Supplement to: Giacinto Libertini, Sex and Aging: A Comparison between Two Phenoptotic Phenomena (ISSN 0006-2979, *Biochemistry (Moscow)*, 2017, Vol. 82, No. 12, pp. 1435-1455)

SUPPLEMENT A (simulation programs, resulting Figs. S1-S12, and raw data of the simulations)

Aging model programs (aging_model_programs.exe and source files)

Warning. The programming language is Microsoft Visual Basic 6.0, which runs under the operating system Windows XP or older version of Windows. However, the executable file works with more modern operating system too. The simulation programs are available solely in the supplementary materials on the site of the journal (http://protein.bio.msu.ru/biokhimiya).

{See also the Movie}

Sex model program (sex_model_program.exe and source files)

Warning. The programming language is Microsoft Visual Basic 6.0, which runs under the operating system Windows XP or older version of Windows. However, the executable file works with more modern operating system too.

Instructions. The numerical results of the simulations are given in:

1) C:\ReportFile1.txt (results of a single simulation);
2) C:\ReportFile2.txt (results of each group simulation);
3) C:\ReportFile3.txt (mean and SD for each group of simulation).

A small technical notice is necessary. With the options:

Loop with $\log_{10}N$ = [...] to [...] step. 5
No. iterations (from 1 to 10,000) [...],

if the number of iterations is not small, the graphic display of simulations may disappear after some simulations (due to PC power limits) and program commands freeze. This does not mean that the program is blocked: it continues to run till the end. It is necessary to await the end of the simulations and then see the results in the aforesaid files 2 and 3.

Raw data

{For the section "Raw data", see Excel file and the movie}

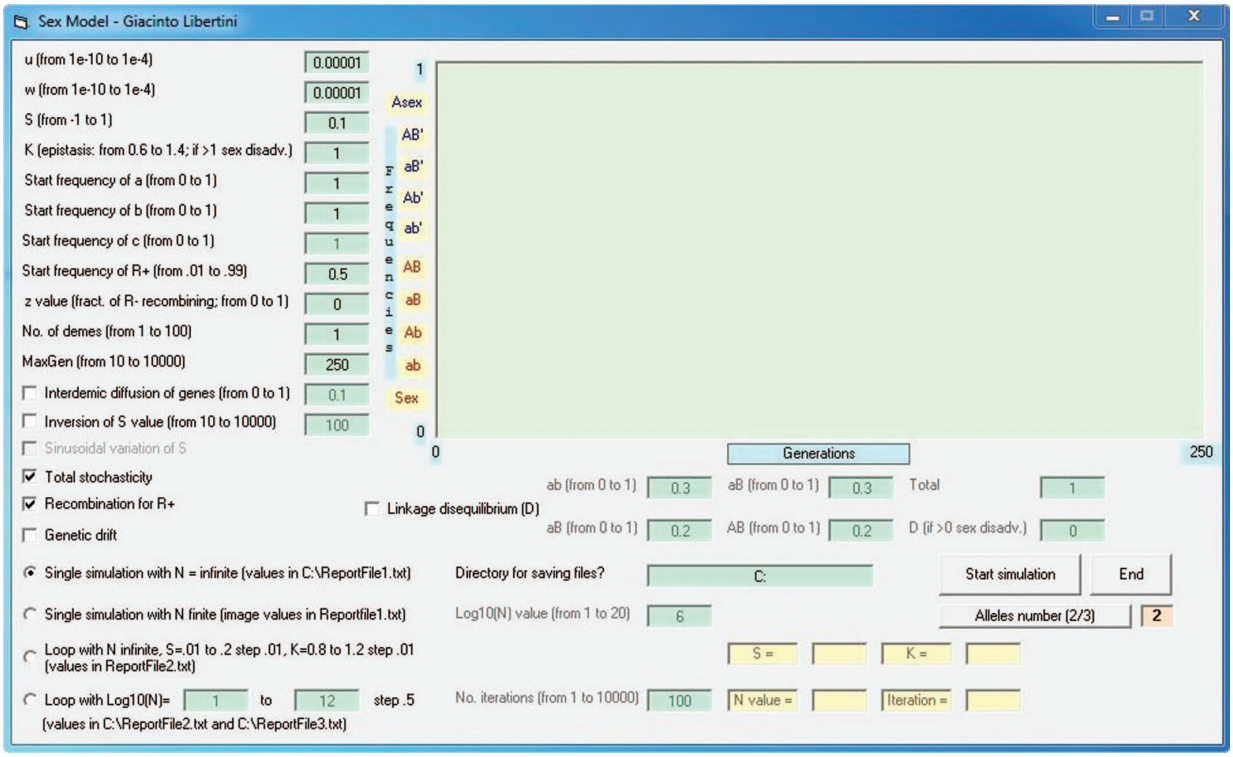


Fig. S1. An image of the program interface.

