D.J. Catcheside

GENETICS SOCIETY OF AUSTRALIA

22nd GENERAL MEETING

UNIVERSITY OF ADELAIDE

28th to 29th AUGUST, 1975

A. GENERAL INFORMATION

1. PAPERS

Papers will be presented in the Fisher lecture theatre at the northern end of the R.A. Fisher building (No. 23 on the plan) and when sessions are concurrent, also in the Mawson lecture theatre in the Mawson building (No. 20 on the plan).

2. DEMONSTRATIONS

Demonstrations will be on display in the 2nd and 3rd year laboratories on the ground floor of the Genetics Department at the southern end of the R.A. Fisher building.

3. REFRESHMENTS

Morning and afternoon tea and coffee will be available in the 2nd year laboratory on the ground floor of the Genetics Department at the southern end of the R.A. Fisher building.

4. DISPLAYS OF ANIMALS

Marsupials and other native mammals which are being used for genetical work in Adelaide will be on display in Tutorial rooms 1 & 2, on the ground floor of the Genetics Department.

5. ACCOMMODATION AND MEALS

Accommodation has been arranged at St. Mark's College, Kermode St., North Adelaide. The College is situated to the west of St. Peter's Cathedral and is 10-15 minutes walk from the University.

Breakfast is from 8 - 8.45 a.m. on week days and 8.30 - 9.15 a.m. on Sundays. Dinner is also available but this should be ordered on the morning of the day required.

Lunch is available in the Union (No. 17 on plan) and in the Staff Club (No. 7 on plan). All members of the Society will be honorary members of the Union and of the Staff Club over the period of the meeting in compliance with the licencing laws, so that they may use the facilities available. In the Union building, the Bistro serves meals until 9 p.m. and the Tavern Bar is open until 10 p.m.

6. SOCIAL ARRANGEMENTS

(1) A Mixer will be held in the Dining Room on the 4th floor of the Union building on Wednesday, 27th August from 8 - 11 p.m. The entrance to the Dining Room is on the southern side of the Union facing the Bragg Laboratories (No. 11 on plan). Please wear your name tags.

(2) The Society Dinner will be held in the Staff Club on Thursday, 28th August at 7 for 7.30 p.m.

(3) The Annual Business Meeting will be held in the Fisher lecture theatre on Friday, 29th August at 8.30 p.m.

(4) Visit to Winery and Barbecue. Buses will leave St. Mark's College at 9.30 a.m. on Saturday 30th August and will return to the city before 5 p.m.

7. PUBLICATIONS

Copies of the Proceedings of the Eucaryote Chromosome Conference held in Canberra in May 1974 are now available and will be on sale to members of the Society at a special discount price.

8. PARKING

Permits are necessary for parking in the University grounds. A small number of permits are available on request.

9. TRADE DISPLAY

The following companies are exhibiting a range of materials of interest to members in the 1st year laboratory on the ground floor of the Genetics Department.

CARL ZEISS PTY. LTD.
MEDOS COMPANY PTY. LTD.
WATSON VICTOR LTD.

10. BANKING AND POST OFFICE FACILITIES

Banking and Post Office facilities are available in the Hughes Building on the southern side of Hughes Court adjacent to the Staff Club.

11. NAME TAGS

We would be grateful if members would return their name tags to us at the end of the meeting.

B. LECTURE PROGRAMME

THURSDAY, 28TH AUGUST

SESSION 1 — Fisher Lecture Theatre

9.00 - 10.15 Invited Lecture

W.J. Peacock - "The Chromosomes of Drosophila - Organization of Genes and Non-Genes"

Chairman - S. Smith-White

10.15 - 10.45 TEA/COFFEE

SESSION 2 — Fisher Lecture Theatre

10.45 - 12.45 Short Papers — Chairman - D.G. Catcheside

10.45	George L.G. Miklos R.N. Nankivell	DNA studies in three species of grasshopper
11.05	Pamela Dunsmuir	Highly repeated DNA in *Macropus rufogriseus*
11.25	R. Appels W.J. Peacock	Chromosomal organization of highly repeated DNA in Drosophila
11.45	J.M. Dearn	Geographic variation in nuclear DNA content for three grasshoppers
12.05	G.W. Grigg	Specific cleavage of 5 bromouracil-containing DNA by high temperature hydrolysis
12.25	Barry J. Richardson Barry G. Rolfe, William E. Poole	Phage-mediated transgenosis of the galactose-1-phosphate uridyl transferase locus using kangaroos as a model system for gene therapy

12.45 - 2.00 LUNCH

SESSION 3A — Fisher Lecture Theatre

2.00 - 3.40 Short Papers — Chairman - G.L.G. Miklos

2.00	J.A. Sved	A model for the explanation of a high mutation phenomenon in terms of spatial organization of chromosomes
2.20	M.C. Deland	ERG defective mutants of *Drosophila melanogaster*
2.40	B.W. Holloway Heidi Rossiter	The origin of aeruginocin tolerant mutants of *Pseudomonas aeruginosa*
3.00	John Watson	Suppression in *Pseudomonas aeruginosa*
3.20	Barbara Mills	A mutation causing plasmid instability in *Pseudomonas aeruginosa*

SESSION 3B — Mawson Lecture Theatre

2.00 - 3.40 Short Papers — Chairman - B. Boettcher

2.00	N.S. Mina	Electrophoresis markers in the domestic fowl
2.20	Roger S. Holmes	Genetics of peroxisomal enzymes in the mouse
2.40	A.H.D. Brown A.C. Matheson	Estimation of the mating system of *Eucalyptus obliqua* L'Hérit using allozyme polymorphisms
3.00	Kay Pearse	Geographic variation of morphometric and allozymic characters in the common brown butterfly *Heteronympha merope merope*
3.20	Lincoln H. Schmitt	Rat races on off-shore islands of South Australia

3.40 - 5.00 TEA/COFFEE AND DEMONSTRATIONS

FRIDAY, 29TH AUGUST

SESSION 4 — Fisher Lecture Theatre

9.00 - 10.15 Invited Lecture

A.M. Clark - "Environmental Mutagenesis"

Chairman - M.J.D. White

10.15 - 10.45 TEA/COFFEE

SESSION 5 — Fisher Lecture Theatre

10.45 - 12.45 Short Papers — Chairman - B. John

10.45	B. Boettcher	Australia antigen in Australian aborigines
11.05	J.A. Bishop	Ecological genetics of 'warfarin' resistance in *Rattus norvegicus*
11.25	P.G. Johnston G.B. Sharman D.W. Cooper	Expression of glucose-6-phosphate dehydrogenase allozymes in tissues and cultured fibroblasts of kangaroos
11.45	D.W. Cooper J.L. VandeBerg G.B. Sharman Carmel Freeman Jennifer A. Marshall Graves	A third state of the kangaroo X-chromosome; partial activity
12.05	Jennifer A. Marshall Graves	Preferential loss of chromosomes from somatic cell hybrids
12.25	R.M. Hope	Marsupial somatic cell genetics

12.45 - 2.00 LUNCH

SESSION 6A — Fisher Lecture Theatre

2.00 - 4.00 Short Papers — Chairman - J. Thomson

2.00	M.J.D. White	Is *Moraba virgo* a hybrid?
2.20	J. Dempsey M.W. Westerman	Studies of the B-chromosome of *Phaulacridium vittatum*
2.40	Graham C. Webb	Banding phenomena in grasshopper chromosomes
3.00	Jon Martin	Cytogenetics of Chironomidae - the *Chironomus australis* group

3.20	Max King D.L. Hayman	An annual cycle in chiasma frequency in the lizard *Phyllodactylus marmoratus*
3.40	David D. Shaw	Inter- and intraspecific karyotype diversity in the genus Caledia (Orthoptera: Acrididae)

SESSION 6B — Mawson Lecture Theatre

2.00 - 3.40 Short Papers — Chairman - J.H. Bennett

2.00	R. Frankham	Selection for sex-linked polygenes in Drosophila
2.20	David A. Briscoe	Linkage disequilibrium in Spanish populations of *Drosophila melanogaster*
2.40	Frank Nicholas	Inheritance of liability to disease: heritability estimates for a single locus model
3.00	L.R. Piper	The number and effects of sternopleural chaetae genes on a segment of the third chromosome of *Drosophila melanogaster*
3.20	J.W. James	Some aspects of open nucleus breeding systems

3.40 - 5.00 TEA/COFFEE AND DEMONSTRATIONS

ABSTRACTS

SESSION 2

MIKLOS, George L. Gabor and NANKIVELL, R.N.
Department of Population Biology, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

DNA STUDIES IN THREE SPECIES OF GRASSHOPPER

On the Australian mainland, there are three species of grasshopper in the genus *Atractomorpha*. They are *A. similis*, *A. australis* and an unnamed species *A. species one*. The chromosomes of *A. similis* possess large heterochromatic telomeric blocks on all autosomes whereas the other two species lack these blocks completely. The relative DNA contents of *A. similis* and *A. australis* are in the ratio 1.3 to 1.0.

By means of CsCl centrifugation in the presence of Actinomycin, we have isolated a large cryptic satellite from *A. similis*, and when this satellite was xeroxed and the complementary RNA hybridised to meiotic chromosomes *in situ*, the satellite reannealed exclusively to the large telomeric blocks. We have not been able to isolate any satellites from *A. australis*.

We are examining the hypothesis that the large telomeric blocks in *A. similis* are involved in the control of recombination.

DUNSMUIR, Pamela
Genetics Department, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

HIGHLY REPEATED DNA IN MACROPUS RUFOGRISEUS

Two distinct satellite DNAs, amounting to 25% of total nuclear DNA, have been isolated from the red-necked wallaby, *Macropus rufogriseus*. The physical properties of native, single-stranded and renatured molecules have been studied using bouyant density centrifugation. The homogeneity of each satellite fraction has been examined using melting characteristics of native and renatured DNA, renaturation kinetics, and susceptibility to cleavage by a sequence specific endonuclease. These data suggest that sequence heterogeneity exists in both fractions.

