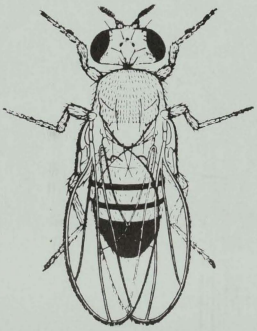
The Genetics Society of Australia

24th General Meeting

PROGRAM & ABSTRACTS



Monash University

26 – 27th August, 1977

GENERAL INFORMATION

PAPERS

Sessions will be held in Rotunda Lecture Theatres R1, R2 and R7 (Building No. 7 on map in Guide to Monash). Would speakers please give their slides (50 mm square only) to the projectionist, numbered and in order, before their session begins.

DEMONSTRATIONS

These will be set up in the Foyer of the Rotunda Theatre Block. Included will be a Teacher's Desk, containing items of interest and help for those organizing laboratory and tutorial classes in Genetics.

TEA AND COFFEE

Morning and afternoon tea and coffee, with biscuits, will be available in the Foyer of the Rotunda.

LUNCH

Delegates may use the facilities of the Union Building (No. 9 on Guide), where lunch is available from 12 - 2.00 p.m. on weekdays, and 12 - 3.00 p.m. on Saturdays (when the Union Grill Room alone will be open). The cash cafeteria in Howitt Hall (No. 39) will also be open for lunch from 12 - 1.45 p.m. The closest hotels to Monash are the Monash Hotel Motel at 2,077 Dandenong Road, and the Notting Hill Hotel on the corner of Fern Tree Gully and Gardiner Roads. Both serve a counter lunch.

ACCOMMODATION

Members who have booked into the Monash Halls of Residence should check in and out at the Halls Administration Office, between Roberts and Richardson Halls off Normanby Road (see map at end of programme). Payment should be made before leaving at this office, which is open from 9 a.m. to 10 p.m. on weekdays and 9 a.m. to 9 p.m. on weekends. Rates are $9-50 per night for a single, serviced room and breakfast. Lunch and dinner are available at the cash cafeteria in Howitt Hall (see map). Meal hours are as follows:

Breakfast	8.00 a.m. - 9.00 a.m.
Lunch	12.00 noon - 1.45 p.m.
Dinner	5.45 p.m. - 7.30 p.m.

Incoming mail for delegates should be addressed care of The Genetics Society Meeting, Monash University Halls of Residence. It will be distributed to the alphabetical pigeon holes of the Hall in which the delegate is booked.

MONASH UNIVERSITY CLUB

Delegates will be able to use the Club's facilities, except for lunch. The Club is licenced and is close to the Rotunda and Union Building (No. 45 in Guide). The Club's bar is open from 11.30 a.m. - 8.30 p.m. on Mondays to Thursdays, and 11.30 a.m. - 10.00 p.m. on Friday. Dinner is available from 5.30 p.m. - 8.00 p.m. The Club is closed on weekends.

When signing in, please wear your name-tag, and tell the doorman that you are from the Genetics Society Meeting.

POST OFFICE AND BANKS

These are located in the Union Building (No. 9 in Guide). They are closed on weekends.

PARKING

Ample free parking is available on campus on the right (east) side of the main entrance on Wellington Road. There are also areas of free parking at the Halls. Other areas, where signposted, are for permit holders only, and are patrolled regularly.

PUBLIC TRANSPORT

Monash campus is served by bus from the 'bus loop' off Wellington Road (see Guide), connecting with suburban train lines.

Sinclairs buses on Route 630 travel between the loop and Huntingdale Station, on the Dandenong line, at about half hourly intervals up to 11.30 p.m. This is the easiest and most regular service.

Ventura buses on Route 703 ply between Clayton Station, the Monash bus loop, along Blackburn Road past Monash Halls, and Syndal Station on the Glen Waverley line. This is the only route servicing the Halls, and terminates at about 9 p.m. on weekdays, 7 p.m. on Saturdays, and there is no Sunday service.

All suburban trains pass through Flinders Street Station in the city. Delegates should leave at least an hour to travel to and from the city by public transport.

Details of timetables and routes will be available from the Registration Desk at the meeting.

ANNUAL BUSINESS MEETING

This will be held at 5.30 p.m. on Friday 26th August in Rotunda Theatre R1. The remainder of Friday evening is free.

SOCIAL EVENTS

Mixer: An informal gathering will be held in the Deakin Hall Common Room (see map at end of programme) on Thursday 25th August at 8.00 p.m. This year, we will be joined by delegates from the Human Genetics Society Meeting.

Melbourne Theatre Company: "The Merchant of Venice" is playing at 8.15 p.m. on Friday 26th August at the Athenaeum Theatre, 188 Collins Street in the city. Members who ordered tickets will receive them when registering.

Annual Dinner: This will be held at 7.00 p.m. for 7.30 p.m. on Saturday 27th August in the Farrer Hall Dining Room, Monash Halls. Enter off Normanby Road (see map at back of programme). Students giving a paper or a demonstration will receive a complimentary ticket.

Chateau Tahbilk Picnic: On Sunday 28th August, a wine-tasting and barbecue will be held at the Chateau Tahbilk, Nagambie. A bus will leave from Normanby Road outside the Monash Halls at 9.30 a.m. sharp. It will return to the Halls by 6.00 p.m., calling into the TAA city terminal en route at about 5.30 p.m.

48th ANZAAS CONGRESS

This is to be held from 29th August to 2nd September at the University of Melbourne.

The Genetics Society is sponsoring a Symposium on "The Genetical Consequences of Environmental Hazards" jointly with Section 11 (Zoology). Details are given at the end of this programme.

XIV INTERNATIONAL CONGRESS OF GENETICS

The Congress will be held in Moscow on 21st-30th August 1978. Copies of the Second Announcement and Registration Forms are available from the Registration Desk.

ACKNOWLEDGEMENTS

TAA, who are arranging airline travel for delegates, having kindly donated the printing of this programme.

The local committee thank staff of the Department of Genetics at Monash for their assistance. In particular, we thank Mrs Jenny Elliston and Mrs Sandra Batton for excellent secretarial help.

