D.F. Calcheinde

GENETICS SOCIETY OF AUSTRALIA

18th GENERAL MEETING

Brisbane, 20-21 May, 1971.

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PROGRAMME

Sessions will be held in the Biological Sciences Lecture Theatres (B1 and G12)

Thursday 20 May

8.30-9.00 a.m. Registration (Biological Sciences Building)

SESSION 1A

Evolutionary Genetics. Chairman: Dr. Wharton B. Mather.

9.00 a.m. ✓	Webb, G.C. Department of Genetics, University of Melbourne.	Has polyploidy occurred in the evolution of the Dermaptera ?
9.30 a.m. ✓	Martin, J. Department of Genetics, University of Melbourne.	Inversion polymorphism in *Chironomus staegeri*.
10.00 a.m. ✓	Angus, D. Genetics Laboratory, Zoology Department, University of Queensland.	Selective mating and stable equilibrium in *Drosophila tetrachaeta*.
10.30 a.m.	MORNING TEA.	

Population Genetics. Chairman: Dr. R.D. Brock.

11.00 a.m.	Latter, B.D.H. Division of Animal Genetics, CSIRO Epping. N.S.W	Genetic divergence and population variability.
11.30 a.m.	Franklin, I.R. Division of Animal Genetics, CSIRO Epping. N.S.W.	Allozyme variation in natural populations of *Drosophila melanogaster*.
12.00 a.m.	James, S.H. Department of Botany, University of Western Australia.	Neutral allele manipulation as a tactic in evolution.

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*Paper to be read by the author underlined.

SESSION 1B

Thursday 20 May — Plant Genetics. — Chairman: Prof. S. Smith-White

11.00 a.m. ✓	Darvey, N.L. School of Botany, University of New South Wales.	Nucleolus and chromosome association studies in hexaploid wheat.
11.30 a.m. ✓	Pryor, A.J. Genetics Section, Div. of Plant Industry, CSIRO Canberra.	Genetics and biochemistry of catechol oxidase in maize.
12.00 a.m. ✓	McWhirter, K.S. Department of Agricultural Botany, University of Sydney.	Variegated pericarp in Sorghum bicolor.
12.30 p.m. ✓	Shepherd, K.W. Department of Agronomy, Waite Agricultural Research Institute, Sth Australia.	Genetic control of endosperm proteins in wheat and rye.

LUNCH

SESSION 2A

Population Genetics. — Chairman: Dr. W.R. Scowcroft.

2.00 p.m.	Sheldon, B.L. Milton, M.K. Division of Animal Genetics, CSIRO Epping. N.S.W.	Some results of scutellar bristle selection bearing on canalisation, dominance and genetic correlation.
2.30 p.m.	Winston, J.A. Department of Mathematics, La Trobe University, Vic.	Mutation survival, dominance and assortative mating.
3.00 p.m.	Sved, J. School of Biological Sciences, University of Sydney.	Tests for heterosis in Drosophila melanogaster.
3.30 p.m.	AFTERNOON TEA	

SESSION 2A (cont'd)

Population Genetics. Chairman: Dr. B. Latter.

4.00 p.m.	Bundgaard, J. Department of Genetics, La Trobe University, Vic.	A simultaneous study of several selection components in *Drosophila melanogaster*.
4.30 p.m.	Scowcroft, W.R. Division of Plant Industry, CSIRO Canberra.	The effective number of loci in selection response.
5.00 p.m.	Karlsson, L.J. Barker, J.S. Department of Animal Husbandry, University of Sydney.	Effects of population size and selection intensity on responses to disruptive selection.

SESSION 2B

Biochemical Genetics. Chairman: Dr. H.T. Clifford

2.00 p.m.	Kinnear, J.F. Martin, M.D. Department of Genetics, University of Melbourne.	Gene activity in insect development: The relation between the haemolymph proteins of the larva and adult in *Calliphora*.
2.30 p.m.	Thomson, J.A. Voitl, B.D. Department of Genetics, University of Melbourne.	Gene activity in insect development: Larval and adult haemolymph esterases in *Calliphora*.
3.00 p.m. ✓	Sin, Y.T. Department of Genetics, University of Melbourne.	Gene activity in insect development: Patterns of nuclear RNA and protein in larval tissues of *Calliphora*.
3.30. p.m.	AFTERNOON TEA	

Biochemical Genetics. Chairman: Prof. P.A. Parsons.

4.00 p.m. ✓	Daday, H. CSIRO Canberra.	Biochemical basis of differentiation in chicken embryos.
4.30 p.m. withdrawn	Jha, K.K. Department of Genetics, Research School of Biological Sciences, A.N.U.	The regulation of purine metabolism in *Neurospora*.
5.00 p.m. ✓	Chew, G.K. Department of Genetics, La Trobe University, Vic,	Phosphoglycerate kinase and tetrazolium oxidase polymorphism in *Drosophila*.

8.00 p.m. Presidential address.

Prof. M.J.D. White,
Department of Genetics,
University of Melbourne.

Genetic models of speciation.

SESSION 3A

Friday 21 May Biochemical Genetics. Chairman: Dr. J.A. Thomson

9.00 a.m. ✓ Vandeberg, J.L. Cooper, D.S. Sharman, G.B. Poole, W.E.
Department of Genetics,
La Trobe University, Vic.

Inherited variation in marsupial phosphoglycerate kinase and its bearing on X-inactivation.

9.30 a.m. ✓ Cooper, D.W. & G.B. Sharman
Department of Genetics,
La Trobe University, Vic.

~~A proposed mechanism of~~ X-inactivation in eutherian and marsupial mammals.

10.00 a.m. ✓ Shineberg, B.
Division of Plant Industry,
CSIRO Canberra.

Degraded lactose repressors.

10.30 a.m. MORNING TEA

Microbial Genetics. Chairman: Prof. D.G. Catcheside

11.00 a.m. ✓ Miss Stanisich, V.A. Holloway, B.
Department of Genetics,
Monash University.

Sex factors mutants of Pseudomonas aeruginosa.

11.30 a.m. ✓ Mr. Krishnapillai, V.
Department of Genetics,
Monash University.

Restriction of Pseudomonas aeruginosa phages by multiple antibiotic resistant R-factors.

12.00 a.m. ✓ Mr. Kretschmer, P.J. Egan, J.B.
Department of Biochemistry,
University of Adelaide.

Suppressor system in Staphylococcus aureus.

12.30 p.m. ✓ Mr. Woods, W.H. Egan J.B.
Department of Biochemistry,
University of Adelaide.

Mapping the integration site of coliphage 186.