Each satellite DNA fraction has been localized in nuclei and on metaphase chromosomes by *in situ* hybridization. The chromosomal distribution of the satellites differentiates the sex chromosomes which have sequences of only one satellite, from the autosomes, which have sequences of both satellites in the centromeric heterochromatin. C-banding techniques also show this differentiation of the centromeric heterochromatin of sex chromosomes from autosomes.

APPELS, R. and PEACOCK, W.J.
Division of Plant Industry, CSIRO, Canberra, A.C.T.

CHROMOSOMAL ORGANIZATION OF HIGHLY REPEATED DNA IN DROSOPHILA

Hydroxylapatite chromatography of renatured DNA has been used to analyse the organization of highly repeated sequences in the genome of *Drosophila melanogaster*. The major findings arising out of the study are that (1) the known satellite DNA species must be organized, *in vivo*, in large blocks of homogeneous repeated sequences, (2) the 1.705 g/cc satellite (repeating

sequence $\begin{matrix} 5' \text{ AGAAG } 3' \\ 3' \text{ TCTTC } 5' \end{matrix}$ is covalently linked to main band sequences as well as to other satellite sequences, (3) a highly repeated DNA species with a high T_m has been found in addition to the previously described satellites and (4) renatured DNA banding at a density of 1.692 g/cc has been shown to be a complex mixture of satellites. The last point is particularly important in relation to some reports suggesting that 1.692 g/cc renatured DNA is centromeric DNA with "repeated" regions dispersed amongst "non-repeated" regions. The results complement analyses carried out on native DNA and will be discussed in relation to the native DNA data.

DEARN, J.M.
Department of Population Biology, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

GEOGRAPHIC VARIATION IN NUCLEAR DNA CONTENT FOR THREE GRASSHOPPERS

Abstract on page 30.

GRIGG, G.W.
CSIRO Division of Animal Genetics, Epping, N.S.W.

SPECIFIC CLEAVAGE OF 5 BROMOURACIL - CONTAINING DNA BY HIGH TEMPERATURE HYDROLYSIS

The substitution of 5 bromouracil (5BU) for thymine nucleotide in DNA sensitises it to hydrolysis at 100°. The breakage is specific, with one break point per 5BU residue, and efficient (>80% of 5BU have associated breaks when the DNA is heated overnight at 105°). It is independent of pH in the range 7 to 9, the presence of BDTA and exposure to light. The potential use of this reaction in DNA sequencing and the detection of repair replication will be discussed.

RICHARDSON, Barry J., ROLFE, Barry G. and POOLE, William E.
Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

PHAGE-MEDIATED TRANSGENOSIS OF THE GALACTOSE-1-PHOSPHATE URIDYL TRANSFERASE LOCUS USING KANGAROOS AS A MODEL SYSTEM FOR GENE THERAPY

Western grey kangaroos are deficient for the enzyme galactose-1-phosphate uridyl transferase (GPUT), the enzyme usually deficient in humans suffering from galactosemia. Liver and blood samples were taken from two animals before 10^{14} λ gal^+ phage particles were injected into the caudal vein. Daily blood samples were taken and the animals killed after 7 days. Various tissues were assayed for kangaroo and *E. coli* GPUT activity. Liver muscle and kidney contained the *E. coli* enzyme, brain and spleen did not. The level of viable phage particles remained high in the blood until the primary immune response occurred between the 3rd and 4th day.

SESSION 3A

SVED, J.A.
School of Biological Sciences, University of Sydney, N.S.W.

A MODEL FOR THE EXPLANATION OF A HIGH MUTATION PHENOMENON IN TERMS OF SPATIAL ORGANISATION OF CHROMOSOMES

High rates of production of recessive lethal mutations have previously been found in crosses of *Drosophila melanogaster* to flies from the Hunter Valley wineries of N.S.W. Male recombination has been shown to be associated with this, in line with findings from several other laboratories. Following a recent report by Kidwell & Kidwell (*Nature 253*: 755), a high level of female infertility has also been found, and it has been shown that all three effects occur non-reciprocally, i.e. when the winery flies are used as male and the laboratory stock as female, but not *vice versa*. A simple model of genotype-cytoplasm interaction has however been ruled out as an explanation following the results of further crosses.

A model will be put forward which proposes that chromosomes are organised spatially, presumably by attachment to the nuclear membrane, and that the above phenomena are related to a mis-matching of spatial organisation of chromosomes handed down from the two strains. The model implies a direct inheritance of spatial organisation in some as yet undetermined manner. Tests are being made for non-random disjunction of non-homologous chromosomes, which is a possible prediction of the hypothesis, although preliminary tests with the X-chromosome and chromosome II have been negative. The possibility that the male- and female-derived chromosomes mutate at different rates is also being investigated.

DELAND, Michael C.
Department of Genetics, Monash University, Clayton, Vic.

ERG DEFECTIVE MUTANTS OF DROSOPHILA MELANOGASTER

Three laboratories have been independently using the methods of single step mutation as part of their own research into the visual system of *Drosophila melanogaster*. Gotz's laboratory in Tübingen, Germany, has been studying the optomotor response; Pak's laboratory at Purdue in the U.S. has concentrated on the electrophysiological and biophysical analysis of the visual process; and Benzer's group at Caltech has been concerned with various aspects of the behaviour of the organism.

Each group concentrated initially on the X chromosome. To co-ordinate their locus designations and nomenclature each laboratory supplied representative alleles of each sex linked locus for inter-laboratory complementation tests. The tests, carried out at Purdue, used the electroretinogram (ERG) as the criterion of complementation. This paper will present the results of these tests and describe the array of existing mutants at each locus.

The search for ERG defective mutants has been extended to the autosomes. The mutation schemes and the methods used to detect mutants will be discussed.

HOLLOWAY, B.W. and ROSSITER, Heidi
Department of Genetics, Monash University, Clayton, Vic.

THE ORIGIN OF AERUGINOCIN TOLERANT MUTANTS OF PSEUDOMONAS AERUGINOSA

Mutants of *Pseudomonas aeruginosa* which are not killed by aeruginocins (*tol* mutants) have been isolated and characterized. Some of these mutants evidently do not arise by simple base pair change as concomitant mutations to auxotrophy are found at frequencies up to 5%. The *tol* loci and the corresponding auxotrophic locus are often not cotransducible, although the two loci show high coinheritance in conjugation. Linkage of some such auxotrophic markers to nearby other markers may show significant reduction. This evidence is consistent with the view that this type of mutation arises by insertion of a length of DNA into the bacterial chromosome. A class of phage resistant mutants with similar characteristics has also been found in which reversion of the associated auxotrophy to prototrophy is associated with acquisition of phage sensitivity. Again the data support an insertion sequence hypothesis for the origin of these mutants. Experiments to substantiate this hypothesis will be described, as well as the implications of this type of mutation for genetic variability in bacteria.

WATSON, John
Department of Genetics, Monash University, Clayton, Vic.

SUPPRESSION IN PSEUDOMONAS AERUGINOSA

A suppressor mutant of *Pseudomonas aeruginosa* strain PAT has been isolated. The strain, which was initially selected as a temperature-sensitive mutant, has been shown to suppress two auxotrophic alleles. The suppressor locus, designated *sup* 1, has been found to be cotransducible with three *thr* loci on the strain PAT linkage map. The suppressor mutation has been used to isolate suppressor-sensitive (*sus*) mutants of the virulent phage E79 and the R factor R18. When suppressor mutants are selected for directly, they are found to be of two types. One class, like the original mutant, is temperature-sensitive while the second class is temperature-insensitive. The mutations giving rise to each of these classes of suppressor are very closely linked and are probably located in the same gene. The *sup* 1 alleles of strain PAT also express suppressor activity when transferred into strain PAO. When the *sus* mutant of R18 is transferred into *Escherichia coli* strains carrying *sup* D, *sup* F or *sup* C, the R factor mutation is not suppressed. This suggests that the suppressor is not of the amber or ochre types.

MILLS, Barbara
Department of Genetics, Monash University, Clayton, Vic.

A MUTATION CAUSING PLASMID INSTABILITY IN PSEUDOMONAS AERUGINOSA

A temperature sensitive mutant of *Pseudomonas aeruginosa* unable to maintain the plasmid R38 was isolated following mutagenesis of strain PAO1669 carrying R38. After EMS treatment, mutants tolerant to aeruginocin 41 were selected, and the maintenance mutant was isolated from these. The inability to maintain R38 was due to a host mutation, designated *ris*$^-$. The *ris*$^-$ mutation also affected the stability of one other plasmid in the same compatibility group as R38, and of four plasmids of other compatibility type. The mutation did not affect the ability to transfer R38 at the restrictive temperature. After growth of the mutant at the restrictive temperature, variants could be isolated which had lost all known R38-coded functions except for one drug resistance marker, which became stably maintained.

SESSION 3B

MINA, N.S.
CSIRO Division of Animal Genetics, Epping, N.S.W.

ELECTROPHORESIS MARKERS IN THE DOMESTIC FOWL

Arguments have been frequently raised around the question of whether the theoretical level of homozygosity after a number of inbreeding generations is actually attained.

Electrophoresis markers have provided a useful tool for numerous studies of natural and domestic populations of various organisms aimed at explaining the ways by which variations may be maintained.

In the present work, highly inbred lines of the domestic fowl (F>0.95) were used in an attempt to compare the expected vs observed heterozygosity. Eight inbred lines were used, as well as 2 control, 2 selection, and 6 "synthetic" populations of White Leghorn and Australorp.