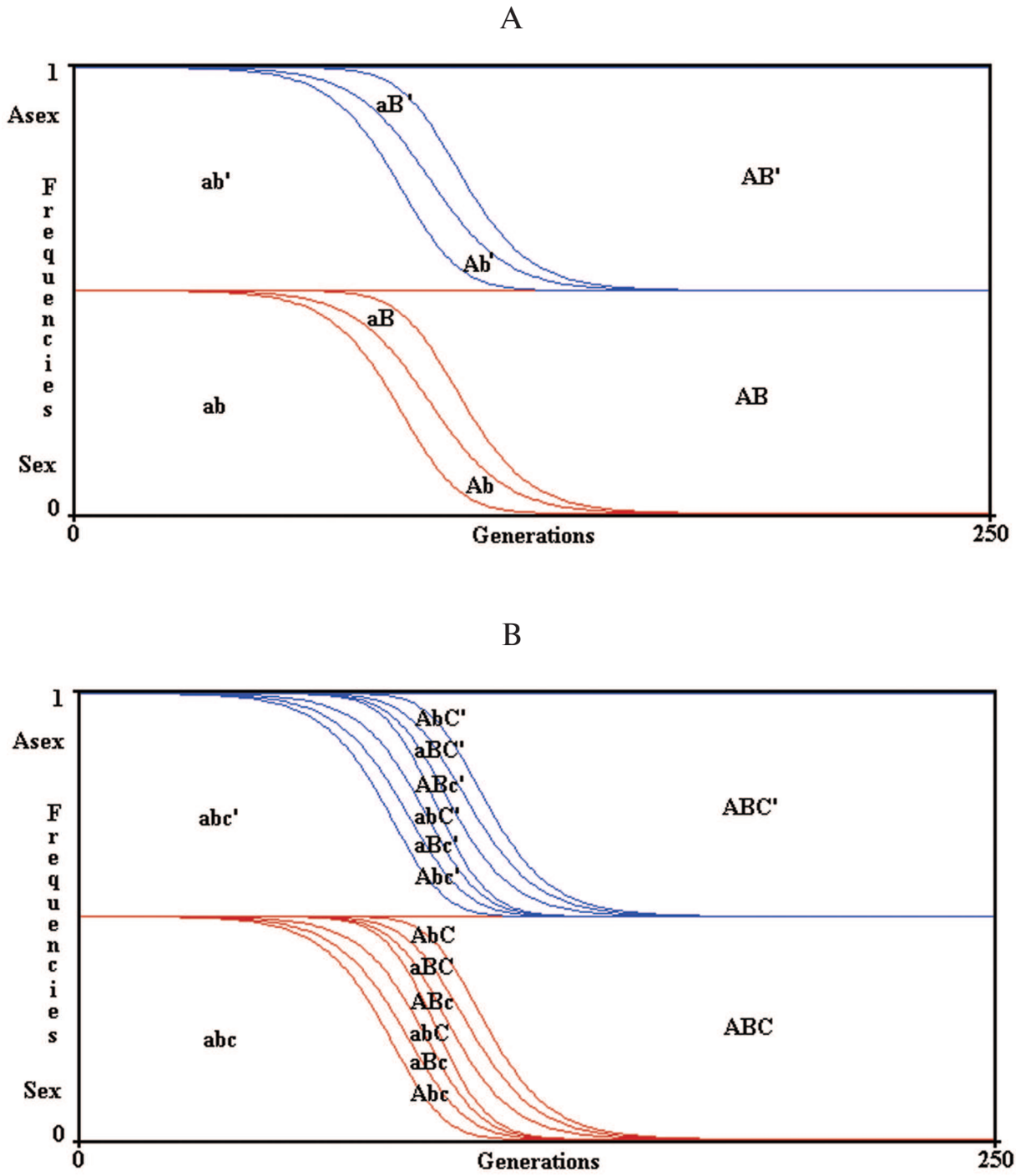


Fig. S2. A) 2G case; B) 3G case. In both examples and in the following figures, if not specified otherwise: $u = w = 0.00001$; $s = 0.1$; $k = 1$; $D = 0$. The value of R+ after 250 generations ($P_{R+,250}$) is 0.499997620408316 in the first case and 0.499998194700698 in the second case. The slight differences between these values and 0.5 (the frequency of R+ at generation 0) are due to the little positive linkage disequilibria caused by mutations. The frequencies of R+ and R– at generation 0 ($P_{R+,0}$; $P_{R-,0}$) are 0.5 to give to sex and asexual individuals the same starting conditions. With any other value as well (for example, $P_{R+,0} = 0.6$; $P_{R-,0} = 1 - P_{R+,0} = 0.4$), the model shows that in infinite populations there is no significant variation from the initial frequencies of R+ and R–, as predicted by Maynard Smith [4]. The simulations, in this and in the following figures, have been extended up to 250 generations, which is sufficient to stabilize combination and R+ values (except for Fig. S10, simulation series with $s = 0.01$).

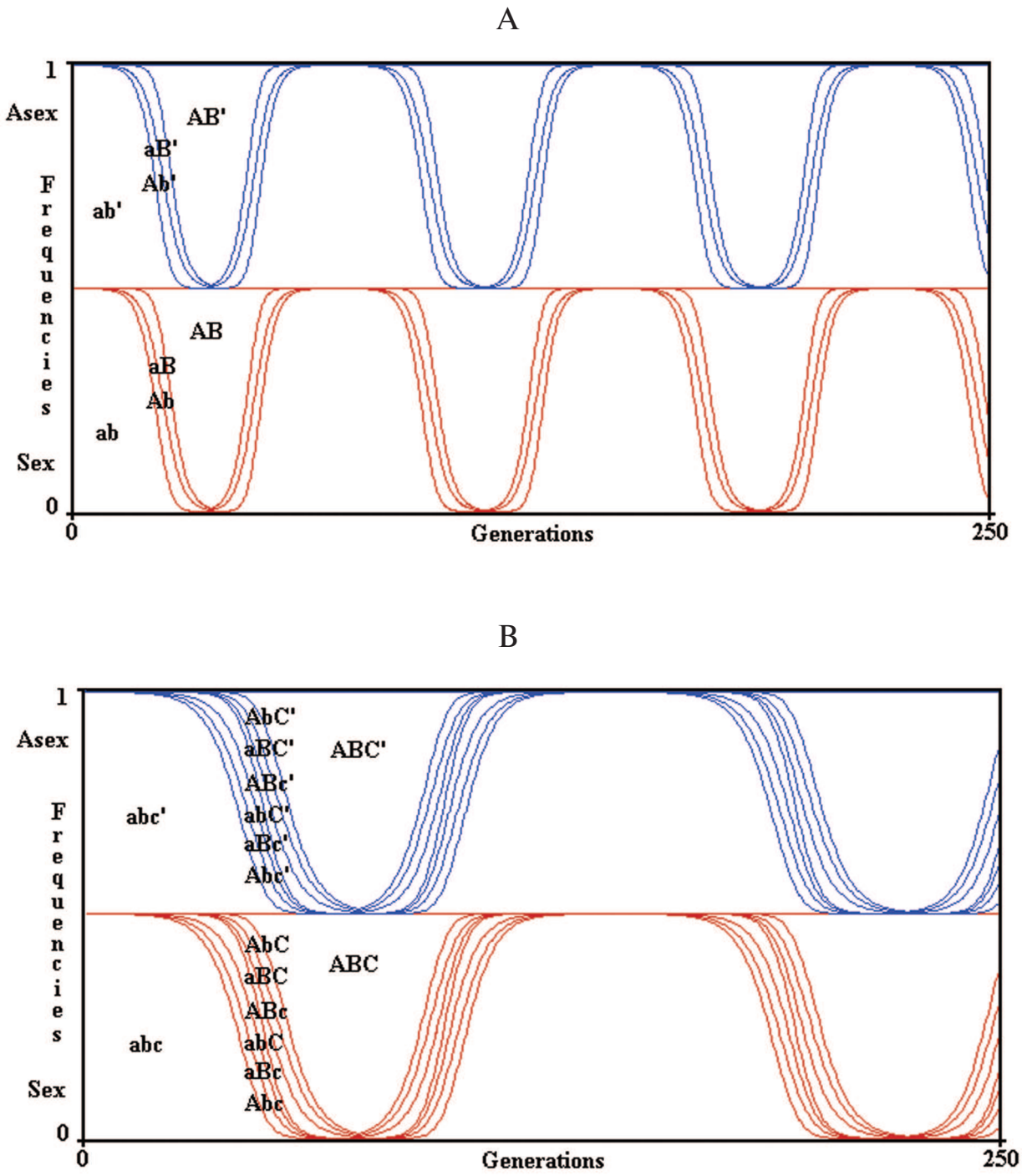


Fig. S3. Effects of the oscillations of *s*. A) 2G case; B) 3G case. In the simulations, *s* value oscillates from –0.1 to +0.1 every 150 generations. The model shows that in infinite populations any oscillating value of *s* cannot be sufficient to justify sex.

