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Moya, A., A.Barbera and J.Dopazo. Universidad de Valencia, Espana. Simulation of the larval competition process.

The present work is an attempt to bring light on the relevance of Wallace's (1981) "biological space unit". The validation procedure was the simulation of the larval competition process, where the medium is divided into K preexisting biological space units. The following assumptions were made: (i) This simulation has no replacement. (ii) Once one larva occupies a biological space unit it will remain in it. This occupation will be at random, taking into account the relative frequency of genotypes before the random number is generation. (iii) Once the larva is inside a unit an intrinsic probability of survival exists, which is obtained from a normal distribution for each genotype. The mean value and standard deviation used for each genotype are obtained from experimental data on Drosophila. (iv) The process ends when the units are exhausted. Then the survivors of each genotype are counted, and the relative viability for each is calculated.

This simulation is a first attempt to find density- and frequency-dependent selection using Wallace's concept. For this reason several values of biological space units (density-dependent selection) and different genetic compositions (frequency-dependent selection) were essayed.

The programming used was PASCAL. The abbreviations used for the parameters were the following:

- N : number of total larvae
- K : number of biological space units
- N_1 : number of larvae of genotype 1
- N_2 : number of larvae of genotype 2
- m_1 : intrinsic viability of larvae of genotype 1
- m_2 : intrinsic viability of larvae of genotype 2
- s_1 : standard deviation of m_1
- s_2 : standard deviation of m_2
- V_1 : viability larva-to-adult of genotype 1
- V_2 : viability larva-to-adult of genotype 2

The results showed that no frequency-dependent selection existed in this kind of simulation (at least when these assumptions). On the contrary, positive density-dependent selection was generated, according to the available biological space unities. Table 1 shows the mean value of viability according to genetic composition for each density. As can be seen, no differences appear between the viabilities of genotypes 1 and 2 due to the similarity of m_1 and m_2. Results not shown here indicate that neither do reductions in the values of s_1 and s_2 statistically permit differences to be on between the viabilities for the different frequencies of the same genotype and density. The same occurs when the mean values of the frequencies are taken and the viabilities of genotypes 1 and 2 are compared. Great differences between m_1 and m_2 will permit differences between V_1 and V_2 to be found and only when other additional parameters are taken into account will it be possible to detect some kind of frequency-dependent selection. More simulations are needed.

Table 1. Results of the simulations: mean viabilities with standard errors. $m_1 = 0.755$, $s_1 = 0.378$, $m_2 = 0.760$, $s_2 = 0.380$

N	n*	K	V_1	V_2
20	19	4	0.19630 ± 0.04638	0.15945 ± 0.02600
		8	0.32514 ± 0.05515	0.25372 ± 0.05427
		12	0.35762 ± 0.02643	0.38887 ± 0.03730
		16	0.50645 ± 0.04924	0.56807 ± 0.04152
		19	0.62756 ± 0.02937	0.63428 ± 0.03918
30	14	6	0.11469 ± 0.01595	0.11158 ± 0.03164
		12	0.26000 ± 0.02799	0.24654 ± 0.02940

Table 1 (contin.)

N	n*	K	V_1	V_2
		18	0.39002 ± 0.03610	0.42584 ± 0.02954
		24	0.47445 ± 0.03206	0.59281 ± 0.03643
		29	0.61254 ± 0.03290	0.59318 ± 0.04483
40	19	8	0.10161 ± 0.01282	0.12610 ± 0.01833
		16	0.26831 ± 0.02801	0.28024 ± 0.02342
		24	0.40296 ± 0.02798	0.33257 ± 0.03474
		32	0.47619 ± 0.03331	0.49050 ± 0.03612
		39	0.59710 ± 0.02394	0.64023 ± 0.02412
50	16	10	0.14573 ± 0.01596	0.11992 ± 0.01388
		20	0.22489 ± 0.02269	0.23789 ± 0.01761
		30	0.38186 ± 0.02159	0.34837 ± 0.03453
		40	0.47197 ± 0.03047	0.51342 ± 0.02742
		49	0.62752 ± 0.02343	0.57838 ± 0.03744
60	19	12	0.13127 ± 0.01544	0.14540 ± 0.01876
		24	0.24562 ± 0.02005	0.25008 ± 0.01861
		36	0.35685 ± 0.03174	0.38115 ± 0.01816
		48	0.50787 ± 0.01634	0.53117 ± 0.03397
		59	0.59681 ± 0.01882	0.59052 ± 0.01538
70	17	14	0.12178 ± 0.01341	0.10846 ± 0.01586
		28	0.25899 ± 0.01385	0.21884 ± 0.02080
		42	0.35761 ± 0.02267	0.40287 ± 0.02263
		56	0.48298 ± 0.03544	0.52257 ± 0.02168
		69	0.66098 ± 0.02802	0.62936 ± 0.02067

* = number of genetic compositions for each pair of N, K.

References: Wallace, B. 1981, Basic Population Genetics, Columbia University Press, New York.

Nahmias, J. and G.C.Bewley. North Carolina State University, Raleigh, North Carolina USNA. Catalase-specific CRM in flies euploid and aneuploid for the cytogenetic region 75D-78A.

Generation of segmental aneuploids spanning the entire genome of Drosophila melanogaster has demonstrated that polytene chromosome region 75D-78A is the only segment in the genome exhibiting a dosage sensitive response to catalase activity with a hyperploid to euploid ratio of 1.54 (1). This result has suggested that this region is the site for the catalase structural gene, Cat^+. Analysis of catalase turnover rates using the irreversible inhibitor 3-amino-1,2,4-triazole has attributed this dosage effect to a 1.4 fold increase in the rate of enzyme synthesis while the rate of enzyme degradation remains constant (1). In the present study, we report that this dosage effect is also reflected by an analogous increase in the number of enzyme molecules as evidenced by quantitating levels of catalase-specific cross reacting material (CRM) using antiserum from rabbits injected with purified catalase antigen (2).

Segmental aneuploids were generated by crosses between stocks L131 and R153 which carry (Y;3) translocations with autosomal breakpoints at 75D and 78A respectively (1). Male progeny euploid and hyperploid for region75D-78A were homogenized at a concentration of one fly per 10 µl of 10 mM sodium phosphate buffer (pH 7.0) containing 0.1% Triton X-100 and 5 µl were applied to each well of a 1% agarose gel containing monospecific antibodies against catalase (2). Gels were stained for catalase activity and the area underneath each rocket was estimated. The ratio of 3-dose to 2-dose flies obtained was 1.52 (Fig. 1). This result demonstrates that the 50% increase in activity observed in 3-dose vs. 2-dose flies is not attributed to structural modifications of the enzyme molecules but rather to differential rates of enzyme accumulation to the steady state.