Six polymorphic loci were surveyed; three of the egg-white proteins (Ov, G_3, and G_2), two of the serum proteins (Tf, and Pa), and a serum enzyme (Es).

Gene frequency data were collected; average heterozygosity per population over all loci, and Nei's genetic distance were computed. The results, so far, will be presented and discussed. Possible association between these markers and some important traits in poultry production is also raised.

HOLMES, Roger S.
School of Science, Griffith University, Nathan, Q'land.

GENETICS OF PEROXISOMAL ENZYMES IN THE MOUSE

Peroxisomes are single membrane bound subcellular organelles occurring predominantly within liver and kidney cells in mammalian tissues and which contain enzymes involved with hydrogen peroxide metabolism. The genetics of three of these peroxisomal enzymes, L-α-hydroxyacid oxidase (HAOX), D-amino acid oxidase (DAOX) and catalase (Ct) have been investigated in the mouse. (HAOX) is a flavoprotein enzyme which catalyses the reaction: $R\text{-}CHOH\text{-}COO^- + O_2 \rightarrow R\text{-}CO\text{-}COO^- + H_2O_2$. DAOX is also flavoprotein, catalysing the reaction: $R\text{-}CH.NH_3^+ \quad COO^- + O_2 \; H_2O \; R\text{-}CO\text{-}COO^- + NH_4^+ + H_2O_2$; whereas Ct is a tetrameric haemenzyme catalysing the reaction: $2H_2O_2 \rightarrow 2H_2O + O_2$.

Previous studies have shown mouse liver and kidney HAOX isozymes (HAOX-A_4 and B_6 respectively) to be encloded by separate genetic loci (Hao-I and Hao-2 respectively) (Duley and Holmes, 1974; Holmes and Duley, 1975). In contrast, multiple forms of Ct were shown to be encoded by a single locus (Ce). Genetic analyses, using NZC and C_s^b inbred strains of mice which exhibited homozygous phenotypes for HAOX-A_4'/Ct-A_4 (Hao-I^b/Ce^a) and HAOX-A_4/Ct-A_4' (Hao-I^a/Ce^b) respectively, demonstrated genetic linkage on chromosome 2 (7.4% recombination frequency) of the mouse for the loci encoding these enzymes.

Further genetic analyses have been carried out using NZC and BALB/C inbred strains which exhibit homozygous phenotypes for HAOX-A_4'/DAOX-A_4' (Hao-I^b/Dao-I^b) and HAOX-A_4/DAOX-A_n (Hao-I^a/Dao-I^a) respectively.

The results and significance of these studies will be reported and discussed.

Duley, J.A. and Holmes, R.S. (1974) *Genetics 76*: 93-97.
Holmes, R.S. and Duley, J.A. (1975) in "Isozymes-I. Molecular Structure" C.L. Markert, ed. Academic Press, N.Y. pp 191-211.

BROWN[1], A.H.D. and MATHESON[2], A.C.
[1] Division of Plant Industry, CSIRO, Canberra City, A.C.T.
[2] Division of Forest Research, CSIRO, Yarralumla, A.C.T.

ESTIMATION OF THE MATING SYSTEM OF EUCALYPTUS OBLIQUA *L'HÉRIT USING ALLOZYME POLYMORPHISMS*

Seeds from populations of *Eucalyptus obliqua* were assayed for their allozyme genotype at three loci (alcohol dehydrogenase, malate dehydrogenase and acid phosphatase) as members of half-sib arrays to obtain quantitative estimates of three mating system parameters. These were (i) the proportion of seed derived from self-pollination as distinct from the proportion randomly outcrossed, (ii) the allele frequency in the pollen, and (iii) the within population heterogeneity for the frequency of detectable outcrosses. The rate of selfing varied between loci and populations, but overall suggested that up to 24% of viable seed may derive from self-fertilization. This level of partial self-fertilization together with local variation in the mating system yielded an observed average inbreeding coefficient (Wright's fixation index) of 0.123 for these loci. In addition, the populations showed substantial differences in gene frequency at each locus.

PEARSE, Kay
Department of Genetics, La Trobe University, Bundoora, Vic.

GEOGRAPHIC VARIATION OF MORPHOMETRIC AND ALLOZYMIC CHARACTERS IN THE COMMON BROWN BUTTERFLY, HETERONYMPHA MEROPE MEROPE

H. merope merope is found in Eastern Australia from Expedition Range in Central Queensland to Flinders Range in South Australia. A number of wing characters as well as two autosomal allozymes (Phosphoglucomutase (PGM) and Glutamate-Oxaloacetate Transaminase (GOT) have been examined in 17 populations.

Differences in gene frequencies between sexes have been found for PGM. This and other variation, both temporal and geographical, is described and discussed.

SCHMITT, Lincoln H.
Department of Genetics, University of Adelaide, S.A.

RAT RACES ON OFF-SHORE ISLANDS OF SOUTH AUSTRALIA

In South Australia, the Southern Bush-rat (*Rattus fuscipes greyii*) inhabits many off-shore islands as well as three large, separate areas on the mainland. A simple model is presented which predicts the relative amount of genetic variability expected in the isolated populations, as well as the pattern of genetic variation between populations. The model presumes the existence of a large, panmictic ancestral population, which was fragmented into the present day populations. Starch gel electrophoresis has been used to detect genetic variation in *R. f. greyii*. In all, 16 genetic loci have been studied. The findings are in reasonable agreement with the predictions of the model and also suggest that genetic drift has been an important factor in determining the amount of genetic variation on the off-shore island populations.

SESSION 5

BOETTCHER, B.
Department of Biological Sciences, University of Newcastle, Shortland, N.S.W.

AUSTRALIA ANTIGEN IN AUSTRALIAN ABORIGINES

In a group of full-blood Australian aborigines the incidence of asymptomatic Australia antigen (Au) carriers is over 20%. The incidence is higher among males than females, and is higher among juveniles than adults.

Investigation of HL-A histocompatibility antigens among the group has established a significant deficiency of the antigen W15 among Au carriers.

The data can be explained in terms of an Au immune response locus closely-linked, and in linkage disequilibrium, with the Four locus of the HL-A system, where Au carriers are homozygous for an allele which does not lead to an immune response to Au. Because a similar deficiency of W15 has been observed among Au carriers in Europe it is proposed that the association between Au and W15 has not arisen by chance, but indicates that selection involving both the LA and Au immune response alleles is operating. The study provides support for Blumberg's model that the potential for becoming an Au carrier is a simple recessive Mendelian character.

BISHOP, J.A.
Department of Genetics, University of Liverpool, U.K.

ECOLOGICAL GENETICS OF 'WARFARIN' RESISTANCE IN RATTUS NORVEGICUS

The brown rat is a widespread agricultural pest in the U.K. and the anticoagulant drug 'Warfarin' is used to control population numbers. Warfarin has the advantage that it is tasteless to rats and is "ecologically acceptable". It inhibits the synthesis of several vitamin K-dependent clotting factors and rats die from generalised internal bleeding.

Inevitably, after its intensive use in rodent control, genetically-determined resistance to the drug has developed and is now known from a number of countries. Most out-breaks of resistance apparently result from establishment of separate mutants. In two resistant forms from U.K. (from near Glasgow, and in the Welsh borders) different alleles at one locus are involved. In rats from Wales the character for resistance is dominant but the character of vitamin K requirement is nearly recessive. Homozygous resistants have a dietary vit-K requirement 10-20 times greater than the other genotypes and succumb to deficiency diseases.

The ecological implications are being examined during field studies in the Welsh country of Powys. In the Welsh borders there seems to be a mosaic of populations of varying sizes (5-500+). The species breeds at any time of the year but most movements liable to result in dispersal of genes occur in late summer and autumn. Chance establishment of wandering males in other populations is a major factor in this. Evidence from one population indicates that in an environment lacking Warfarin the heterozygote has lower fitness than the susceptible.

JOHNSTON, P.G., SHARMAN, G.B. and COOPER, D.W.
School of Biological Sciences, Macquarie University, North Ryde, N.S.W.

ESPRESSION OF GLUCOSE-6-PHOSPHATE DEHYDROGENASE ALLOZYMES IN TISSUES AND CULTURED FIBROBLASTS OF KANGAROOS

The structural gene coding for glucose-6-phosphate dehydrogenase is sex-linked in kangaroos as in other mammals. Electrophoretic studies of G6PD in tissues of known female heterozygotes show expression of only the maternally derived allele. This is consistent with the hypothesis that dosage compensation in kangaroos is achieved by paternal X-inactivation. The tissue results contrast with those obtained from primary uncloned cultured fibroblasts where apparent interaction products were observed indicating activity of both X-chromosomes.

COOPER, D.W., VANDEBERG, J.L., SHARMAN, G.B., FREEMAN, Carmel and MARSHALL GRAVES[1], Jennifer A.
School of Biological Sciences, Macquarie University, North Ryde, N.S.W.
[1]Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

A THIRD STATE OF THE KANGAROO X-CHROMOSOME; PARTIAL ACTIVITY

Primary mass cultures of cells have been grown from explants of organs of kangaroos of the species *Macropus giganteus* and *Macropus parryi*. When electrophoresis is used to type the PGK *A* allozymes of mass cultures from females heterozygous at this locus, the maternally derived allele is seen to be fully expressed and the paternally derived one partly expressed. When clones are grown from these cultures, they have the same electrophoretic pattern as the mass culture. Each cell accordingly possesses a fully active maternally derived gene and a partly active paternally derived one. It appears that the kangaroo X, or part of it, can exist in a state of partial activity. Like the inactive X, the partly active X replicates later than its fully active homologue.

Blood muscle cultured cells
G6PD – – full?
PGK – partial partial X paternal expression.
Both types of polymorphism not in same species.