LUNCH

SESSION 3B

Friday 21 May — Miscellaneous. Chairman: Dr. K. McWhirter.

9.00 a.m.	Craddock, E. School of Biological Sciences, University of Sydney.	A compound hybrid zone in *Didymuria*.
9.30 a.m.	Ford, J.H. School of Biological Sciences, Flinders University, S.A.	Nuclear degeneration: A causal sequence of events.
10.30 a.m.	MORNING TEA	
	Recombination. Chairman: Assoc. Prof. S. Barker.	
11.00 a.m.	Westerman, M. Department of Genetics, La Trobe University, Vic.	The effect of X-Irradiation on chiasma frequency in *Chorthippus brunneus*.
11.30 a.m.	Hawke, A. Scowcroft, W. Plant Industry, CSIRO Canberra.	Effect of density on recombination in *Drosophila melanogaster*.
12.00 a.m.	Byrne, O.P. Hawke, A. Plant Industry, CSIRO Canberra.	Effect of density on chiasma frequency in the locust *Chortoicetes terminifera*.
	LUNCH	

SESSION 4A

Microbial Genetics. Chairman: Prof. M.J.D. White.

2.00 p.m.	MacPhee, D.G. Department of Genetics, La Trobe University, Vic.	Effects of R-factors on radiation repair in *Salmonella*.
2.30 p.m.	Brink, N.G. School of Biological Sciences, Flinders University, S.A.	Tryptophan transport in various mutant strains of *Neurospora crassa*.
3.00 p.m.	Hull, R.R. Reeves, P.R. Department of Microbiology, University of Adelaide.	Sensitivity of Bacteriophage λ to colicin Ca42-E2.

SESSION 4A (cont'd)

3.30 p.m.	Stevenson, I. Department of Developmental Biology, A.N.U. Canberra.	Genetic implications from the fine structure of nuclear division in *Paramecium*.
4.00 p.m.	AFTERNOON TEA.	
4.30 p.m.	Business Meeting.	

SESSION 4B

Human and Behavioral Genetics. Chairman: Dr. O.R. Byrne.

2.00 p.m.	Wallace, D.C. Queensland Institute of Medical Research.	The genetic map of the human X chromosome, with a report of a study of the linkage relationships of the Lesh-Nyhan Locus.
2.30 p.m.	Angell, R. Prince Henry Hospital and Prince of Wales Hospital, Randwick.	Chromosomal polymorphism of the Y chromosome in Australian aboriginal and white populations.
3.00 p.m.	McKenzie, J.A. Parsons, P.A. Department of Genetics, La Trobe University, Vic.	Variations in mating propensities in selected strains of *Drosophila melanogaster*.
3.30 p.m.	Parsons, P.A. Department of Genetics, La Trobe University, Vic.	Morphology and behavior of mice and men.
4.00 p.m.	AFTERNOON TEA	
4.30 p.m.	Business Meeting.	

AgS no 18

polyploidy?

HAS POLYPLOIDY OCCURRED IN THE EVOLUTION OF THE DERMAPTERA ?

2n 12
4n 24 25
6n 36

XO
XY
X_1X_2Y
$X_1X_2X_3Y$

By G. C. Webb

Department of Genetics,
University of Melbourne

chrom. apparently without localised Xtra.

The widely accepted view that the earwigs have evolved by polyploidy has been recently re-expounded by Henderson(1970)but the theory suffers from certain weaknesses, the most notable being the requirement that polyploidy arose independently in different superfamilies in the higher Dermaptera (suborder Forficulina).

Y chrom. polymorphism

Recently obtained results which do not agree with the polyploidy hypothesis have been found the higher Dermaptera from eight indigenous Australian species and from the introduced Forficula auricularia (Webb and White, 1970). These results include a report of the lowest chromosome count in the higher Dermaptera; 2n ♂ = 10 (8 + XY) in Labidura riparia;the third different chromosome count for this "cosmopolitan species". An XO species is also reported for the first time: previously all male Dermaptera were believed to require a Y chromosome and the case for polyploidy is considerably weakened by this finding particularly as the diploid number, 2n ♂ = 19 (18 + X) is above that of the primitive diploid number (around 12) on the polyploidy hypothesis.

In addition a species of Hemimeris (suborder Hemimerina) investigated by White (unpublished) has 2n ♂ = 7(X_1X_2Y + 4); which indicates that multiple sex chromosome mechanisms may arise in lower Dermaptera by agencies other than polyploidy.

The case for polyploidy in the Dermaptera appears to be confounded by the above new evidence.

References

Henderson, S.A. Chromosoma,31, 139 (1970).
Webb, G.C. and White, M.J.D. Experientia, 26, 1387 (1970).

INVERSION POLYMORPHISM IN CHIRONOMUS STAEGERI

By J. Martin.

Department of Genetics,

University of Melbourne.

Chironomus staegeri is distributed through most of North America. The inversions in this species show a number of unusual characteristics, including marked deficiency of heterozygotes; considerable non-random association of inversion systems, whether linked or non-linked; and the occurrence together of rare sequences.

The results further indicate that the species may be in the process of splitting into three parts, which may already have achieved a considerable degree of isolation.

SELECTIVE MATING AND STABLE EQUILIBRIUM IN DROSOPHILA TETRACHAETA

By D.S. Angus

Genetics Laboratory
Zoology Department
University of Queensland

It is well established that among some species of Drosophila, polymorphic for chromosomal inversions, that individuals which are chromosomally heterozygous may have a selective advantage over homozygous individuals from the same populations.

Drosophila tetrachaeta is a chromosomally polymorphic species found in New Guinea which has two alternative gene sequences on chromosome 5. These sequences are separated by a simple inversion involving about 30% of the chromosome. All natural populations so far sampled appear to be in Hardy-Weinberg equilibrium with respect to karyotypes involving this inversion.

Investigation of the relative mating success of male karyotypes taken from a laboratory culture of the Bisianumu population demonstrated that heterozygous males were more successful than either of the homozygous males. The advantage enjoyed by the heterozygous males was independent of the females' karyotype.

A stable equilibrium frequency for the inversion was calculated from the differences in relative fitness of the males. This frequency did not significantly differ from, and could account for, that found in the natural populations at Bisianumu.

GENETIC DIVERGENCE AND POPULATION VARIABILITY

By B.D.H. Latter

Division of Animal Genetics

CSIRO Epping, N.S.W.

Natural selection for an intermediate level of gene or enzyme activity has been shown to lead to a high frequency of heterotic polymorphisms in populations subject to mutation and random genetic drift. The model assumes a symmetrical spectrum of mutational variation, with the majority of variants having only minor effects on the probability of survival. Each mutational event produces a variant which is novel to the population. Allelic effects are assumed to be additive on the scale of enzyme activity, heterosis arising whenever a heterozygote has an expected level of activity closer to optimal than that of other genotypes in the population.