PROGRAMME

(Names of speakers are underlined)

FRIDAY 26 AUGUST

REGISTRATION — Rotunda Theatre Foyer
8.30 - 9.15

GUEST LECTURE — Rotunda Theatre R1
9.15 - 10.30 — Chairman: Professor Max Clark

"Evolutionary Problems Posed by Repetitive DNA"

Professor Alan Robertson, University of Edinburgh

TEA AND COFFEE
10.30 - 11.00

SESSION 1 — Rotunda Theatre R1
11.00 - 12.40 — Chairman: Professor Max Whitten

11.00	R. Frankham and D.A. Briscoe	Unequal crossing over as a source of quantitative genetic variation
11.20	G.G. Foster, M.J. Whitten, C. Konovalov, and R.H. Maddern	Current status of genetic control of *Lucilia cuprina*
11.40	K.M. Summers and A.J. Howells	The biochemical nature of the eye colour mutants of the Australian sheep blowfly, *Lucilia cuprina*
12.00	W.L. Gerlach and W.J. Peacock	Molecular probes for investigating the evolution of polyploid wheat
12.20	Ruth Rofe	Chromosome evolution in marsupials

LUNCH
12.40 - 2.00

SESSION 2A — Rotunda Theatre R1
2.00 - 4.00 — Chairman: Professor David Catcheside

2.00	M.J. Hynes	Mutations in the controlling region of a structural gene in *Aspergillus nidulans*
2.20	Joan M. Kelly and M.J. Hynes	Mutations affecting carbon catabolite repression in *Aspergillus nidulans*
2.40	J.A. Thomson	Genetics of the cotyledonary storage proteins in *Pisum sativum*
3.00	W.R. Scowcroft and J.D. Pagan	Nitrogen fixation in D-amino acid mutants of *Rhizobia*

3.20	Miriam Fischer and W.R. Scowcroft	Cauliflower mosaic virus - Infectivity and genetic variability
3.40	C.R. Datson and N.G. Brink	The influence of the maternal genome on early development in *Drosophila*

SESSION 2B — Rotunda Theatre R2
2.00 - 4.00 — Chairman: Professor Barrie Latter

2.00	Kerry Rathie and Frank Nicholas	Artificial selection with differing population structures
2.20	J.A. Sved	Further studies on the inheritance of hybrid dysgenesis in *Drosophila melanogaster*
2.40	Alan Wilton	A measure of heterosis for the X-chromosome in *Drosophila melanogaster*
3.00	Stephen McKechnie and Phillip Morgan	The alcohol dehydrogenase polymorphism in *Drosophila melanogaster*: Spatial heterogeneity of environmental substrates
3.20	Jay Hetzel and Frank Nicholas	Genotype - environment interaction for growth in mice
3.40	B.J. McGuirk	Response to selection for fleece weight in Merino sheep

TEA AND COFFEE, DEMONSTRATIONS
4.00 - 5.30

ANNUAL BUSINESS MEETING — Rotunda Theatre R1
5.30

SATURDAY 27 AUGUST

GUEST LECTURE — Rotunda Theatre R1
9.15 - 10.30 — Chairman: Professor Geoff Sharman

"Cytogenetic Studies of Marsupials"

Dr David Hayman, University of Adelaide

TEA AND COFFEE
10.30 - 11.00

SESSION 3A — Rotunda Theatre R1
11.00 - 12.40 — Chairman: Professor Michael White

11.00	Elizabeth Dennis, Pamela Dunsmuir and W.J. Peacock	Fine structure of the 1.708 satellite DNA of the red-necked wallaby *Macropus rufogriseus*

11.20	Lee Venolia	Satellite DNA in the wallaroo (*Macropus robustus robustus*) and its use as a probe in kangaroo phylogeny
11.40	G.L.G. Miklos, P.R. Baverstock, C.H.S. Watts, M. Gelder, R. Warnock, and M. Yamamoto	Studies on satellite DNA function
12.00	Judith Helen Ford	Cytogenetics of human male infertility
12.20	Grant R. Sutherland	Fragile sites on human chromosomes

SESSION 3B — Rotunda Theatre R2
11.00 - 12.40 — Chairman: Professor Stuart Barker

11.00	Ian R. Bock	Degrees of sexual isolation amongst four *Drosophila* species
11.20	D.J. Colgan and D.S. Angus	Hybrid sterility in *Drosophila melanogaster*
11.40	G.R. Murray	Possible pheromonal effects on egg-laying in *Drosophila*
12.00	Janice McDonald	Genetic control of the courtship display of *Drosophila melanogaster*
12.20	B.L. Sheldon and M.K. Evans	Chromosomal and lethal analysis of scutellar bristle selection lines in *Drosophila*

LUNCH
12.40 - 2.00

SESSION 4A — Rotunda Theatre R1
2.00 - 3.20 — Chairman: Dr Jim Peacock

2.00	R. Appels and W.J. Peacock	The highly repeated DNA sequences near ribosomal genes of *Drosophila melanogaster*
2.20	A.R. Lohe	Evolutionary stability of highly repeated DNA locations in the heterochromatin of *Drosophila*
2.40	M. Yamamoto	Studies on the functions of heterochromatin in *Drosophila melanogaster*
3.00	K. Kongsuwan	DNA loss during C-banding of *Lilium* chromosomes

SESSION 4B — Rotunda Theatre R2
2.00 - 3.20 — Chairman: Dr Ross Crozier

2.00	Jon Martin, B.T.O. Lee, R. Ananthakrishnan and E. Harts	Further data on the speciation in *Chironomus oppositus*

2.20	C. Moran and D.D. Shaw	Chromosomal polymorphism, racial parapatry and introgression in *Caledia captiva* (Orthoptera: Acridinae) in south-east Queensland
2.40	R.B. Halliday	Electrophoretic variation and sibling species relationships in Meat Ants (*Iridomyrmex purpureus*)
3.00	D.G. Bedo	Sibling speciation in the blackfly *Simulium ornatipes*

SESSION 4C — Rotunda Theatre R7
2.00 - 3.20 — Chairman: Dr John Thomson

2.00	B.A. Evans and A.J. Howells	Control of pteridine eye pigment synthesis in *D. melanogaster*: Eye colour mutants with altered levels of the first enzyme of the pathway
2.20	B.L. Sheldon and L.W. Bobr	Effects of U.V. irradiation of poultry sperm: (i) Fertility, hatchability and egg production traits
2.40	M.H. Thorne and B.L. Sheldon	Effects of U.V. irradiation of poultry sperm: (ii) Chromosome study
3.00	L.R. Piper	Some problems in parasite resistance genetics