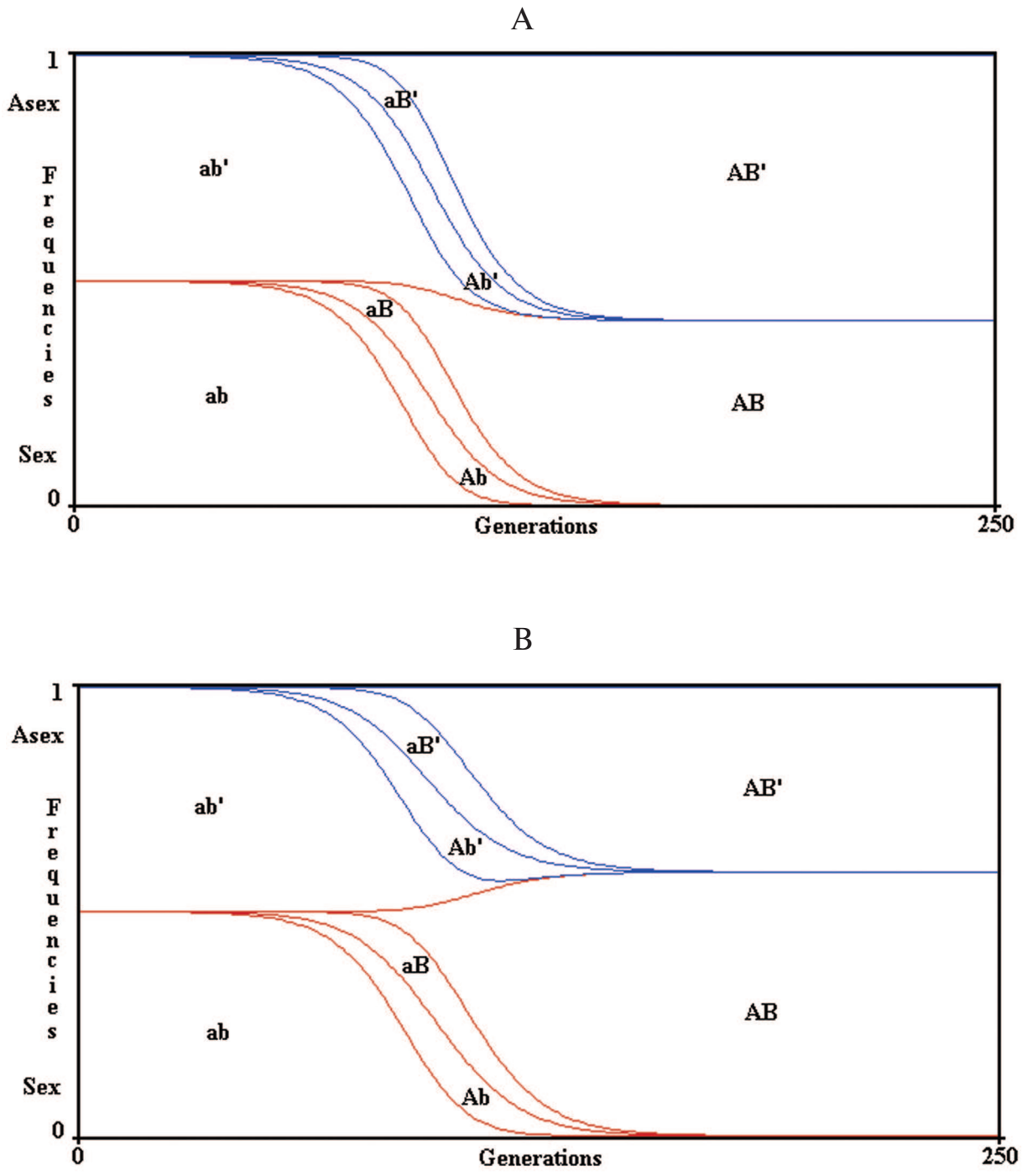


Fig. S4. Effects of the variations of k. 2G case. A) $k = 1.03$ (positive epistasis): sex is disadvantageous; B) $k = 0.97$ (negative epistasis): sex is advantageous. If the absolute value of $(1 - k)$ is greater, the disadvantage or advantage of sex increases proportionally.

