GENETICAL SOCIETY OF GREAT BRITAIN

ABSTRACTS of Papers read at the HUNDRED AND FORTY-SECOND MEETING of the Society held on 12th JULY 1963, at the CHESTER BEATTY RESEARCH INSTITUTE, FULHAM ROAD, LONDON, S.W.3.

GENETICS OF ROUGHNESS IN *SALMONELLA TYPHIMURIUM*

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

Roughness segregated normally when nineteen rough mutants in multiply marked stocks of *Salmonella typhimurium* LT2 were crossed with smooth strains, using colicine factors *colI* and *colE1* to obtain fertility ; in 13 mutants (*rouA* class) linked to *ile* (isoleucine requirement) and in six mutants (*rouB* class) to *try* (tryptophan requirement).

All the *rouB* mutants were sensitive to Felix's anti-O phage ; some *rouA* mutants were resistant. An anti-*rouB* rabbit serum agglutinated only *rouB* mutants ; anti-*rouA* sera agglutinated both *rouA* and *rouB* mutants.

The rough mutants were obtained by prolonged incubation in broth ; colony selection after exposure to N-ethylmethane sulphonate ; or selection with virulent phage PLT22 or with Felix's O phage.

The typical rough characters—rough-looking growth on agar, clumping during growth in broth, inagglutinability by anti-smooth (O-4) serum but auto-agglutination in 0·85 per cent. saline, negative Millon's reaction—are attributed to rough somatic lipopolysaccharide which contains glucose and galactose but lacks mannose, rhannose and abequose, present in wild-type smooth lipopolysaccharide. However, phenol extracts of two *rouA* mutants (Drs Beckman and Westphal, at Freiburg) yielded typical macromolecular rough lipopolysaccharide and a relatively low-molecular-weight fraction containing glucose, galactose, mannose, rhamnose and abequose and with smooth serological specificity.

PLASMID ASSOCIATIONS IN *SALMONELLA TYPHIMURIUM*

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

An Hfr derivative (Zinder, Rockefeller Institute) of *Salmonella typhimurium* LT2 was infected with various plasmids and crossed to an F- strain. Colicine factors *colI*, *colE1* and *colE2* were represented in c. 20 per cent., 50 per cent. and 15 per cent. respectively, of chromosomal recombinants, whatever the Hfr locus selected. A resistance factor, *R3ND*, conferring resistance to sulphonamides, tetracycline and streptomycin (*sul-r, tet-r and str-r*), (Datta, 1962, *J. Hyg.*, *60*, 301) was also transmitted as a unit without apparent linkage to any chromosomal locus. A higher than random proportion of chromosomal recombinants acquired two, three, or all four plasmids. Interrupted mating experiments confirmed the map inferred from linkage data, but did not reveal a chromosomal location for any plasmid.

Phage P22 grown on this Hfr strain transduced either the *sul-r* and *sr-rt* characters together or the *tet-r* character alone. Most such transductants could not transmit resistance by conjugation (Watanabe, 1963, *Bact. Rev.*, *27*, 87). Some transductants had acquired *colE1* or *colE2* ; this co-transduction indicates association of the plasmids concerned in the Hfr donor strain.

Some transductants, phage-resistant, but not phage-producing, presumably carried defective P22 prophage. When crossed, in *col*-factor-mediated conjugation, the transduced resistance character and defective lysogenic character segregated together, closely linked to *pro*, the site of attachment of normal prophage P22 (S. Smith, unpublished).

MITOTIC RECOMBINATION IN YEAST

B. S. COX
Department of Genetics, University of Liverpool

Diploid yeast, heterozygous at a given locus, is known occasionally to revert to homozygosity. For example, a diploid heterozygous for the gene ad_2 (a recessive determining adenine requirement and a red colouration) forms white colonies when grown on agar medium. A number of these colonies may be found, on close examination, to include red sectors or spots composed of cells homozygous for ad_2. These cells have usually been described as being the result of mitotic crossing-over. Experiments are reported in which red sectors have been isolated from diploids heterozygous for ad_2 and a number of linked and unlinked markers. The results suggest that the majority of sectors may be the result of mitotic non-disjunction rather than mitotic crossing-over. Diploids of reciprocal genotypes have been isolated from sectored colonies, but not in significant frequency.

