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A DIFFERENCE BETWEEN HETEROKARYONS AND HETEROZYGOUS DIPLOIDS OF *ASPERGILLUS NIDULANS* IN COMPLEMENTATION AND ENZYME FORMATION

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A series of mutants unable to utilise sorbitol has been described previously (C. F. Roberts, *J. gen. Microbiol.*, *30*, 1963). These mutants are unusual in that they are all non-complementary when combined in balanced heterokaryons while some pairs do complement in the corresponding heterozygous diploids.

The mutants are all recessive and represent three functionally distinct but closely linked (0·01 per cent. recombination) loci spanned by a deletion. Quantitative growth tests confirm the difference in complementation of the mutants in heterokaryons and diploids.

The oxidation of sorbitol by intact organisms involves an inducible enzyme system. Non-complementary pairs of mutants fail to form this system in both heterokaryons and diploids. Complementary pairs of mutants form the system in diploids (having about 75 per cent. of the activity of wild type controls) but the same pairs of mutants fail to form the system when combined in heterokaryons.

Complementation thus occurs when genes are combined in the same nuclei but cannot take place across the cytoplasm between genes in different nuclei.

INTER-ALLELIC COMPLEMENTATION *IN VITRO* THROUGH PROTEIN-PROTEIN INTERACTION

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The complementing mutants am^1 and am^3 of *Neorospora crassa* each produce a defective variety of the NADP-linked glutamate dehydrogenase. The am^1 variety has no activity, while the am^3 variety can be activated by high concentrations of glutamate in the presence of NADP but is probably quite inactive *in vivo*. The two mutant proteins are very similar physically and chemically, but can be partially separated on a column of diethylaminoethyl-cellulose. When they are mixed at *p*H 7·4 no detectable interaction occurs, but when the *p*H is adjusted for a short time to 5·8 and then readjusted to 7·4 the proteins interact to form an active enzyme which is very similar in specific activity and other properties to that found in am^1+am^3 heterocaryons. The yield of activity per unit protein is dependent on the ratio of the interacting proteins (about 3 parts of am^1 to 1 of am^3 is optimal), but is not strongly dependent either on protein concentration or on time of treatment at *p*H 5·8. It is believed that the complementation product consists of hybrid aggregate molecules, and some evidence suggests that more than one active hybrid form may exist. Preliminary ultracentrifuge analysis has failed to provide any evidence for a dissociation-reassociation model of hybrid formation, though it is clear that the enzyme has a sub-unit structure. The complementation product is evidently very similar in sedimentation characteristics to the interacting proteins and to wild type enzyme.

PARTIAL REVERTANTS AT THE *AM* LOCUS IN *NEUROSPORA CRASSA*

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The amination deficient, *am*, mutants in *N. crassa* are unable to synthesise normal glutamic dehydrogenase. Ninety-four backmutant strains induced in *am*-3 by ultra-violet irradiation were assayed for glutamic dehydrogenase. Fourteen of these strains possess less than 20 per cent. of normal enzyme activity. A genetic analysis has shown that all the backmutations are in or close to the *am* locus. A biochemical investigation shows that all the partial revertants produce glutamic dehydrogenase different from that of the wild type. Furthermore the partial revertants can be classified into six distinct groups. The members of each group produce a unique variety of glutamic dehydrogenase different from the varieties produced by the other groups. Some of the genetical, enzymatic and complementation characteristics of the partial revertants will be discussed.

SIX INDEPENDENTLY SEGREGATING LOCI ASSOCIATED WITH NITRATE REDUCTASE IN *ASPERGILLUS NIDULANS*

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Forty mutants obtained by U-V irradiation of a prototrophic strain of *A. nidulans* are unable to use nitrate but can use nitrite as a nitrogen source. Heterokaryon complementation tests divide the mutants into seven groups, and linkage studies show that at least six separate locis are involved, none of which is closely linked to another. All the mutants have abnormal nitrate reductase activity when grown under conditions inducing appreciable activity in the wild type. Possible explanations will be discussed, and work in hand will be described.

MORPHOLOGICAL AND PHYSIOLOGICAL POPULATION DIFFERENTIATION OF *ANTHOXANTHUM ODORATUM* ON THE PARK GRASS EXPERIMENT, ROTHAMSTED

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The Park Grass Plots at Rothamsted have continuously received different fertiliser treatments since 1856, and different liming treatments since 1903. The various treatments have led to wide differences in the botanical composition and appearance of the plots. *Anthoxanthum odoratum* is present on most of the plots. The plots, which measure approximately 40 yards by 20 yards, present an ideal situation for the investigation of possible population differentiation over short distances and during known periods of time. Spaced plant trials and box experiments, using population samples of *A. odoratum* from the plots, show that significant population differentiation has occurred in a number of morphological characters, including vegetative and inflorescence height, yield, plant posture, leaf size and panicle size ; some of these differences are closely correlated with obvious physiognomic characters of the vegetation of the plots. Significant differences also exist between populations for such physiological characters as response to contrasting soil conditions, date of flowering, and disease susceptibility ; these physiological differences are closely correlated either with the contrasting soil conditions of the plots or with the physiognomy of the vegetation.

