection), and mutation, along which we describe the detailed treatments in the following. We assumed that each of g_i , b_{ij} , c_i is considered as a single locus so that the model consists of in total $n(n+2)$ loci. Free recombination is assumed between all pairs of two loci in the main text, but essentially identical results were obtained when this assumption was violated (see below).

In the developmental process, each individual develops as defined given their embryo genotype and the environment (see the Model section), resulting in the adult phenotype ($\vec{x}_v$).

In the reproduction process, we first calculated the fitness of each individual by $w_i = \exp(-|\vec{x}_v - \vec{X}_i|^2/2\sigma^2)$. Next, we calculated the frequency of each allele at each locus in the gene pool, or population. Let W_i be the fitness of the i th individual and let us assume that the i th individual has the a_{ik} -th allele at the k th locus. Then, the allele frequency of the j th allele at the k th locus, P_{jk} , is given by

$$P_{jk} = \frac{\sum_i W_i \delta_{a_{ik},j}}{\sum_i W_i}, \quad (1)$$

where δ_{ij} equals to 1 when $i = j$, otherwise, 0. Assuming no linkage disequilibrium among different loci, the expected frequency of individuals that have the b_i -th allele at the i th locus is given by $\prod_i P_{b_i,i}$. Given the expected frequencies, the next generation was produced by a multinomial distribution, following the Wright–Fisher model.

In the mutation process, we added mutations following the procedure described in the Model section.

Although we assumed free recombination between all loci in the main text, essentially the same results should be obtained when the assumption of free recombination is violated, unless the mutation rates are so high that multiple mutations interfere to each other. To confirm this, we assumed complete linkage for each i (i.e., g_i , b_{ij} , and c_i) so that there are essentially n unlinked loci in total. Biologically, this may represent a situation in which the expression level of type-G genes is controlled by *cis*-regulatory regions

that is completely linked to the corresponding type-G gene. Table S2 shows the results for this setting, demonstrating that the quantitatively very similar results to Table 1 in the main text were obtained. It is indicated that our results should be less affected by linkage given the low mutation rates assumed in this study.

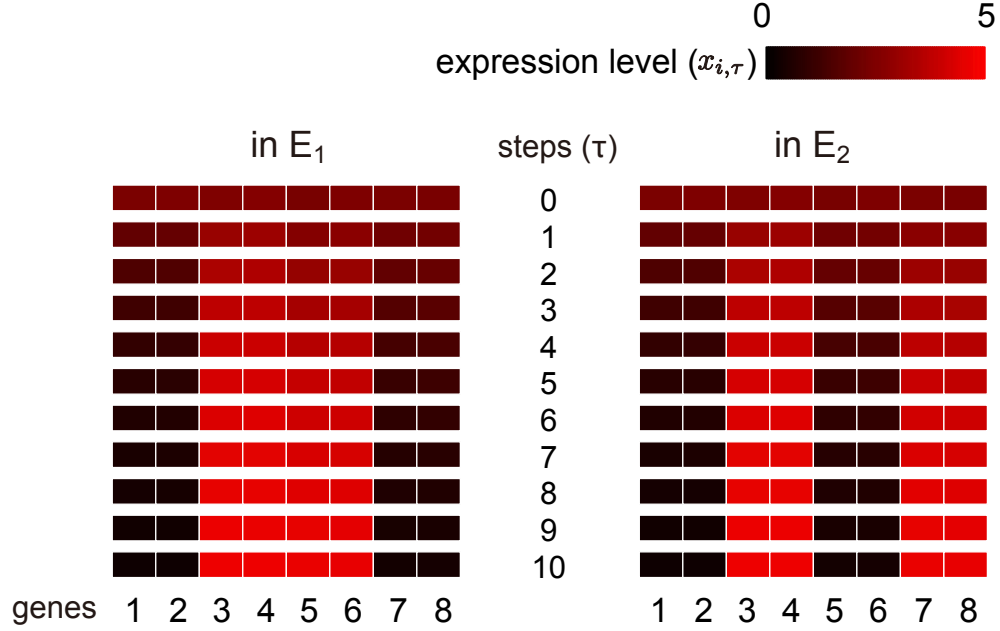


Figure S1: Changes of the expression level of n type-G genes through the development in each of the two environments, from embryo ($\tau = 0$) to adult ($\tau = 10$). The shown pattern is obtained at time point ∇ III of Figure 1 in the main text.