MARSHALL GRAVES, Jennifer A.
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

PREFERENTIAL LOSS OF CHROMOSOMES FROM SOMATIC CELL HYBRIDS

Preferential segregation of chromosomes from interspecific cell hybrids is a process of great importance for somatic genetic analysis, yet it is very poorly understood. Several hypotheses have been tested by analysis of chromosome loss in mouse x hamster hybrids. In these hybrids, hamster chromosomes are preferentially and progressively eliminated over a long period of growth. A large number of clones were recovered which had a full (or nearly full) set of mouse chromosomes, and very diverse partial sets of hamster chromosomes. Certain hamster chromosomes were retained more frequently than others, but the growth rate of clones did not appear to be related to the set of hamster chromosomes present.

These data do not support hypotheses that disparity of growth rates of phase times of the parent cells determines chromosome loss, nor the hypothesis that cells carrying certain hamster chromosomes are at a selective disadvantage. It is suggested that chromosome loss may be the result of continuing errors in replication or distribution of hamster chromosomes in hybrid cells.

HOPE, R.M.
Department of Genetics, University of Adelaide, S.A.

MARSUPIAL SOMATIC CELL GENETICS

Somatic cell hybridization provides an experimental approach for comparing marsupial and eutherian mammals with respect to the organization and regulation of their genetic material. The distant evolutionary relationship between eutherians and marsupials, and the karyotypic 'simplicity' of most marsupial species, lead to the prediction that eutherian x marsupial hybrids would be well suited for genetic analysis, and would yield information over and above that readily obtainable from human x rodent hybrids. For example, enzymes that tend to be conservative in the variation of their molecular structure amongst eutherian species (e.g. mitochondrial enzymes) and are therefore of limited use as genetic markers in man x rodent hybrids, have been shown by electrophoresis to be distinct, in many cases, from their marsupial counterparts. The analysis of eutherian (human) x marsupial hybrids may lead to the chromosomal assignment of the genes determining these and other enzymes in species belonging to both these groups. The compilation of gene assignments to autosomes and sex chromosomes in selected marsupial species will complement studies on karyotypic differences amongst these species, and will lead to an assessment of the extent to which genetic re-arrangements have accompanied evolution.

A number of *Sendai* virus mediated fusions between various combinations of eutherian and marsupial cells have been carried out. The marsupial cells were either diploid fibroblasts, lymphocytes, or from established cell lines, including drug resistant derivations of the line PTK2. Of five PTK2 clones that were resistant to 10µg/ml of 6-thioguanine, three were HGPRT deficient and sensitive to Littlefield's HAT selective medium. Two clones, resistant to 22µg/ml 5-bromodeoxyuridine, were also HAT sensitive. These 'mutant' cell lines had similar karyotypes to PTK2. The eutherian cells used were either diploid fibroblasts or were from drug resistant established cell lines of human or mouse origin. Experiments using radioactively labelled cells have clearly shown that *Sendai* virus attaches to and fuses marsupial cells with human and mouse cells. Both heterokaryons and synkaryons have been observed, but as yet no proliferating hybrids have been obtained. Possible reasons for this are discussed.

SESSION 6A

WHITE, M.J.D.
Department of Genetics, University of Melbourne, Parkville, Vic.

IS MORABA VIRGO *A HYBRID?*

Moraba virgo, the only grasshopper species which reproduces exclusively by parthenogenesis, is a diploid with a karyotype that is extensively heterozygous for a number of chromosomal rearrangements and for late-replicating DNA segments in two chromosome pairs. It is also hemizygous for a small X_2 chromosome.

White and Webb have interpreted most of the heterozygosity (and in particular the heterozygosity for late-replicating segments) as having arisen since the origin of the parthenogenetic method of reproduction, which is of a type that does not permit genetic recombination. On the other hand, Hewitt (*Heredity 34*: 117-123) has put forward an entirely different interpretation, according to which *M. virgo* would have arisen by hybridization between the two bisexual species 'P196' and 'P169'.

The evidence for and against the Hewitt hypothesis will be discussed on the basis of distribution, karyotypes, DNA replication patterns and phenotypes of triploid hybrids between *virgo* and the 2 bisexual species and of diploid laboratory hybrids between P196 and P169. Some evidence from gel electrophoresis of hemolymph proteins will also be presented.

DEMPSEY, J. and WESTERMAN, M.W.
Department of Genetics, La Trobe University, Bundoora, Vic.

STUDIES OF THE B-CHROMOSOME OF PHAULACRIDIUM VITTATUM

Preliminary studies on the La Trobe campus population of *Ph. Vittatum* suggested a temporal variation in the B-chromosome frequency in this population. Sequential sampling during the 1975 meiotic season confirmed this and established that the B-chromosome affects recombination by increasing Mean cell chiasma frequency.

Preliminary molecular studies indicate that the DNA from B-containing populations exhibits a light satellite DNA under neutral CsCl centrifugation.

WEBB, Graham C.
Department of Population Biology, Research School of Biological Sciences, Canberra, A.C.T.

BANDING PHENOMENA IN GRASSHOPPER CHROMOSOMES

G-banding in the normal chromosome complement of a variety of grasshoppers produces only a few lightly-stained gaps in otherwise darkly stained chromosomes. Some of these gaps correspond to secondary constrictions. The gaps may be used to trace chromosomal rearrangements in some cases. The short arms of certain small chromosomes in the Australian plague locust, *Chortoicetes terminifera*, become lightly stained and flared after G-banding. In contrast to the normal complement large supernumerary chromosomes in *C. terminifera* show a relatively spectacular pattern of alternating light and dark G-bands which are not present in some other species.

C-banding in the normal complement of grasshoppers is usually in the centromere regions but in one species many unusual interstitial bands have been found. Correctly C-banded supernumerary chromosomes are difficult to obtain by current techniques which generally yield mixtures of G- and C-banding in the same cells.

MARTIN, Jon
Department of Genetics, University of Melbourne, Parkville, Vic.

CYTOGENETICS OF CHIRONOMIDAE - THE CHIRONOMUS AUSTRALIS *GROUP*

Cytological studies of material included under the name *Chironomus australis* reveal that three species are present. These are *Ch. australis* with 4 polytene chromosomes, and *Ch. duplex* and *Ch. occidentalis* both with only 3 polytene chromosomes. *Ch. australis* and *Ch. duplex* occur in south-eastern Australia, while *Ch. occidentalis* occurs in south-western Australia. *Ch. duplex* and *Ch. occidentalis* are quite polymorphic but *Ch. australis* is polymorphic only for a sex linked heterochromatic band.

Aspects of the cytological relationships and of the polymorphisms of *Ch. duplex* will be discussed.

KING, Max and HAYMAN, D.L.
Department of Genetics, University of Adelaide, S.A.

AN ANNUAL CYCLE IN CHIASMA FREQUENCY IN THE LIZARD PHYLLODACTYLUS MARMORATUS

Observations of the chiasma frequency in individuals from field populations of *Phyllodactylus marmoratus* have been made at regular intervals over two and a half years. These have demonstrated the presence of an annual cycle in chiasma frequency with an August maximum of some 29 chiasmata per cell and a January minimum of 21 chiasmata per cell.

The cycle occurs in two chromosome races of the species. Observations have been made on chiasmata distribution and the male and female reproductive cycles to examine the implication of this variation in chiasma frequency in the reproductive biology of the species.

SHAW, David D.
Department of Population Biology, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

INTER- AND INTRASPECIFIC KARYOTYPE DIVERSITY IN THE GENUS CALEDIA (*ORTHOPTERA:ACRIDIDAE*)

The genus *Caledia* contains only two species - *C. captiva* and *C. species nova 1.* The former is distributed from Southern Papua, across the Torres Strait to the Cape York Peninsula, down the Eastern Seaboard as far South as Southern Victoria. The latter species has only been found on the Oriomo plateau of Southern Papua where it is found in close association with *C. captiva.*

The karyotypic organisation of these two species in Papua is quite different in its basic structure and similarly, populations of *C captiva* in Australia and Papua can be grouped into four zones with respect to their karyotypic organisation. Chromosomal variability is most marked in Southern Queensland where all twelve chromosomes - including the X - have been involved in centromeric repositioning which converts the basic acro- and telocentric chromosomes into metacentric elements. Some of these centric adjustments have become fixed structural homozygotes whereas others are still polymorphic.

Populations of *C. captiva* from New South Wales and Victoria are again, highly polymorphic for intrachromosomal rearrangements but not necessarily the same ones as found in Southern Queensland.

The nature of this complex polymorphism will be discussed together with the results of inter-population studies and the effects of the polymorphism upon the recombination system.

SESSION 6B

FRANKHAM, R.
School of Biological Sciences, Macquarie University, North Ryde, N.S.W.

SELECTION FOR SEX-LINKED POLYGENES IN DROSOPHILA

The mechanism of dosage compensation affects the rate of response to selection for sex-linked genes. The extent of this effect will be considered.

Experimental evidence which indicates that dosage compensation is complete for abdominal bristle polygenes will be presented.

The results of selection on sex-linked abdominal bristle effects in

(a) both sexes, and in
(b) males only in lines with attached-X females will be presented and discussed.

BRISCOE, David A.
School of Biological Sciences, Macquarie University, North Ryde, N.S.W.

LINKAGE DISEQUILIBRIUM IN SPANISH POPULATIONS OF DROSOPHILA MELANOGASTER

Two enzyme-coding loci on the second chromosome of *D. melanogaster* are in strong linkage disequilibrium in Spanish wine cellar populations. This disequilibrium is associated with the presence of an inversion which suppresses recombination over the entire length of 2L, and with genes affecting a quantitative character (sternopleural chaeta number).

NICHOLAS, Frank
Department of Animal Husbandry, University of Sydney, N.S.W.