Those sectors which cannot be ascribed to non-disjunction seem likely to be the result of a gene-conversion type of recombination mechanism operating at mitosis. There is no evidence that markers unlinked to ad_2 recombine at the same time.

GENETICS OF THE ANAPHYLACTOID REACTION IN RATS

H. KALMUS, J. M. HARRIS and G. B. WEST
Galton Laboratory, University College, London: School of Pharmacy, Bristol, and Department of Pharmacology, School of Pharmacy, London

A single injection of dextran or egg white produces hyperemia, pruritis and œdema in the face, ears and paws of most laboratory rats. This reaction resembles an anaphylactic reaction but no prior sensitisation is necessary. Rats which do not react in the described way even after repeated injections were found in some Wister albino colonies and pure strains of reactors and non reactors were bred. The difference appears to be caused by a recessive autosomal gene *dx* which in the homozygous state prevents the reaction ; *Dx dx* and *Dx Dx* animals are reactors. The gene was outbred into other strains and segregates independently of the fur colour genes *c*, *p*, and *a*. In 14 colonies of different origin non-reactivity occurred in three Wistar strains at frequencies of 17·5, 23·4 and 100 per cent. Two of these colonies were maintained by brother sister matings and the third as a closed population.

BARR BODIES IN RELATION TO PLOIDY AND NUCLEAR SIZE

U. MITTWOCH
Galton Laboratory, University College, London, W.C.1

The formula proposed by Harnden, $B = x - p/2$, where $B =$ the number of Barr bodies, $x =$ the number of X-chromosomes, and $p =$ the ploidy of the cell, holds for the maximum number of Barr bodies in cells with even ploidy numbers, but cannot be applied where p is uneven. Triploid cells with XXY sex chromosomes have previously been reported either to lack sex chromatin, or to contain it.

A triploid/diploid fibroblast culture with XXX sex chromosomes, which has recently been established by Dr Ellis, contained, in addition to cells with single Barr

bodies, 64 out of a 1000 cells with double Barr bodies (both were at the nuclear membrane in 26 cells). Measurement of DNA content, carried out in conjunction with Dr N. B. Atkin, indicated that some double Barr bodies occurred in triploid as well as in cells with higher ploidy, and that they were absent in diploid cells. It is concluded that triploid cells may contain the same maximum number of Barr bodies as diploid ones, although the incidence of such cells may be smaller.

Measurements of nuclei have shown that cells with Barr bodies are on an average somewhat smaller than those without. A comparison has been made between nuclear sizes in fibroblasts with XX and XY sex chromosomes with a view to determining the possible significance of this finding.

GENE LOCALISATION IN MAN: THE USE OF GENETIC MARKERS IN CASES OF CHROMOSOMAL ABNORMALITY

S. D. LAWLER
Department of Clinical Research, Royal Marsden Hospital, London

There are three well-established autosomal linkages in man. Recent advances in human cytogenetics together with the numerous genetic markers already known provide the means for an attempt at gene localisation.

As yet there has been only suggestive, but not conclusive, evidence that any gene is carried on a particular autosome. The application of the study of genetic markers in various cases of chromosomal abnormality will be discussed.

THE RECONSTRUCTION OF EVOLUTION

A. W. F. EDWARDS and L. L. CAVALLI-SFORZA
International Laboratory of Genetics and Biophysics, Naples, Pavia Section: Instituto di Genetica, Universita di Pavia

Darwin's theory of evolution invites us to believe that closely similar species are closely related. In cases in which there is no fossil record, or other means of following evolutionary history, this concept provides the only means of drawing inferences about the course of evolution, and it is important to see whether it can be defined sufficiently precisely to be used for estimating the most likely form of an evolutionary tree solely from data on the similarities and differences between species. A detailed consideration of this problem leads to the conclusion that the following principle may be employed :

THE PRINCIPLE OF MINIMUM EVOLUTION

The most plausible estimate of the evolutionary tree is that which invokes the minimum nett amount of evolution.

