FIGURE 1.—Single locus clines at equilibrium under weak selection. Curve A, a codominant locus, Equation 3. Equation 6 is similar: selection is approximately as effective in the center, but only $1/2$ as effective at the edge: the cline will be $\sqrt{(2/3)}$ as steep. Curve B, a dominant locus, equation (8). Distance is measured in standardized units of $\sigma/4\sqrt{s}$.
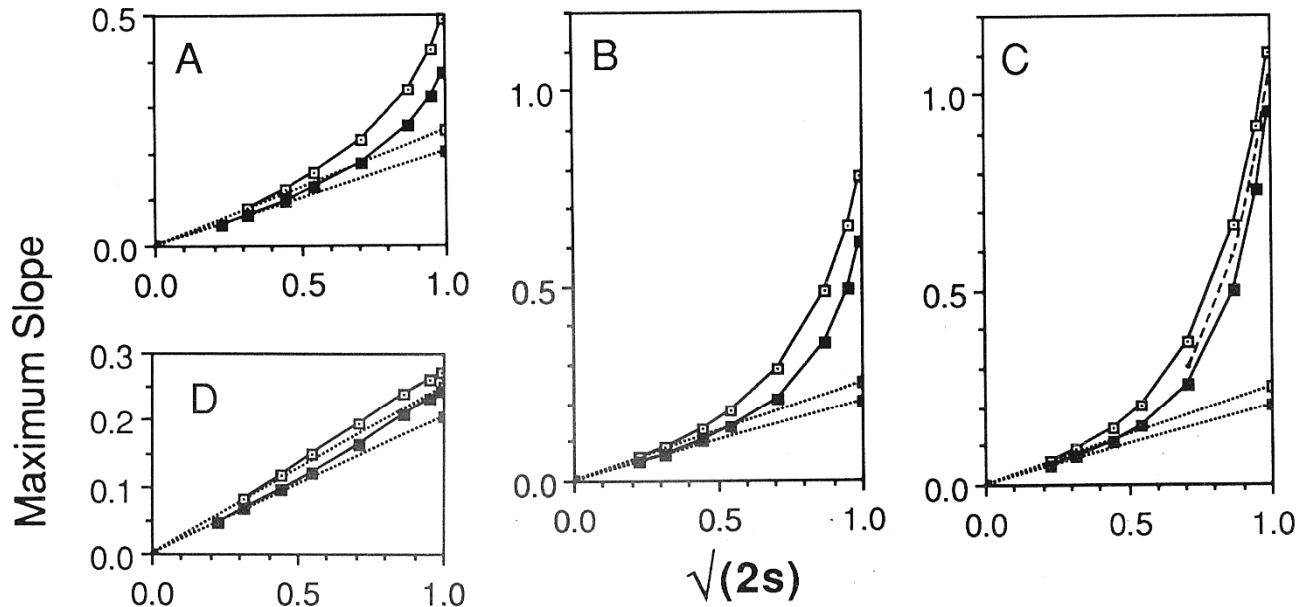
FIGURE 2.—Maximum slope (standardized by multiplying by σ) in simulated tension zones plotted against selection, $\sqrt{(2s)}$. (A) 1 locus; (B) 2 loci; (C, D) 3 loci; (A)–(C) all have the standard order reproduction–migration–selection; (D) has an alternative order of reproduction–selection–migration. The lines represent all dominant (open squares), and all codominant (filled squares) clines. In (C) the mean slope (dashed line) of clines in a zone with 1 codominant locus and 2 dominant loci is also plotted. The low s approximations for dominant genes ($\sqrt{[s/8]}$, upper dotted line), and codominant genes ($\sqrt{[s/12]}$, lower dotted line) are also shown in each figure.
