

The Genomes of Recombinant Inbred Lines

Karl W. BROMAN, *Department of Biostatistics, Johns Hopkins University, USA*, E-mail: kbroman@jhsph.edu

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Abstract: Recombinant inbred lines (RILs) are formed by crossing two inbred strains (e.g., of mice), followed by repeated sibling mating (or, in some plants, selfing) to produce a new inbred line whose genome is a mosaic of the genomes of the initial strains. RILs can be powerful tools for genetic mapping. Recently, members of the Complex Trait Consortium have proposed the development of a large panel of eight-way RILs in the mouse, derived from eight genetically diverse parental strains. The use of such 8-way RILs will require a detailed understanding of the relationship between alleles at linked loci on an RI chromosome. We have extended the work of Haldane and Waddington (1931) on two-way RILs and describe the map expansion, clustering of breakpoints, and other features of the genomes of multi-way RILs as a function of the level of crossover interference in meiosis. The problem concerns the absorption probabilities of a Markov chain with a very large number of states.

References

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