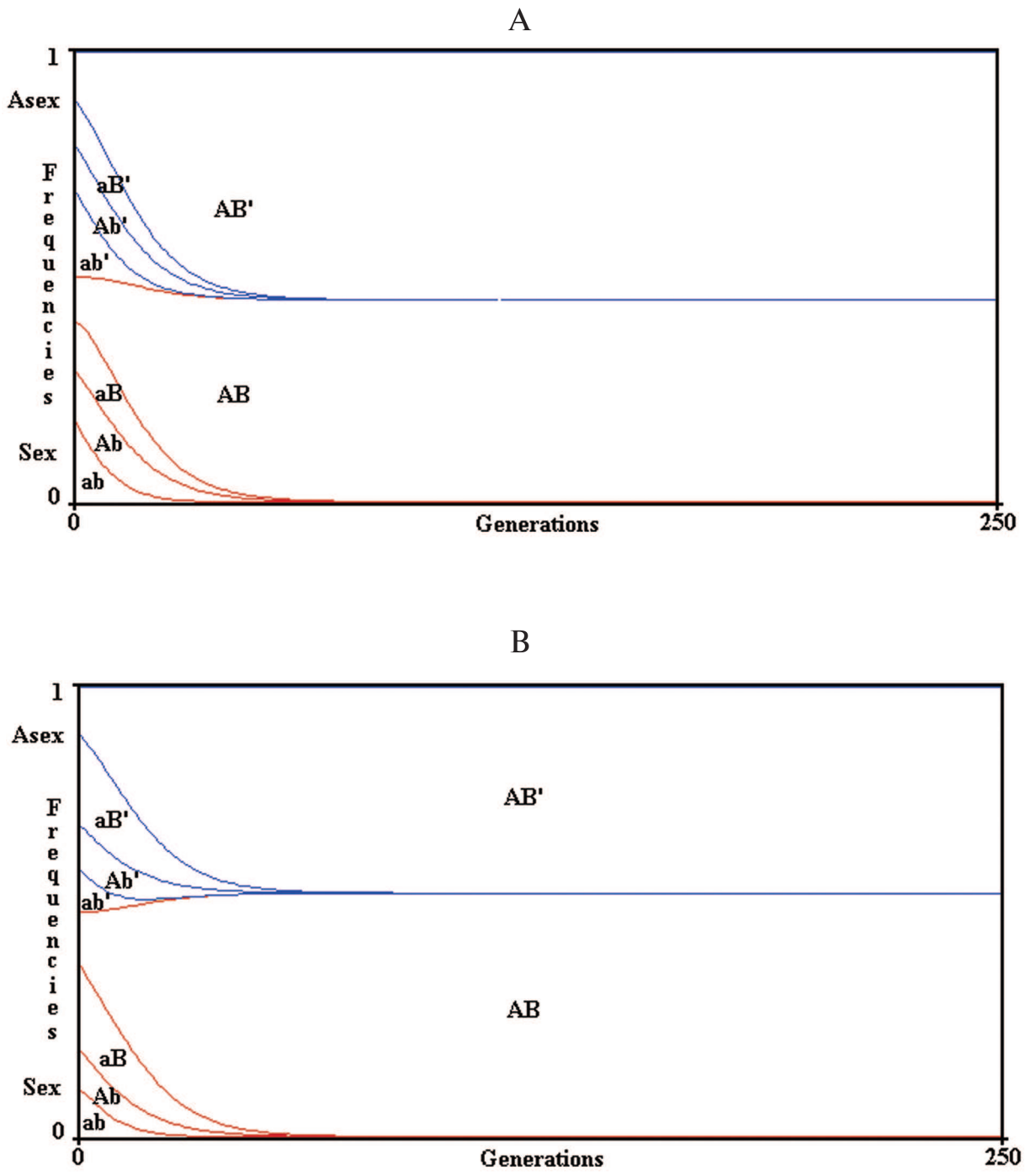


Fig. S5. Effects of the variations of *D*. 2G case. A) $D = +0.04$ (positive linkage disequilibrium): sex is disadvantageous; B) $D = -0.04$ (negative linkage disequilibrium): sex is advantageous. If the absolute value of *D* is greater, the disadvantage or advantage of sex increases proportionally.

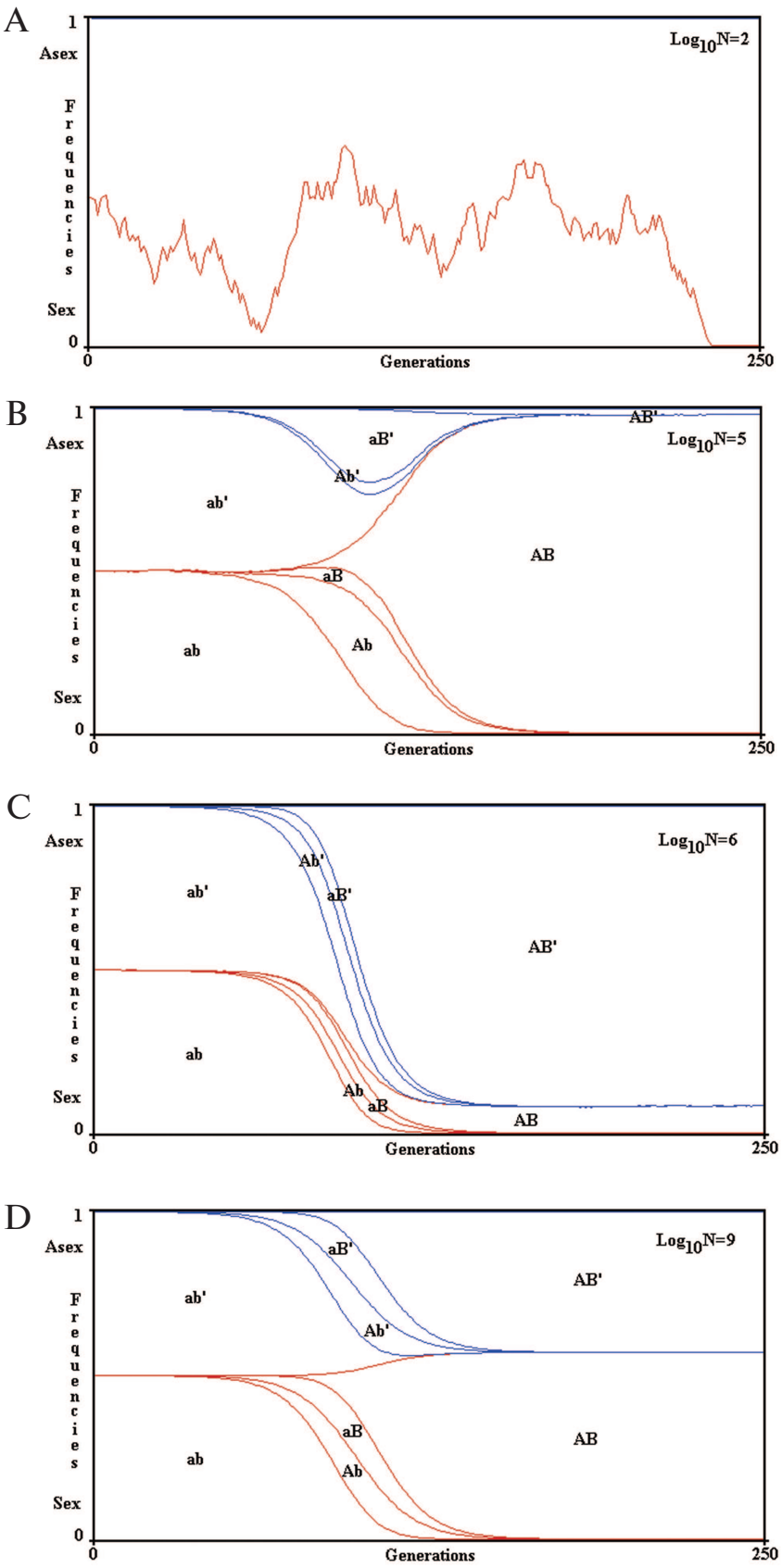


Fig. S6. 2G case, single simulations in finite populations. A) $\log_{10}N = 2$; B) $\log_{10}N = 5$; C) $\log_{10}N = 6$; D) $\log_{10}N = 9$. In the case (A), only genetic drift determines the fluctuation of R+ and R– values. In the cases (B), (C), and (D), the prevalence of R+ or R– is determined by the random antecedence of mutation onset in R+ or R–.

