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Dependence of the Crossing Time on the Sequence Length in a Diploid Discrete-Time Mutation-Selection Model for a Finite Population¹ WONPYONG GILL², Pusan Natl Univ — This study examined the crossing time in the diploid discrete-time mutation-selection model in a finite population for a range of dominance parameters and selective advantages by switching on a diploid, asymmetric, bridged landscape, from an initial state, a steady state in a diploid, bridged landscape. The dependence of the crossing time on the sequence length was examined for a fixed extension parameter, which was defined as the mean Hamming distance from the optimal allele of the initial steady state divided by the sequence length. The boundary between the deterministic and stochastic regions in the diploid discrete-time mutation-selection model was characterized using the same formula as that in the haploid discrete-time mutation-selection model. The crossing time in a finite population with various population sizes, dominance parameters and selective advantages began to deviate from the crossing time for an infinite population at the critical sequence length. The crossing time for a finite population in the stochastic region was found to be an exponentially increasing function of the sequence length, whose rate was unchanged, regardless of changes in the population size, dominance parameter and selective advantage with a fixed extension parameter.

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