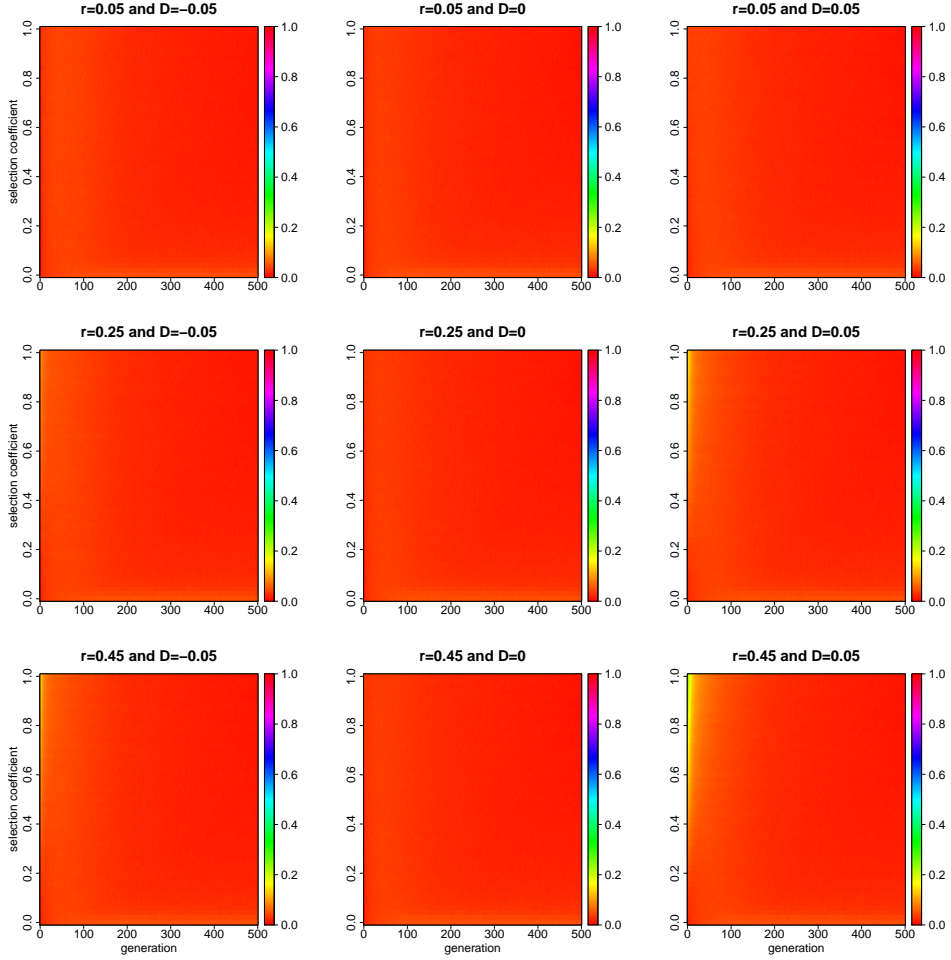RESULTS WITH DIFFERENT GENE ACTIONS

FIGURE 1. Dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_\mathcal{A}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely dominant. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 500$, $s_\mathcal{B} = 0.05$, $h_\mathcal{A} = 0$ and $h_\mathcal{B} = 0.5$.
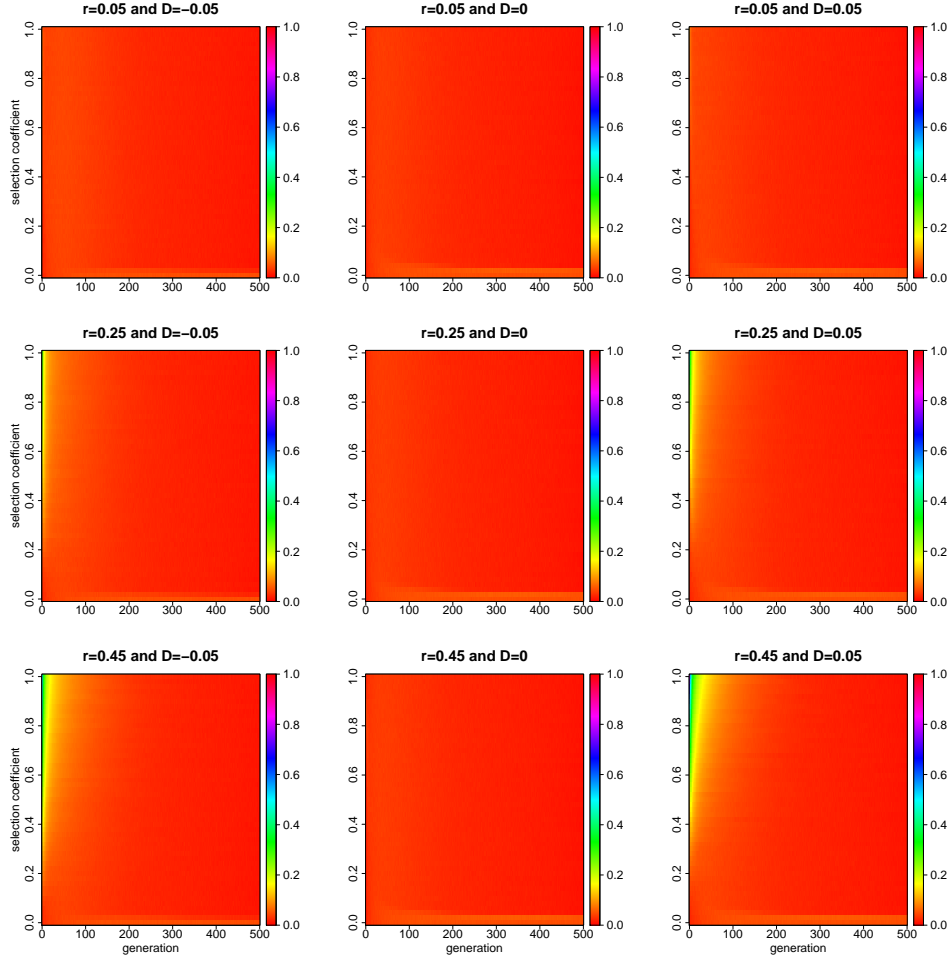
FIGURE 2. Dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_\mathcal{A}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population initially in different levels of linkage disequilibrium when gene action at locus $\mathcal{A}$ is completely recessive. We generate $M = 10^5$ independent realizations in Monte Carlo simulation and adopt $N = 500$, $s_\mathcal{B} = 0.05$, $h_\mathcal{A} = 1$ and $h_\mathcal{B} = 0.5$.

We simulate the dynamics of the Hellinger distance $H(\pi_1^{(v)}, \pi_1^{(f)})$ simulated with the varying selection coefficient $s_\mathcal{A}$ and recombination rate r over 500 generations under the two-locus Wright-Fisher model with selection for the population of 500 individuals initially in different levels of linkage disequilibrium in the following two particular scenarios according to the types of gene action at locus $\mathcal{A}$: completely dominant ($h = 0$) in Figure 1 and completely recessive ($h = 1$) in Figure 2, respectively. These illustrations confirm the conclusions we have achieved in our work and also

show that the difference in the behaviour of the two-locus Wright-Fisher model between viability and fecundity selection is more significant for completely recessive gene action than completely dominant gene action.