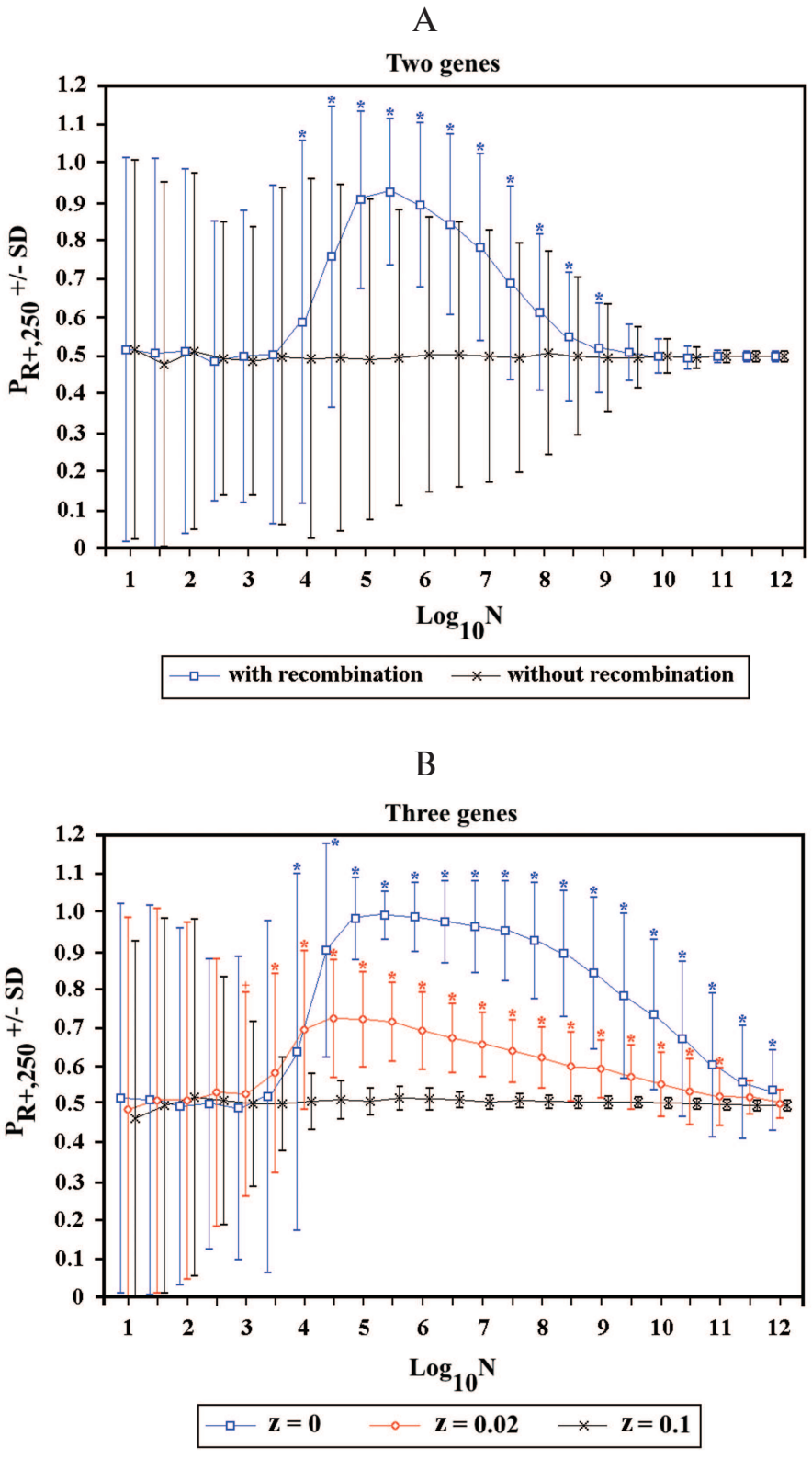


Fig. S7. Effects of the recombination in finite populations. A) 2G case; B) 3G case. The mean and standard deviation (SD) are reported for each point. For the series of simulations with recombination, an asterisk indicates a significant difference ($p < 0.001$) for each point compared to the corresponding point of simulations without recombination. In this and in the subsequent figures, to avoid the superimposition of SD bars, the symbols of the first and of the second series have been shifted slightly to the left and to the right, respectively. In addition, the results are always those obtained during the first runs of simulations. (Repetitions of the simulations for each series gave results that were equivalent to those of the first runs. However, these results have not replaced those of the first runs.)

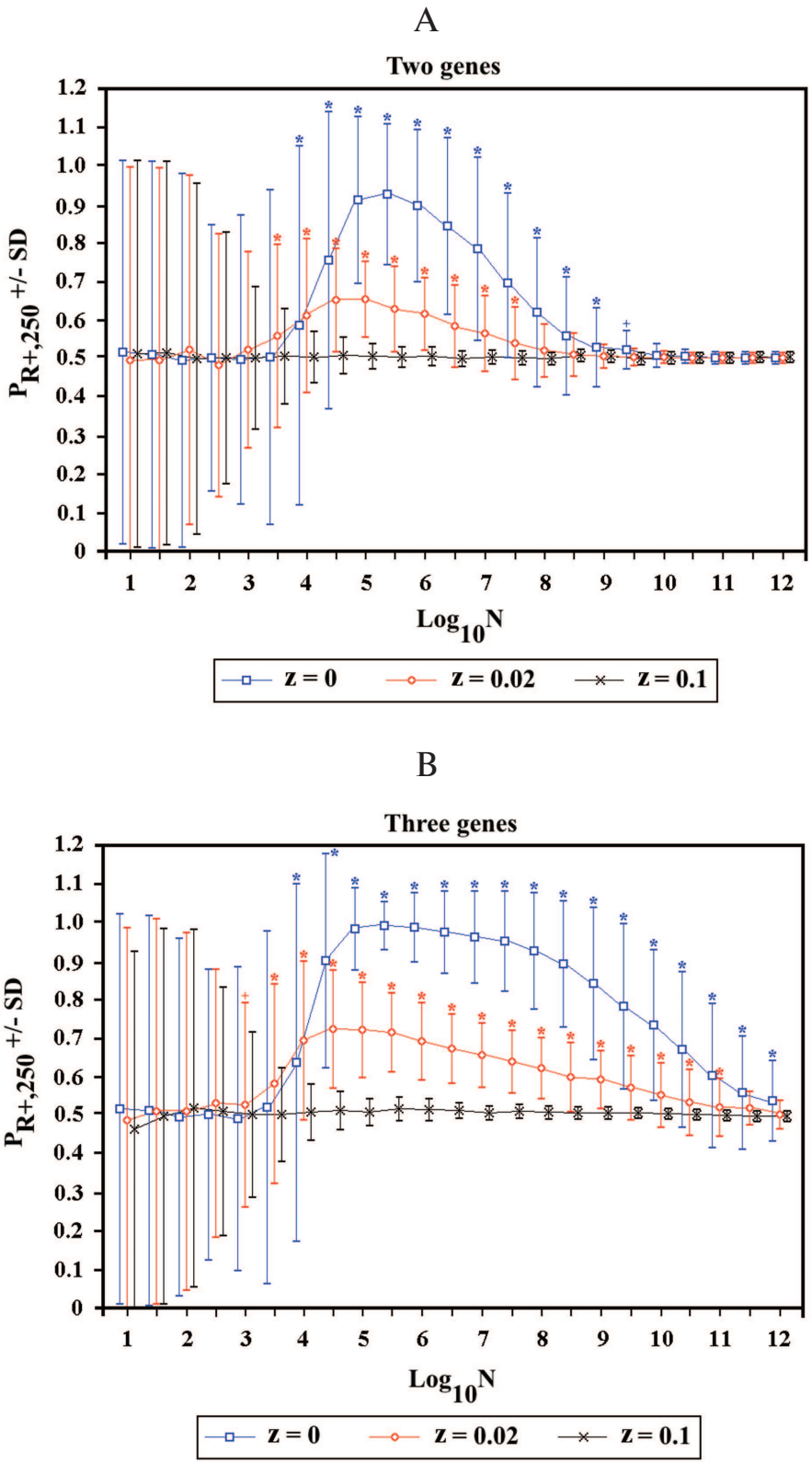


Fig. S8. Effects of the variations of z. A) 2G case; B) 3G case. The two series with $z = 0$ are the same as in Fig. S7 with recombination. When $z = 0.02$ the advantage for R+ individuals is greatly reduced, and when $z = 0.1$, there is no advantage. In these and in the subsequent figures, an asterisk or a cross indicate a significant difference ($p < 0.001$ and $p < 0.01$, respectively) for each point compared to the corresponding point of simulations without recombination in Fig. S7, a and b.

