GENETICAL SOCIETY OF GREAT BRITAIN

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ANEUPLOIDY IN YEAST

B. S. COX
Botany School, University of Oxford

In 1958, Bevan reported that a strain of yeast, heterozygous for an adenine requirement which confers a red colour when present in the homozygous condition, produced many colonies with red sectors when it was plated on complete nutrient agar. It has been possible to demonstrate, through the existence of partial heterozygosity in the haploid offspring, that this diploid was a tetrasomic of constitution 2n+2=AD/ad/ad/adl. It has been shown that the frequency of sectoring of this and other aneuploids can be very much higher than that of normal heterozygous diploids, but that the frequency varies between one aneuploid and another, and even between different sub-cultures of the same aneuploid strain. It is suggested that fluctuations in the chromosome complement are responsible both for the appearance of the red sectors themselves and also for some of the variation in the frequency with which they appear. Experiments are also described which suggest that some of this variation may be due to cytoplasmic factors.

THE ASSOCIATION OF CHROMOSOMES IN HAPLOID COTTON

G. KIMBER
Plant Breeding Institute, Cambridge

The chromosomes of the allotetraploid cottons derived from the Asiatic diploids (A genome) are larger than those derived from the American diploids (D genome). Analysis of meiosis in polyhaploids of *Gossypium barbadense* reveals that whilst there is no bivalent formation there is a frequent association of chromosomes of dissimilar size and a less frequent association of chromosomes of a similar size.

The evidence from polyhaploids and from certain interspecific hybrids points to the possibility of genetic control of intergenomic chromosome pairing in the allotetraploid cottons, similar to that in *Triticum æstivum*. Since earlier data on *Nicotiana tabacum* hybrids can be similarly interpreted, the genetic control of the cytologically diploid behaviour of allopolyploids may be a frequent occurrence.

CHANGES IN FERTILITY AND VIGOUR ASSOCIATED WITH SELECTION FOR EAR EMERGENCE IN *LOLIUM*

J. P. COOPER
Welsh Plant Breeding Station, Aberystwyth

Selection for early and late ear emergence in Irish and Kent ryegrass has produced rapid and continued response for six generations. Although the selection differential is similar in both directions, the realised heritability is always higher in the late lines. Both the selection differential and the heritability are greater in Kent than in Irish, possibly because of less stringent agronomic selection in the past. Back-selection, which was started in each line after the first generation, indicates that considerable potential genetic variation can be carried within four foundation plants.

Male and female fertility have declined in all lines by the 6th generation, and in some cases severely reduced the possible selection differential. The variation in fertility both *between* and *within* plants was also increased in the selection lines. Although the mating system employed results in slight inbreeding no regular depression in such criteria of vigour as leaf size, tiller number or dry weight per seedling could be detected, nor was there any regular correlated response in these characters.

GENETIC AND ONTOGENETIC VARIATION IN THE GROWING FORM OF THE DOMESTIC FOWL

A. G. COCK
A.R.C. Poultry Research Centre, Edinburgh, 9

In a population of mixed breed origin, selection in opposite directions for relative length of shank (tarsometatarsus) has been carried out, using $\log y_{10} - 0{\cdot}4 \log x_{10}$ as an index, where y_{10} and x_{10} are shank length and body weight at 10 weeks of age. Two generations of selection have produced a divergence of 0·031 (equivalent to 7·5 per cent. difference in relative shank length) between the selected lines, the realised heritability being 0·55. A correlated response (in the opposite direction) in relative shank width has occurred.

The ontogenesis of these differences in form will be discussed. It will be shown that : (i) over the period 2-10 weeks the relative growth-rate (k) of $\log y$ with respect to $\log x$ is approximately constant within individuals, with a mean value close to 0·4. (ii) In the initial population, variation in k between individuals is highly significant, but does not account for all the variation in $\log y$ at a fixed $\log x$ (the regression lines do not pass, within the limits of error, through any single point). (iii) Although the selection applied has been partly directed towards changing k, in the first generation at least, no divergence in k has occurred.

THE SYNDROME OF CONGENITAL DEAFNESS WITH ABNORMAL ELECTROCARDIOGRAM

G. R. FRASER
M.R.C., Population Genetics Research Unit, Oxford
P. FROGGATT
Department of Social Medicine, Queen's University, Belfast

One type of recessively inherited congenital deafness is found to be associated with qualitative and unique abnormalities in the electrocardiogram. These have not been found to be correlated with any identifiable biochemical or pathological lesion either in life or post-mortem. The syndrome may be associated with an undue predisposition to fainting attacks in childhood which have in some cases terminated fatally.

The clinical and genetical features of this syndrome are discussed in relation to five families found during a survey of deaf school-children.