Experimental evidence in support of the model is reviewed. A survey of published data concerning polymorphic loci in man and Drosophila suggests that an alternative model, based on the superiority of hybrid molecules, is not generally applicable; 13 loci giving rise to hybrid zones on electrophoresis have a mean frequency of heterozygotes of $0.22 \pm .06$, compared with a value of $0.23 \pm .04$ for 16 loci classified as producing no hybrid enzyme.

A new measure of genetic divergence between populations is proposed, which is readily interpreted genetically, and increases approximately linearly with time under centripetal selection, drift and mutation. The parameter is closely related to the rate of amino-acid replacement observed over the long-term evolutionary history of the computor populations studied.

ALLOZYME VARIATION IN NATURAL POPULATIONS OF DROSOPHILA MELANOGASTER

By I.R. Franklin

CSIRO Epping, N.S.W.

Allele frequencies at 10 loci have been measured in two populations of D. melanogaster collected in the Hunter Valley, N.S.W. These two populations, located at Wineries about 5 miles apart, differ in frequency at several loci. Two pairs of loci, Esterase-6 and Tetrazolium Oxidase on the third chromosome, and Alcohol dehydrogenase and α-glycerophosphate dehydrogenase on the second, show significant linkage disequilibrium. The implications of these findings are discussed.

NEUTRAL ALLELE MANIPULATION AS A TACTIC IN EVOLUTION.

By S.H. James

University of Western Australia

A computer model of genomic organization, deriving from that proposed by Kauffman (1969) is described. The operation of the model allows a broad system of analogies to be developed. In this system of analogies, neutral allele analogs can be defined and some of the possibilities resulting from their manipulation are demonstrated. In particular, it is shown that in this model, neutral alleles at other loci may be used to neutralize initially non-neutral mutations, and some of the evolutionary implications of this phenomenon are indicated.

NUCLEOLUS AND CHROMOSOME STUDIES IN HEXAPLOID WHEAT

By N.L. Darvey, and C.J. Driscoll.

School of Botany,

University of N.S.W., Sydney.

Four nucleolar bodies arising from the two pairs of satellited chromosomes (1B,6B) are produced in each telophase nucleus. The probability that these fuse depends in part on the spatial proximity of the telophase satellited chromosomes.

The distances between satellites in materials deficient for two homologous or two non-homologous satellites were measured. The materials were not pre-fixed with cold water and hence chromosomes retained a normal metaphase configuration. The results supported the conclusions drawn from earlier studies on pre-fixed materials together with other studies on nucleolar fusion (Gen. Soc. Aust. 1970) There was no evidence for somatic association in hexaploid wheat.

Studies at meiosis indicate that nucleolar fusion is always complete at zygotene, except in cases where homologous chromosomes failed to associate (asynapsis), e.g. by colchicine treatment.

Nucleolar fusion is complete at zygotene in de-synaptic material of nullisomic 5D or di-isosomic $5B^{L}$. This suggests that homologous chromosomes had associated pre-synaptically, but that the monitoring effect of genes in homoeologous group 5 had a limiting effect on synapsis.

The pre-zygotene fusion of nucleoli in material with varying numbers of satellited chromosomes is being currently studied and some results will be presented.

Class Control MH
I + ++
II + +
III – –
non migrating migrating
kinetics non linear sigmoid

GENETICS AND BIOCHEMISTRY OF CATECHOL OXIDASE IN MAIZE

By A.J. Pryor

Division of Plant Industry, CSIRO,

Canberra.

The Catechol Oxidase gene (Cx) has been located in chromosome 10 less than 0.2 recombination units from the endosperm marker du$_1$. Three electrophoretic variants, (the Slow and Fast migrating forms and a Null), are specified by the alleles Cx^S, Cx^F, Cx^N respectively.

As interaction occurs between catechol oxidase and a'modifer' which is probably an endogenous phenolic substrate. The enzyme and modifer are functionally isolated until cellular disruption, when the interaction leads to changes in the kinetics and electrophoretic migration of the enzyme. The modifier content in the seedling is genetically determined by genes other than Cx, and in addition is reduced ten-fold by treatment of seed with maleic hydrazide.

The system seems to possess many of the requirements of a biochemical mechanism for hypersensitive disease resistance and should allow for a rigorous test of several models.

VARIEGATED PERICARP IN SORGHUM BICOLOR

By K.S. McWhirter

Department of Agricultural Botany,

The University of Sydney.

A variegated pericarp phenotype, consisting of red stripes on a white background occurs in certain Sorghum bicolor stocks (calico sorghum). This phenotype is of interest because of the apparent homology with the variegated pericarp phenotype in maize.

A variegated phenotype can be produced by either a "pattern" allele (such as P^{mo}, mosaic pericarp, in maize) or by a genetic system characterised by a high rate of mutation in somatic and germinal tissues (such as P^{vv} variegated pericarp in maize.)

In this preliminary study the variegated pericarp phenotype in sorghum is shown to depend on somatic and germinal mutation of an allele Y^v (variegated pericarp) to the dominant Y (self red pericarp), occurring at high frequency. Somatic mutation, producing conspicuously sectored red/variegated inflorescences, occurred frequently but/ in none of the instances was there evidence of twin somatic sectors. Somatic mutation of Y^v to Y occurred more frequently in homozygous (Y^vY^v) than in heterozygous(Y^vy) genotypes.

The genetic system producing variegated pericarp in sorghum bears many similarities to the variegated pericarp system in maize. A common origin of the genetic elements involved in the two mutable gene systems might be inferred from the homology of phenotypes and similar modes of operation of the mutable gene systems.

GENETIC CONTROL OF ENDOSPERM PROTEINS IN WHEAT AND RYE

used nulli-tetra
e.g. 0 1A 4 1B

By K.W. Shepherd

Department of Agronomy

Waite Agricultural Research Institute

Hexaploid wheats possess a complex mixture of electrophoretically different gliadin (storage) proteins in the grain, whereas diploid rye, a relative of wheat, possesses few of these proteins. In an analysis of chromosome deficient stocks of hexaploid wheat it was shown that most, if not all, of its gliadin proteins are controlled by genes on chromosomes 1 and 6 of each of the A,B, and D genomes. Thus at least two chromosomes (1and 6) must have been associated with the equivalent proteins of the ancestral diploid from which the three wheat genomes are believed to be derived. However, although diploid rye is thought to have come from this same diploid progenitor, in an analysis of lines having single pairs of rye chromosomes added to the wheat genome it was found that the gliadin proteins of rye are controlled by gene(s) on just one rye chromosome(V).