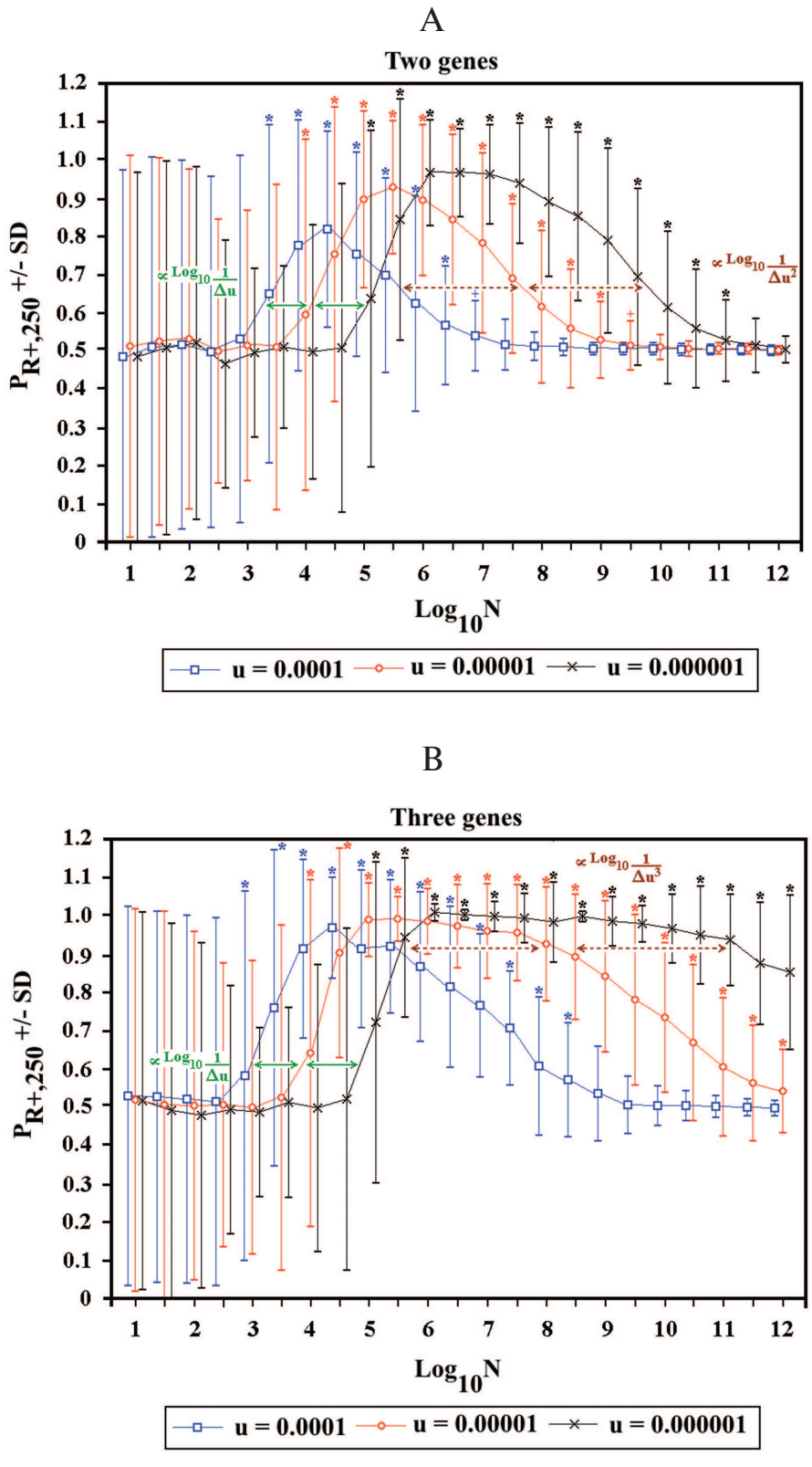
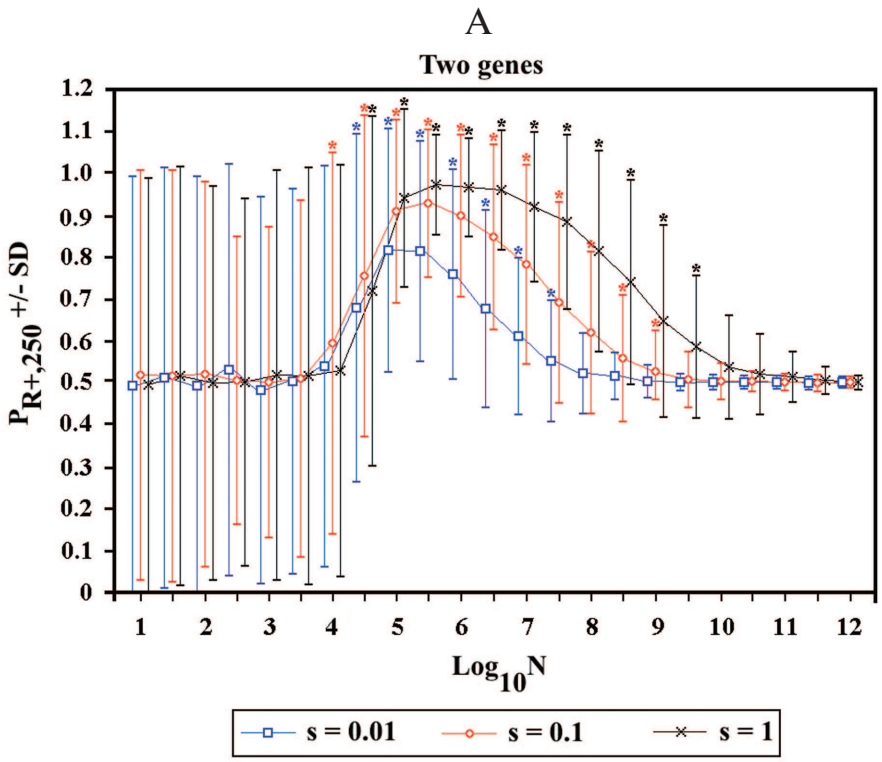


Fig. S9. Effects of the variations of u. A) 2G case; B) 3G case. The distance between the left sides of the curves is proportional to $\log_{10}(1/\Delta u)$, while for the right sides the distance is proportional to $\log_{10}(1/\Delta u2)$ in (A) and to $\log_{10}(1/\Delta u3)$ in (B). A variation of u modifies the curve of sex advantage. In particular, the left side is shifted to the left by an increase of u, and *vice versa*, in proportion to u (sex advantage is conditioned by mutation onset, which is proportional to u). The right side is shifted to the right or left in proportion to u^2 in the 2G case and to u^3 in the 3G case (sex advantage fades when two – in the 2G case – or three – in the 3G case – mutations arise at the same time and these events are proportional to u^2 and u^3, respectively).



