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REPLICATION OF THE GENETIC MATERIAL

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Complementary daughter strands of opposite polarity are synthesised simultaneously as a replication fork advances along a replicating DNA molecule. Current models of how this is achieved, and the role of DNA polymerases and DNA ligase in the process will be discussed. Recent work on membrane-bound DNA polymerising activities responsible for the replication of bacterial and bacteriophage DNA will be reviewed, as well as evidence concerning the roles of several distinct components of such complexes. Finally the mechanisms by which replication is initiated and the genomes of mature bacteriophage particles are generated will be considered.

GENETIC HETEROZYGOSIS TRANSFERABLE BY DNA AND ITS RELATION TO RECOMBINATION MECHANISMS

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A common feature of many proposed models for incorporation of heterologous genetic material into a genome is a stage at which a DNA hemiduplex from one parent has interrupted, and become covalently attached to, a corresponding DNA strand in the other parent. A repetition of this process at another point along the same strand eliminates the overlap and inserts a piece of the foreign strand. An equivalent event on the complementary pair of strands results in a potential single crossover recombinant. These alternative processes are essentially deduced from the types of stable end products observed.

A semi-stable penumococcal transformant strain bearing sulfonamide-resistance determinants from two parents has been obtained which bears DNA showing some evidences of having the intermediate structure first mentioned. Markers from the relevant region of the DNA are found in dosage one and one-half times the normal amount, strains manifesting the allelic ratios, 3 : 0, 2 : 1, 1 : 2, and 0 : 3 being represented. This would call for a structure of three strands instead of two (the intermediate referred to) or a region triplicated instead of duplicated in tandem. Since there is no evidence in favor of a tandem duplicate in the normal stable strains, it is presently considered that these semi-stable strains bear a three-stranded DNA region which, by virtue of some unknown feature of the particular marker involved, usually replicates unchanged but at a finite rate can complete the recombinational rearrangement to form stable normal transformants.

SOME FEATURES OF THE GENETICS OF MAMMALIAN RNA VIRUSES

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The RNA viruses of animals and plants exhibit a diversity of structure and mode of replication, commensurate with their biological differences. Few generalisations

are appropriate, therefore, about the nature and organisation of the genome of RNA viruses. A brief comparative account will be given of results of genetic experiments with foot-and-mouth disease virus, influenza virus, Newcastle disease virus, poliovirus, Semliki forest virus, sindbis virus and reovirus, which together with vesicular stomatitis virus, represent the main taxonomic groups of mammalian RNA viruses.

More detailed consideration will be given to current work with vesicular stomatitis virus (VSV). In the case of this virus a large number of spontaneous and induced temperature-sensitive mutants have been classified precisely by genetic complementation tests. This classification and other data concerning the biochemical properties of the mutants will be discussed in relation to the information they provide about the VSV genome. Consideration will also be given to experiments concerned with the nature of the genetic recombination observed in this and other RNA virus systems.

STUDIES ON BASE SEQUENCE HOMOLOGY BETWEEN DIFFERENT INFLUENZA STRAINS

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A method will be described which allows the synthesis and isolation of minus strand RNA of influenza virus which is sufficiently free of viral plus strand RNA to permit the use of annealing as a measure of cross relationships between different myxoviruses. Minus strands of a variety of influenza virus strains, labelled or unlabelled, have been hybridized with labelled or unlabelled plus strands of different myxoviruses. The results indicate the extent of genetic relationships between a variety of strains. Some physical properties of the hybridization products will be described.

GENETIC REGULATION OF AMMONIA TRANSPORT IN *ASPERGILLUS NIDULANS*

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The synthesis of a number of enzymes and uptake systems in *Aspergillus* is subject to ammonia repression. The *ammI*$^-$ mutations on chromosome IV and the *ammE*^{c} mutations on chromosome II result in general ammonia derepression. The ammonia derepression is accompanied by abnormalities of ammonia transport in the mutants.