CHROMOSOME NUMBER VARIATION WITHIN A *RUBUS* PLANT

G. HASKELL and N. N. TUN
Genetics Department, Scottish Horticultural Research Institute, Invergowrie, Dundee

One abnormal stunted seedling occurred in the thornless segregants of an F_2 progeny from a cross between Merton Thornless (*R. craniensis*) and Himalaya Giant (*R. procerus*). Cytological investigations showed this seedling to be unstable in somatic chromosome number (root-tips and stipules), with a range of $2n=9$ to 46 ; the mode was at the pentaploid level ($2n=35$). The range in chromosome numbers decreased, while the actual numbers of cells with 35 chromosomes increased as the

plant aged. Both parents and sibs were constant tetraploids of 2n=28. Tests showed that viruses did not cause the instability.

Within root-tips for the aneuploid series there was a correlation between cell size and chromosome number of $r=0{\cdot}65$, significant at the 5 per cent. level. It is suggested that because *Rubus* chromosomes are more or less alike, introduction or removal of individual chromosomes into a cell is comparable to introducing or removing equivalent amounts of DNA to give proportional changes in cell size. It has been suggested by other workers that the amount of DNA affects cell size in a strictly polyploid series in rats.

Somatic chromosome number variation in the vegetative system may be another facet of the reproductive versatility in the genus *Rubus*.

A LATENT GENE CONTROLLING DDT SENSITIVITY IN *HOREDUM*

J. D. HAYES
Welsh Plant Breeding Station, Aberystwyth

Barley gives a distinct reaction to spraying with DDT. Certain varieties are resistant and do not manifest any external symptoms of damage, while susceptible varieties suffer severe chlorosis. Resistance to DDT in cultivated barley (*H. vulgare*) is controlled by a single recessive gene (*ddt*) and it appears to be distributed at random through the commercial varieties. Populations of wild barley (*H. spontaneum*) have also revealed similar variability in their reaction to DDT spray, which indicates that the gene does not appear to have had any selective advantage in the evolution of the barley crop.

Under severe DDT treatment, susceptible genotypes of barley are eliminated while resistant genotypes remain unharmed. The possibility of linking this phytocidal action with male sterility (*ms*) has led to the proposal that a system of breeding hybrid barley on a field scale could be developed.

The genetic control for reaction to DDT for barley leads to a consideration of the possible existence of similar control systems in other crops and also for other chemicals.

GENETIC RECOMBINATION IN *SALMONELLA TYPHIMURIUM* MEDIATED BY CERTAIN COLICINE FACTORS

H. OZEKI, S. HOWARTH, S. M. SMITH and B. A. D. STOCKER
Guinness-Lister Research Unit, Lister Institute of Preventive Medicine, London S.W.1

When one genetically marked sub-line of *Salmonella typhimurium* LT2 transmits colicine factor I to another sub-line at high frequency (10^{-1}) rare recombinants in respect of various chromosomal genes are produced. If colicine factor E1 is also being transmitted their frequency is increased fifty-fold, to c. 10^{-6}.

In such recombination pairs of genes which can be co-transduced by phage PLT22 usually remain coupled; if recombination results from transfer of part only of one chromosome into a " merozygote " (cf. *Hfr* mating in *Escherichia coli* K-12) the fragment transferred must be larger than that carried by a transducing phage particle.

When the parent strains differ in many characters recombinants selected for possession of one selective marker from each parent may be of many different types in respect of other markers. This suggests that at least some recombinants arise by recombination between two complete chromosomes. The relative frequency of various recombinant classes has been used to map four nutritional loci (*adC*, *proA*, *metA* and *tryB*), streptomycin-resistance, the H_1 and H_2 flagella antigen loci and two loci for production of flagella; the arrangement sought was that which accounted for the common recombinant classes by a minimum number of cross-overs. The map obtained is a single line or loop.

COLICINOGENY-CONFERRED FERTILITY IN *ESCHERICHIA COLI* K-12

R. C. CLOWES
Microbial Genetics Research Unit, Hammersmith Hospital, London, W.12

In *Escherichia coli* K-12, genetic transfer is mediated by the presence of a fertility factor, *F*, which determines the donor state. In *Salmonella*, Ozeki and Stocker have recently shown that a similar donor state is initiated by the *recent* transfer of a colicinogenic factor, I. In K-12, this same colicinogenic factor promotes the donor state in strains devoid of *F*. The colicinogeny fertility system in K-12 differs from that in *Salmonella* in two main respects. Firstly, there is no enhancement of fertility when transfer of colicinogeny I is made to potential donors, already colicinogenic for a second colicine, E1. Secondly, the donor state is readily stabilised and does not require recent transfer of colicinogeny I.