This principle will be discussed, the system of estimation to which it leads expounded, and some examples of its application given.

SOME POLYGENES

J. M. THODAY, J. B. GIBSON and S. G. SPICKETT
Department of Genetics, University of Cambridge

We speak of polygenic variation when we have to use variance comparisons to demonstrate significant segregation of heritable differences affecting a continuous character. Attempts to locate relevant genes in linkage groups using the methods outlined by Thoday (*Nature*, 1961, *191*, 368) will only be successful with loci making sufficiently large contributions to variance relative to other sources combined. Such methods may therefore only detect and locate a biased sample of " more effective "

polygenes, but knowledge of such locations must add greatly to our understanding of quantitative genetics.

The location and some effects of 15 polygenes in *D. melonagaster*, 13 influencing sternopleural chaeta number, one influencing fly size and one influencing both will be described. They occupy at least 10 loci.

An example will be given showing how much light can be thrown on the genetic control of a quantitative difference by studies of the differing effects of some of the individual genes concerned once they are located and can be handled separately in breeding programmes.

INHERITANCE OF LYMPH PROTEIN FRACTIONS IN *DROSOPHILA*

E. M. PANTELOURIS and E. J. DUKE
Zoology Department, Queen's University, Belfast, Northern Ireland

The experiments to be reported were carried out with various mutant laboratory stocks of *Drosophila melanogaster* and with wild stocks of the same species and of *D. funebris* collected locally. The hæmolymph from third instar larvæ produced, by starch electrophoresis with a discontinuous buffer system, a pattern with up to seven distinct protein bands ; the present investigation was concerned with only three of the faster fractions, to be denoted A, B and C.

Not only the wild stocks, but also most of the standard mutant stocks comprised more than one phenotype, and there was a clear difference between the two species tested. By examining samples from the F_1 and F_2 of pair-matings, it was established that the presence of fraction A depends on a sex-linked dominant factor, whilst the presence of B and C depends on two other linked autosomal dominant genes.

THE ACTION OF TUMORIGENIC TREATMENTS AND PROTECTIVE AGENTS ON MELANOTIC TUMOUR FORMATION IN *D. MELANOGASTER*

B. BURNET
A.R.C. Poultry Research Centre, Edinburgh

The *tu bw : st su-tu* strain of *Drosophila melanogaster* carries a melanotic tumour gene on the second chromosome and a specific tumour suppressor on chromosome three. Plaine and Glass (*Science*, 1957, *126*, 683-689) showed that penetrance of this tumour is greatly increased by X-ray treatments or by an excess of l-tryptophan in the diet, and that the effect of these treatments can be counteracted by l-cysteine. They suggest that both tumorigenic treatments act upon the tryptophan peroxidase-oxidase mediated reaction, the product of which, formylkynurenine, interferes with the action of the suppressor gene. Current investigations using chemically defined germ-free media do not support these propositions since tryptophan and X-ray treatments operate through temporally distinct developmental events, and studies on the protective effect of l-cysteine, l-methionine and cystamine point rather to a genetically controlled defect of sulphur metabolism.

EFFECTS OF ENVIRONMENTAL MANIPULATION ON THE PENETRANCE OF MELANOTIC TUMOURS IN SUPPRESSED AND UNSUPPRESSED STRAINS OF *D. MELANOGASTER*

J. H. SANG
A.R.C. Poultry Research Centre, Edinburgh

If X-rays and excess tryptophan both increase tumour penetrance in the *tu bw : st su-tu* strain by inhibiting the action of the suppressor gene, it should follow that

strains not carrying the suppressor would have a different reaction to environmental treatments. Tests with germ-free, synthetic diets containing excesses or deficiencies of individual nutrients show that the majority of treatments affect tumour penetrance in the same way, whether or not the *su-tu* gene is present. This suggests that these treatments influence the expression of the tumour gene directly, rather than through the suppressor. Since many metabolically unrelated treatments are similarly effective, it also seems unlikely that they operate directly through a specific metabolic pathway. The general implications of these results for tumorigenesis will be considered.