The rates of influx and efflux of ammonia and methylammonium in the wild type and mutants have been studied using ^{15}N-ammonia and ^{14}C-methylammonium. The response of these strains to toxic concentrations of methylammonium in the presence of various nitrogen sources has been determined. The experimental observations suggest the following hypothesis: In *Aspergillus* the level of an active transport ammonia influx system is regulated by ammonia repression. The level of an ammonia efflux system is regulated by ammonia induction. The *ammI* gene determines a structural component of the influx system and the mutations result in a lower rate of influx. The *ammE* gene is a regulator gene for the efflux system and the mutations result in constitutive efflux. The response to toxic concentrations of methylammonium and the general ammonia derepression of these mutants are secondary consequences of their abnormal ammonia transport.

IMMUNOCHEMICAL ANALYSIS OF NITRATE REDUCTASE IN *ASPERGILLUS NIDULANS*

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Biochemical and genetic investigations of the regulation of nitrate reductase in *Aspergillus nidulans* have revealed two interesting features: (1) the enzyme participates in the control of its own synthesis (D. J. Cove and J. A. Pateman, *J. Bacteriol.*, 1969, *97*, 1374), and (2) five unlinked loci (*cnx*) specify a cofactor common to both nitrate reductase and xanthine dehydrogenase (J. A. Pateman *et al.*, *Nature (Lond.)*, 1964, *201*, 58). Immunochemical analysis of these characteristics has been undertaken in an attempt to determine the structural integrity required for autoregulation, and the nature of the *cnx*-specified cofactor. *Aspergillus* nitrate reductase is a molybdoflavoprotein which is probably a dimer of molecular weight approximately 190,000 (D.W. MacDonald, Ph.D. Thesis, University of East Anglia, 1969). Examination of the enzyme has thus far indicated that the dimeric structure is necessary for the correct regulation of enzyme synthesis. An integral feature of the molecular dimerisation appears to be the involvement of the *cnx*-specified component. In *Neurospora* recent *in vitro* studies provided evidence which was interpreted to support the hypothesis that nitrate reductase and xanthine dehydrogenase share a common sub-unit (P. A. Ketchum *et al.*, *Fed. Proc.*, 1970, *29*, 333Abs.; P. A. Ketchum *et al.*, *Proc. Nat. Acad. Sci.*, 1970, *66*, 1016; A. Nason *et al.*, *Proc. Nat. Acad. Sci.*, 1970, *65*, 137) Their evidence is, however, compatible with alternative interpretation. In *Aspergillus*, this considerable structural relationship does not appear to exist. Immunochemical evidence on the possible nature of the *cnx* product and its participation in the structure and function of nitrate reductase in *Aspergillus* will be discussed.

LOCATION OF *trpR* IN THE *thr* REGION OF *SALMONELLA TYPHIMURIUM*

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Two- and three-point transduction crosses have been used to map mutations in the *thr* region of *S. typhimurium*. The results are compatible with the order: *smo—trpR —thr* (O, D, C, A, B) as given earlier for *E. coli* (Taylor A. L., *Bact. Rev.*, *34*, 155, 1970).

BIOCHEMICAL STUDIES ON MUTANTS IN THE *ad-1* GENE IN *SCHIZOSACCHAROMYCES POMBE*

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Ramirez, Friis and Leupold (*Proc. Internat. Congr. Genetics*, *1*, 7, 1963) have shown that mutants in the *ad-1* gene of *S. pombe* map in either of two distinct regions, designated $ad\text{-}1_A$ and $ad\text{-}1_B$ which are at opposite ends of the gene. Complementation tests indicated the existence of three complementation groups. Mutants in the first group map in both regions and do not complement. Mutants in the second group map in the $ad\text{-}1_A$ region and complement strongly in all pairwise combinations with

those in the third group which map in the *ad-1*$_B$ region. Some of the latter group of mutants show weak complementation with each other. Biochemical studies on the wild type and selected mutants indicate that the non-complementing mutants and the complementing *ad-1*$_A$ mutants lack glycineamide ribotide synthetase whereas the wild type and the complementing *ad-1*$_B$ mutants possess this activity. The wild type and some complementing *ad-1*$_A$ mutants also appear to possess a second activity, aminoimidazole ribotide kinocylohydrase which is lacking in the complementing *ad-1*$_B$ and the non-complementing mutants. It is proposed that the *ad-1* gene codes for a bifunctional enzyme which catalyses two distinct steps in purine biosynthesis. The properties of this enzyme and that produced by some of the complementing mutants will be discussed.

