NOTES AND COMMENTS

THE 2×2 GENOTYPE-ENVIRONMENT TABLE

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If two genotypes or groups of genotypes, G_0 and G_1 , are raised in each of two environments, E_0 and E_1 , the four resulting phenotypes may, in respect

	G ₀	G ₁	Mean
$\begin{array}{cccccccccccccccccccccccccccccccccccc$	m+d+e+g m+d-e-g	m-d+e-g m-d-e+g	m+e m-e
Mean	m+d	m-d	m

TABLE 1

of any quantitative character, be expressed in terms of four parameters. In table 1, m stands for the overall mean, d represents the average genotypic

TABLE 2

	G ₀ G ₁		G ₀		G1
E ₀		00	d+e+g	01	e
E1	•	10	d	II	g

effect, e the average environmental effect, and g the genotype-environment interaction. These parameters were recently used by Mather and Morley Jones (1958) in their study of genotype-environment interactions in quantitative inheritance.

In the following we will compare in terms of d, e and g the *relative* magnitudes of the phenotypic values, to be labelled 1, 2, 3 and 4 in descending order. For ease of inspection table 1 may be transformed into table 2 by adding to its elements -m+d+e+g and dividing by 2.

Haldane (1946) compared the relative magnitudes without the use of parameters, and dealt with $3 \stackrel{!}{=} 6$ situations, left after assigning the largest phenotypic value to oo. This implies (table 2) e+g>0, d+g>0, and d+e>0, *i.e.* not more than one of the parameters is allowed to become

negative, and its absolute value must be smaller than the value of the two positive ones. Haldane's six types can be described as follows :----



Mather and Morley Jones (*loc. cit.*) took all three parameters as positive in that they omitted the modulus sign from the inequalities, and therefore did not cover all possible situations.

The present author proposes a modified approach as (1) it seems more consistent to take the same two parameters as positive in all cases, and as (2) it is customary in biometrical genetics to define d as non-negative. Let us define d and e as non-negative and consequently allow only g to take sign. This means that the four phenotypic values must be arranged in table 1 so that $oo+10\ge 01+11$, as $d\ge 0$, and $oo+01\ge 10+11$, as $e\ge 0$. Then with g<0 four new sequences of magnitude arise, viz. 3' (d>-g>e)as a counterpart of 3 (d>g>e), etc., in which oo is not the largest phenotype. The 6+4 = 10 types have been listed in table 3. Inspecting this table with the help of table 2 we see :—

- 1. Table 3 is symmetrical for d > e, *i.e.* 10>01, and e > d, *i.e.* 10<01.
- 2. g>0 implies that oo is the largest phenotype, g<0 that 11 is the smallest.
- 3. If g>0, then 00-10>|01-11| and 00-01>|10-11|. This means that G_0 is the less stable genotype and at the same time E_0 the most differentiating environment. If g<0 this holds for G_1 and E_1 respectively.
- 4. If d > |g| and d > e (cases 1*a*, 3 and 3'), then G_0 is the highest "yielder" irrespective of environment: G_0 shows unconditional superiority. If in additon |g| > e (cases 3 and 3'), then G_0 and G_1 have their highest values in different environments. Thus the superiority of the environment is conditioned by the genotype. This may be described as conditional superiority of the environment.

If e > |g| and e > d (cases 1b, 2 and 2'), then E_0 shows unconditional superiority. If in addition |g| > d (cases 2 and 2'), then

TABLE 3

The possible comparisons in terms of the parameters d, e and g (cf. Table 1), of four phenotypes obtained by raising two genotypes in each of two environments. The phenotypic values have been labelled 1, 2, 3 and 4 in descending order of magnitude. The parameters d and e have been defined as non-negative. A line indicates equality of phenotypic values. Type numbers have been added to the cases where all four values are different.



 E_0 and E_1 induce the "better performance" in different genotypes. Thus the superiority of the genotype is conditioned by the environment : conditional superiority of the genotype.

If |g| > d and |g| > e (cases 4a, 4a', 4b and 4b'), then there is no unconditional superiority of either kind : *specific adaptation*.

Turning now to the cases of two or more phenotypic values being equal, we find that each of them corresponds uniquely to a parameter equality (cf. table 2) :—

d = -g	$\therefore 00 = 01$	e = -g .	00 = 10
$\mathbf{d} = \mathbf{g}$	IO = II	$e = g$ \therefore	01 = 11
d = g = o	$ \therefore \begin{cases} 00 = 01 \\ 10 = 11 \end{cases} $	$e = g = o$ $\therefore \left\{$	00 = 10 01 = 11
d = e	10 = 01	d = e = -g	$\therefore 00 = 01 = 10$
d = e = 0	. ∫10 = 01	$\mathbf{d}=\mathbf{e}=\mathbf{g}$	$\therefore 01 = 10 = 11$
<u> </u>	(00 = 11)	$\mathbf{d} = \mathbf{e} = \mathbf{g} = \mathbf{o}$	$\therefore 00 = 01 = 10 = 11$

It should be noted that d = 0, e = 0 or g = 0 does not in itself lead to equality of phenotypic values. The different cases, apart from oo = oi = 10 = 11, have been inserted in table 3.

Change in environment or selection in populations of genotypes may cause the different types to pass into each other. When by some selection device g is increased, *e.g.* type 4a', changes into 3', 1a, 3 and 4a respectively. Decrease of d leads from, *e.g.* type 1a via 1b to 2 or 2', depending on whether g>o or g<o. When we then allow d to become negative, we obtain e>-d>|g| and finally -d>e>|g|. These types derive from 1b and 1a by interchanging the columns. Having defined d as non-negative, however, the selection result will under the present approach make the particular population change its label G_0 into G_1 or *vice versa*.

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