TEA AND COFFEE
3.20 - 3.40

SESSION 5A — Rotunda Theatre R1
3.40 - 5.00 — Chairman: Dr Viji Krishnapillai

3.40	Robert Saint and Barry Egan	Restriction map of coliphages P_2 and 186
4.00	J. Carrigan and V. Krishnapillai	Suppressible transfer deficient mutants of a *Pseudomonas aeruginosa* R plasmid
4.20	K.M. Oakley and G.D. Clark-Walker	Analysis of high petite frequency mutants in the yeast *Saccharomyces cerevisiae*
4.40	S.F. Delaney	Isolation of auxotrophs of the blue-green alga, *Anacystis nidulans*

SESSION 5B — Rotunda Theatre R2
3.40 - 5.00 — Chairman: Professor Hewson Swift

3.40	A.K.M.R. Islam, K.W. Shepherd and D.H.B. Sparrow	Wheat-barley hybrids and isolation of addition lines
4.00	G.E. Hart, A.K.M.R. Islam and K.W. Shepherd	Isozyme expression in wheat-barley addition lines

4.20	S. Durvasula and N.L. Darvey	C-banding in the evaluation of chromosome pairing in a 5B-mutant wheat-rye polyhaploid
4.40	N.C. Subrahmanyam	Genetic control of chromosome pairing in *Hordeum*

SHERRY, DEMONSTRATIONS
5.00

ANNUAL DINNER — Farrer Hall Dining Room
7.00 for 7.30

DEMONSTRATIONS

Rotunda Theatre Foyer

Sarah E. Ashmore and Alan R. Gould
Approaches to somatic cell genetics using low chromosome number Composites

Elizabeth Dennis and J.I. Menzies
Rodents of Papua New Guinea

W.M. Ellis, R.J. Keymer and D.A. Jones
Ecological studies on the polymorphism of cyanogenesis in populations of *Lotus corniculatus* in Anglesey, Wales

C.B. Gillies
Pachytene chromosomes of annual *Medicagos*

C.B. Gillies
Serial section reconstruction of meiotic chromosomes at the ultrastructural level

Ken C. Reed
A 'thought' experiment: Isolation of mammalian structural genes by molecular cloning

R. Rofe, P. Baverstock, D.L. Hayman and M. Gelder
Chromosome studies in marsupial gliders (genus *Petaurus*)

W. Dorsey Stuart and David Porter
An improved *in situ* hybridization method

Philip Ward
Genetic variation and social behaviour in a species complex of ponerine ants

M.J.D. White, G.C. Webb, N. Contreras, J. Cheney, W.J. Peacock and R. Appels
Genetic systems of the parthenogenetic grasshoppers *Warramaba virgo* and *Xiphidiopsis lita*

M.J. Whitten
The Australian sheep blowfly, *Lucilia cuprina*, for illustrating the basic concepts in genetics

K. Williams and G. Robson
Genetic analysis of *Dictyostelium discoideum* using the parasexual and sexual cycles

ABSTRACTS

GUEST LECTURE

PROFESSOR ALAN ROBERTSON
Institute of Animal Genetics, University of Edinburgh. Commonwealth Visiting Professor at University of Sydney, Sydney, N.S.W.

EVOLUTIONARY PROBLEMS POSED BY REPETITIVE DNA

While evolutionists have been involved in a somewhat sterile neutralist-selectionist argument, the molecular biologists have been producing a vast amount of evidence on DNA organization in higher organisms which poses challenging questions. This includes the multiplicity of loci coding for proteins, for the protein-making machinery, for regulatory loci (which we may think we detect though we know little about precise function) and finally for the highly repeated satellite fractions, about whose function we have still only speculation. As an interested onlooker in this field, I want first of all to summarize the present evidence, to consider some of the problems it presents to the evolutionist and to examine some of the new mechanisms which have been suggested.

SESSION 1

R. FRANKHAM and D.A. BRISCOE
School of Biological Sciences, Macquarie University, North Ryde, N.S.W.

UNEQUAL CROSSING OVER AS A SOURCE OF QUANTITATIVE GENETIC VARIATION

A marked homozygous line was constructed and used to found abdominal bristle selection lines (3 high, 3 low and controls) to measure the contribution of "mutations" to selection response. Two of the low lines each exhibited a period of rapid response to selection in females but not in males, together with a corresponding series of other sex-limited changes. All these changes were shown to be due to the X chromosomes in these two lines and the X chromosomes in these two lines were shown to carry *bb* alleles while the Y chromosomes did not. Evidence for similar changes is to be found in other reports.

Since the changes occurred at the multiple copy tandemly duplicated rRNA locus and since *bb* mutations are known to be partial deficiencies of this locus, it is argued that the *bb* alleles in our low lines were generated by unequal crossing over.

G.G. FOSTER[1], M.J. WHITTEN[2], C. KONOVALOV[1] and R.H. MADDERN[1]
[1] CSIRO Division of Entomology, Canberra, A.C.T.
[2] Department of Genetics, University of Melbourne, Parkville, Vic.

CURRENT STATUS OF GENETIC CONTROL OF LUCILIA CUPRINA

Two types of chromosome rearrangements (compound autosomes and male-limited translocations) and one type of conditional lethal mutation (eye colour mutations) are presently being developed for their potential as major genetic control weapons against *Lucilia cuprina*.

A trial during 1975-76 of the compound strain *C(5L)2; C(5R)1* indicated that this strain was not fit in the field; the most likely cause for this was an insufficiently broad genetic background in the strain. Current research in the radiation genetics of *L. cuprina* is aimed at solving this problem.

The other type of strain being developed, called "translocation-male/eye colour" (TM/EC) strains, are made by using Y-autosome (σ -limited) translocations to limit the expression of certain eye colour mutations to females. We thus have true-breeding strains, for example, in which females are homozygous for a white and a yellow-eyed mutation, while males are heterozygous for these mutations and for a multiple Y-autosome translocation. The mutant females can survive in cages, so the strain can be mass-reared, but they are unable to survive in the field. Males, which appear wild-type can survive and mate in the field, transmitting their eye mutations to their female offspring. Persistant releases of this type of strain can lead to a high proportion of mutant females in a population. The inability of these females to survive and reproduce, combined with the partial sterility caused by the translocation, can lead to levels of genetic death in excess of 90%. Ecological studies suggest that this should be enough to suppress sheep blowfly populations under most conditions.

Preliminary results of a trial of TM/EC strain during 1976-77 are presented, and plans for the 1977-78 season are discussed.

K.M. SUMMERS and A.J. HOWELLS
Department of Biochemistry, Faculty of Science, Australian National University, Canberra, A.C.T.