B CHROMOSOMES AND THEIR DNA SEQUENCE IN GRASSHOPPERS

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The DNA from 6 British populations of the European mottled grasshopper, *Myrmeleotettix maculatus*, has been examined by CsCl gradient centrifugation. Each population has a satellite DNA which constituted from 4 to 6 per cent. of the total DNA. All these populations possess B chromosomes. Populations without B chromosomes do not have a satellite DNA. Each satellite has a different density in CsCl representing base compositions of 25 to 35 per cent. GC.

Two of the satellite DNA fractions have been examined in detail by reassociation kinetics and temperature melting. RNA has been transcribed enzymatically from the satellite and attempts to hybridise it to other satellite DNA peaks will be described.

AN ANALYTICAL STUDY OF THE ORIGIN OF THE GENETIC CODE

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The codon catalogue subdivides into two eight-membered sub-catalogues according to " quartet coding-character ". " Monocoding " quartets code for one amino acid only; " heterocoding " ones have more than one coding-sense. The two subcatalogues display high and identical symmetries, governed by six simple letter-parity and letter-exclusion rules. An exploration of possible mechanisms underlying these observations has led to the conclusion that polynucleotide hybridization played a central role in the origin of the genetic code. Two types of hybrid (2-strand) sequence, the one predominated by G-C pairs and the other by A-U pairs, particularly at their termini, provide a well-defined mechanism for the establishment of two eight-membered sets of " primordial transfer-polynucleotides ". The one set will have G and C as letter-l's, the other will have A and U; letters 2 and 3 being subsequently acquired by base-addition. Thus a sequestering of primordial transfer polynucleotides into two subsets by physicochemical differences between the two types of hybrids accounts for subcatalogues and for four of the six catalogue rules. A regular form of " coding anomaly ", displayed by an anomalous sequestering, by this mechanism, of codons for the Thr, Ser (U_1C_1) His/Gln and Asp/Glu quartets, appears to generate the remaining pair of rules.

The mechanism is supported by Skoog's study of cytokinins in tRNA's, and by evidence that some metabolically inactive polypeptides may be coded almost entirely by one of the tRNA subsets. The nature of these confirmations will be discussed.

TEMPERATURE-SENSITIVE MUTANTS OF HUMAN ADENOVIRUS TYPE 5

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Temperature sensitive mutants of adenovirus type 5 have been isolated from stocks of virus mutagenised by nitrous acid, hydroxylamine and 5-bromodeoxyuridine. Most of these mutants are very stable and show little sign of leakiness or reversion to wild type, and are well suited for complementation and recombination analysis.

To date, complementation tests have been carried out with ten mutants, and nine complementation groups have been determined. In many of the crosses extremely efficient complementation was found. A preliminary analysis of recombination has been made with four of the mutants at the permissive temperature. Recombination occurred in all crosses, with the proportion of wild type recombinants ranging from 0·5 per cent. to 7·6 per cent. ($< 2 \times 10^{-4}$ per cent. wild type in single infections). Progeny tests confirmed that in all cases true recombinants were obtained. Recombination with other *ts* mutants is currently being carried out. The results of the complementation and recombination analyses will be presented and discussed.

One of our prime interests lies in using the *ts* mutants to identify the set of gene functions involved in the oncogenic activity of the human adenoviruses. To this end we are comparing the transforming ability of the *ts* mutants with that of the wild type, at non-permissive and permissive temperatures. Preliminary results concerning transformation of rat embryo cells with some *ts* mutants will be presented.

GENETIC STUDIES WITH TEMPERATURE-RESTRICTED MUTANTS OF HERPES SIMPLEX VIRUS

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Temperature sensitive mutants (*ts*) of Herpes simplex Type 1 virus (Glasgow strain 17) were isolated from virus grown in BHK21/C13 cells in the presence of BUdR. The type 17 parent strain used was specially selected to give, in later work, the immediate potential for three factor crosses. The *ts* mutants obtained replicate at 31° C., some at 36° but none at 38°; wild type virus replicates efficiently at all three temperatures. Nine *ts* mutants so far isolated have been studied by complementation and recombination tests.

