

GENETICAL SOCIETY OF GREAT BRITAIN

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ECOLOGICAL DISTRIBUTION OF GENETICAL VARIATION IN SOUTHERN SCOTLAND

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The data are derived from over 200 sites and consist of (a) ecological notes on the sites (floristics, altitude, rainfall, etc.) and (b) means for plant characters of populations derived from the sites after cultivation in trial. Analyses indicate that the relationships between the two groups of data are highly significant. Several species were isolated from each site and the interspecific correlations of plant characters are interesting. Thus sites which contained both *Potentilla erecta* and *Festuca ovina* (tetraploid) tended to have them in comparable sizes, *i.e.* both big or both little. It is argued that interspecific correlation of this type can only result from simultaneous selection within the two species by related environmental factors.

COMPETITIVE ABILITY OF NATURAL POPULATIONS OF *TRIFOLIUM REPENS* AND ITS RELATION TO DIFFERENTIAL RESPONSE TO SOIL FACTORS

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Recently attention has been drawn to the genetic determination of competitive ability of varieties of crop species, and the effect of soil factors upon this. Information concerning the response of natural populations, where response may be correlated with natural habitat conditions, would evidently be of interest.

Natural populations of *T. repens*, taken from contrasting soils, have been grown on those soils either separately or as pairs of contrasting populations. Differential response to the soils was found to be more marked under the competitive conditions of mixed planting, and most marked under field conditions of interspecific competition. The response of each population was closely related to its native soil conditions. The relative competitive ability of the various populations was found to be dependent upon the soil used; this might be regarded as genotype-environment interaction and is amenable to physiological analysis. Such analysis has shown that differences in response to calcium, magnesium, phosphate and iron are involved and that differential response to these nutrients is due mainly to differences in uptake.

The results throw light upon the physiological basis of population differentiation in response to soil factors and also lead to speculation on the role of competition in relation to natural selection.

EVOLUTION IN THE ROSTRATE VIOLETS—I

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The group (typical examples of which are the common dog-violets *V. riviniana* and *V. canina*) consists of some 30 species, and its total range covers the temperate regions of the whole northern hemisphere. Of the species so far counted, at least 13

are diploid, 6 are tetraploid and 2 hexaploid. Their relationships are being investigated both morphologically and by studies of meiosis in interspecific hybrids (*a*) between the European species and (*b*) between the European and N. American species. It is hoped eventually to include the Asiatic species, and to build up a picture of the evolutionary history of the group as a whole.

EVOLUTION IN THE ROSTRATE VIOLETS—II

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Meiotic studies of hybrids involving 15 species by the authors and by D. M. Moore have shown that the tetraploid and hexaploid species all behave as allopolyploids. It has been possible to interpret the relationships between the species in terms of their constituent genomes, some of which are referable to known diploid species while others are as yet unidentified. A close relationship between the genome of one diploid Eurasiatic species with that of the American diploids has been established. Some of the results from hybrids between the diploid species are, however, not consistent with a simple genomic interpretation and these will be discussed.

INTERCHANGE HETEROZYGOSITY IN ANTHOXANTHUM

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Cytological studies show that the condition of interchange heterozygosity known to occur in the tetraploid *Anthoxanthum odoratum* ($2n = 20$) is typical of the species as such. No homozygotes have been found in natural populations in Britain. It is postulated that the heterozygotes are not the product of gradual accumulation of interchanges but are the result of a hybrid origin. The F_1 hybrid between putative diploid ancestors, *A. alpinum* and *A. puellii* ($2n = 10$) is heterozygous for several large interchanges. Pairing between the sets of these species is continued in their artificial amphidiploid which both cytologically and morphologically resembles *A. odoratum*. Disjunctional orientation of multivalents controls the segregation of the parents' sets, one of each of which passes to each gamete. Zygotes are thus alike in their basic constitution and all will be heterozygous for interchanges.

THE EVOLUTION OF A PATTERN IN DROSOPHILA

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Continued selection for an increase in the number of bristles and ocelli in the *ocelli-less* mutant of *Drosophila subobscura*, which is variable for the number of bristles and ocelli on top of the head, has resulted in the appearance of a new pair of bristles. These bristles always arise at a specific site and have a definite orientation. The "neomorphs" are normally absent in the Drosophilidæ but they are present in a family closely related to it, namely the Aulacigastridæ.

A hypothesis is postulated to explain the origin of neomorphs in terms of an unvarying "prepattern" which determines the positions of these structures, and of a common "precursor" of bristles and ocelli which must be present in the required amount if structures are to be formed. It is suggested that if the amount of the precursor is increased to a certain threshold, a new bristle is formed in response to a peak of the prepattern which is present in the wild-type flies, but to which wild-type cells are not competent to respond.

NON-RANDOMNESS OF MITOTIC RECOMBINATION IN YEAST

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Mitotic recombination allows homozygosis at loci previously heterozygous and for any given locus this will occur spontaneously with a certain frequency. This frequency can be increased considerably by ultraviolet radiation. If the event is a random one, simultaneous homozygosis at two or more loci will occur at a rate equal to the product of their separate probabilities. In strains heterozygous for a number of genes, multiple homozygotes occurred at a rate too high to be consistent with this hypothesis. It is suggested that the process takes place between all homologous chromosomes in a dividing nucleus when a certain set of conditions obtains. That homozygosis did not result from non-disjunction or partial haploidisation was shown by including two sets of linked markers in the strains used; those that became homozygous at one locus were not generally homozygous at the linked locus.

FERTILITY AND CHROMOSOME PAIRING IN AUTOTETRAPLOID RYE

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Fertility in autotetraploids depends in part on the frequency and distribution of multivalents and other chromosome configurations at meiosis. These frequencies and distributions in turn depend on the chiasma frequencies—as is shown in a recent theoretical model presented by Durrant (1960). Since chiasma frequencies are known to be under genotype control one should expect heritable variation in the distribution of multivalents and hence in the fertility of autotetraploids.

The work described confirms such variation among autotetraploids produced from F_2 families in rye. Evidence is also produced showing that heritable variation in the distribution pattern of multivalents at meiosis, and hence in plant fertility, can be independent of chiasma frequencies. Finally from the standpoint of breeding for high fertility in tetraploid rye our evidence shows that the most effective selection would be for high quadrivalent frequencies.

PARTITION OF THE D GENOME IN TRITICUM

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Partition of genome D of *Triticum aestivum* by analysis of the genetic effects of individual D chromosomes on a common background constituted by genomes AB of *T. durum* requires some knowledge of the relative frequencies of aneuploid and euploid gametes from pentaploid hybrids.

A comparison of the direct and indirect estimates of the frequencies of male and female gametes from such hybrids indicates that certation is the main cause of the elimination of some chromosomal types from the selfed and backcross progenies. Not only are euploid pollen grains much more successful than aneuploid, there being an inverse relationship between success and degree of aneuploids, but there is specific complementation between pollen grains and styles having identical genomic constitutions. These results together with the marked instability of the additional chromosomes in haplosomics and diplosomics suggest that each of the genomes of this established allopolyploid still functions as an integrated unit.

A re-appraisal of the methods of partition analysis and alien chromosome addition studies shows that the genomic pattern of the allopolyploid series within the genus *Triticum* permits two types of partition analysis of the genomes in *T. aestivum*.