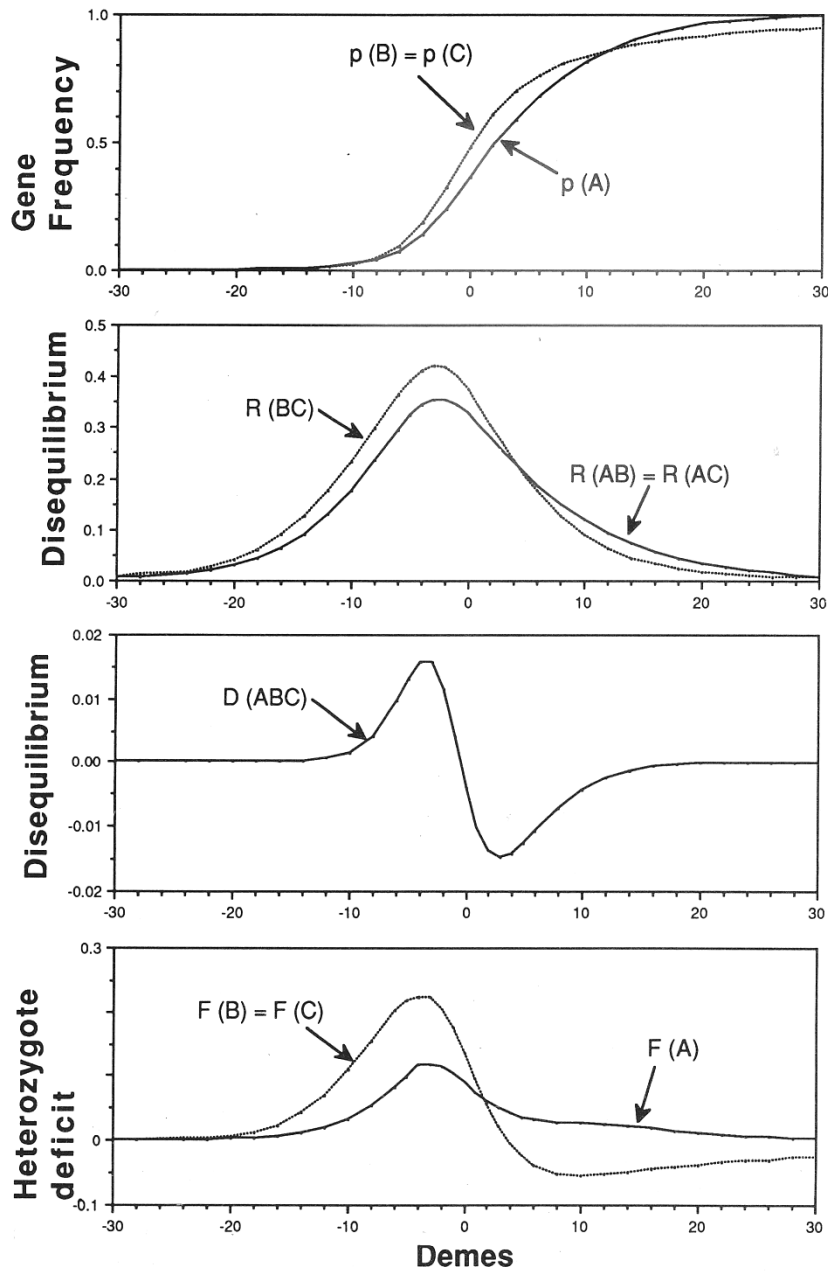
FIGURE 3.—Simulated three-locus tension zone consisting of one codominant locus (*A*) and two completely dominant loci (*B*, *C*). Such a hybrid zone occurs in Heliconius (MALLET and BARTON 1989). The clines are stabilized by frequency-dependent selection, $2s = 0.5$ per locus, and migration, $\sigma^2 = 15$ demes per generation. The figure shows variation along a demic continuum of all the parameters needed to reconstruct the genotypic distributions. Only the central section of the simulation is shown out of a total of 150 demes modeled. The simulation has been running for 250 generations since contact between fixed populations, has stabilized in shape and is moving to the left at a constant speed of ~0.20 demes (~0.051 dispersal distances, σ) per generation. At lower selection pressures such a zone would separate into a stationary *A* cline and a pair of rapidly moving clines, *B* and *C*. Top to bottom: gene frequencies; two-way disequilibria, R_{IJ}; three-way disequilibrium D_{ABC} (defined as in SLATKIN 1972); and heterozygote deficits, F_{IS}.
