Models of inversion polymorphism

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Three models of inversion polymorphism are discussed. Each employs
the assumptions of the standard two locus model, together with the
following:

    (a)   only paracentric chromosomal inversions are considered;

    (b)   recombination is suppressed within the inverted segment of
          inversion heterozygotes;

    (c)   inversions, whether in heterozygotes or homozygotes, have
          no effect on fitness.

The equations which result from these assumptions are recurrence
relations giving the frequencies of standard and inverted gametotypes in
terms of the gametic frequencies of the previous generation. Genotypic
fitness coefficients and recombination ratios are the underlying
parameters. Comparisons are made with other similar equations and
alternative interpretations of inversion polymorphism as a one locus
phenomenon are shown to be naive.

The only difference between the three models is that model 1 [1]
assumes the inversion includes both fitness determining loci, model 2 [2]
assumes the inversion includes one locus, and model 3 assumes the inversion
lies between the two loci. Since model 3 is a mathematical generalization
of model 2 which in turn generalizes model 1, the discussion proceeds
largely in terms of model 3.

The method of analysis is to find the equilibrium points of the
recurrence relations and investigate their stability. It is found that
there are only three classes of non totally polymorphic equilibria

(equilibria with at least one gametotype absent) called cases A, C, H . There are also three classes of totally polymorphic equilibria, cases J, L, M , but case L is shown to be rare because it requires a restriction on arbitrary fitness parameters. Case M provides an example of rigid inversion polymorphism. Case J is a bridge between case M which is unstable for small recombination and case J of model 2.

Case A is shown to be unstable. This disproves a recent conjecture that recombination altering mechanisms are selected for only if the equilibrium mean fitness is a decreasing function of recombination. Using the analysis of other boundary equilibria it is argued that both allelic and structural polymorphism will be maintained. A counterexample is given to the conjecture that recombination reducing mechanisms increase the mean fitness over a long time.

References

[1] Michael A.B. Deakin, "A model for inversion polymorphism", *J.
          Theoret. Biol.* 35 (1972), 191-212.

[2] Michael A.B. Deakin and Rodney B. Teague, "A generalized model of
          inversion polymorphism", *J. Theoret. Biol.* 48 (1974), 105-123.