INHERITANCE OF LIABILITY TO DISEASE: HERITABILITY ESTIMATES FOR A SINGLE LOCUS MODEL

Recent studies on inheritance of liability to disease have illustrated that it is often difficult to distinguish between single-locus and multifactorial models of inheritance. In practice, many workers have assumed the latter, and (following Falconer, 1965) have estimated heritability from the incidence of the disease among relatives of affected individuals. But how valid is Falconer's estimate of heritability if the data in reality result from a single-locus mode of inheritance?

In an attempt to answer this question, the expected incidence of a particular

condition in relatives has been determined theoretically for the general two-allele single-locus model (incorporating various levels of penetrance, dominance and the possibility of non-genetic causes). Estimates of heritability from these incidences have been compared with the true value of heritability defined as that portion of the total phenotypic variance that is additive genetic.

In general, it appears that Falconer's estimate is a considerable overestimate of true heritability when the incidence of the condition in the overall population is relatively low. The implications of these results will be considered in relation to other potential estimators of heritability.

PIPER, L.R.
Division of Animal Genetics, CSIRO, Epping, N.S.W.

THE NUMBER AND EFFECTS OF STERNOPLEURAL CHAETAE GENES ON A SEGMENT OF THE THIRD CHROMOSOME OF DROSOPHILA MELANOGASTER

A genetic analysis of the *sepia* to *scarlet* segment of the third chromosome of *D. melanogaster* has been performed using a modified form of the method proposed by Thoday (1961).

The basic principles of Thoday's method were retained but two changes which substantially improve the resolution were included. First, the marker chromosome used to detect recombinants was constructed by back-crossing for several generations the required markers into a chromosome derived from a stock selected to the limit for low sternopleural chaetae count. The second improvement derives from using the distribution of the largest gap between ordered normal variates to assist in classifying the recombinants into distinct sub-groups.

The particular third chromosome analysed was extracted from the Kaduna cage population and in a "high" sternopleural chaetae background, homozygotes had a mean count of 29.4. In the same background the homozygous marker stock count was 15.2. The estimate of the number of genes in the *sepia* to *scarlet* segment was eight, with effects ranging from 0.7 to 1.1 chaetae.

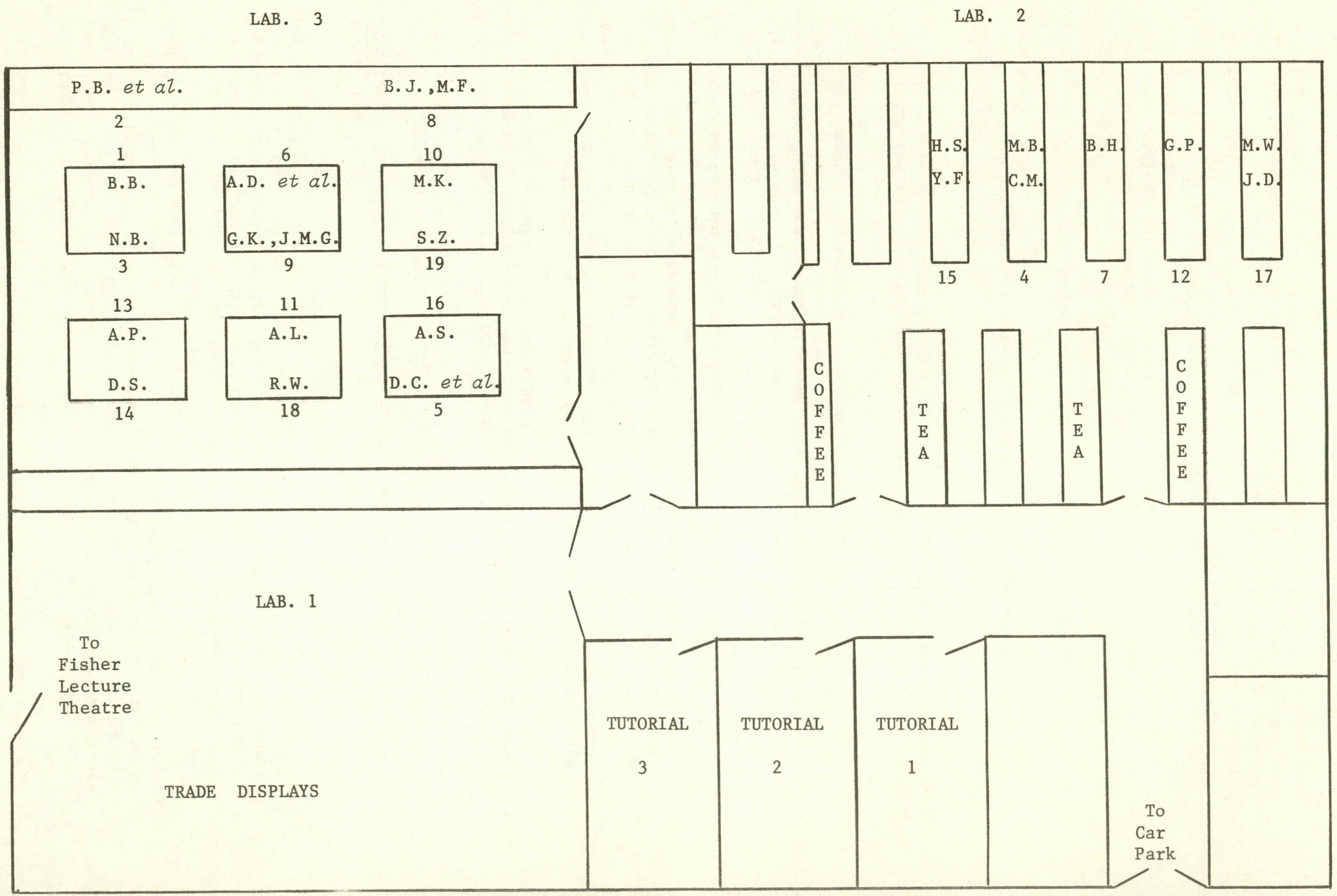
At least for this quantitative character, the observed genetic variation seems likely to result from the action of a fairly large number of loci.

JAMES, J.W.
School of Wool and Pastoral Sciences, University of New South Wales, Kensington, N.S.W.

SOME ASPECTS OF OPEN NUCLEUS BREEDING SYSTEMS

Traditional animal breeding systems are usually hierarchical, with gene flow from the higher levels to the lower. Recently there has been increased interest in systems in which there is some reverse gene flow, especially in co-operative schemes. In this paper a simple model system is analysed to determine optimum rates of gene flow in both directions through females, it being assumed that gene flow through males remains unidirectional. The optimum size of the male breeding nucleus is related to selection intensities in the two sexes, and the relative importance of the steady-state gain is assessed. The effect of partly opening the sire breeding nucleus on the effective size of the population (with respect to inbreeding) is also dealt with.

PLAN OF DEMONSTRATIONS AND DISPLAYS



DEMONSTRATION ABSTRACTS

1. BARLOW, B.A.
School of Biological Sciences, Flinders University, Bedford Park, S.A.

TRANSLOCATION HETEROZYGOSITY AND SEX RATIO IN VISCUM

Several African species of *Viscum* show permanent, sex-linked translocation heterozygosity. Male plants of *V. fischeri* have $2n = 23$ and constantly produce 7 bivalents and a multivalent chain of 9 chromosomes at meiosis. Regular assortment results in transmission of 11- and 12-chromosome genomes via the pollen. Female plants have $2n = 22$ and are homozygous for the 11-chromosome genome. The multivalent chain in the males is a consequence of reciprocal translocations, one of which was Robertsonian and one of which involved the chromosome carrying the sex determination factors.

There is a constant female-predominant sex ratio of approximately 2:1 in *V. fischeri*. It is suggested that the ratio is maintained by gamete selection, and that the genes involved have been linked with the sex determination system through the system of translocations.

Both *V. hildebrandtii* and *V. engleri* ($n = 14$) are polymorphic with regard to the chromosome associations which have been found. These include 12II ⌀4; 11II ⌀6; 10II ⌀4 ⌀4; 10II ⌀8; 9II ⌀4 ⌀6 and 6II ⌀4 ⌀6 ⌀6. The translocation heterozygosity is not associated with a distortion of the sex ratio in favour of female plants, as occurs in *V. fischeri* Engl., and it is suggested that the chromosomal polymorphisms in these species are associated with the differentiation and adaptation of biotypes.

Translocation heterozygosity is also indicated in several species of *Viscum* in South Africa.

2. BAVERSTOCK, Peter R., HOGARTH, Jane T. and WATTS, C.H.S.
Division of Animal Science, Institute of Medical and Veterinary Science, Adelaide, S.A.

CHROMOSOME STUDIES OF NATIVE AUSTRALIAN RODENTS

An extensive chromosome analysis of the majority of the native rodents has revealed three areas of general interest -

(i) Chromosome "growth" in *Notomys cervinus*

The basic Pseudomyid karyotype is mainly acrocentric (e.g. *Pseudomys fumeus, Notomys alexis*). Some have one or two subacrocentric autosomes due to pericentric inversions (e.g. *P. delicatula*). *Notomys cervinus* is unique in possessing an almost entirely subacrocentric karyotype. C-banding reveals, however, that the majority of the short arms are heterochromatic. It is argued that because all other Pseudomyids, including the closely related *N. alexis*, have a mainly acrocentric karyotype, the *N. cervinus* condition is derived. Hence the heterochromatic short arms are due to "growth".

(ii) X-chromosome variation in *N. alexis*

At least three different X-chromosomes are encountered in *N. alexis* - a metacentric, a submetacentric and a subacrocentric. Chromosome measurements, C-banding and G-banding suggest that these are related to each other by inversions, deletions of heterochromatin and deletions of euchromatin.