Table S1: Proportion of successful runs (S_p) and average waiting time (T_p) for the development of phenotypic plasticity. The following parameters were fixed in all simulation runs: $p_g = p_b = p_c = 10^{-7}$, $\mu_g = \mu_b = \mu_c = 0.1$, $v = 10$, $\alpha = 0.2$, $\sigma = 5.0$, and $N = 10,000$. In the shaded rows, we set $\vec{X}_1 = (0, 0, 5, 5, 5, 5, 0, 0)$ and $\vec{X}_2 = (0, 0, 5, 5, 0, 0, 5, 5)$ (i.e., the results are the same for the two shaded line).

focal parameter	$T = 1$		$T = 10$		$T = 100$		$T = 1,000$		$T = 10,000$		$T = 100,000$		$T = 1,000,000$	
	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time
$\vec{X}_1 = (0, 0, 0, 5, 5, 5, 5, 0)$ and $\vec{X}_2 = (0, 0, 0, 5, 5, 5, 0, 5)$	1	401N	1	401N	1	399N	1	492N	1	906N	0.998	1692N	0.993	7672N
$\vec{X}_1 = (0, 0, 5, 5, 5, 5, 0, 0)$ and $\vec{X}_2 = (0, 0, 5, 5, 0, 0, 5, 5)$	1	366N	1	366N	1	372N	1	469N	0.998	848N	0.994	1715N	0.979	7594N
$\vec{X}_1 = (0, 5, 5, 5, 5, 0, 0, 0)$ and $\vec{X}_2 = (0, 5, 0, 0, 0, 5, 5, 5)$	1	371N	1	373N	1	373N	0.999	465N	0.996	827N	0.992	1894N	0.97	7871N
$\vec{X}_1 = (5, 5, 5, 5, 0, 0, 0, 0)$ and $\vec{X}_2 = (0, 0, 0, 0, 5, 5, 5, 5)$	1	403N	1	401N	1	402N	0.999	497N	0.993	745N	0.987	1920N	0.976	8221N
$\vec{X}_1 = (0, 0, 0, 0, 5, 5, 0, 0)$ and $\vec{X}_2 = (0, 0, 0, 0, 0, 0, 5, 5)$	1	391N	1	388N	1	390N	0.999	397N	1	634N	0.998	1227N	0.99	5129N
$\vec{X}_1 = (0, 0, 0, 5, 5, 5, 0, 0)$ and $\vec{X}_2 = (0, 0, 0, 5, 0, 0, 5, 5)$	1	372N	1	373N	1	376N	1	435N	0.997	756N	0.999	1483N	0.989	6301N
$\vec{X}_1 = (0, 0, 5, 5, 5, 5, 0, 0)$ and $\vec{X}_2 = (0, 0, 5, 5, 0, 0, 5, 5)$	1	366N	1	366N	1	372N	1	469N	0.998	848N	0.994	1715N	0.979	7594N
$\vec{X}_1 = (0, 5, 5, 5, 5, 5, 0, 0)$ and $\vec{X}_2 = (0, 5, 5, 5, 0, 0, 5, 5)$	1	364N	1	360N	1	363N	1	457N	0.999	960N	0.996	2015N	0.982	8835N
$\vec{X}_1 = (5, 5, 5, 5, 5, 5, 0, 0)$ and $\vec{X}_2 = (5, 5, 5, 5, 0, 0, 5, 5)$	1	356N	1	361N	1	360N	1	487N	0.997	906N	0.99	2241N	0.98	9952N

Table S2: Proportion of successful runs (S_p) and average waiting time (T_p) for the development of phenotypic plasticity. The following parameters were fixed in all simulation runs: $\vec{X}_1 = (0, 0, 5, 5, 5, 5, 0, 0)$, $\vec{X}_2 = (0, 0, 5, 5, 0, 0, 5, 5)$, $p_g = p_b = p_c = 10^{-7}$, $v = 10$, $\alpha = 0.2$, $\sigma = 5.0$, and $N = 10,000$. In the shaded rows, we set $p_g = p_b = p_c = 10^{-7}$ (i.e., the results are the same for all three shaded line), and one of the three parameters was changed in the other rows.

