NOTES AND COMMENTS

THE USE OF THE DIALLEL CROSS ANALYSIS FOR INVESTIGATING SPECIES DIFFERENCES

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The diallel cross analysis first proposed by Jinks in 1954 is now generally accepted as a useful and powerful device for investigating the nature of genetic differences controlling quantitative characters. It has been widely used to investigate differences between inbred lines and between varieties within numerous species. It is clear that the analysis could also be useful in the investigation of variation between more distantly related parents or populations, in particular between species, when it could be expected to throw some light on the nature of the genetic differences by which separate species have diverged during the course of their evolution. The results should enable us then to describe, with respect to particular characters, the divergence of specific genotypes in strictly genetic terms, that is with respect to the dominance, interaction and other properties of genes or gene systems which distinguish them.

TABLE 1

Time (in days) between germination and the development of the second leaf in six rye species and species hybrids

	<i>c</i>	<i>a</i>	<i>m</i>	<i>v</i>	<i>d</i>	<i>t</i>
<i>c</i>	1.21					
<i>a</i>	9.66	7.50				
<i>m</i>	9.80	16.65	12.41			
<i>v</i>	14.25	9.48	7.10	7.35		
<i>d</i>	19.18	11.55	24.75	31.91	25.90	
<i>t</i>	3.30	10.47	16.11	15.70	20.43	2.33

c = *S. cereale* ; *a* = *S. ancestrale* ; *m* = *S. montanum* ;
v = *S. vavilovii* ; *d* = *S. dighoricum* ; *t* = *S. turkestanicum*.

The present brief report demonstrates the use of such a diallel analysis applied to one of many characters being investigated in species within the genus *Secale*. The character in question is the average length of time between germination and the development of the second leaf in genotypes produced from crosses within and between the species. The seeds were obtained from crosses between at least three pairs of plants within and between each species. Because of the shortage of seeds, particularly in some interspecific crosses, the seeds were mixed. Seeds were then sown in two replicates with 10 seeds each.

There was excellent correspondence between replicates and an analysis of variance showed highly significant differences between genotypes ($P = < 0.001$). The W_r/V_r graphs (see Jinks, 1954) from the pooled data (table 1) indicate how these differences are determined. In fig. 1 the W_r/V_r

FIGS. 1 and 2.— W_r/V_r regressions for the interspecific diallel cross. In fig. 1 (top), the complete 6×6 , and, in fig. 2 (bottom), with *S. vavilovii* removed.

regression has a slope of 0.58 ($P = 0.05-0.10$), and is interpreted as indicating non-allelic interaction between parental gene combinations. Following the procedure of Jinks (1954), the removal of *S. vavilovii* from the diallel table gives the W_r/V_r graph for a 5×5 diallel shown in fig. 2. Here the W_r/V_r

regression is significant ($P = < 0.01$) and has a slope not significantly different from 1.0. Only the removal of *S. vavilovii* from the 6×6 data gives this result and it is concluded therefore that the interaction, in the main at least, is between *S. vavilovii* and the other species, whose genes act in additive fashion with dominance and little or no interaction. In terms of dominance, *S. ancestrale* has most dominant genes and in decreasing order, *S. dighoricum*, *S. montanum*, *S. cereale*, and *S. turkestanicum*.

For this character the analysis provides therefore a classification of species differences in purely genetical as distinct from morphological or physiological terms. Similar analyses have been carried out, and are being carried out, on a number of other morphological and cytological characters in these species. These analyses help towards gaining a better understanding of the nature of specific differences and provide, wherever practicable, an extremely useful device that could be widely used for such investigations.

REFERENCE

- JINKS, J. L. 1954. The analysis of continuous variation in a diallel cross of *Nicotiana rustica* varieties. *Genetics*, 39, 767-788.

AN EXTENSION OF THE USE OF ORTHOGONAL COEFFICIENTS IN PARTITIONING GENETIC VARIANCES

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1. INTRODUCTION

In this paper, we propose to develop a method for partitioning genetic variances in diploids and autotetraploids with two alleles. Li (1957) has reported a method for partitioning the variances of such genotypic arrays, which he called "the method of successive linear regressions". This method can of course be extended to higher auto-2n-ploids with two alleles.

2. THE USE OF ORTHOGONAL COEFFICIENTS

We now consider a different approach to partitioning the genetic variance, which makes use of orthogonal coefficients. Cockerham (1954) presents the partitioning of the variance of a two-factor genotypic array in diploids when epistasis is present. In order to work out the breakdown of the total variance, he makes use of orthogonal coefficients. By subtracting the linear component from the total genetic variance of a diploid array, we get the quadratic component which cannot be anything but the dominance component; thus, if we break down the variance of a diploid genotypic array into its linear and quadratic components by means of a suitable set of orthogonal coefficients, then it is clear that we must get genetically meaningful components, *i.e.* the additive and dominance components.

We shall show that the method remains valid for an autotetraploid array with two alleles, *i.e.*, we shall prove that a suitable orthogonal partitioning of the variance leads, in this latter case, to the conclusion that the two-, three- and four-gene effects are in fact regressions of the second, third and fourth degree respectively.