A comparison has been made of genetic transfer in K-12, mediated either by *F* (in the F^+ state), or by colicinogeny I. Preliminary results show that the main difference is one of frequency, the *F* mediated cross being one hundred times as fertile as the corresponding I cross. Among the recombinants, seven unselected markers are transferred at similar frequencies, suggesting that the size of the chromosomal fragments transferred may be similar in both types of crosses.

A GENE DETERMINING PRESENCE OR ABSENCE OF ε-N-METHYL-LYSINE IN *SALMONELLA* FLAGELLAR PROTEIN

B. A. D. STOCKER and M. W. MCDONOUGH
Guinness-Lister Research Unit, Lister Institute of Preventive Medicine, London, S.W.1

R. P. AMBLER
Department of Biochemistry, University of Cambridge

Only twenty amino-acids are common in proteins, possibly because there are only twenty different amino-acid-specifying base-groups in DNA.

Salmonella flagella, of many different antigenic types, consist of the protein flagellin. Some, but not all, flagellins contain the uncommon amino-acid ε-N-methyl-lysine (NML). The antigenically distinct phase 1 and 2 flagellins produced by a diphasic *Salmonella* both contain, or both lack, NML.

The H_1 and H_2 genes determining, respectively, the phase 1 and 2 flagellar antigens, were transduced between diphasic strains differing in NML character. The NML character of both the flagellins of a recombinant was that of the parent strain which provided its H_1 gene. This indicated that NML character was determined at H_1 or at a closely linked locus. By suitable crosses recombination between H_1 and NML was later obtained.

The H_1 and H_2 genes probably determine, respectively, the complete amino-acid sequences of phase 1 and 2 flagellins. The control of presence or absence of the uncommon amino-acid NML in a flagellar protein by a gene other than that which specifies the amino-acid sequence of the protein is compatible with the hypothesis that only twenty different amino-acid-specifying groups occur in DNA.

PAIRING INTERACTION AS A POSSIBLE BASIS FOR NEGATIVE INTERFERENCE

G. A. MACCACARO and W. HAYES
Microbial Genetics Research Unit, Hammersmith Hospital, London, W.12

The most plausible current theory of negative interference supposes that chromosome pairing is discontinuous and random, and that recombination occurs only within those small regions where effective pairing occurs. Thus recombination in two intervals would occur with greater than random frequency if these intervals

were so close as frequently to lie within one effectively paired region. The length of such regions has been estimated, in *Aspergillus* and phage, to be of the order 10^4 double nucleotides of DNA. The unique features of conjugation in *E. coli* K-12 enable distances between loci on the chromosome of the ♂ parent to be measured in absolute terms, independently of the recombination process. A study of the correlation between recombination in two intervals, in this system, has revealed a significant degree of negative interference which extends over a region of chromosome at least 10^6 double nucleotides long. Since there is evidence that effective pairing is unlikely to be continuous over such long regions, an interaction between different, small, regions of pairing is postulated to account for the effect. An explanation is offered of some anomalies between recombination data emerging from transductional and conjugal crosses involving the same strain and genetic loci.

MUTATIONS AFFECTING THE *A* MATING TYPE LOCUS IN *COPRINUS LAGOPUS*

P. R. DAY
John Innes Institute, Bayfordbury, Hertford, Herts.

The *A* mating type locus of *Coprinus* controls the formation of clamp connections. Clamp bearing heterokaryons are only formed between strains with different *A* alleles. Mutations which enable a presumed haploid monokaryon to form clamp connections spontaneously were recovered from fruit bodies produced by common *A* heterokaryons. Similar mutants were also recovered among recombinants in crosses involving markers closely linked with the *A* locus.

Three out of four mutations tested are either very close to the two sub-units of the *A* locus or involve one of them. Stocks carrying them show no detectable *A* incompatibility reaction and will dikaryotize all *A* tester stocks. The fourth is a mutation at an unlinked locus. The mutant gene appears to be a recessive suppressor since stocks carrying it are unable to dikaryotize common *A* tester stocks.

THE INHERITANCE AND SURVIVAL OF THE XASTA (*Xa*) MUTANT OF *DROSOPHILA MELANOGASTER*

W. J. WHITTINGTON and W. E. PEAT
School of Agriculture, University of Nottingham

The Xasta condition in *D. melanogaster* is determined by a semi-dominant wing mutation which is lethal when homozygous. The heterozygote has a wing with a deeply cut edge. Early cytological analysis showed that the condition was inseparable from a translocation between the right arms of chromosomes 2 and 3 and that two inversions were also present.

The present investigation has considered the results of single crosses involving Xasta and its survival in small population cages with or without the inversions. The results clearly demonstrate the existence of a state of balanced polymorphism in the population, probably controlled by the inversions.