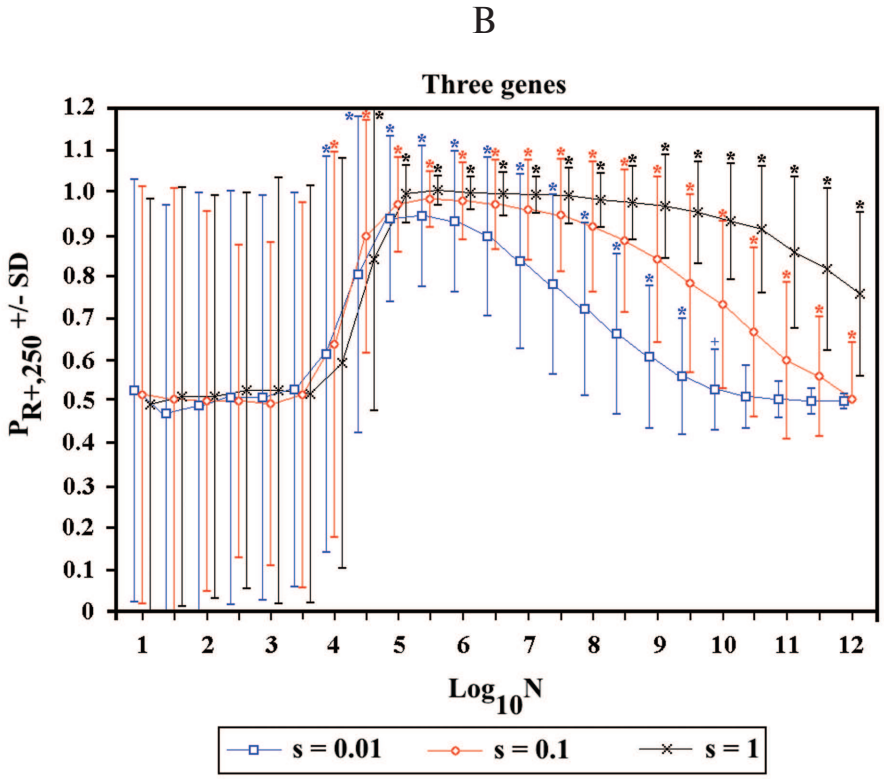


Fig. S10. Effects of the variations of *s*. A) 2G case; B) 3G case. With $s = 0.01$, simulations have been extended to 2000 generations. A variation of *s* modifies, in proportion, only the right side of the curve of sex advantage.

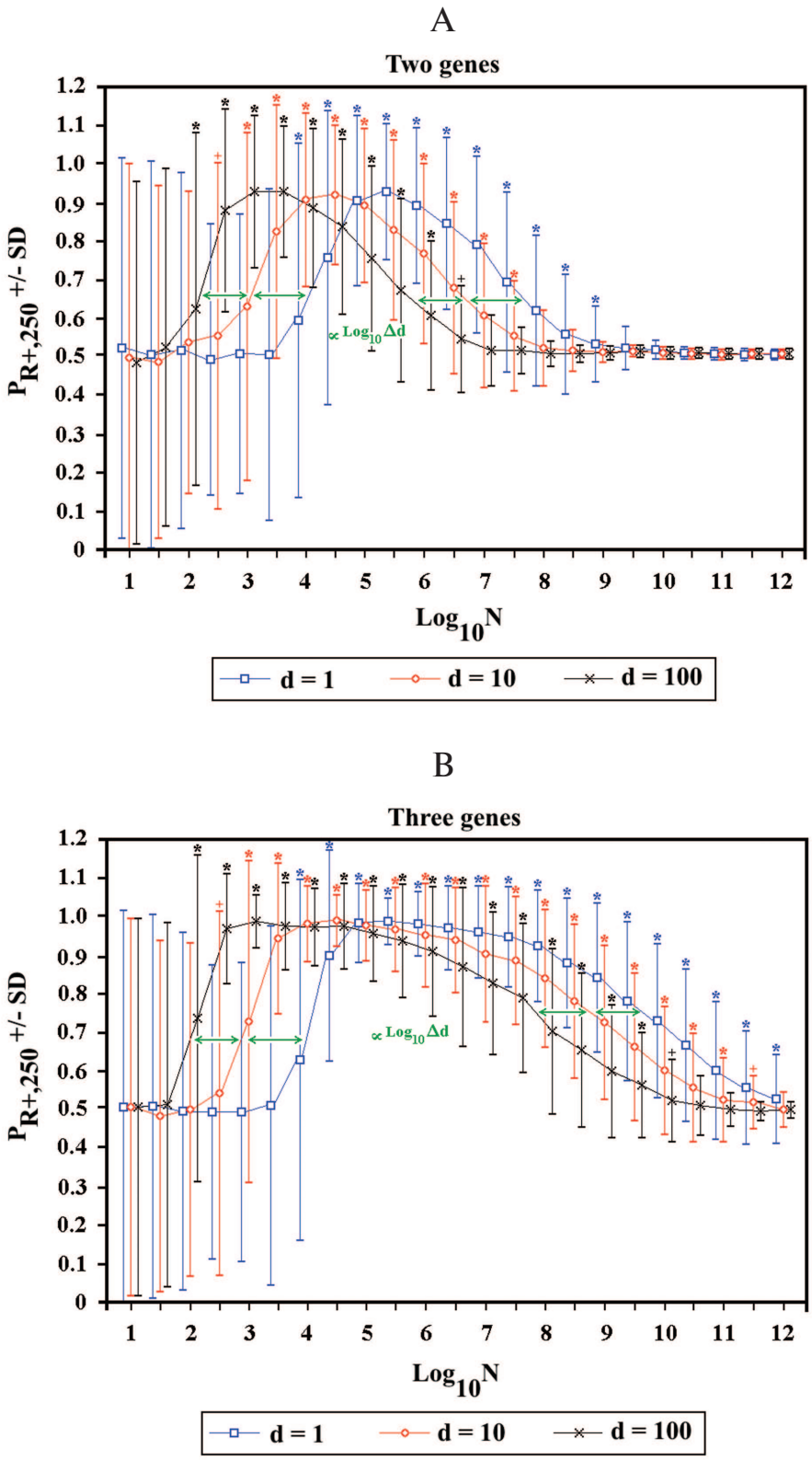
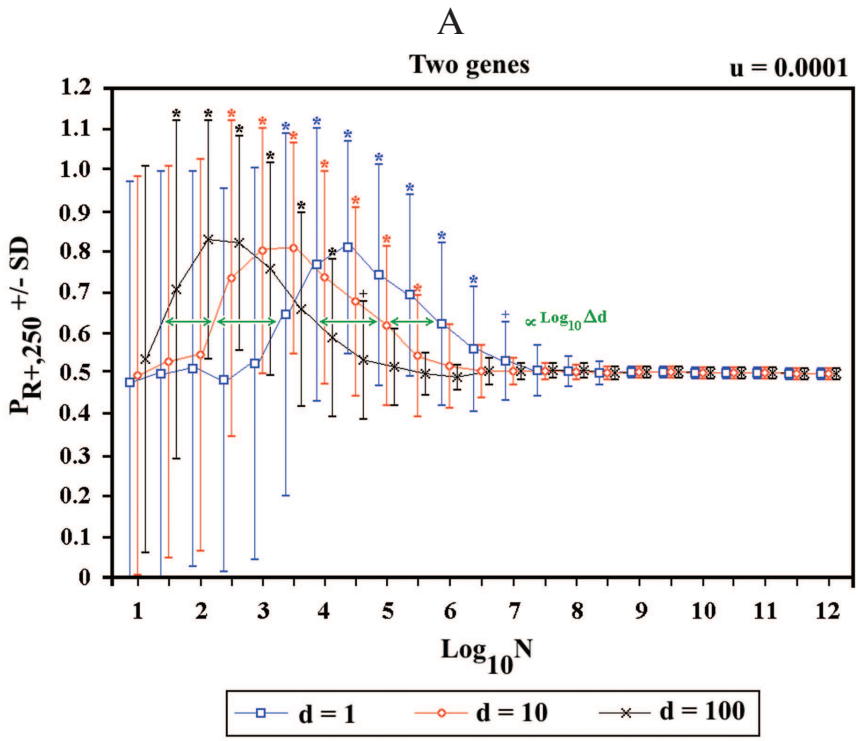