Complementation: From a comparison of the frequencies of productive complexes at the non permissive temperature in heterologous (*ts* A × *ts* B) and homologous (*ts* A × *ts* A and *ts* B × *ts* B) infection it has been possible to assign the nine mutants to eight complementation groups.

Recombination: Three factor crosses of the type *ts* A *Syn* × *ts* B *syn* have been performed in all possible combinations (the *Syn*/*syn* alleles affect plaque morphology) and the frequencies of the ts^+ recombinants measured. From this data a provisional linear linkage map incorporating all nine of the *ts* mutants and the *Syn* marker has been constructed.

COMPETITION BETWEEN DIFFERENT STRAINS OF SCRAPIE AGENT AND THEIR INTERACTION WITH THE HOST GENOTYPE

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Techniques have been developed for separating some strains of Scrapie agents from natural mixtures. These techniques involve passage in two genotypes of mice

each of which delays replication of a different component of the mixture and thus permits a high degree of separation by serial passage.

After 21 passages in sheep the SSBP/1 Scrapie source was transmitted to mice and the two component Scrapie agents, 22A and 22C, were separated using VM and C57BL mice. These two agents have very different biological properties as measured by incubation period, type of host gene effect and distribution of damage in the brain. In VM mice, 22A had a short incubation (204 ± 3 days; $\approx 10^4 LD_{50}$ intracerebrally) whereas 22C had a long incubation (443 ± 4 days; $\approx 10^4 LD_{50}$ i.c.).

Evidence will be presented of competition between 22A and 22C when these separated agents are used for mixed infection of VM mice. These results support the hypothesis that there is a limited number of replication sites within susceptible cells and/or a limited number of susceptible cells.

A DIRECT MEASURE OF THE TIME AND FREQUENCY OF ALLELIC RECOMBINATION IN *USTILAGO MAYDIS*

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In experimental studies on the mechanism of recombination it is desirable to have a method for detecting recombination under physiological conditions which do not permit genetic replication or cell growth. This can be done in heteroallelic diploids of Ustilago which carry non-complementing mutants in the structural gene for nitrate reductase, and are also homozygous for a mutant lacking nitrite reductase activity. Occasional allelic recombination (gene conversion) results in the production of active nitrate reductase. This reduces nitrate to nitrite which is excreted by the cells and can be detected in very small amounts in the medium. The method is sensitive enough to detect one recombinant per 10^4 diploid cells.

The method has been used to examine the time and frequency of recombination which is stimulated by treatment of cells with gamma rays. Active recombinant genes appear 4·5 hours after irradiation. Experiments with high doses of radiation strongly suggest that recombination occurs only in surviving cells, although it is known that non-viable cells containing an active gene are quite capable of synthesising nitrate reductase. The results provide support for the hypothesis that the synthesis of one or more of the enzymes involved in recombination repair is induced after the cells have been irradiated, and that in normal mitotic cells these enzymes are repressed.

APPLICATION OF NUMERICAL TAXONOMIC METHODS TO POSITIONS OF HYBRIDS IN RELATION TO THEIR PARENTS

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Plant positions in phenetic hyperspace may assist the breeder in choosing parents for a desired hybrid (Whitehouse, *Genet. Agrar.*, *23*, 61). For this, generalisations about hybrid positions are needed. As test data that of Ramon (*Univ. Kansas Sci. Bull.*, *47*, 863) on hybrids of *Haplopappus* species (reduced by principal component analysis to three main axes of variation, X, Y, Z) were used.

Hybrids usually lie about midway between the parents but displaced laterally 25 to 40 per cent. (here 37 per cent.) of the mean interparental distance (here 7·04), due to dominance effects. The hybrid swarm was found to be centred not on the midpoint (parental centroid taken as origin) but on a point (Mean Parental centroid-Hybrid Vector) at X, Y, Z, of 0·63, 1·33 and 0·86. The degree of this displacement

is almost independent of the magnitude of the interparental distance. The dispersion (root mean square distance) of the swarm about the parental control was 2·76, and about the Mean-Vector 2·14 (a moderate but useful gain).