(iii) C-banding behaviour of Supernumeraries of three Phylogenetically distinct Species

(a) *Uromys caudimaculata*
Specimens from the northern tip of Cape York, Qld. possess $2n = 46$ chromosomes. At meiosis there are 23 bivalents. Specimens from further south have larger numbers of chromosomes (up to $2n = 55$), mainly due to the addition of metacentrics. Karyotype analysis shows that the increased number is not due to Robertsonian translocations, suggesting that the extra chromosomes are B-chromosomes. All of the proposed B-chromosomes show intense C-banding.

(b) *Mastacomys fuscus*
Most specimens have a typical Pseudomyid karyotype ($2n = 48$ - mainly acrocentric). One specimen from Mt. Kosciusko had $2n = 49$ due to the addition of a small acrocentric. The single acrocentric showed intense C-banding.

(c) *Rattus fuscipes*
Most *R. fuscipes* have $2n = 38$ chromosomes. However many specimens from Victoria and southern N.S.W. have $2n = 39$ due to the addition of a small metacentric. The additional metacentric shows a complete absence of C-banded material. A similar situation has been found by others for B-chromosomes of *R. rattus*.

3. BRINK, N.G.
School of Biological Sciences, Flinders University, Bedford Park, S.A.

USE OF PRIMARY EMBRYONIC CELL CULTURES FOR STUDYING LETHALS IN DROSOPHILA

Many non-complementing lethal mutations in *Drosophila* are polyphasic even when the genetic background is made relatively homogeneous. This may suggest that the various alleles have different expressions depending on their position within the gene, or it may imply that certain non-complementing lethal mutants in fact occur in different genes which has implications for the one gene, one band hypothesis.

The development of a technique for establishing primary embryonic cell cultures from individual *Drosophila* embryos, may enable the primary developmental lesion to be identified particularly in the case of some embryonic and larval lethals. This may be detected as absence or variation in frequency of cell types or alterations in cell structure. Wild type cell cultures are being quantified in this way and they are to be compared with a series of autonomous polyphasic lethals, some alleles of which cause death during embryogenesis. Four non-complementing groups of polyphasic lethals are being investigated. Two occur in the white-zeste region (ZW1 and ZW3) and two somewhere in the region 2E. 2F on the salivary gland chromosome.

The demonstration shows how these lethals are being genetically analysed, the procedure for establishing cell cultures and some pictures of normal and mutant cell cultures.

4. BULL, M.[1] and MURPHY, C.[2]
[1]School of Biological Sciences, Flinders University, Bedford Park, S.A.
[2]Department of Zoology, University of Adelaide, Adelaide, S.A.

BACK-PATTERN POLYMORPHISM IN FROGS OF THE GENUS RANIDELLA

Seven of the eight species of the "*signifera*" group in the leptodactylid frog genus *Ranidella* are known to be polymorphic for back pattern. Two common morphs, ridged and lyrate, are present in all these species.

Using breeding data from *R. insignifera* Main (1965) proposed a one locus, two allele model of inheritance with lyrate dominant to ridged. Data from an additional 135 crosses within and between two Western Australian species confirm Main's model for *R. insignifera*, suggest a similar inheritance system for *R. pseudinsignifera* back-pattern morphs, and furthermore suggest that the loci involved occupy homologous positions in the two genomes, and have analogous, if not identical alleles. The most probable explanation is that this is an ancient polymorphism which has been present in these species for 400,000 years and probably longer.

Previous work by Walker (1966) suggested that adult *R. insignifera* homozygous for the recessive allele, ridged, tolerate warm dry conditions more successfully than lyrate phenotypes. This property is now demonstrated for *R. signifera* adults as well. In addition the hypothesis that ridged tadpoles develop more rapidly to metamorphosis, and thus are fitter in years when the breeding ponds dry early, is supported by experimental data. But during tadpole growth in conditions of low climate stress, the lyrate forms appear to competitively inhibit the growth of the ridged forms.

However a model for maintenance of this polymorphism relying on selection favouring one and then the other form in alternate years seems unlikely, especially considering the present day geographical range and the past history of the species, with the associated experience of considerable changes in climatic conditions.

5. COOPER, D.W., JOHNSTON, P.G., VANDEBERG, J.L., SHERMAN, R.F., MAYNES, G.M. and GUAT KIN CHEW[1].
School of Biological Sciences, Macquarie University, North Ryde, N.S.W.
[1]Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

THE FREQUENCY OF POLYMORPHISM FOR SEX LINKED ENZYME LOCI COMPARED TO THE FREQUENCY OF POLYMORPHISM FOR AUTOSOMAL LOCI IN MARSUPIALS

Unlike eutherians, kangaroos and perhaps marsupials use paternal X-inactivation as their mode of X-chromosome dosage compensation. Heterozygotes may therefore have one of two phenotypes, one identical with that of one homozygote, the other identical with that of the contrasting homozygote. The two phenotypes are equally frequent amongst the heterozygotes and so the selective coefficient of the heterozygote is equal to the mean of the selective coefficients of the two homozygotes. If this constraint is placed upon the conditions for the maintenance of a selectively balanced polymorphism at an X-linked locus, it is immediately apparent that balance through overdominance is not possible and balance through selection in opposite directions in the two sexes is very unlikely.

The frequency with which particular enzyme loci show polymorphism in marsupials has been determined. There is no detectable difference between sex linked and autosomal loci with respect to this frequency. This implies that, on the assumption of fixed selective coefficients, balancing selection is not the principal cause maintaining polymorphisms in marsupials. Whether more complex selective regimes such as frequency dependent and density dependent selection or environmental heterogeneity could lead to balanced polymorphism in marsupials remains to be determined.

6. DANIEL, Arthur, LAM-PO-TANG, R., STEWART, L. and GRAS, L.
Cytogenetics Unit, Prince of Wales Hospital, Randwick, N.S.W.

ROBERTSONIAN TRANSLOCATIONS IN MAN

Centric fusion translocations were first proposed by Robertson in 1916 to correlate changes in chromosome morphology with certain taxonomic relationship in insects. The concept involved the inclusion of two entire longarms in the translocation product. The generally accepted model for Robertsonian Translocations (R.T.) has been breakage immediately adjacent but on opposite sides of the centromere in the two chromosomes involved and exclusion of one centromere from the major translocation product. A possible model for some specific RT's e.g. t(21;21) in man, has been isochromosome formation. In recent years these mechanisms have been reassessed and a number of not necessarily exclusive alternatives have been proposed:

(i) that an R.T. may be the result of unequal reciprocal translocation White 1961 (Hirschhorn & Cohen, 1969);

(ii) that the centromeres simply fuse or that neither is lost appearing as a single centromere under light microscopy (Hsu & Mead, 1969);

(iii) that an abnormal recombination event occurs between homologous regions, e.g. the repeated 18 and 28S ribosomal cistrons in man, resulting in a dicentric translocation product (Ferguson-Smith, 1967, 1971).

Electron microscopy studies on a human t(D;G) (Barnicot *et al.*, 1963) and on some mammalian metacentric chromosomes, (Comings & Okada, 1970), have provided support for the concept that both centromeric regions are included in R.T.'s. Also C banded R.T.'s in the mouse often appear to have four heterochromatin masses instead of the regular two seen in the telocentric chromosomes, (Chen & Ruddle, 1971). This quadripartite structure in some metacentrics can also be seen in a heterochromatin stained karyotype of *Mus poschiavinus* from Forejt 1973. In man Niebuhr (1972c) studied five balanced Robertsonian Translocations. Heterochromatin staining showed four masses in all of the translocations except one a t(15;21) where six masses were seen and it was likely that the satellites of the chromosome 21 were incorporated.

This suggests that many Robertsonian Translocations are dicentric but before any real distinction can be made between the possible mechanisms of origin the regular breakpoints will have to be determined.

In man many studies on R.T.'s are being published with Q and/or G banding but without heterochromatin staining and therefore, the dicentric nature or otherwise of various Robertsonian Translocations has not been

commented upon. In this study the structure of the region surrounding the centromere was examined by C, G and Q banding in as many Robertsonian Translocations as were available from the N.S.W. Registry of Chromosome Abnormalities to indicate whether:

(a) R.T.'s commonly had their breakpoints in the shortarm and if so, what is the likely mechanism, and

(b) whether the structure of the centromere region influenced the segregation of the chromosome.

7. HALLIDAY, R.B.
Department of Genetics, University of Adelaide, Adelaide, S.A.

DISTRIBUTION AND GENETIC VARIATION IN MEAT ANTS (IRIDOMYRMEX PURPUREUS)

The species *I. purpureus* consists of a number of recognisable colour forms, of uncertain taxonomic relationships. Gel electrophoresis of enzymes to reveal polymorphic gene loci is one approach to the problem of clarifying this situation. Two loci have been identified (*Amy* and *Es-1*) which appear to have alleles at substantially different frequencies in some of the colour forms examined. In particular the "red form" of the meat ant appears to be reproductively isolated from the "blue form". This is also suggested by their differences in nest form and geographic distribution.

8. JOHN, B. and FREEMAN, M.
Department of Population Biology, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

CHROMOSOME VARIATION IN THE GENUS TOLGADIA

Abstract on page 30.

9. KELLOW, G.N. and MARSHALL GRAVES, J.A.
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

USE OF CELL HYBRIDIZATION TO STUDY THE MECHANISM OF UV-INDUCED CHROMOSOME DAMAGE

Virus-mediated cell fusion provides a convenient and useful approach for the study of nuclear-cytoplasmic interactions. This work makes use of the technique to investigate possible modes of action of ultra-violet light in the production of chromosome aberrations other than via the accepted phenomenon of direct DNA damage. The general method employed involves the irradiation of one parental line prior to fusion, followed by an analysis of the karyotypes of the subsequently formed hybrid clones and the detection of aberrations in the unirradiated set. Extensive use is made of trypsin-Giemsa banding for proper identification of the chromosomes.