It was shown that the reduced vegetative vigour and fertility of wheat nullisomics deficient in turn for each pair of group 1 chromosomes, could be largely overcome by substituting rye chromosome V for the deleted wheat chromosomes. Thus rye V is genetically related to the three group 1 wheat chromosomes.

To account for these results it is necessary to modify the commonly accepted pathway for the evolution of wheat and rye genomes.

SOME RESULTS OF SCUTELLAR BRISTLE SELECTION BEARING ON CANALISATION, DOMINANCE AND GENETIC CORRELATION.

By B.L. Sheldon and M.K. Milton

CSIRO Epping, N.S.W.

Five high and five low scutellar bristle lines were derived from Oregon RC and selected for periods up to 150 generations. The sc' allele was introduced into subsamples of these lines at about generation 40, an extra dose of sc+ was introduced into other subsamples at generation 134 and the correlated responses in abdominal chaetae were followed for most of the period. Correlated responses in bristle number at other positions on the head and thorax were scored occasionally. Crosses between the low and high lines are being studied at present. Most of the results are consistent with the model that canalisation at 4 scutellar bristles in wild type flies is brought about by a control genotype, regulating the activity of the scute locus. This genotype has apparently not been affected by selection in these lines, the responses, in one line up to a mean of about 14 bristles, being due to selection of other modifier genes. Dominance of + to sc has been altered to some extent, but not disrupted, by selection, at least to generation 40. A positive correlated response in abdominals occurs in all lines but some lines show a decrease in the proportion of total bristle resources being used for abdominals.

TESTS FOR HETEROSIS IN DROSOPHILA MELANOGASTER

By J. Sved

School of Biological Sciences,

University of Sydney.

A population cage test for heterosis has been carried out in D. melanogaster which is similar in design to the experiment of Sved and Ayala (Genetics 66 : 97) on D. pseudoobscura. The results indicate that homozy osity of the entire second chromosome causes a depression in fitness of the order of 85%. A preliminary experiment on the effect of crowding carried out using larval samples from the cages has given a significant reduction in homozygote viability, unlike previous experiments which failed to demonstrate any effect of crowding. The results are discussed from the point of view of Wallace's "hard" and "soft" selection.

A SIMULTANEOUS INVESTIGATION OF SEVERAL SELECTION COMPONENTS IN DROSOPHILA MELANOGASTER.

By J. Bundgaard.

Department of Genetics and Human Variation

La Trobe University.

The total dynamics of a 4, chromosome polymorphism in Drosophila melanogaster has been studied in various genetic situations using an experimental system by which it was possible to get optimal information about the sexual, fecundity and zygotic selection patterns simultaneously in each generation. Data revealed that the selection component of major importance for the dynamics of this genetic system was sexual selection. Both the zygotic and sexual selection component behaved in a frequency dependent way but the latter was the component responsible for the stability of the polymorphism. Fecundity selection was of very minor importance for the total dynamics of this system.

The results are discussed in relation to the study of selective forces in natural populations.

THE EFFECTIVE NUMBER OF LOCI IN SELECTION RESPONSE

By W.R. Scowcroft

CSIRO Canberra

The quantitative identification and location of chromosomal regions contributing to the response to selection for both increased and decreased scutellar microchaetae in Drosophila melanogaster has been carried out by a recombinational subdivision of the X, IInd and IIIrd chromosomes. The correlated genetic effects on scutellar bristles, which shows a correlated response to selection for microchaetae, were also studied.

The genetic changes following selection for increased chaetae involved two regions on each of the IInd and IIIrd chromosomes, while selection for reduced microchaetae caused genetic changes at three sites on the IInd and two on the IIIrd chromosome. There were no significant genetic changes involving the X chromosome. Interaction did occur between the located "genes" which in one case suggested duplicate gene action and in an other complementary gene action.

There was some direct correlation between the changes affecting microchaetae and those affecting scutellar bristles. Other genetic changes that affected scutellar bristles were manifested as interactions unfavourable to the direction of selection but which had no effect per se. These results will be interpreted along with other similar analyses in relation to the number, location, and size of gene effects and the nature of gene interaction involved in quantitative genetic theory.

EFFECTS OF POPULATION SIZE AND SELECTION INTENSITY ON RESPONSES TO DISRUPTIVE SELECTION

By L.J. Karlsson and J.S. Barker

Department of Animal Husbandry

University of Sydney

With the exception of the work of Thoday and his collaborators, experimental disruptive selection has not been found to lead to sexual isolation between the rwo parts of the the population. In the experiment to be reported, the effects ofpopulation size and intensity of selection (for sternopleural bristle number in D.melanogaster) on responses to disruptive selection, on degree of sexual isolation, and on mating behaviour have been investigated, Four treatments were used:

High number, high selection - 40 pairs selected from 1600 pairs (1 replicate).

High number, low selection - 40 pairs selected from 80 pairs (two replicates).

Low number, high selection - 8 pairs selected from 320 pairs (two replicates.)

Low number, low selection - 8 pairs selected from 16 pairs (four replicates).

Selected high and low parents in each line in each generation were put in a mating chamber and matings recorded, so that mating behaviour parameters (mating speed and copulation duration) and isolation indices were calculated for every generation.

In the high number, high selection treatment, the two parts of the line were distinct subpopulations (no migration between them) by generation 3. Significant sexual isolation was found in four of the 17 generations of selection, but the regression of isolation index on generations was not significant. Results for the other treatments were more variable, but with no tendency to the development of sexual isolation.

THE RELATION BETWEEN THE HAEMOLYMPH PROTEINS OF LARVA AND ADULT IN CALLIPHORA

By J.F. Kinnear and M.D. Martin.

Department of Genetics

University of Melbourne

The striking contrast at both cell and tissue levels between embryogenesis and larval development on the one hand, and imaginal differentiation and morphogenesis during metamorphosis on the other, led historically to the idea that two relatively distinct sets of genes must be involved in these processes (1) Recent evidence of limited protein synthesis during imaginal development in the pupa (2) has suggested the importance of re-utilisation of larval protein at this stage. This implies (a) a major difference in the kind of gene activity in the pupa compared with the larva and (b) that adult proteins should be largely derived from the polypeptides of larval tissues.

The haemolymph serves as a link between the storage proteins of the fat body and the developing imaginal tissues. Changes from the larval to the adult spectrum of plasma proteins occur stepwise, but are quantitative rather than qualitative. The relation between the major protein species involved has been investigated immunologically, and at the polypeptide level, electrophoretically.