Considerable environmental or other variation is present, whose removal would be worthwhile. An influence of the angle of interparental line to the axes is present, but complex. The methods could be extended to many dimensions.

BIOMETRICAL GENETICAL ANALYSES OF HYBRID VIGOUR

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Two possible causes of heterosis are of interest to the practical breeder, namely, genes dispersed between the parents of an F_1 which show directional dominance and overdominance due to the superiority of the heterozygous state *per se*. Both may be complicated by epistasis, linkage and genotype × environment interactions but these complications do not radically affect the expectation that heterosis due to dispersed dominants can be fixed by inbreeding and that due to overdominance can not.

Biometrical genetical models are available which specify the heterosis expected on crossing two inbred lines in terms of components of family and generation means which allow for the effects of additive, dominance and epistatic effects of the genes, their distribution between the inbred lines, their linkage relationships and their interaction with the environment. From the observed means of the families and generations that may be raised by selfing, backcrossing or sib-mating the F_1 these components may be estimated and their contributions to the observed heterosis evaluated. Given sufficient families and generations the direction of dominance, the kind of epistasis and the type of linkage of the genes responsible for the heterosis can be determined.

However, to evaluate the role of overdominance it is usually necessary to estimate the components of variation within and between families as well as the components of their means.

The contribution that the biometrical genetical approach can make to the understanding and practical exploitation of heterosis will be illustrated by the analysis of examples chosen from flowering plants.

THE POSSIBLE BIOCHEMICAL BASIS OF HETEROSIS

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Surveys of wild populations using gel electrophoresis techniques have shown that enzyme polymorphisms are very common. It is tempting to speculate that they are maintained by heterozygous advantage. While it is possible to imagine that having two separate " allelic " enzymes with somewhat different properties might sometimes be more advantageous than having only one of them, the most obvious basis for heterozygous advantage at the enzyme level is the formation of an interallelic hybrid enzyme. Such hybrids are, indeed, formed more often than not in heterozygotes when the enzyme is normally a dimer or higher oligomer. The difficulty lies in showing not only that the hybrid enzyme differs significantly in its properties from either homomeric enzyme, but that these differences are of adaptive significance. Evidence on these points is lacking. One can, however, make a convincing theoretical argument. In an outbreeding population a new enzyme monomer produced by a new allele will be initially represented mostly in hybrid molecules and will therefore tend to be selected, if at all, primarily on the basis of hybrid advantage. Thus the population will tend to accumulate enzyme varieties which are " good " in hybrids rather than by themselves.

BREEDING HYBRID WHEAT

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The breeding of hybrid wheat is still at a developmental stage. No hybrid wheat varieties have yet been used commercially anywhere in the world. There is as yet no accepted practice of hybrid wheat breeding as such.

The utilisation of hybrid wheat varieties will only be worth doing if they can give agricultural benefits that cannot be achieved by the use of pure-line varieties. In practice the most important benefit would be heterotic increases in yield.

The cost of seed production of hybrid varieties is likely to be higher than that of pure-line varieties so that the heterotic yield increase of a hybrid variety over the highest yielding pure-line variety in current use at the time of the hybrid's introduction would have to be sufficiently large to pay for any increased cost of seed and still leave a larger profit for the grower than that obtained from the pure-line variety. Thus the actual increases in yield obtained from hybrid varieties that would be economically viable will depend on the cost of seed to the farmer.

There is, at present, no reason to suppose that the improvement in yield of pure-line varieties cannot be continued. If this is so then the yield advantage of any hybrid variety will in the course of time be reduced sufficiently to make the hybrid variety uneconomic. Hybrid varieties will thus only make a lasting contribution to agriculture if they can be improved at a rate as fast or faster than pure-line varieties so that their agronomic advantages are maintained.

The breeding of hybrid wheats thus raises three fundamental questions. Can large heterotic increases in yield be achieved; can these increases be maintained over ever improving pure-line varieties and can the production of hybrid varieties be economically viable?