THE BIOCHEMICAL NATURE OF THE EYE COLOUR MUTANTS OF THE AUSTRALIAN SHEEP BLOWFLY, LUCILIA CUPRINA

The sheep blowfly has been subjected to considerable genetic analysis and manipulation as part of the investigation into possible methods of genetic control carried out by the Division of Entomology, CSIRO. Seven eye colour mutants, at 6 loci, have been discovered. This paper reports recent studies of the biochemistry of eye pigmentation in *L. cuprina* which have led to the elucidation of the nature of the biochemical defects associated with these eye colour mutants.

The eyes of *L. cuprina* contain the brown pigment, xanthommatin, which has been found in all species of Diptera analysed, and some yellow pteridines, although the bright red drosopterin group is missing. The onset of xanthommatin pigmentation occurs midway through metamorphosis, as has been found for *Drosophila melanogaster*. Developmental patterns of accumulation for the xanthommatin precursors tryptophan, kynurenine and 3-hydroxykynurenine have been established for wild type.

Examination of levels of these precursors in the mutants has revealed homologies with mutants of *D. melanogaster*. *Yellowish* of *L. cuprina* accumulates tryptophan and, like *vermilion* of *D. melanogaster* has negligible tryptophan oxygenase activity *in vitro*. *Yellow* accumulates kynurenine, like *cinnabar* of *D. melanogaster*, suggesting that it lacks kynurenine hydroxylase. *White* of *L. cuprina* lacks all eye pigment classes and may be defective in transport of pigment precursors like *white* of *D. melanogaster*. The *topaz* locus, with alleles *topaz*^{1} and *topaz*^{2}, may be responsible for a protein involved in transport of xanthommatin precursors, like the *scarlet* locus of *D. melanogaster*. *Tangerine* is thought to involve a block in the final step in xanthommatin formation, like *cardinal* of *D. melanogaster*. *Tangerine* mutants accumulate 3-hydroxykynurenine. *Grape* is apparently a pteridine mutant with xanthommatin formation virtually normal.

This clarification of the biochemical nature of the eye colour mutants of *L. cuprina* provides a basis for further studies on the developmental control of eye pigment synthesis in Diptera. In addition, it will assist researchers at CSIRO to include these visually defective eye colour mutants in their genetic control programme for the sheep blowfly.

W.L. GERLACH and W.J. PEACOCK
CSIRO Division of Plant Industry, Canberra, A.C.T.

MOLECULAR PROBES FOR INVESTIGATING THE EVOLUTION OF POLYPLOID WHEAT

Hexaploid wheat *Triticum aestivum* (2n=42), is an allopolyploid containing three informationally similar genomes. It is accepted that the A genome (2n=14) was provided by a diploid wheat (*Triticum*) species and the D genome (2n=14) by *Aegilops squarrosa* but the origin of the B genome is not clear. A satellite DNA containing a highly repeated sequence with long pyrimidine tracts has been isolated from the hexaploid wheat variety Chinese Spring. It is predominantly located at defined, major sites on the B genome chromosomes and has therefore been used as a molecular probe for assaying the proposed donors of the B genome. Use of this satellite sequence also provides an insight into the evolution of the chromosomes of homoeologous group 4 in wheat.

The isolation and initial characterization of a further, complex satellite DNA containing at least 3 different sequence classes will be reported.

RUTH ROFE
Department of Genetics, University of Adelaide, Adelaide, S.A.

CHROMOSOME EVOLUTION IN MARSUPIALS

Giemsa G-banding techniques produce distinctive light and dark staining bands along the length of the mammalian chromosome. Such G-bands are useful for examining chromosome changes as the characteristic pattern of a chromosome segment appears to be conserved over long evolutionary periods, even if the position of the segment in the karyotype is changed.

Prior to the development of chromosome banding techniques Hayman and Martin proposed that in the marsupials there was an ancestral karyotype of 14 chromosomes, animals retaining complements of this basic form occurring in the extant Australian and American superfamilies of marsupials.

This paper discusses results of G-banding karyotypes from eight marsupial species, each with the hypothesized basic form complement. Among the eight species, each of the Australian superfamilies are represented and the results are used to determine whether the proposed basic form karyotype remains evident with G-banding.

Information from the results of C(centromeric)- and N(nucleolus organizer)-banding relevant to the evolution of these chromosomes is also discussed.

SESSION 2A

M.J. HYNES
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

MUTATIONS IN THE CONTROLLING REGION OF A STRUCTURAL GENE IN ASPERGILLUS NIDULANS

The synthesis of the acetamidase enzyme of *A. nidulans* is subject to regulation by multiple control circuits. Mutations adjacent to the structural gene, *amdS*, affecting regulation of enzyme synthesis have been isolated and shown to have *cis* but not *trans* effects. One of these (*amdI9*) results in increased inducibility by a metabolite of acetate. A second mutation (*amdI18*) results in elevated enzyme levels under all growth conditions. A third

mutation (*amd*I93) leads to loss of induction by the ω-amino acids, β-alanine and γ-aminobutyric acid, which has been shown to be mediated by the unlinked positive regulatory gene, *amd*R. The *amd*I93 lesion is epistatic to *amd*R constitutive regulatory mutations, and therefore apparently defines the site of action of the product of this gene. Deletion mapping of the *amd*S gene shows that the regulatory mutations map together at the centromere distal end of the gene.

JOAN M. KELLY and M.J. HYNES
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

MUTATIONS AFFECTING CARBON CATABOLITE REPRESSION IN ASPERGILLUS NIDULANS

Strong selection techniques are available in the fungus, *Aspergillus nidulans*, for the isolation of mutant strains altered in their response to carbon catabolite repression. Mutations that result in either increased or decreased sensitivity to carbon catabolite repression have been isolated.

Mutations in three separate genes, *cre*A in linkage group I, and *cre*B and *cre*C in linkage group II, result in derepressed levels of some enzymes of carbon catabolism, and altered levels, without affecting the response to carbon catabolite repression, of others. The mutant strains are hypersensitive to the toxic analogues fluoroacetamide, fluoroacetate and allyl alcohol in the presence but not in the absence, of a source of carbon catabolite repression; and the enzymes acetamidase, acetyl CoA synthase and alcohol dehydrogenase show derepressed levels, in the presence of sucrose, in the mutant strains. Isocitrate lyase shows a similar decreased sensitivity to carbon catabolite repression in the mutant strains. In addition to these effects, other enzymes have altered levels, but are not altered in their response to carbon catabolite repression, in the *cre*B and *cre*C mutant strains. The *cre*B and *cre*C mutant strains grow less well than wildtype on sole carbon sources such as quinate and lactose, and this is reflected in lowered levels of quinate dehydrogenase and β galactosidase under these conditions. These enzymes are, however, still subject to carbon catabolite repression in the mutant strains, when glucose is added. The *cre*B and *cre*C mutant strains have elevated levels of extracellular protease activity in both the presence and the absence of glucose.