(1) Wigglesworth, V.B. 1961. Roy.Ent.Soc.Lond. Symp.No.1, 103
(2) Dinamarca, M.L. and Levenbook,L. 1966. Arch.Biochem.Biophys. 117:110

LARVAL AND ADULT HAEMOLYMPH ESTERASES IN CALLIPHORA

By J.A.Thomson and B.D. Voitl

Department of Genetics

University of Melbourne.

Extensive polymorphisms for plasma esterases occurs in natural populations of C. stygis, at least 3 genetics systems being involved. The most complex of these controls a variable series of isozymes, function of at least one of which appears obligatory for normal development beyond hatching. The variant enzymes of inbred strains and their crosses have been used in a systematic study of the relation between larval and adult esterases. The work confirms the evidence of Pantelouris and Downer (1) that quantitative rather than qualitative changes occur at metamorphosis, but their implication that such data can provide critical evidence that no new genetic activity is involved in the transition is questioned.

(1) Pantelouris, E.M. and Downer, R.G.H. 1969.
J. Insect Physiol. 15: 2357

PATTERNS OF NUCLEAR RNA AND PROTEIN IN LARVAL TISSUES OF CALLIPHORA

By Y.T. Sin.

Department of Genetics,

University of Melbourne.

Patterns of nuclear RNA and protein in larval tissues of Calliphora. Previous work from this laboratory (1) has provided evidence of major changes in the amount and nature of nuclear inclusion RNP in the larval fat body and salivary gland. Changes in this material, and in chromosome dispersion, can be correlated with activity of these cells in protein synthesis.

At the light microscope level, the nuclear RNP of each tissue has a characteristic form and distribution. The major RNA and protein species of these inclusion bodies has been examined electrophoretically (2) in conjunction with studies on the acidic proteins and histones of the chromatin at the same stages. The data provide a basis for a preliminary analysis of the genetic significance of the developmental sequence shown by the nuclear RNP.

(1) Thomson,J.A. and Gunson, N.M. 1970. Chromosoma 30: 193
(2) Collaboration in some of these experiments with F. Paula Imray is gratefully acknowledged.

BIOCHEMICAL BASIS OF DIFFERENTIATION IN CHICKEN EMBRYOS

By H. Daday.

CSIRO Canberra

This paper will concern the mechanisms of cell aggregation and involvement of protein during embryo development.

PHOSPHOGLYCERATE KINASE AND TETRAZOLIUM OXIDASE POLYMORPHISMS IN DROSOPHILA

By G.K. Chew

Department of Genetics

La Trobe University, Melbourne.

Two enzyme systems have been studied in Drosophila (1) phosphoglycerate kinase, using starch gel electrophoresis, and (2) tetrazolium oxidase using polyacrylamide gradient gel electrophoresis. Phosphoglycerate kinase (PGK) polymorphism has not been previously reported in Drosophila. It was found to be polymorphic in *D. melanogaster* in this study. It appears to be a two allele autosomal system, the faster migrating form being the more common. Heterozygotes show both bands but no hybrid band is observed, so that the enzyme may be a monomer. Wild populations of *D. melanogaster*, *D. simulans* and *D. immigrans* were examined. A male-specific fluorescent substance was observed when PGK was being studied. Some observations on it will be reported. Two forms of Tetrazolium oxidase were observed in *D. melanogaster*. Heterozygotes for this enzyme possess an intermediate band which suggests a dimeric structure for this enzyme. A comparison between *D. melanogaster* and *D. simulans* populations is being carried out.

INHERITED VARIATION IN MARSUPIAL PHOSPHOGLYCERATE KINASE AND ITS BEARING ON X-INACTIVATION

By J.L. VandeBerg, D.W. Cooper
G.B. Sharman and W.E. Poole.

Department of Genetics

La Trobe University, Melbourne.

An electrophoretic survey of red cell phosphoglycerate kinase in marsupials has been initiated. All species examined so far have a major form of the enzyme which appears as an intense band after staining. Some species possess a slower moving minor band as well. Family data, along with population data, indicate that in those species where polymorphisms exist, the major band is inherited in a sex-linked manner, with the paternally derived X-chromosome being inactive in somatic cells of females. The minor band appears to be inherited in a codominant autosomal fashion. Evolutionary implications will be discussed.

major component:

P.		N		VE	
♀	♂	♀	♂	♀	♂
N	VE	4	5	0	0
VE	N	2	1	2	3

VE is faster than N

borne on X paternal X inactive

minor component: (V slow) autosomal. SF × S → S & SF

X-INACTIVATION IN EUTHERIAN AND MARSUPIAL MAMMALS

By D.W. Cooper and G.B. Sharman

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Dosage compensation in eutherian mammals is achieved by inactivation of either the maternally derived or the paternally derived X chromosome (random X-inactivation or "Lyonization"). Studies on the X chromosomes of hybrid kangaroos show that the paternally derived X is always late labelling, which suggests that dosage compensation in marsupials is achieved by inactivation of the paternal X. This conclusion is supported by studies on sex linked enzyme differences, which also suggest that marsupials and eutherians have sex linked genes in common. A model for the evolution of random X-inactivation in eutherians will be presented.

Used:

			X relative size
Wallaroo	Macropus robustus	robustus	1·0
Euro	"	erubescens	1·5
Red K.	"	rufus	2·0

Hybrids.

Hybrids Sharman	♀	♂	late labelling X
	Red	Euro	Euro
	Euro	Wallaroo	Wallaroo

Theory

control'g element in Macrops. not detachment ∴ pat. X not active.

Glucose 6 Phosphate dehydrogenase

parent ♀	parent ♂	♀ S	♀ F	♂ S	♂ F
E	W	1	0	1	0
W	R	0	2	0	1

in Eutherians

? detachment of control'g element & random reattachment.

Searle's translocation in mouse example of paternal X inactivation

But XO mice, which have X from father, are not inactivated.

PARTIALLY DEFECTIVE LACTOSE REPRESSOR MUTANTS OF ESCHERICHIA COLI

By B. Shineberg

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The lactose repressor protein has two functions: to bind to the DNA of the lac operator and to mediate the effect of inducer in de-repressing the repression of the lac genes. While considerable genetic variability has been obtained in the repressor with respect to its affinity for inducers, variability with respect to its DNA binding function has tended to be limited to mutants whose function is completely impaired. The examination of a sample of mutants, capable of growth on phenyl-β-galactoside, revealed considerable variability in this basic function. Its nature and significance is discussed.