Two refinements of the technique are being introduced to provide further information. The fluorescent stain Hoechst 33258 is being used to stain differentially sister chromatids following growth in 5-bromodeoxyuridine. Permanent staining can be achieved by the additional use of Giemsa. The

resultant preparations permit the detection of sister chromatid exchanges. The second refinement is the use of enucleate cells formed by treatment with cytochalasin B and subsequent centrifugation. The remaining "cytoplasts" may be irradiated and fused with whole cells to form "cytohybrids".

10. KING, Max
Department of Genetics, University of Adelaide, Adelaide, S.A.

CHROMOSOME RACES IN THE GEHYRA VARIEGATA - PUNCTATA *SPECIES COMPLEX*

The gekkos *Gehyra variegata* and *Gehyra punctata* are species possessing an extraordinarily low vagility, but with a vast Australia wide distribution. Evidence has been obtained for the existence of six distinct chromosome races: 2n=44 N.A., 2n=44 S.A., 2n=42 W.A., 2n=40 W.A., 2n=40 E.A. and 2n=38 E.A. Specimens from these races are morphologically distinct yet show considerable variation between populations. The chromosome morphology suggests that chromosomal evolution has been by centric fusion rather than fission, and that the races have evolved as entities in a single complex rather than in the current taxonomic groupings.

The chromosome race distribution is of interest, in that the range of a race at a particular locality is proportional to the area of the geographic feature on which that population lives (mountain range, rock outcrop, drainage system or forest type). In addition to this, the complex distribution of the central Australian populations suggests that the present day distributions are relics of more continuous populations, (and probably race radiations) isolated by aridity.

11. LOHE, Allan
Genetics Department, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

SATELLITE DNAs OF DROSOPHILA SIMULANS

Abstract on page 31.

12. PETERS, G.B.
Botany Department, School of General Studies, Australian National University, Canberra, A.C.T.

GERM-LINE POLYSOMY IN FIELD AND LABORATORY POPULATIONS OF THE PYRGOMORPHINE GRASSHOPPER ATRACTOMORPHA SIMILIS (*BOLIVAR*)

Two-hundred and fifty adult males were collected from seven sites in the Atherton Tableland and adjacent coastal plain of north Queensland.

Meiotic tissue from 217 males was examined, and 25% were found to be polysomic for the megameric number 9 autosome, which is easily recognised by its distinctive large heterochromatic segments. These segments always appear highly condensed in 2 of the homologues, but are less condensed in any additional copies. In polysomic individuals, the 2 denser homologues usually occur as a bivalent, sometimes as univalents, but never as part of a multivalent. The extra homologues also usually form bivalents and univalents. They may form multivalents and do so with increasing frequency the higher the level of polysomy.

States of polysomy in the field range from tri- to octosomic, although there is some variation within individuals. Nevertheless, no significant difference exists between the 7 populations in respect of the level of polysomy.

Gut cecae from a sample of germ-line polysomic males contained mitotic cells of normal chromosome number.

From these 7 populations, 30 males were selected containing 1 or more extra number 9 autosomes. These were mated to virgin females of unknown chromosomal constitution from the same population mixture. In the F_1, the percentage of adult males containing polysomic germ cells was approximately double that in the field sample, and considerably higher levels of polysomy were observed. Within-individual variation was also increased.

This response indicates that there must be a genetic component to the causative mechanism responsible for the production of germ-line polysomy.

13. PRYOR, A.J.
Division of Plant Industry, CSIRO, Canberra, A.C.T.

THE CHARACTERIZATION AND DISTRIBUTION OF GC-RICH SEQUENCES IN THE DNA OF MAIZE

Thermal denaturation profiles of maize DNA are heterogeneous indicating the presence of DNA species with a Tm that is about 10°C higher than the bulk of the DNA i.e. DNA species with about 65% GC content as compared to 42% for the bulk of the DNA.

The GC-rich sequences are distributed widely throughout the total DNA. This was demonstrated by a comparison of unsheared and sheared DNA. Three methods allowed the same conclusion. Some purification of the GC-rich DNA was achieved by hydroxyapatite chromatography under conditions of partial denaturation. Only DNA molecules containing double stranded regions (i.e. GC-rich) are retained on the column. The denaturation and renaturation characteristics of this fraction indicate that the GC-rich DNA is possibly a repeated sequence of length greater than 100 base pairs.

14. SMYTH, D.R.
Department of Genetics, Monash University, Clayton, Vic.

"C-BANDS" IN CHROMOSOMES OF LILIUM

If centromeric C-bands, discovered in mammalian chromosomes, are a fundamental aspect of chromosome structure, they should be detectable in chromosomes of most species. We have obtained analogous bands in chromosomes of *Lilium*, a genus of plants. The method is based on that used in animals, but omits any alkali pretreatment. Air-dried squashes of chromosomes from root tips are made and treated in saline/sodium citrate at 60°C for 10-60 minutes. Staining in buffered Giemsa reveals heavily-stained regions at or near all centromeres and nucleolar organizers. The mechanism of C-banding in plant and animal chromosomes might have a common basis, and depend on the location of DNA of highly repeated sequence in these regions. These sequences at, or near, centromeres might have a role in chromosome movement.

15. STACE, Helen M. and FRIPP, Yvonne J.
Department of Genetics, La Trobe University, Bundoora, Vic.

FLORAL POLYMORPHISMS IN EPACRIS IMPRESSA *LABILL*

Epacris impressa is considered taxonomically to be a single species. It is remarkably polymorphic for flower colour, with pink and white variants being most common; a less common scarlet variant also exists. There are populations monomorphic for each corolla colour, as well as polymorphic populations presenting two or more corolla colours. The monomorphic populations throughout Victoria consistently show divergent characters with respect to corolla colour, corolla length, time of flowering and ecological preference. However, populations polymorphic for corolla colour show intermediate characteristics especially in mean corolla length and also in flowering time.

We propose two alternative views of this species structure:

1. There is a superspecies consisting of several discrete races or species that are characterised in the first instance by monomorphic corolla colour; and the polymorphic populations are the product of hybridization between races or species.

2. There is a single species which can exist in a polymorphic state in some habitats or in a monomorphic state in other habitats as a result of local selections. A consequence of the latter is divergence in flowering times which thus acts as a primary pre-mating barrier in sympatric situations.

In either case polymorphic populations provide a route for gene flow between the monomorphic populations.

16. STOCKER, Ann J.
Department of Genetics, University of Melbourne, Parkville, Vic.

THE REARING OF RHYNCHOSCIARA *AND ITS USEFULNESS IN CYTOLOGICAL & BIOCHEMICAL STUDIES*

For research and teaching in the biochemical and cytological aspects of development, *Rhynchosciara* has many features to recommend it. It is a large Dipteran with synchronous larval development. It's polytene chromosomes are well-developed in three different larval organs. These chromosomes form large RNA and DNA puffs during larval life which can be correlated with morphological and biochemical events. Many can be induced by specific substances such as hormones, heat, etc.

Rhynchosciara is easier than any other Diptera for student practical work. The main principles of gene action in relation to chromosome structure can be readily observed under the student microscope. In comparison to a conventional organism such as *Drosophila*, students can easily learn to inject *Rhynchosciara* and follow the expansion of induced puffs.

Labelled nucleic acid precursors can also be readily injected and their distribution along the chromosome followed. Sufficient material can be taken from an organ type of a single larva for electrophoretic analysis.

A disadvantage of *Rhynchosciara* is its sex-determination mechanism in which one female produces only 1 sexual type of progeny. This means that

a large number of groups must be kept for breeding. A further disadvantage is that *Rhynchosciara* requires a large amount of care. Since we are successfully raising this Dipteran in Melbourne, we would be glad to send larvae to other Universities and Colleges in Australia for teaching purposes in order to maximize the use of our stocks.

17. WESTERMAN, M. and DEMPSEY, J.
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

SUPERNUMERARY HETEROCHROMATIN IN PHAULACRIDIUM MARGINALE

Population samples of the New Zealand grasshopper *Phaulacridium marginale* taken from both North and South Islands are known to be polymorphic for extra heterochromatin. They may be present in the chromosome complement as either B-chromosomes or as extra segments on the four smallest autosomes or as both together. Presence of the different B's and/or segments in a population is stable from year to year and appears to be negatively correlated with annual rainfall. The ability of this species to tolerate many different polymorphisms for extra heterochromatin appears to be restricted to "central" populations.

The possible role of this extra heterochromatin in the control of chiasma frequency will be illustrated by data from one particular population in which to date 38 of the possible 108 different karyotypes have been observed.

18. WHITE, Richard J.
Department of Genetics, University of Adelaide, Adelaide, S.A.

MULTIVARIATE ANALYSIS OF A POLYMORPHISM

The "medionigra" gene in the Scarlet Tiger Moth, *Panaxia dominula* (L.), has been used extensively in the United Kingdom for research into the selective mechanism responsible for the maintenance of a polymorphism (Ford, 1971, *Ecological Genetics*).

In the only naturally polymorphic colony (Cothill) the gene is not completely recessive, allowing heterozygotes to be identified and accurate gene frequency estimates to be made.

In various colonies where the gene has been introduced it is tending towards recessiveness (Sheepstead Hurst) or dominance (Pewsey, Hinksey Hill). In the former case it becomes difficult to monitor the gene's frequency as homozygotes for the "medionigra" gene are rare.

Multivariate analysis of a large number of phenotypic characters has revealed a number of variables affected by the gene. This knowledge permits optimal recognition of heterozygotes (even in the field) and allows quantification of the changes in dominance.