MITOCHONDRIAL COMPLEMENTATION

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Mitochondrial complementation (enhancement of activities of enzyme(s)) in artificial mixtures of mitochondria of un-related lines of maize, wheat and barley has been demonstrated (Srivastava *et al.*, *Genetics*, *63*, 611). Mitochondrial complementation reflects heterosis or hybrid vigor in the sense that the 1 : 1 mixture of parental mitochondria exhibit oxidative and phosphorylative activities which parallel those of mitochondria of the hybrid. These findings are of utmost importance from the points of view that: (1) Complementation by mitochondria may provide an operational means for the study of heterosis, and (2) Complementation by mitochondria may prove to be a useful tool in evaluating potential combining ability of heterotic and non-heterotic individuals in a breeding project.

Results of studies of kinetics of mitochondrial complementation in maize and wheat suggest that a particle-to-particle contact between mitochondria from two genetically different sources is a physical basis of complementation. Recent studies reveal that conformation of membrane bound enzymes (alpha-ketoglutarate dehydrogenase, adenosine triphosphatase and cytochrome oxidase) is involved during complementation. The exact nature of interaction between membrane bound enzymes from the parents remain unknown; however, some conformational change of the enzymes appears to occur upon direct contact between the particles. When the proper conformation, required for enhanced activity in the mixture of mitochondria, is apparently altered by Na-deoxycholate or diethylstilbesterol or parachloromercuribenzoate, complementation is not accomplished. These results

will be discussed with the point of view that sulfhydryl groups of the membrane bound enzymes may be involved in internal hydrogen bonding to maintain a proper conformation of the active site(s) in the complementing mixture of mitochondria.

Mitochondria from the hybrids seem to be polymorphic and of importance in maintaining high efficiency, heterosis and intracellular homeostasis in such organisms. The plausible relationship of mitochondrial polymorphism (heterogeneity) to complementation and heterosis will be considered.

THE EXPLOITATION OF HYBRID VEGETABLES IN COMMERCE

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Generally speaking, hybrid vegetables outyield ordinary straight varieties of the same crop, but now, with the trend towards mechanised horticulture, the associated uniformity of hybrids is an added and important advantage. For a hybrid to be successful, sufficient seed must be produced to meet potential demand and succeeding generations must be constant for all characteristics. This means, therefore, that the parents must be stable, uniform and true-breeding.

Within vegetables, we find all three types of sexual reproduction, (i) obligate self-fertilisation, (ii) obligate cross-fertilisation and (iii) a mixture of both. Since self-fertilisation produces uniformity, it is only within the self-fertilised group that we have ready made parent lines. The difficulty arises in the production of hybrid seed. Emasculation followed by hand-pollination is the only method at present by which this can be achieved, and therefore, to produce hybrid seed on a commercial scale, plants must possess flowers which are easily emasculated before anthesis and must produce fruits having many seeds.

Crops which habitually cross-pollinate are quite variable from plant to plant and, therefore, the first step in a hybridisation programme is the production of uniform inbred lines. Since these plants are self-incompatible, self-fertilisation can only be achieved by " bud-pollination ". Selection at each generation for both commercial characters and high self-incompatibility, produces, after 5 or 6 generations, uniform inbred lines suitable as potential parents. By making use of the self-incompatibility, hybridisation is easily achieved by interplanting the two parents. The commercial exploitation depends on facilities available for reproducing the parents and the amount of seed obtained by bud-pollination.

Crops belonging to the third group are again variable from plant to plant but since they are self-fertile, inbred lines are easily produced. Hybridisation can be achieved by emasculation and hand-pollination in those crops which lend themselves to the technique, while with others, use has to be made of male-sterility.

THE SUPPRESSION OF HOMEOLOGOUS PAIRING BY B CHROMOSOMES IN *LOLIUM* HYBRIDS

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In the hybrid between *Lolium temulentum* and *L. perenne* (both $2n = 2x = 14$) chromosome pairing and chiasma formation between homeologous chromosomes is effective and extensive. Cells with seven bivalents at first metaphase are common. When B chromosomes from *Lolium perenne* are introduced the pairing between homeologues is drastically reduced. The implications of these results for the synthesis of wheat type amphidiploids are discussed.