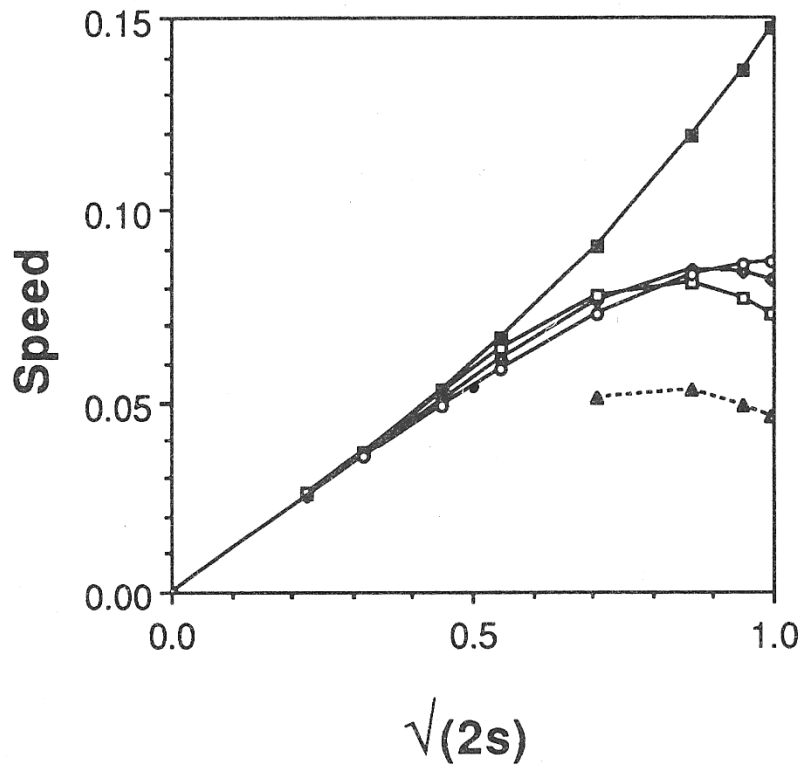
FIGURE 4.—Cline movement due to dominance. Curves show movement speeds of tension zones (measured in units of dispersal distances, σ, per generation) plotted against selection pressure, $\sqrt{(2s)}$. Open symbols and solid lines: circles, 1 dominant locus; diamonds, 2 dominant loci; squares, 3 dominant loci; triangles and dashed lines, 1 codominant and 2 dominant loci. All are for the standard order (reproduction–migration–selection) except for the upper curve (filled squares) which is for 3 dominant genes with the order reproduction–selection–migration. Cline movement due to advantage of one of the homozygotes also shows an approximately linear dependence on $\sigma\sqrt{s}$ (BARTON 1979).
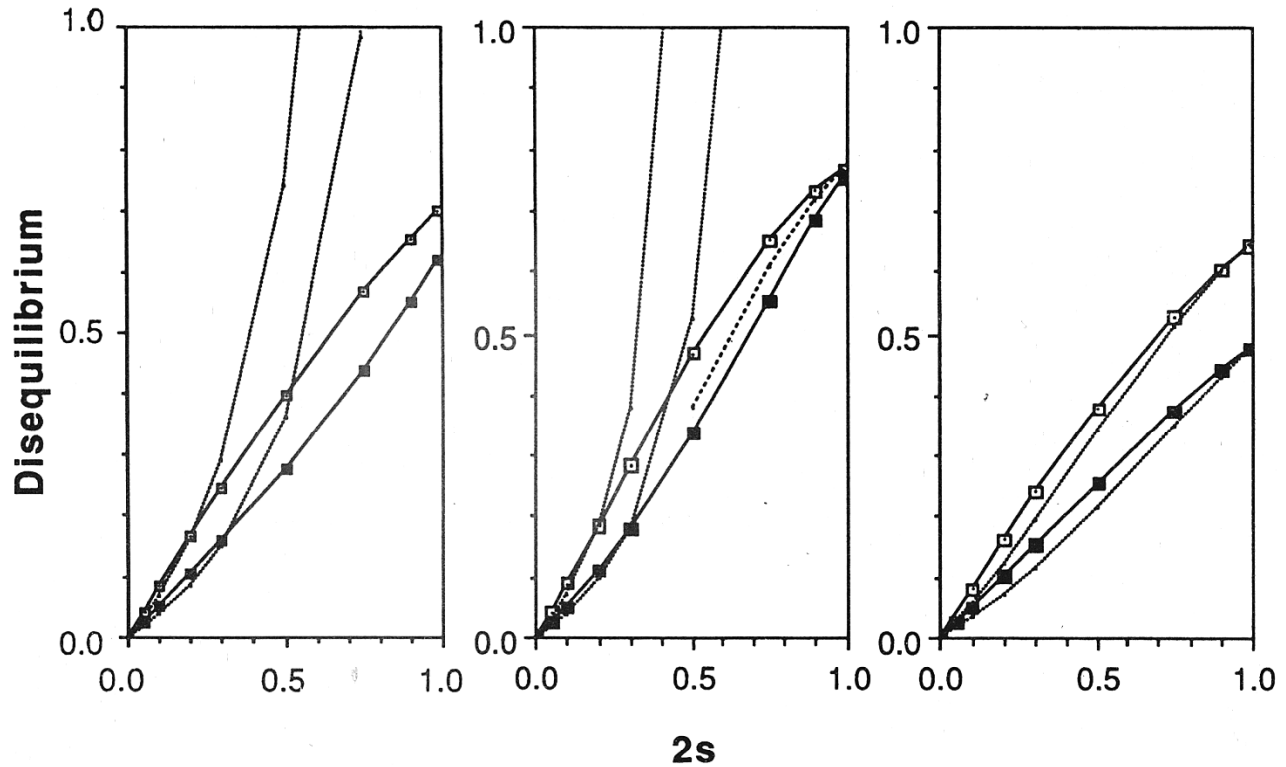
FIGURE 5.