SEX FACTOR MUTANTS OF PSEUDOMONAS AERUGINOSA

By V.A. Stanisich

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Males of P. aeruginosa strain PAT have been isolated which harbour mutants of the FP2 sex factor and are defective in both sex factor and host chromosome transfer to recipient bacteria. Another mutant of FP2 designated $FP^{\oplus}$ is known to mediate chromosome transfer between male bacteria such that matings of the type $FP^{\oplus}$ x FP^{+} show at least a thousand fold increase in recombinant formation over that observed in FP^{+} x FP^{+} matings. These defective FP2 factors can be transferred to recipient strains when males heterozygous for the two mutant sex factors $FP_d FP^{\oplus}$ are constructed, suggesting that $FP^{\oplus}$ can provide the function(s) defective in FP_d male strains.

Wild type (FP^{+}) or mutant males ($FP^{\oplus}$ or FP_d) are distinguishable from recipient bacteria (FP^{-}) by their greater precipitability at PH5 This characteristic of male strains is a sex factor coded function. The properties of a male strain not showing this precipitation responses will be discussed.

	FP^-	FP^+	% initial
FP^-	−	+	3
FP^+	+	−	95
$FP^{\oplus}$	+	+	1.5
FPd	−	−	0.5

extended plating

$FP^+ \times FP+$	$10^{-7}-10^{-8}$
$FP^- \times FP+$	$<10^{-8}$
$FP+ \times FP-$	$10^{-3}-10^{-6}$
$FP^{\oplus} \times FP-$, $\times FP+$, $\times FP^{\oplus}$	$10^{-2}-10^{-6}$

about ½ of these are FPd.

R FACTORS, PHAGES AND HOST-CONTROLLED MODIFICATION (HCM) IN P. AERUGINOSA

By V. Krishnapillai

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Three R factors R91, R18, and R68 arising from P. aeruginosa strains isolated in a Burns Unit were transferred to P. aeruginosa strain PAO and tested for their ability to restrict the replication of 50 temperate phages. R91 had no effect on any of those phages while R18 restricted phages 39, 227, and 228 (EOP reductions of 10^{-5} -10^{-9}) and R68 restricted phage G101 (EOP reduction of 10^{-1}). R18 was unable to modify phages 39 and 228, while it was able to partially modify phage 227. These two R factors had no effect on the replication of the Salmonella phage P22 in S. typhimurium.

Complementation tests for restoration of restriction function, made by transferring R18 or R68 into restriction-deficient bacterial mutants, indicated that the HCM systems controlled by the host and R factor genomes were unrelated.

The R18 R factor protects against induction of the UV-inducible phages 39,228 or the UV-inducible aeruginocins produced spontaneously or following UV-irradiation by bacteria lysogenic for phage 39 or 228. Such effects were not observed on the UV non-inducible phage 227 and the same aeruginocins in 227- lysogens.

These results demonstrate the extent of genes coded for by R factors in addition to the traditionally encountered drug resistance genes.

SUPPRESSOR SYSTEM IN STAPHYLOCOCCUS AUREUS

By P. Kretschmer and J.B. Egan

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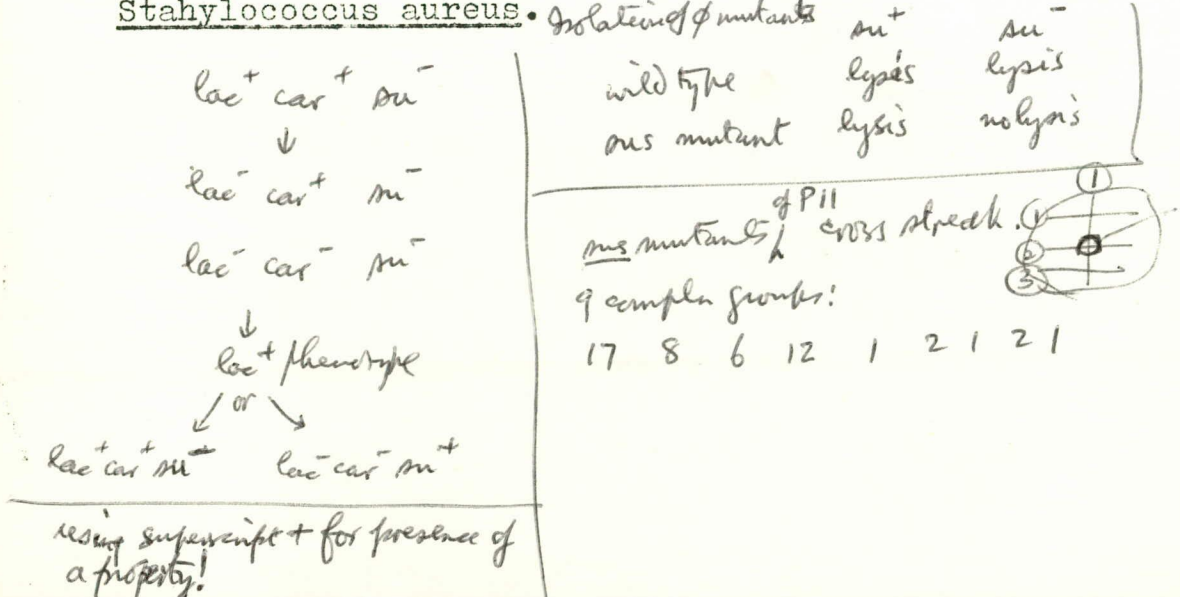
A suppressor host mutant in Staphylococcus aureus strain NCTC 8325 has been isolated. Bacteria containing two independently isolated mutations in the unlinked Z and car genes affecting lactose fermentation were tested for spontaneous single-step reversion to Z^+ car phenotype. Two such Z^- car mutants reverted at a frequency of 10^{-8}, suggesting a single mutation (suppressor) had resulted in the phenotypic reversion.

One of these mutants was used to isolate suppressor sensitive (sus) mutants of the temperate staphylococcal phage P11; that is, phage which could grow on the revertant but not on the original bacterial strain. The mutants so far obtained (after UV, hydroxylamine or nitrosoguanidine mutagenesis) fall into 8 complementation groups, a fact which strongly indicates that the suppression is of the classical nonsense translation type.

Further sus mutants of P11 are being isolated with the aim of studying the biochemical genetics of phage infection in Stahylococcus aureus.