THE PRODUCTION AND POTENTIAL OF F_1 HYBRID BARLEY

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Several systems of producing F_1 hybrid barley are being studied; the most promising at present utilize a recessive gene for male sterility (*ms*). The difficulty of maintaining and multiplying the male sterile stocks can be overcome in several ways. In one system a closely linked combination of *ms* with an informational gene aids the identification and removal of male fertile plants from segregating populations. Another system utilizes balanced tertiary trisomic (BTT) plants in which the normal complement of chromosomes carries the *ms* gene and the extra interchanged chromosome carries the dominant gene for fertility. A BTT stock when selfed, produces (*a*) male sterile diploid plants, which can be used as the female parent in the production of F_1 hybrids, and (*b*) male fertile BTT plants which produce functional pollen that is haploid and all *ms*.

Attempts are being made to combine the essential elements of both systems so that male sterile diploid plants and male fertile trisomic plants can be separated automatically. This requires an interchange chromosome having the locus for male sterility, the informational gene and the translocation breakpoint all closely linked.

Over 200 stocks containing *ms* genes, a large number of interchanged chromosomes, and informational genes are available for incorporation into this system provided the required linkage can be secured.

Cytoplasmic male sterility is not being pursued but the possibilities of chemically inducing male sterility or restoring fertility are being actively studied.

Wind pollination of male sterile stock in Britain is generally poor and variable, but genetic variation appears to be sufficient to permit fairly rapid improvement by selection.

Evidence for heterosis is still meagre. However, by using the BTT techniques, sufficient quantities of F_1 hybrid seed is now becoming available for large scale experiments. Crop density investigations are providing valuable information on the effects of spacing on the expression of heterosis.

INTERCONVERSION BETWEEN LAC PHENOTYPES IN A STRAIN OF *KLEBSIELLA AEROGENES*

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Klebsiella aerogenes strain VgA harbours a Lac^+ plasmid carrying an fi^+ sex-factor repressor gene but no active sex factor. This plasmid can be transferred to *E. coli* with the help of an added sex factor. On MacConkey Lactose Agar (MLA) VgA colonies are typically red (L+), but about 10^{-1} are colourless (L−). Such L− colonies, when purified on MLA, give revertants to a pink intermediate colony type (*L*−/+) and to the original phenotype (L+). All three phenotypes can grow in lactose as sole carbon source, but they differ strikingly in their ability to grow on lactose after growing on another sugar. L+ cells and those which have reverted from L− to L+ show virtually no lag when transferred from glucose or other sugars to lactose. L− cells show a lag of 5-6 hours when transferred from glucose to lactose, but none when transferred from raffinose to lactose. L−/+ cells, in contrast, show a very long lag when transferred from raffinose to lactose, and a shorter lag when transferred from glucose to lactose. Similar results are obtained in diauxy tests with pairs of sugars. These growth reactions appear to be manifestations of catabolite repression. The Lac^+ plasmid could only be transferred from L+ donors to various strains of *E. coli* K12, suggesting that part of the plasmid was missing or inactivated

in L− and L−/+ cells. Recently, transfers from an L− line to a Lac⁻ K12 strain have given three Lac⁺ phenotypes resembling L⁺, L−/+ and L− on MLA and showing similar patterns of catabolite repression.

NON-RANDOM X-CHROMOSOME EXPRESSION IN EQUINE HYBRIDS

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Fibroblast clones derived from skin biopsies from one female mule (*E. caballus* ♀ × *E. asinus* ♂) and two female hinnies (*E. asinus* ♀ × *E. caballus* ♂) have been typed for the sex-linked enzyme glucose-6-phosphate dehydrogenase (*Gd* E.C.1.1.1.49). Out of 303 clones studied 51 showed hemizygous expression of Gd^D, 246 hemizygous expression for Gd^H while six showed expression of both alleles. Sub-clones from two of these six mixed clones demonstrated that the apparent heterozygosity was due not to expression of both loci in a single cell, but to a mixture of cells. The significance of these results in relation to the single active X-hypothesis and the complemental X-hypothesis will be discussed.