19. ZOBRIST, Stephanie
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

STUDIES ON RADIORESISTANT AND RADIOSENSITIVE STRAINS OF DROSOPHILA MELANOGASTER

From a massmated laboratory population of *Drosophila melanogaster* lines were selected for resistance and sensitivity following irradiation with 90 or 120 krad of γ-rays. The response to selection was asymmetrical in both cases but in opposite directions. Thus in the experiment with 120 krad the selection for resistance and in the 90 krad experiment the selection for sensitivity was more successful. These responses to selection are related to the initial mortality of the base population to the dose used. The established lines were then used for recombination, split dose and low dose experiments. Subsequently the different sensitive and resistant lines were separately massmated and the selection pressure intensified by using a lower dose (60 krad) to increase sensitivity and a higher (150 krad) to enhance resistance.

LATE ABSTRACTS

DEARN, J.M.
Department of Population Biology, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

GEOGRAPHIC VARIATION IN NUCLEAR DNA CONTENT FOR THREE GRASSHOPPERS

A polymorphism for the presence of a supernumerary chromosome segment is being utilized to examine the nature and significance of nuclear DNA variation in three species of grasshopper. *Praxibulus* sp., *Kosciuscola cognatus* and *Kosciuscola usitatus* have overlapping distributions which exhibit altitudinal zonation in the higher regions of S.E. Australia. All three species are polymorphic for a large supernumerary heterochromatic chromosome segment on the smallest pair of autosomes (S_{11}). An analysis of the geographic variation for this polymorphism indicates that the supernumerary heterochromatin is not neutral as some authors have suggested. The temporal and spatial patterns of the observed variation suggest a number of hypotheses for the role of the chromosome segment in natural populations and these are currently being tested. It is proposed that intrapopulation polymorphisms for supernumerary DNA provide useful experimental models for studying the significance of nuclear DNA variation.

JOHN, B. and FREEMAN, M.
Department of Population Biology, Research School of Biological Sciences, Australian National University, Canberra, A.C.T.

CHROMOSOME VARIATION IN THE GENUS TOLGADIA

1. The genus *Tolgadia* includes three species of short horned grasshoppers which are well defined morphologically though one of them (*sp. 1*) has not yet been named. All are endemic to Australia and are hygrophilous, occurring only in high rainfall areas. *sp. 1* has a very restricted distribution and is known only from areas in the Northern Territory and the Kimberlies with an annual rainfall in excess of 47 inches. The other

two species, *bivittata* and *infirma*, are more widespread extending from northern Queensland to northern Western Australia. *Infirma* has the widest range and is capable of occupying much drier habitats despite the fact that unlike *bivittata* and *sp. 1* it is brachypterous.

2. The three species are also well defined cytologically. All of them have a neo XX/neo sex chromosome mechanism involving an X⌒3 fusion in *sp. 1* and *bivittata* and an X⌒2 fusion in *infirma*. In addition *bivittata* is homozygous for two autosomal fusions, 1⌒4 and 2⌒5. The karyotypes are thus:

sp. 1 - 2n = 22♂ 22♀ (X⌒3)

bivittata - 2n = 18♂ 18♀ (X⌒3, 1⌒4, 2⌒5)

infirma - 2n = 22♂ 22♀ (X⌒2)

3. *Infirma*, the most widespread and least habitat restricted species, differs from *sp. 1* and *bivittata* in two other respects:

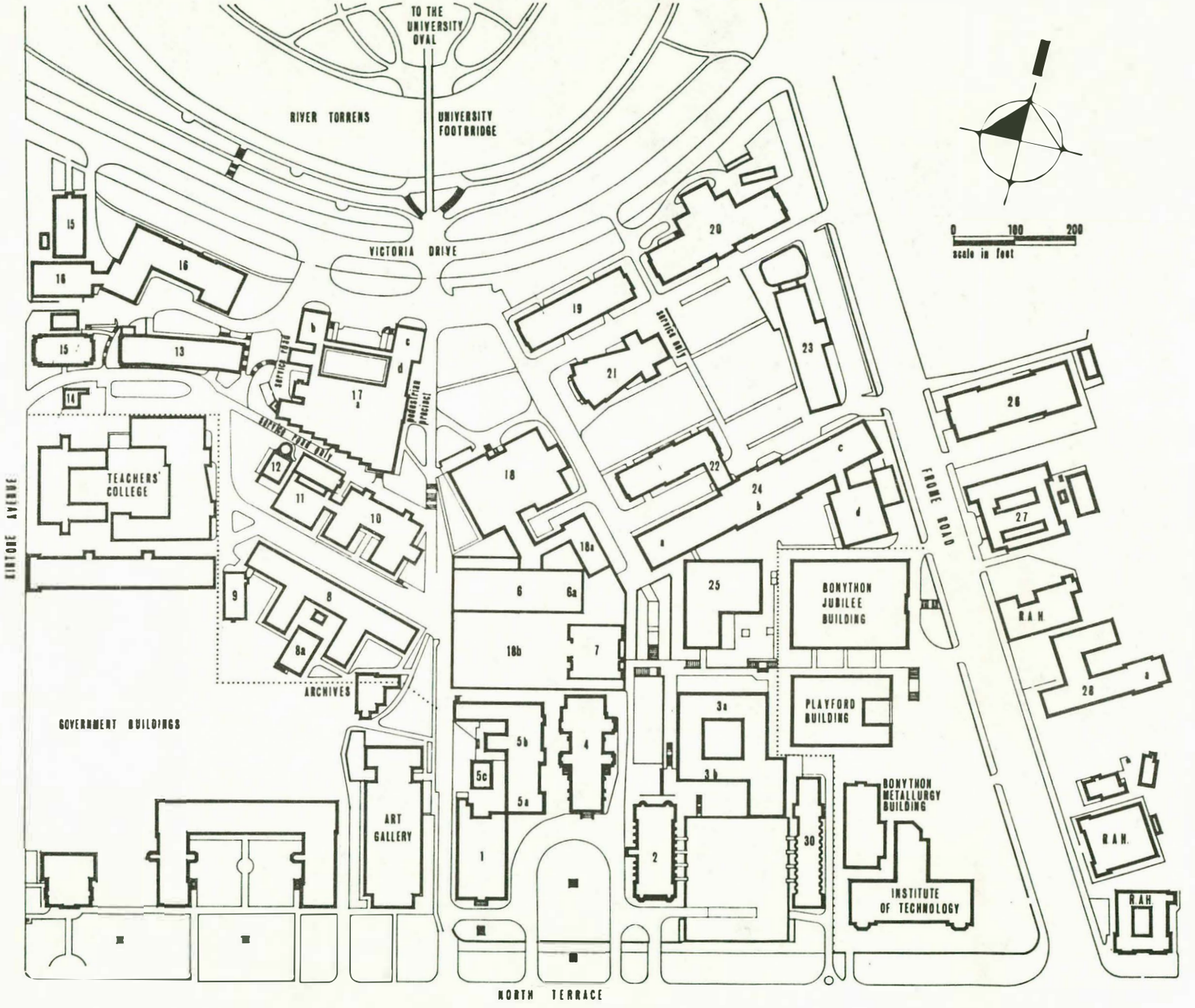
(i) It has a significantly higher mean cell chiasma frequency, $\bar{x}$ 14.6 versus 13.8 (*sp. 1*) and 13.7 (*bivittata*).

(ii) At least some of its populations are polymorphic for a supernumerary heterochromatic segment on the smallest autosome. When present this segment leads to a significant elevation of mean cell chiasma frequency, $\bar{x}$ 15.7 (+ segment) v. 14.6 (standard).

LOHE, Allan
Genetics Department, Research School of Biological Sciences,
Australian National University, Canberra, A.C.T.

SATELLITE DNAs OF DROSOPHILA SIMULANS

Most of the satellite DNA species of *Drosophila simulans* are different to those of a sibling species, *Drosophila melanogaster*, as judged by their buoyant densities in CsCl. Several satellites of *Drosophila simulans* have been purified and their chromosomal locations mapped by cytological hybridisation. However, hybridisation has shown that the *Drosophila simulans* satellites studied are still closely related to those in *Drosophila melanogaster*.



THE UNIVERSITY OF ADELAIDE

KEY TO PLAN

1. Mitchell Building: Administration.
2. Bonython Hall.
3. Napier Building:
   a. Economics, Commerce.
   b. Arts Departments.
4. Elder Conservatorium: Music.
5. Prince of Wales Building:
   a. Administration.
   b. Psychology.
   c. Administration.
6. Library.

6a. Computing Science.

7. Staff Club.
8. Physics.

8a. Maintenance and Physics Workshops.

9. Mawson Institute, Physics, Mathematical Physics.
10. Darling Building: Biochemistry.
11. Bragg Laboratories: Physics.
12. Observatory.
13. Organic Chemistry.
14. Maintenance Superintendent's Residence.
15. C.S.I.R.O.
16. Johnson Laboratories: Physical and Inorganic Chemistry.
17. The Union:
   a. Refectories.
   b. Lady Symon Building.
   c. George Murray Building.
   d. Union Bookshop.
18. Barr Smith Library.

18a. Architecture, Horace Lamb Lecture Theatre and Library.

18b. Adult Education, Architecture, Computing, Health Service, Library (partly still under construction).

19. Benham Laboratories: Botany.
20. Mawson Laboratories: Geology, Economic Geology.
21. Union Hall.
22. Mathematics Building.
23. R. A. Fisher Laboratories: Genetics, Zoology.
24. Engineering Building:
   a. Civil Engineering.
   b. Electrical Engineering.
   c. Chemical Engineering.
   d. C.S.I.R.O. Civil and Electrical Engineering.
25. Mechanical Engineering.
26. Medical School: Anatomy, Pathology, Physiology, Microbiology.
27. Dental School and Hospital.
28. Institute of Medical and Veterinary Science:
   a. Verco Lecture Theatre.
29. Physical Education: At Mackinnon Parade.
30. Ligertwood Building: Law, Classics, Philosophy.
31. Waite Agricultural Research Institute at Urrbrae: Agricultural Science.