THE RELATIONSHIPS OF THE CHROMOSOMES OF *TRITICUM ÆSTIVUM* THAT PAIR NON-HOMOLOGOUSLY, AT MEIOSIS, IN THE ABSENCE OF CHROMOSOME V (5B)

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Non-homologous meiotic chromosome pairing takes place in *Triticum æstivum* ($2n = 6x = 42$) in the absence of a particular chromosome pair, V (5B). Non-homologous meiotic recombination results in the production of changes, relative to the original chromosome structure, that must formally be recognised as translocations. By identifying the chromosomes involved in translocations, arising in this way, it is possible to determine which chromosomes paired and recombined non-homologously in the chromosome V (5B)-deficient parent.

The chromosomes concerned were identified in 23 translocations, of which nine were certainly of independent origin. All the translocations were between homœologues, that is between genetically corresponding chromosomes of the component genomes of the complement of *T. æstivum*. Consequently it can be inferred that the non-homologous pairing takes place between homœologues. This confirms the hypothesis that an activity of chromosomes V (5B) so restricts its specificity that homologues, but not homœologues, are capable of meiotic pairing.

DOMINANCE

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Theories of dominance evolution seem so plausible that they have always been widely accepted, in spite of occasional strong and well-directed criticism. Such criticism was not only valid, it often understated the case. In particular, Fisher's theory of the selection of dominance modifiers collapses under critical examination, and most of his evidence is irrelevant. Such selection would be a second-order effect of so low a magnitude that it would be swamped by random fluctuations, and would probably be too low to be effective against mutation of the modifying genes.

The idea that, in general, dominance is an evolutionary phenomenon is rejected. It springs from the assumption that there should primarily be a quantitative relationship between gene dose and activity. This assumption is without foundation, for differentiation produces within one organism variations in gene activity among cells with the same gene dose, and within one cell gene activity may change with time. The control of gene activity producing dominance may be closely related to that determining differentiation, and both may be brought about by control of competition among gene representatives for sites on microsomal particles. When dominance occurs, it would thus be a primary and not an acquired property of the gene.

THE GENETIC VARIATION IN STERNOPLEURAL BRISTLES IN *DROSOPHILA MELANOGASTER*

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A complete description of the genetic variation of a character in a wild population would be in terms of the effects and frequencies of the genes responsible, the interactions between them, the linkage relations and of the forces maintaining their segregation. Experiments will be described which were designed to throw light

on these aspects for sternopleural bristles in *D. melanogaster*. They include investigations of scaling problems, of the nature of selection limits, of the effect of restricted population size, both before and during selection, on these limits and of natural selection on artificially selected populations. Finally, some results will be given referring to the rate of accumulation of new variation by mutation and to the effect of cross-over suppression on the response to selection.

A DIFFERENTIAL ALLOCATION OF RECOMBINANT AND NON-RECOMBINANT CHROMOSOMES TO THE SEXES IN *DROSOPHILA MELANOGASTER*

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Studies in *Drosophila* species assume that estimates of recombination derived from female and male progeny are identical. Where discrepancies occur, this is normally attributed to differences resulting from sampling error, or to a differential sex viability of the marker genes used. A number of experiments to be reported here, however, have indicated such large departures from expectation, that these explanations must be considered suspect. An account will be given of such notable cases and the experiments which have been attempted to investigate the phenomenon.

SOMATIC INSTABILITY IN THE TOMATO

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Instability during development in the tomato leading to variegated sectors on leaves and stems, and to breakdown in meiosis, is described. The precise cause of the conditions is unknown but it appears to have many features in common with several other case of somatic instability in higher plants.

SPECIATION PHENOMENA IN BASIDIOMYCETES

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A brief review will be given of the available data concerning speciation in these fungi. The data included are chromosome number and behaviour, hybridisation, adaptive behaviour, polymorphism and isolating mechanisms. Conclusions from the sparse information available suggest that polyploidy does not seem to be common ; that hybridisation is correlated with the type of mating system ; that adaption may be related to heterocaryosis or a genetic mosaic make-up of the mycelium, as well as to other more usual mechanisms ; that there is little evidence for isolation by distance but that ecological isolation, inbreeding (including amixis) and cryptic speciation (which is not correlated with differences in ecology, mating system or morphology), may be common.