MAPPING THE INTEGRATION SITE OF COLIPHAGE 186

By W.H.Woods and J.Barry Egan

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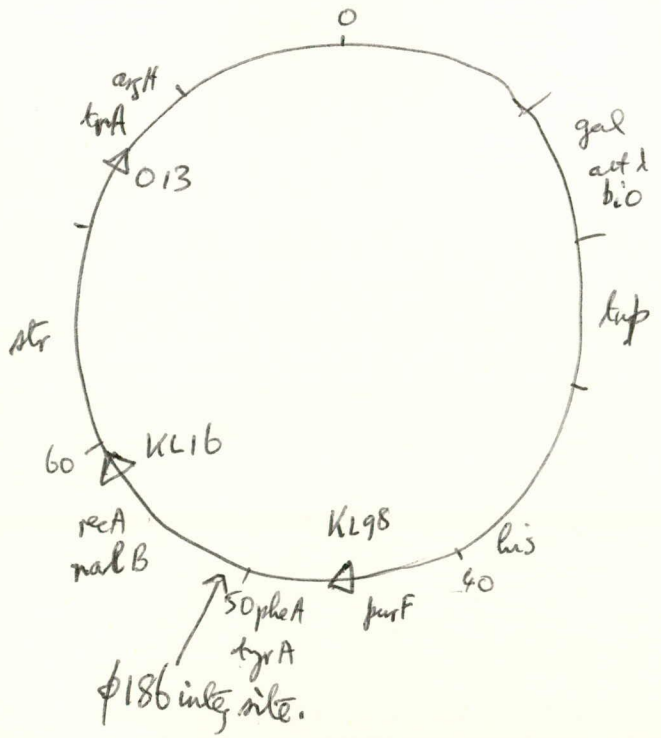
University of Adelaide.

We have found that coliphage 186 is inducible by ultra-violet irradiation but does not undergo zygotic induction in contrast with phage λ which is subject to both these forms of induction. To further investigate the non-zygotic induction of phage 186 it was necessary to establish precisely the integration site of this phage into the E. coli genome.

The integration site has been mapped using Hfr 0-13 and Hfr KL16 conjugation systems, interrupted mating experiments and finally P1 transductions. It is located adjacent to the pheA locus which is at 50 minutes on the E. coli map. We are presently attempting to demonstrate integration of the 186 genome by P1 transductions involving markers spanning the 186 attachment site and ultimately through specialised transductions by phage 186.



φ186 does not cause zygotic induction as φx does, whether φ or ♂ zygotic. no effect on prop. transfer of distal markers.

Donor $x^+ (186)^-$

recipient $x^- (186)^+$

↓

X^+ how many still hydrogenous?

186 site maps between PheA and NalB.
(50 min) (51 min.)

A COMPOUND HYBRID ZONE IN DIDYMURIA

By E. Craddock

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University of Sydney

Several chromosome races of the stick insect Didymuria violescens come into contact and hybridize within a limited area on the northern edge of the Barrington Tops plateau. The consequences of the meiotic behaviour of hybrids from this zone will be discussed and an interpretation of the situation presented.

CAUSAL SEQUENCE OF DIFFERENTIATION IN THE EPACRIDACEAE

By Judith Ford

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Flinders University, S.A.

Following telophase II in anthers of the Styphelieae (Epacridaceae) three of the four microspore nuclei migrate to one end of the cell and degenerate; only one nucleus completes development. In a triploid species Leucopogon juniperinus, this functional nucleus always has a haploid chromosome number of (4) four; univalent chromosomes are excluded from the pollen.

Selection and degeneration of the three nuclei is the result of a causal sequence of events initiated at premeiotic mitosis:

(1) Suppression of elongation of the mitotic anaphase spindle.
→ (2) Establishment of complementary polarity in pairs of sister cells.
→ (3) Initiation of a tripolar spindle at metaphase I of meiosis.
→ (4) Temporal difference between the two second division spindles. (In the special case of L. juniperinus and unequal distribution of chromosomes also results).
(5) Differentiation of 3 of the 4 telophase II nuclei.
(6) Expansion of the "functional" cytoplasm pushes 3 nuclei (found in low-organellar cytoplasm) to one end of the cell and a cell plate is laid down asymmetrically.

In some species specialized chromosome behaviour has amplified the temporal difference between second division spindles leading to a greater stability of the system. Species lacking amplication often exhibit varied degrees of development within each pollen tetrad.

THE EFFECT OF X-IRRADIATION ON CHIASMA FREQUENCY IN CHORTHIPPUS BRUNNEUS (Thunberg).

By Dr. M. Westerman

Department of Genetics and Human Variation,

La Trobe University.

Low doses of X-irradiation can alter chiasma frequency as scored at diplotene-diakinesis if given during discrete periods of prophase I of meiosis. Thus irradiation given during premeiotic DNA synthesis leads to a reduction in mean cell chiasma frequency, while irradiations given in leptotene or zygotene-early pachytene both lead to an increase. The findings of a dose-response experiment will be discussed in relation to a recent scheme (LAWRENCE, C.W. and HOLT, P.D., 1970) which attempts to interpret the action of ionizing irradiations on meiosis.

EFFECT OF DENSITY ON CHIASMA FREQUENCY IN THE LOCUST, CHORTICETES TERMINIFERA

By O.R. Byrne and A. Hawke

Department of Botany

A.N.U. Canberra

Studies on variation in density of the plague locust, Chorticetes terminifera indicate a positive association with chiasma frequency. The effects of temperature and some biochemical metabolites on chiasma number will also be reported.

EFFECT OF DENSITY ON RECOMBINATION IN DROSOPHILA MELANOGASTER

By A. Hawke and W. Scowcroft

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Plant Industry, CSIRO Canberra.

The effect of density on recombination between two linked markers has been investigated and will be reported..Females from crowded cultures have shown a significantly lower recombination percentage compared with females reared solitarily.

no ligase mutants are viable.

EFFECTS OF PLASMIDS ON RADIATION SENSITIVITY OF SALMONELLA TYPHIMURIUM

By D.G. MacPhee

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La Trobe University.

	Protection	Mut effect
Salmonella	+	+
E.coli	0	+

Certain extrachromosomal genetic elements or plasmids have been found to protect strains of S. typhimurium against the lethal effect of ultraviolet irradiation. The same plasmids markedly increase the UV mutability of bacteria carrying them. One possible explanation for these findings is that the plasmids carry a gene (or genes) concerned with repair of radiation damage. Results supporting this hypothesis have been obtained using the drug-resistance transfer factor R-Utrecht. Interactions between R_1-Utrecht and ColE1 (a colicin - determining plasmid which does not protect cells against UV) will be discussed.

R Utrecht protects against all mutagenic agents.

I Damage to DNA needs excision

UV
4 nitroquinoline Oxide (NQO)
Mitomycin C (MC)

II Damage not needing excision

Ionising radiation (X, γ)
Methyl methane sulphate (MMS)
Nitrosoguanidine (NTG)
Thymine starvation in thy mutant.