Another mutation, cre-34, leads to increased sensitivity to carbon catabolite repression of the acetamidase, isocitrate lyase and acetyl CoA synthase. In the absence of a source of repression, the levels of these enzymes are similar to the wildtype in the mutant strain. The cre-34 lesion is epistatic to the *cre*A, *cre*B and *cre*C mutant alleles for its effect on these enzymes. The cre-34 lesion does not reverse the effects of the *cre*B and *cre*C mutant strains onenzymes such as quinate dehydrogenase and β galactosidase.

In heterozygous diploids, the effects of the *cre*A, *cre*B, *cre*C and cre-34 lesions are found to be recessive to the wildtype allele.

Further mutations have been isolated of a "cre type", and it appears that many loci may be involved, either directly or indirectly, in the catabolite repression mechanism.

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

GENETICS OF THE COTYLEDONARY STORAGE PROTEINS IN PISUM SATIVUM

Each of the two main storage protein fractions of peas, legumin and vicilin, is a complex assemblage of holoproteins. The legumin and vicilin fractions each have an apparently non-overlapping range of subunits of very diverse

molecular weights. Diversity within legumin and vicilin arises largely from quantitative differences in subunit composition. The predominant classes of holoprotein are here shown to be genotype specific and qualitatively additive in crosses between lines. In some crosses major quantitative differences between the legumin/vicilin ratios of the parental lines lead to some difficulty in detecting additivity in the fully assembled proteins of the F1 cotyledons. No evidence has been obtained for differential readout from the maternal and paternal genomes in cotyledonary tissue (contrast Davies, *Nature New Biol.* 245:30, 1973).

Variant subunit forms, differing in size and/or charge, have been identified for each of the principal subunit classes of legumin and vicilin. These are being used as markers in an attempt to define the number and kinds of genetic loci involved. The genetic data obtained so far will be discussed in relation to the synthesis, processing and structure of the storage protein molecules.

W.R. SCOWCROFT and J.D. PAGAN
CSIRO Division of Plant Industry, Canberra, A.C.T.

NITROGEN FIXATION IN D-AMINO ACID MUTANTS OF RHIZOBIA

D-amino acid resistant mutants of several *Rhizobium* species have impaired symbiotic properties. The correlation between symbiotic effectiveness and nitrogenase activity was evaluated in mutants of cowpea rhizobia, strain 32H1, resistant to D-alanine and D-norvaline. Among the large number of resistant mutants isolated, a large proportion were defective in symbiosis with *Vigna unguiculata* and/or asymbiotic nitrogen fixation. With only one exception, the symbiotically defective mutants were also deficient for nitrogenase activity in culture, but serological tests indicated that the nitrogenase protein was synthesized. Further examination of these mutants indicated that asymbiotic nitrogen fixation occurred under conditions of reduced O_2 tension in the gas phase and that the extracellular polysaccharides of these mutants may have been altered. These studies indicate a presumptive causal relationship between extracellular polysaccharides and the pleiotropic defects in nodulation and nitrogen fixation in culture.

MIRIAM FISCHER[1] and W.R. SCOWCROFT[2]
[1]Virus Research Ecology Group, R.S.B.S., Australian National University, Canberra, A.C.T.
[2]CSIRO Division of Plant Industry, Canberra, A.C.T.

CAULIFLOWER MOSAIC VIRUS - INFECTIVITY AND GENETIC VARIABILITY

Cauliflower Mosaic Virus (CaMV), a DNA virus, affecting mainly crucifers, might provide a useful system for genetic transformation in plants.

Working with 3 different strains of CaMV we have found consistent production of local lesions on seedlings of hybrid turnip - cv. Just Right - grown under controlled conditions.

Protoplasts of different species of *Brassica* have been isolated using an osmotic solution containing mannitol, sorbitol, $CaCl_2$, $CaH_4(PO_4)_2$, cellulase, driselase.

The presence of nucleases have been detected in the enzymes used in isolation of protoplasts and in plant extracts.

Different methods of inhibiting nucleases have been tried in order to obtain uptake of complete virus particles, and/or viral DNA. Simultaneously, ways of assaying uptake and multiplication of CaMV in protoplasts have been explored.

C.R. DATSON and N.G. BRINK
School of Biological Sciences, Flinders University of South Australia, Bedford Park, S.A.

THE INFLUENCE OF THE MATERNAL GENOME ON EARLY DEVELOPMENT IN DROSOPHILA

The effect of the maternal genome on early development in a number of animal species will be briefly reviewed. In *Drosophila*, several groups of workers have isolated a number of maternal effect mutants, and many of these cause severe abnormalities in embryonic development. This eventually results in death of the embryo. Some of these mutants cannot be rescued by the male genome of the zygote and are known as female sterile mutants.

Recently a temperature-sensitive female sterile mutant has been isolated in our laboratory. This mutant shows periods of temperature sensitivity during the later stages of oogenesis, during the first 9 hours of embryonic development and again during late larval/early pupal development. The mutant appears to cause a general failure in *in vitro* cell determination/cell differentiation rather than produce a specific effect on a particular type of cell determinative event.

On the basis of this investigation and studies on other mutants it is suggested that most female sterile mutants produce abnormalities in early development as a result of a general breakdown in some crucial metabolic/developmental event, rather than cause developmental arrest as a result of the failure of some particular cell type to become determined, thereby upsetting the normal developmental process.

SESSION 2B

KERRY RATHIE and FRANK NICHOLAS
Department of Animal Husbandry, University of Sydney, Sydney, N.S.W.

ARTIFICIAL SELECTION WITH DIFFERING POPULATION STRUCTURES

Using *Drosophila melanogaster*, experimental comparison was made of response to selection for a quantitative character.

i) within an Undivided, large population (treatment U)

ii) within each of 10 sublines which were reconstituted every 6th generation by Crossing after Culling the 5 lowest sublines (treatment CC)

iii) within each of 10 sublines which were reconstituted every 6th generation by Crossing after Retaining all 10 sublines (treatment CR)

The results will be interpreted in terms of:-

a) Wright's shifting balance theory of evolution.

b) The design of artificial selection programmes.