Fig. S11. Effects of the variations of *d*. A) 2G case; B) 3G case. When there is an increase of *d*, there is a shift to the left in both sides of the curves. The shift is proportional to $\log_{10}\Delta d$. The population (now defined as metapopulation) is divided in *d* demes, each composed of *N* individuals, with an interdemic interchange of individuals (*f*) equal to 0.1 per generation. The results show that, in terms of the advantage of sex, a metapopulation is equivalent to a single population of $d{\cdot}N$ individuals.



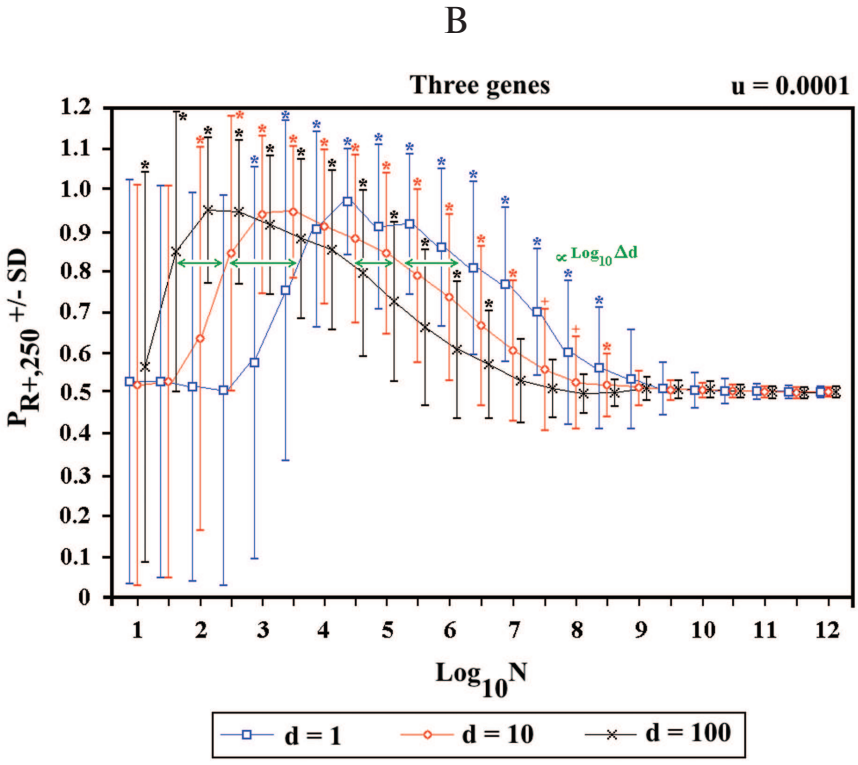


Fig. S12. Effects of the combined variations of *u* and *d*. A) 2G case; B) 3G case. The same conditions as in the previous figure, but the value of *u* is 0.0001 instead of 0.00001. The curves are shifted to the left by a logarithmic unity. In these figures, as in Fig. S11, an increase of *d* shifts both sides of the advantage curves of sex to the left in proportion to $\log_{10}\Delta d$. For the three genes case, sex results advantageous even for values of $\log_{10}N = 1$. This shows that a contemporary variation of *u* and *d* have multiplicative effects and, so, with many demes and high values of *u*, sex is advantageous even with small values of *N*.

SUPPLEMENT B

Modifications of Eqs. (10)-(15), which are necessary when $z > 0$. If the condition "c" is attenuated, namely if $z > 0$, in the 2G case, Eqs. (10), (11), and (12) become:

$$P_{a,n} = P_{ab,n} + P_{aB,n} + z\,(P_{ab',n} + P_{aB',n}); \qquad (10')$$

$$P_{ab,n+1} = 1/2\ P_{ab,n} + 1/2\ \frac{P_{a,n}}{T}\frac{P_{b,n}}{T}\ P_{R+,n}; \qquad (11')$$

$$P_{ab',n+1} = P_{ab',n} - 1/2\ z\ P_{ab,n} + 1/2\ \frac{P_{a,n}}{T}\frac{P_{b,n}}{T}\ z\ P_{R-,n}; \qquad (12')$$

and, in the 3G case, Eqs. (13), (14), and (15) become:

$$P_{a} = P_{abc,n} + P_{aBc,n} + P_{abC,n} + P_{aBC,n} + \\ + z\,(P_{abc',n} + P_{aBc',n} + P_{abC',n} + P_{aBC',n}); \qquad (13')$$

$$P_{abc,n+1} = 1/2\ P_{abc,n} + 1/2\ \frac{P_{a,n}}{T}\frac{P_{b,n}}{T}\frac{P_{c,n}}{T}\ P_{R+,n}; \qquad (14')$$

$$P_{abc',n+1} = P_{abc',n} - 1/2\ z\ P_{abc,n} + \\ 1/2\ \frac{P_{a,n}}{T}\frac{P_{b,n}}{T}\frac{P_{c,n}}{T}\ z\ P_{R-,n}; \qquad (15')$$

with $T = P_{R+,n} + z\ P_{R-,n}$ in both cases.