—Disequilibria. The maximum gametic correlation R is plotted against the per locus selection pressure $2s$. Lines represent values from simulations; all loci dominant (open squares), all loci codominant (closed squares), mean disequilibria when 1 locus is codominant, and 2 others are completely dominant (dashed lines in center graph). Dotted lines represent predictions based on Equation 9 and the actual dp/dx produced in the simulations (Figure 2). Left, 2 loci; center, 3 loci, using the standard order (reproduction–migration–selection); right, 3 loci using the order reproduction–selection–migration.
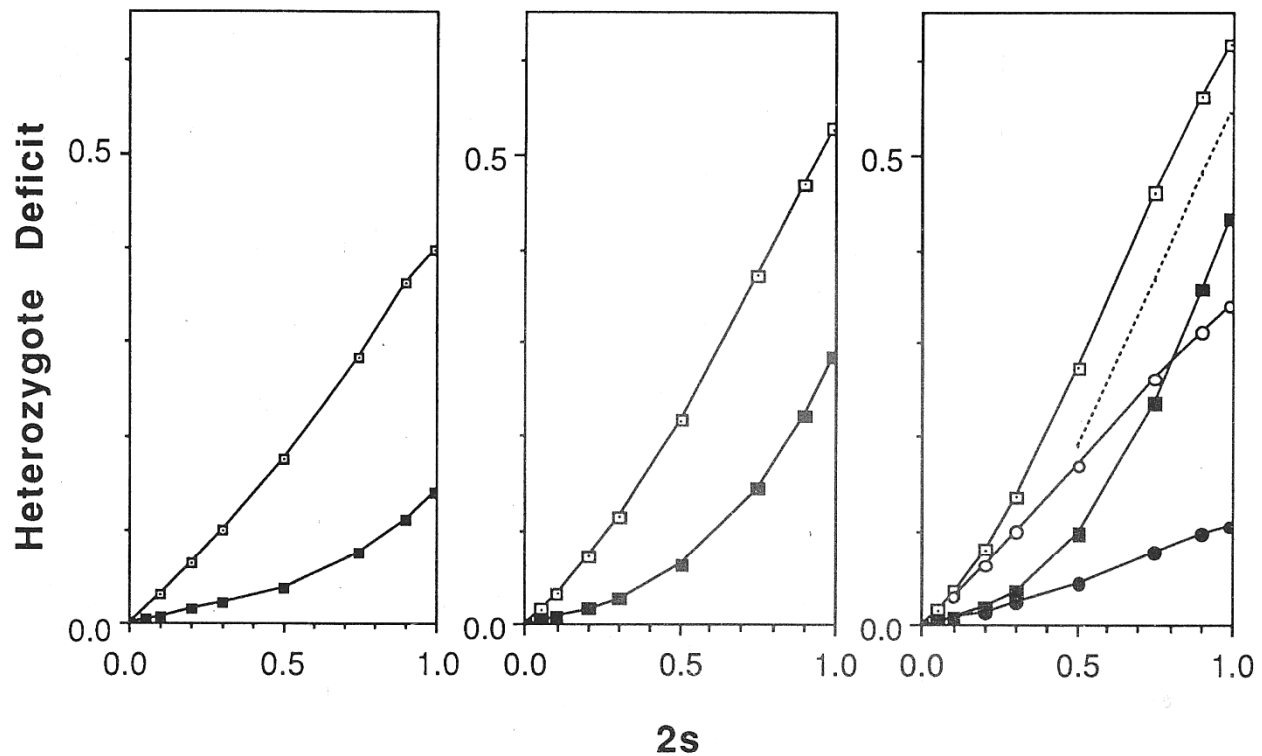
FIGURE 6.—Heterozygote deficit. The maximum heterozygote deficit F is plotted against $2s$. Dominant loci, open symbols; codominant loci, closed symbols. Left, 1 locus; center, 2 loci; right, 3 loci; dashed line indicates 1 codominant and 2 dominant loci. The standard order (reproduction–migration–selection) is plotted in square symbols; the order reproduction–selection–migration is plotted in circles.