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

FURTHER STUDIES ON THE INHERITANCE OF HYBRID DYSGENESIS IN DROSOPHILA MELANOGASTER

The ability to induce male recombination, one of the manifestations of hybrid dysgenesis, has been shown to be transferable between non-homologous chromosomes, analogously to the 'contamination' phenomenon found by Picard (1976) for female sterility. This result suggests the possible existence of

a transmissible factor, such as has also been postulated by Sochacka and Woodruff (1976) who reported the ability to inject male recombination properties from one strain into another. Experiments have been carried out to try to confirm this direct transmission through injection, but have so far been negative. Another possible explanation of the 'contamination' phenomenon is in terms of induced heterochromatin changes in hybrids, such as have been demonstrated in *Nicotiana* by Gerstel *et al.* However no inter-strain differences have been demonstrable for either of the major autosomes using either Q- or C-banding.

ALAN WILTON
School of Biological Sciences, University of Sydney, Sydney, N.S.W.

A MEASURE OF HETEROSIS FOR THE X-CHROMOSOME IN DROSOPHILA MELANOGASTER

Population cage experiments by Sved and others on the fitness of whole autosome homozygotes in *Drosophila* found, that homozygotes have an average fitness relative to the wild-type heterozygotes of about .2. The results to be discussed come from a similar experiment which tested the fitness of X-chromosome homozygotes. They were found to have an average fitness relative to wild-type heterozygotes of about .6.

The heterosis observed in the autosomes could result from either over-dominant genes or deleterious recessives, but the low frequency of deleterious recessives expected on the X-chromosome makes it difficult for this latter model to explain the heterosis observed here. The overdominance model predicts from the autosomal results, that the average relative fitness of X-chromosome homozygotes will be .6 if we assume gene effects are additive and the X-chromosome is half as long as the autosomes. The more realistic assumption of multiplicative gene effects predicts an average fitness of .45. The deleterious recessives model predicts that the average fitness will be .95, although if 50% of these recessives are sex-limited, this prediction also becomes .6.

STEPHEN McKECHNIE and PHILLIP MORGAN
Department of Genetics, Monash University, Clayton, Vic.

THE ALCOHOL DEHYDROGENASE POLYMORPHISM IN DROSOPHILA MELANOGASTER: *SPATIAL HETEROGENEITY OF ENVIRONMENTAL SUBSTRATES*

To better understand the nature of the forces that maintain the alcohol dehydrogenase (*Adh*) polymorphism in *D. melanogaster* we need a greater understanding of the ecology of this organism. Using gas liquid chromatography we have analysed some natural habitats (rotting fruits) of this species and determined the qualitative and quantitative nature of the short-chain alcohols present. *Ethanol* concentrations ranged from 0.25-4.0%; *n-propanol*, 0.02-1.0%; *n-butanol*, 0-0.2%; *iso-propanol*, 0-0.8%; *methanol*, 0-0.06%. Other alcohols were detected but generally at much lower concentrations.

To test for possible selective effects of such alcohol mixtures at the *Adh* locus we have examined larval to adult survival levels under competitive conditions (low yeast levels) on media supplemented with various alcohol mixtures. Three alcohol conditions were chosen: (1) Rotting apple (total alcohol concentration, 0.13%), (2) Grape pile (total concentration, 3.1%), (3) A control medium with no added alcohol. Since temperature is known to influence gene frequencies at this locus we have performed those tests at both high and low temperatures. The results were analysed by multiway contingency χ^2 tests. Our results show that natural levels of alcohol do produce significant changes in gene frequency at this locus. On both alcohol supplemented media the frequency of the F allele decreased at the high temp-

erature, an effect not detected on the control medium.

Results such as these suggest that environmental variation in temperature and alcohol levels may be important selective parameters that influence this polymorphism in nature.

JAY HETZEL and FRANK NICHOLAS
Department of Animal Husbandry, University of Sydney, Sydney, N.S.W.

GENOTYPE - ENVIRONMENT INTERACTION FOR GROWTH IN MICE

Results are reported from two selection lines of mice, where both lines were selected for post-weaning weight gain between 3 and 6 weeks of age, but with one line (SF) being fed *ad libitum* during this period, and the other (SR) fed a restricted amount, (approximately 85% of *ad libitum* food intake). After four generations of selection, the performance of each line was assessed on each feeding level. On restricted feeding, SR had a higher weight gain than SF. However, while this was due to an increased 6 week weight for SF, the improved weight gain for SR was due largely to a decreased 3 week weight.

On *ad libitum*, SF had a higher weight gain than SR. SF ate nearly 5% more food while SR ate 10% less food than controls. Body composition data failed to show any significant differences between the lines on each feeding level at 3 or 6 weeks of age.

Thus, while selection has been supposedly for the same character, on the two feeding levels, selection pressure has been on different component characters, i.e. mainly on 3 week weight with restricted feeding and food intake with *ad libitum* feeding.

These results will be discussed in relation to the genetic correlation between the same character in two environments and the interpretation of genotype - environment interactions.

B.J. McGUIRK
N.S.W. Department of Agriculture, c/- CSIRO Genetics Research Laboratories, Epping, N.S.W.

RESPONSE TO SELECTION FOR FLEECE WEIGHT IN MERINO SHEEP

Selection has been practised for eight generations (23 years) for both increased (Fleece Plus) and reduced (Fleece Minus) hogget clean fleece weight, both derived from the same base flock of medium-wool Merinos. Average annual selection differentials achieved were 0.40 kg/year in the Fleece Plus flock, and 0.45 kg/year in the Fleece Minus.

The heritability of fleece weight in the base population was estimated as 0.40. Steady response has been achieved to selection for reduced fleece weights. When measured as deviations from a randomly selected control flock, realised heritability was estimated as 0.51, 0.47 and 0.39 after 1, 4 and 6 generations of selection.

Initial rates of response in the Fleece Plus flock have not been maintained. Current rates of progress are slow and, depending on seasonal conditions, erratic. Realised heritability after six generations of selection was 0.31.

GUEST LECTURE

DR D.L. HAYMAN
Department of Genetics, University of Adelaide, Adelaide, S.A.

CYTOGENETIC STUDIES OF MARSUPIALS

An outline will be given of chromosome evolution in the marsupials and the problems raised by our present knowledge. The evidence justifying a conservative approach will be considered with respect to the chromosome complement as a whole and the sex-chromosomes in particular.

