

Markov chain in the analysis of the chromosome segment in maize

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A biometric model was designed using the mathematical formalism relating to the discrete absorbent Markov chain in the canonical form, in order to analyse the evolution of the chromosome segment, taking recessive lethal genes linked with the grain yield factors through the generations, as a different approach to the classical mathematical ones. accordance with the theory of absorbent Markov chains, genotypes A, C, F, G, H and I act as absorbent states. Selfing genotype A produces the same cross in the next generation, therefore AA is also an absorbent non-lethal state. The transient states are BB, DD, EE and KK (Figures 1 and 2).

Afterwards, beginning with selfing crosses for independent segregation (loci with very weak linkage, practically independent for the segregation), the selfing crosses AA, CC, FF, GG, HH and II can be recognised as absorbent states, while BB, DD, and EE are equivalent to KK.

Under these conditions, and following Mendel's laws to calculate the resulting probabilities for selfing in the next generation,

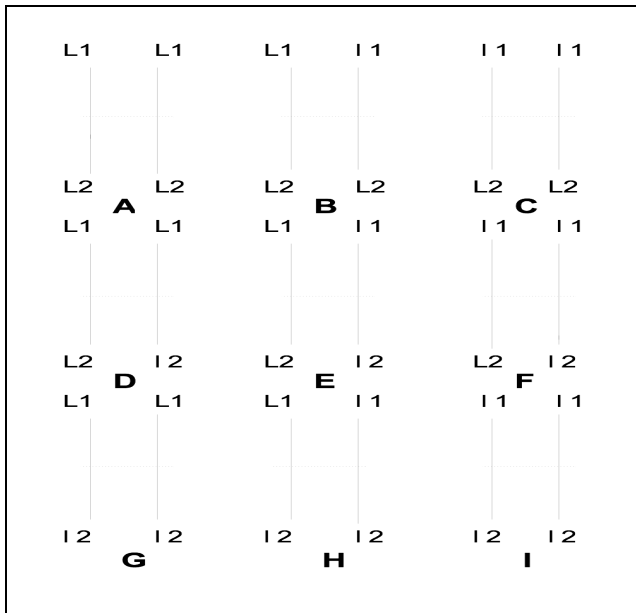


Figure 1. Mean separated chromosomes (really in the same chromosome with negligible linkage).

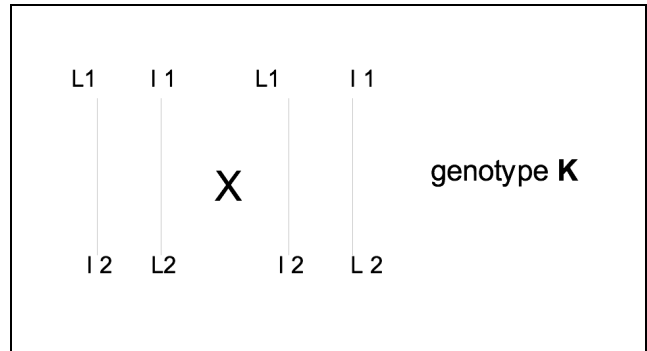


Figure 2. Balanced system (lethal in opposite chromosomes) fully linked loci.

results are given by the transition matrix P written in canonical form. For an absorbing chain, only transient and absorbent states must be considered. The transition matrix P can be written as four sub-matrices: sub-matrix O, a zero matrix of $s(r-s)$ order; sub-matrix Q, providing the probabilities for the transition between transient states; sub-matrix R, denoting the probabilities between transient and absorbent states; and sub-matrix S, $(r-s)(r-s)$ the identity matrix (Figure 3).

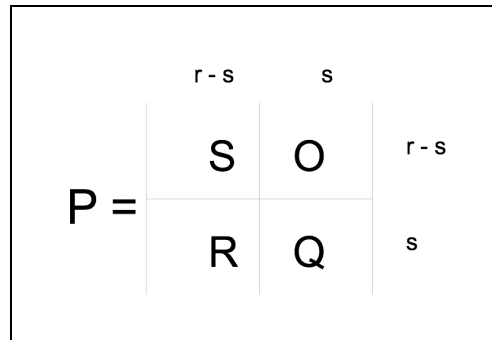


Figure 3. Matrix P, in canonical form; $r = 9, s = 3$.

A chromosome segment containing only recessive alleles remains in the population of two genotypes which have been denoted by A and K. These genotypes can be distinguished easily, with genotype K being an excellent marker for the study of chromosome segments and their association with yield in grain production.