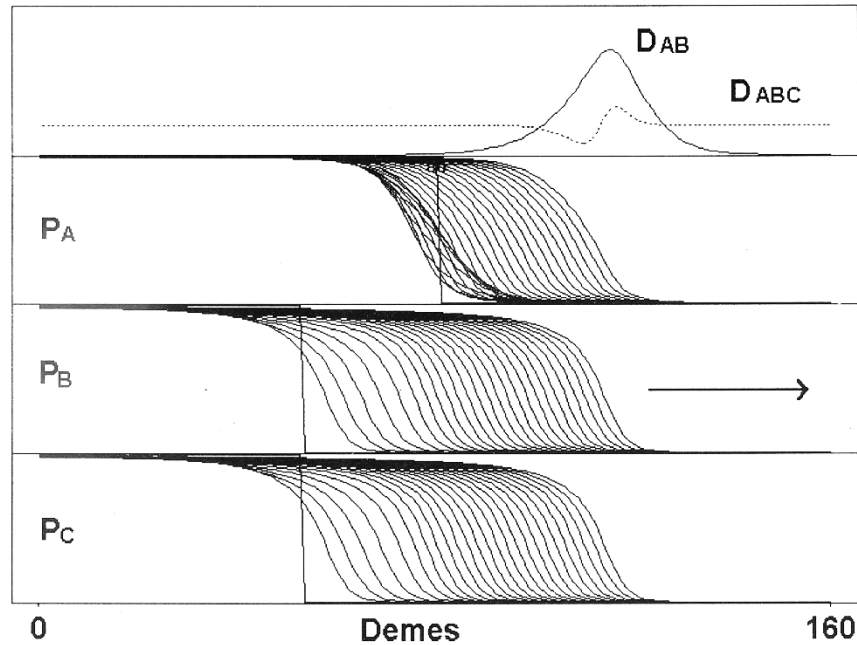
Fig. 16.3   Cline movement as phase III of Wright's shifting balance. The three lower panels show 250 generations of the movement of a three-locus (A, B, C) diploid warning colour cline system (a model of the *Heliconius* three-locus hybrid zone in Tarapoto—see Mallet and Barton (1989*b*) and Mallet *et al.* (1990)) in a linear environment of 160 demes. Each curve represents the gene frequency at ten-generation intervals. These clines are moving to the right under the influence of dominance alone, although adaptive pressures will produce very similar types of cline movement. The simulation starts with two secondary contacts between three patches, a patch on the left fixed for alleles A, B, and C; a central patch fixed for A, b, and c; and a patch on the right fixed for a, b, and c. Initially the identically selected clines at dominant loci B, C move at a constant rate of 0.37 demes per generation towards the symmetrical stationary cline at the codominant locus A. As the dominant clines approach, the A cline is briefly attracted back towards these moving systems. After about 30 generations of cline coalescence, all three clines move off together in the same direction at a reduced velocity of about 0.20 demes per generation. Clines will 'stick together' because of gametic disequilibrium only under conditions of high selection, as here, or if there is epistasis. Selection against foreign phenotypes at each locus is set at 50%, equivalent to heterozygous disadvantage of $s = 0.25$, and is similar to selection observed in *H. erato* of $s \approx 0.23$ per locus (Mallet *et al.* 1990). Gaussian migration is set to $\sigma^2 = 15$ demes^2 per generation. Two-locus gametic disequilibrium under these conditions (top panel) reaches about $D_{AB} \approx +0.09$ (D_{AC} and D_{BC} have similar values), giving a gametic correlation coefficient of $R_{AB} \approx 0.36$ at the centre, and the three-locus disequilibrium varies sigmoidally in the hybrid zone, $D_{ABC} \leq |0.016|$. For further details of the model see Mallet and Barton (1989*a*).