SESSION 3A

ELIZABETH DENNIS, PAMELA DUNSMUIR[1] and W.J. PEACOCK
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FINE STRUCTURE OF THE 1.708 SATELLITE DNA OF THE RED-NECKED WALLABY MACROPUS RUFOGRISEUS

A highly repeated DNA comprising approximately 20% of the total DNA of *M. rufogriseus* has been isolated as a satellite in actinomycin D-CsCl density gradients (Dunsmuir, 1976). This satellite is homogeneous when judged by CsCl density gradients, thermal denaturation profile or reassociation kinetics. Cytological hybridization shows that this satellite DNA is present in the centric heterochromatin of all the autosomes although with minor quantitative differences between chromosomes. This apparently homogeneous satellite is heterogeneous when analysed by restriction endonucleases which recognise specific six, five or four base pair sequences. Two enzymes Bam and Pst cleave all the satellite DNA into a series of fragments of 2500 (monomer) 5000 (dimer) 7500 (trimer) base pairs. Other enzymes Hind III, Xma, Eco R1, Hae II, Hha I cleave only portion of the DNA indicating that various sub-populations of the DNA exist. We have obtained evidence that the various subpopulations of the satellite are not arranged randomly but are clustered in segments on DNA molecules. The different populations of satellite DNA could be arranged on different chromosomes resulting in chromosome specific arrangement of DNA which could be used for homologous chromosome recognition.

Dunsmuir, P. (1976) Satellite DNA in the kangaroo *Macropus rufogriseus*. Chromosoma 56 111-125.

LEE VENOLIA
Department of Genetics, R.S.B.S., Australian National University and CSIRO Division of Plant Industry, Canberra, A.C.T.

*SATELLITE DNA IN THE WALLAROO (*MACROPUS ROBUSTUS ROBUSTUS*) AND ITS USE AS A PROBE IN KANGAROO PHYLOGENY*

DNA isolated from wallaroo liver was fractionated in neutral CsCl gradients to yield a satellite at a buoyant density of 1.709 g/cc, compared to a density of 1.696 g/cc for main band DNA. The satellite which comprises 8-10% of the total DNA, can be most effectively isolated on a large scale from Ag^+-Cs_2SO_4 gradients. ^{3}HcRNA was synthesized from highly purified satellite DNA using *E. coli* RNA polymerase. It was determined that the ^{3}HcRNA sequences are present only in the satellite fraction of the DNA, by hybridizing the cRNA across a fractionated Ag^+-Cs_2SO_4 gradient. Using *Drosophila* DNA as a standard, the satellite cRNA was hybridized to total wallaroo DNA and its subsequent melting temperature determined as 52.3°C in 3 x SSC-50% formamide. The satellite cRNA was also hybridized and melted from DNAs of a number of macropods and related marsupials. No Tm depression was found for

closely related species or sub-species, while the phylogenetically more distant macropods showed a non-specific Tm depression of 3-5°C. However, the percent of the cRNA binding to each marsupial DNA as compared to the binding to wallaroo, does appear proportional to phylogenetic relatedness. The ^{3}HcRNA was also hybridized to cytological preparations of various kangaroos using the *in situ* hybridization technique. The satellite gives a distinctive pattern of grain distribution at the centromeric regions of wallaroo chromosomes. This pattern is largely duplicated in closely related kangaroos, but there are indications of species specific patterns.

G.L.G. MIKLOS[1], P.R. BAVERSTOCK[2], C.H.S. WATTS[2], M. GELDER[2], R. WARNOCK[1] and M. YAMAMOTO[1]
[1]Department of Population Biology, R.S.B.S., Australian National University, Canberra, A.C.T.
[2]Institute of Medical & Veterinary Science, Adelaide, S.A.

STUDIES ON SATELLITE DNA FUNCTION

The major problem associated with unravelling the functions of satellite DNA in eukaryotes has been the lack of direct experimentation on chromosomes which have deletions of, or additions to, the normal satellite complement.

We have used two complementary approaches to studying function. One involves natural populations of specific rodents and grasshoppers which yield a rich and varied source of natural "mutants" of heterochromatin. Another utilises the experimental manipulation of heterochromatin in *Drosophila melanogaster*. The organisms are as follows: a) *Uromys caudimaculatus* (giant white tailed rat). This species occurs naturally with populations having either extra interstitial or telomeric C-bands or a varying number of C-banded supernumerary chromosomes. It provides a "window" for examining DNA variation within the same species, when that DNA variation concerns additions to particular existing chromosomes, or as extra chromosomes. b) *Notomys* species. The four species examined exhibit a large variation in C-banded centromeric heterochromatin, an equivalent variation in satellite DNA content and variation in chiasma frequency in male meiosis. This group provides the potential of examining changes in satellite DNA amount, but little (if any) change in DNA type. c) *Drosophila melanogaster*. The male and female of this organism allows one to specifically test a number of the postulated hypotheses for satellite DNA function - for example, the idea that the specific arrangement of satellites on a chromosome plays a major role in meiotic pairing for segregation.

We find from this integrated approach that it is the meiotic recombination system which is perturbed as the heterochromatin is altered in quantity or position. These systems together reinforce the conclusion that satellite DNA, and possibly heterochromatin deficient in satellite DNA, plays a major role in the meiotic recombination system, a role which can lead to adaptation of populations to their respective environments. Neither the *Drosophila*, rodent or grasshopper findings support a major role for satellite DNA in the more popular hypotheses such as "homologue recognition".

References: Miklos, G.L.G. and Nankivell, R.N. Chromosoma 56, 143-167 (1976). Baverstock, P.R., Watts, C.H.S., and Hogarth, J.T. Chromosoma 57, 397-403 (1976). Yamamoto, M. and Miklos, G.L.G. Chromosoma 60, 283-296 (1977).

JUDITH HELEN FORD
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CYTOGENETICS OF HUMAN MALE INFERTILITY

Male partners of childless couples attending an infertility clinic were unselectively referred to our laboratory for cytogenetic analysis. Conventional giemsa banding and centromeric banding analyses were carried out on peripheral blood cultures. All abnormalities and variants were noted. Testicular biopsy was not performed so meiotic studies were not possible.

Patients were then sorted into 4 groups according to their fertility index: 33 were considered fertile (F.I. = 0-1), 18 had doubtful semen (F.I.= 2-4), 19 had pathological semen (F.I. = 5-9) and 79 had severely pathological semen (F.I. = 10). The patients' histories, endocrinological and cytogenetical results were analysed with respect to their fertility indices.

