The interaction of Selection and Linkage—Heterotic Models I

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Nothing in Biology Makes Sense Except in the Light of Evolution. — Theodosius Dobzhansky

Background | What it is?

In 1960s, we known that:

- Single loci, Selection, Population genetic change
- But two-loci or mulit-loci do not.

So the paper provide some two-loci model.
(need picture)

Background | What it is?

Here are results of Lewontin and Kojima:

1. If the fitnesses are additive between loci, linkage does not effect the final equilibrium state of the population.
2. If linkage is tighter than the value demanded by the magnitude of the epistasis there may be permanent linkage disequilibrium.
3. The rate of genetic chagne with time is affected by the tightness of the linkage.
4. In some cases stable gene frequency equilibria are possible only if linkage is tight enough.

Background | What it is?

Three main modes of selection in natural and artificial populations:

- **Heterotic Models**
- Series optimum selection
- Undirectional selection(Neutral Theory)
  (need picture)

Mathematics of Selection and Linkage | What is the mean?

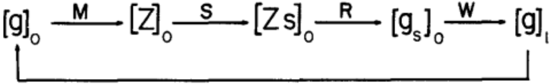

FIGURE 2.—The genetic transformation, T, broken up into its components during a single generation.

Figure 1: The genetic transformation T

Heterotic Selection Model | How to represent?

Evidence:

Heterosis is important, then

$$degree\ of\ heterosis = f(number\ of\ heterozygosity)$$

Hypothesis:

Epistatic(   ) $==>$ interaction of linkage and selection

Test

- Two-locus model
- Five-locus model

Heterotic Selection Model | How to represent?

TABLE 3

Relative fitnesses of the nine genotypes for two-locus heterotic models

	AA	Aa	aa
(a) Model 1: asymmetric heterotic model with epistasis			
BB	.40	.60	.30
Bb	.60	1.00	.50
bb	.50	.70	.40
(b) Model 2: asymmetric partially heterotic model with epistasis			
BB	.5000	.5000	.3750
Bb	.5625	1.0000	.3125
bb	.3750	.4375	.3750
(c) Model 3: mixed overdominance, underdominance model			
BB	.90	.20	.90
Bb	.20	1.00	.20
bb	.90	.20	.90

Figure 2: Relative fitness for two-locus heterotic models

Heterotic Selection Model | How to represent?

TABLE 4

Results of Model 1. Symbols are as explained in the text

R	g_{00}	g_{01}	g_{10}	g_{11}	p	r	D	D'	$\overline{W}$
.00	.50000	.00000	.00000	.50000	.50000	.50000	+.25000	+1.00000	.70000
	.00000	.58333	.41667	.00000	.58333	.41667	—.24306	—1.00000	.70836
.01	.46225	.05195	.01777	.46805	.51420	.48002	+.21543	+.92384	.69014
	.02359	.55936	.38914	.02791	.58295	.41273	—.21700	—.90191	.70378
.02	.42023	.10875	.03871	.43231	.52898	.45894	+.17746	+.82093	.68044
	.04984	.53246	.35855	.05915	.58230	.40839	—.18797	—.79042	.68902
.03	.37049	.17398	.06621	.38932	.54447	.43670	+.13272	+.66717	.67088
	.08051	.50089	.32332	.09528	.58140	.40383	—.15449	—.65799	.67950
.04	.11793	.46211	.28148	.13848	.58004	.39941	—.11374	—.49096	.67038
.06	.20082	.37418	.19621	.22879	.57500	.39703	—.02747	—.12033	.65954
.08	.21773	.35566	.18039	.24622	.57339	.39819	—.01054	—.04616	.65882
.10	.22172	.35125	.17676	.25032	.57297	.39848	—.00659	—.02886	.65878
.30	.22703	.34539	.17195	.25563	.57242	.39898	—.00135	—.00591	.65862
.50	.22766	.34473	.17141	.25620	.57239	.39907	—.00076	—.00327	.65862

Figure 3: Results of Model1

Heterotic Selection Model | How to represent?

TABLE 10

Results of five-locus experiments in Drosophila melanogaster *with genes* se, ss, k, e and ro. *Data of* Dr. Grace B. Cannon

		Population and week								
		Population 20			Population 21			Population 22		
		0	28	50	0	28	50	0	28	50
(a) Gene frequencies										
se		.007	.102	.058	.007	.044	.073	.005	.026	.037
ss		.012	.052	.216	.012	.078	.203	.009	.106	.186
k		.012	.026	.200	.012	.100	.177	.009	.092	.175
e		.012	.013	.174	.012	.133	.219	.009	.106	.181
ro		.007	.064	.084	.007	.066	.094	.005	.026	.048
(b) *D* and *D′* values										
ss–k	*D*		+ .0247	+.1408		+.0610	+.1166		+.0693	+.1328
	D′		+1.0000	+.8980		+.6616	+.8265		+.8426	+.9323
k–e	*D*		− .0003	+.1182		+.0781	+.1231		+.0823	+.1173
	D′		−1.0000	+.8491		+.9008	+.8905		+1.0000	+.8184
ss–e	*D*		+ .0123	+.1154		+.0588	+.0907		+.0810	+.1039
	D′		+1.0000	+.8459		+.8695	+.5721		+.8547	+.7052

Figure 4: Results of five-locus experiments

What about the following and question?

-Epistasis is required in order for linkage to be important in natural selection.

-Five-locus models show *cumulative* effect of the linkage along the chromosome.