Parameters			$T = 1$		$T = 10$		$T = 100$		$T = 1,000$		$T = 10,000$		$T = 100,000$		$T = 1,000,000$	
μ_g	μ_b	μ_c	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time	Prop.	Time
0.01	0.1	0.1	1	368 <i>N</i>	1	366 <i>N</i>	1	372 <i>N</i>	1	463 <i>N</i>	0.995	924 <i>N</i>	0.989	1810 <i>N</i>	0.973	7473 <i>N</i>
0.025	0.1	0.1	1	368 <i>N</i>	1	367 <i>N</i>	1	371 <i>N</i>	1	458 <i>N</i>	0.997	839 <i>N</i>	0.995	1876 <i>N</i>	0.971	7441 <i>N</i>
0.1	0.1	0.1	1	369 <i>N</i>	1	367 <i>N</i>	1	368 <i>N</i>	1	454 <i>N</i>	0.999	827 <i>N</i>	0.995	1883 <i>N</i>	0.98	7892 <i>N</i>
0.25	0.1	0.1	1	367 <i>N</i>	1	365 <i>N</i>	1	366 <i>N</i>	1	468 <i>N</i>	0.999	1055 <i>N</i>	0.998	2503 <i>N</i>	0.981	11403 <i>N</i>
1.0	0.1	0.1	1	354 <i>N</i>	1	356 <i>N</i>	1	356 <i>N</i>	0.999	3342 <i>N</i>	0.988	14288 <i>N</i>	0.958	19198 <i>N</i>	0.478	37036 <i>N</i>
0.1	0.01	0.1	1	3166 <i>N</i>	1	3164 <i>N</i>	1	3174 <i>N</i>	1	3168 <i>N</i>	1	3164 <i>N</i>	1	3170 <i>N</i>	1	3271 <i>N</i>
0.1	0.025	0.1	1	1025 <i>N</i>	1	1024 <i>N</i>	1	1022 <i>N</i>	1	1023 <i>N</i>	1	1044 <i>N</i>	1	1105 <i>N</i>	1	1608 <i>N</i>
0.1	0.1	0.1	1	369 <i>N</i>	1	367 <i>N</i>	1	368 <i>N</i>	1	454 <i>N</i>	0.999	827 <i>N</i>	0.995	1883 <i>N</i>	0.98	7892 <i>N</i>
0.1	0.25	0.1	1	393 <i>N</i>	1	398 <i>N</i>	1	403 <i>N</i>	0.834	7750 <i>N</i>	0.895	13603 <i>N</i>	0.799	22108 <i>N</i>	0.182	40706 <i>N</i>
0.1	1.0	0.1	1	736 <i>N</i>	1	764 <i>N</i>	0.958	2244 <i>N</i>	0	NaN	0	NaN	0	NaN	0	NaN
0.1	0.1	0.01	1	9609 <i>N</i>	1	9678 <i>N</i>	1	9762 <i>N</i>	0.131	38854 <i>N</i>	0	NaN	0	NaN	0	NaN
0.1	0.1	0.025	1	2389 <i>N</i>	1	2379 <i>N</i>	1	2391 <i>N</i>	0.946	9907 <i>N</i>	0.898	21556 <i>N</i>	0.527	34465 <i>N</i>	0	NaN
0.1	0.1	0.1	1	369 <i>N</i>	1	367 <i>N</i>	1	368 <i>N</i>	1	454 <i>N</i>	0.999	827 <i>N</i>	0.995	1883 <i>N</i>	0.98	7892 <i>N</i>
0.1	0.1	0.25	1	153 <i>N</i>	1	149 <i>N</i>	1	152 <i>N</i>	1	160 <i>N</i>	1	222 <i>N</i>	1	365 <i>N</i>	1	1729 <i>N</i>
0.1	0.1	1.0	1	61 <i>N</i>	1	61 <i>N</i>	1	61 <i>N</i>	1	62 <i>N</i>	1	71 <i>N</i>	1	94 <i>N</i>	1	392 <i>N</i>