1 exc	uv^s	mms^r	her (uv)	her^+ (γ)	rec^+
2 res	uv^s	mms^s	her (uv)	her (γ)	rec^+
3 rec	uv^s	mms^s	her^+ (uv)	her^+ (γ)	rec

her = host cell reactivation of ΦES18

uvr-283 ? DNA polymerase mutant

TRYPTOPHANE TRANSPORT IN VARIOUS MUTANT STRAINS OF NEUROSPORA CRASSA

By N.G. Brink

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Flinders University, S.A.

Mutants which are resistant to the amino acid analogues, 4-methyl-tryptophane and para-fluorophenylalanine have been isolated. These strains are defective in tryptophane transport.

Genetic revertants of allele mtr-26 have been isolated, and these are found to be of several types. Firstly, there are the site revertants in which tryptophane uptake is similar to wild type strains. Secondly, some second site (intragenic suppressor) revertants have been found in which the rate of uptake is at a reduced level. The third type of revertant is due to forward mutation at an unlinked suppressor locus and uptake again appears to be at a reduced rate compared with wild type. This suppressor mutation does not appear to be a nonsense suppressor, but is probably due to an alteration in a second uptake system.

In the case of those revertants resulting from intragenic suppression, the second site has been isolated in some cases and is found to be defective in tryptophane transport similar to other mtr alleles.

Colicins act on 1 Ribosomes E3
2 DNA E20
3 Energy A, E1, C, K, Ia, Ib.
Surface receptor on E. coli

SENSITIVITY OF BACTERIOPHAGE λ TO COLICIN CA42-E2

By R.R. Hull and P.R. Reeves

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University of Adelaide

Treatment of E. coli K12 infected by λ C1857 with colicin CA42-E2 resulted in partial inhibition of the infectious process. Uninfected bacteria were killed by colicin with a probability of about five times that of similarly treated λ infected bacteria (loss of plaque forming ability). The λ-DNA, when present in a bacterial cell either as the replicating DNA of infectious phage or as the non-replicating DNA of superinfecting phage was degraded to acid-soluble material following colicin treatment. An analysis of the intermediates of DNA breakdown has revealed that degradation of the DNA to acid-soluble material was preceded by endonucleolytic fragmentation of the chromosome at a limited number of sites. This is the same mechanism of degradation that has previously been observed for E.coli DNA.

GENETIC IMPLICATIONS OF THE FINE STRUCTURE OF NUCLEAR DIVISION IN PARAMECIUM

By I. Stevenson

Department of Developmental Biology

Australian National University

The division process of the ciliate macronucleus is usually described as amitotic; as there are generally no changes in chromatin condensation; or the appearance of chromosomes or comparable spindle elements to those found in the mitotic spindle. Macronuclear amitosis has been studied in Paramecium aurelia with the electron microscope, and the involvement of microtubular elements in each of the three stages of macronuclear amitosis, condensation; elongation; and karyokinesis, has been demonstrated. In the light of ultra - structural observations on amitosis, some concepts of structure and function in the ciliate macronucleus will be discussed.

THE GENETIC MAP OF THE HUMAN X CHROMOSOME, WITH A REPORT OF A STUDY OF THE LINKAGE RELATIONSHIPS OF THE LESCH-NYHAN LOCUS.

By D. Wallace.

Queensland Institute of Medical Research

A large family with a partial deficiency of the enzyme responsible for the Lesch-Nyhan syndrome, Hypoxanthine-guanine phosphoribosyl transferase has been found to be segregating for deuteranopic colour blindness and Xg. This has afforded an opportunity to study the linkage relationships of these 3 X-linked loci. The results of this study will be presented.

CHROMOSOMAL POLYMORPHISM OF THE Y CHROMOSOME IN AUSTRALIAN ABORIGINAL AND WHITE POPULATIONS.

By Dr. R. Angell

Prince Henry Hospital

Randwick N.S.W.

The relative length of the Y chromosome in a group of Aboriginies from Central Australia and a group of Caucasians from Melbourne has been compared. Analysis of the data has demonstrated that the mean length of the Aboriginal Y is significantly shorter than that of the Caucasian Y. Examination of the fluorescence pattern of the Y chromosome using quinacrine mustard has shown a correlation between the extent of the fluorescent segment and the total length of the Y chromosome.

VARIATIONS IN MATING PROPENSITIES IN SELECTED STRAINS OF DROSOPHILA MELANOGASTER

By J.A McKenzie and P.A. Parsons

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La Trobe University, Melbourne.

Mating experiments were carried out by means of multiple choice and male and female choice experiments between 3 lines of D. melanogaster, previously subjected to directional selection for scutellar chaeta number for 73 generations. Mean chaeta numbers of these lines designated A,B and C, were 4,6 and 16 respectively. Line C was homozygous scabrous, sca, and hence sca sca flies were substituted for line C in analogous experiments to determine the importance of the sca locus in the behavioural patterns observed.

Lines A and B mated essentially at random with each other but line C showed extremely high female receptivity and low male mating propensity compared with A and B. Mating propensities within the lines are much more equivalent indicating an adaptation of the thresholds of the sexes of the 3 lines.

The mating behaviour of the homozygous sca sca stock paralleled that of line C in all respects, but was not as extreme as line C. It would thus appear that the difference in the mating behaviour of line C, and A and B may be partially involved with the region of the sca locus.

MORPHOLOGY AND BEHAVIOUR IN MICE AND MEN

By P.A. Parsons

Department of Genetics and Human Variation

La Trobe University

Three inbred strains of mice and their hybrids were assayed for open field activity, open field emotionality, exploratory ability, initial reaction to shock, and learning in a conditioned avoidance apparatus. In general, strains Balb/c and C57Bl were extreme for all traits and C3H intermediate. The same was found for weight in that Balb/c > C3H > C57Bl. Skeletal variability was assayed by scoring the presence or absence of 25 minor skeletal variants. Computing measures of divergence between strains gave the same order. Hybrids mostly fell between the inbred strains, with the exception of traits associated with learning which showed heterosis often associated with homeostasis.

Admitting that the number of strains is limited, the data allow one naively to argue for a correlation between skeletal morphology, weight and behavioural traits, which may not be unreasonable since skeletal variants are presumably associated with variants of the muscular, nervous and vascular systems, and hence with behaviour. This result, if substantiated, would support theories of relationships between morphology (somatotypes) and behaviour in man, and agrees with the associations found between morphological and behavioural divergence in the genus Drosophila.

(This work was done in collaboration with Wendy Kellock and Astrid Rose.)