Eighteen sex chromosome abnormalities were found (13 were 47,XXY) and all were associated with severely pathological semen. Six autosomal abnormalities were found, 4 had severely pathological sperm, 1 mosaic had doubtful sperm and 1 mosaic was fertile.

Heterochromatic variants were recorded in 97 patients, 4 of whom were fertile and 93 sub-fertile. Of these variants, only those affecting the number nine chromosome were significantly increased in the sub-fertile group and the frequency of these was highly correlated with the degree of pathology.

The significance of these findings in the aetiology of sub-fertility will be discussed.

GRANT R. SUTHERLAND
Cytogenetics Unit, Department of Histopathology, Adelaide Children's Hospital, North Adelaide, S.A.

FRAGILE SITES ON HUMAN CHROMOSOMES

Heritable fragile sites have been described on a number of human chromosomes. These include chromosomes 2, 9, 10, 11, 12, 16, 17 and 20. A similar site on the X chromosome at band q27 or 28 is associated with a form of X-linked mental retardation. The frequency of observation of lesions at these sites has been found to vary according to the type of culture medium in which the lymphocytes used for chromosome study are grown. Lesions at the sites are seen most frequently when the lymphocytes are cultured in medium 199 and Eagle's MEM but are only rarely seen when the following media are used: RPMI 1640, Ham's F10, Eagle's basal, CMRL 1969. Lesions at the fragile site are not detected in fibroblast-like cells cultivated from skin biopsies regardless of the type of culture medium in which they are grown. Work on the fragile sites in lymphocytes will be presented. It has been found that the addition of either folic acid or thymidine to medium 199 and Eagle's MEM cause the lesions to disappear. The addition of the folic acid antagonist methotrexate to Ham's F10 causes the lesions to appear. The significance of these findings with relation to chromosome structure and clinical diagnosis will be discussed.

SESSION 3B

IAN R. BOCK
Department of Genetics and Human Variation, La Trobe University, Bundoora, Vic.

DEGREES OF SEXUAL ISOLATION AMONGST FOUR DROSOPHILA *SPECIES*

Drosophila bipectinata, D. parabipectinata, D. malerkotliana and *D. pseudoananassae* are four members of the *melanogaster* species group occurring in south-east Asia; *bipectinata* and *pseudoananassae* also occur in New Guinea and Australia. Morphologically the species are very similar, and comprise the "*bipectinata* species complex". Females of the four species are virtually indistinguishable, but males may be distinguished by the structures of the sex-combs and the abdominal coloration. Interspecific crosses may be effected within the complex in all six pairwise combinations although there is no evidence of hybridization in nature. The most easily obtained cross is *bipectinata* X *parabipectinata*, which yields larvae showing complete synapsis of maternal and paternal polytene chromosome complements and an F_1 with equal numbers of sterile males and fertile females; the F_1 male testes are of normal size but the spermatozoa are immotile. The most difficult cross is *malerkotliana* X *pseudoananassae* which yields larvae showing extensive asynapsis of the polytene chromosome complements and very few F_1 females only. Amongst the remaining four crosses results intermediate between these extremes are obtained. Analysis of the hybrid polytene chromosomes together with the results of the interspecific crosses permits some inferences to be drawn regarding the relative degrees of phylogenetic separation of the four species.

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[2]Department of Biological Sciences, University of Newcastle, Shortlands, N.S.W.

HYBRID STERILITY IN DROSOPHILA MELANOGASTER

A new type of hybrid sterility was investigated in *D. melanogaster*. Crosses between strain 27 ♂♂ from Para Wirra, South Australia, and Canton S ♀♀ result in sterile ♂ and ♀ progeny. The phenomenon is curable by cold shock of the parents and larvae. Heat shock and antibiotics produce no observable effects. The sterility is transmissible by injection and ingestion of homogenates from affected flies. The hybrid sterility was also demonstrated with three other geographic strains but the degree of sterility varied between strains. Further studies have shown that the sterility is characteristic of the Para Wirra population. Models are proposed to explain the maintenance of a postulated sterility substance in the cytoplasm.

G.R. MURRAY
School of Biological Sciences, University of Sydney, Sydney, N.S.W.

POSSIBLE PHEROMONAL EFFECTS ON EGG-LAYING IN DROSOPHILA

A description of a series of experiments designed to determine if there is any olfactory effect of a large number of flies on the fecundity of flies physically separated from them.

A number of stocks of *D. melanogaster* and *D. simulans* were studied.

Results are not clear-cut, but generally indicate that egg-laying was increased by the olfactory presence of other flies.

Attempts were also made to select for positive and negative response of fecundity to olfactory presence.

JANICE McDONALD
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GENETIC CONTROL OF THE COURTSHIP DISPLAY OF DROSOPHILA MELANOGASTER

The genetic control of the stereotyped courtship display of *D. melanogaster* was investigated in lines selected over 40 generations for and against the wing vibration component of the display. Of the two lines selected for increased percentage wing vibration only one responded. However both lines selected for decreased percentage wing vibration responded to selection. The realized heritability of percentage wing vibration was estimated from the first ten generations of selection to be 0.1074 for one line and 0.1956 for the other. Biometrical analysis of parent, hybrid and backcross generations was carried out using extreme selected lines. The generation means were entirely consistent with an additive gene effects model. No directional dominance was found, although ambi-directional dominance may have been present. The absence of directional dominance was unexpected on the basis of theories of 'genetic architecture' which predict some dominance of gene loci for traits associated with 'fitness'.

The orientation, scissoring, licking and attempted copulation components of the courtship display were analysed in the selected lines. Orientation was unaffected by selection. The other three components changed in the same direction as wing vibration, indicating that these components are linked to wing vibration. Selection may have acted on variability in the performance threshold of these linked components.

B.L. SHELDON and M.K. EVANS
CSIRO Genetics Research Laboratories, Epping, N.S.W.

CHROMOSOMAL AND LETHAL ANALYSIS OF SCUTELLAR BRISTLE SELECTION LINES IN DROSOPHILA

Eight selection lines have mean scutellar bristle numbers in females of about 7, 11, 13, 15, 22, 9, 12, 20. The first five of these (Group 1) trace back through different histories to the same original selected Oregon RC female with 5 bristles mated to an Oregon RC male with the normal 4 bristles. The other three lines (Group 2) are independent high mass selection derivatives of Oregon RC. The pattern, as well as the size, of the long term response will be shown to be very variable between lines. Large increases in response following long periods of little or no response occur in several of the lines, particularly the two highest. The nature of the rare "mutational" or "recombinational" events responsible for this is of particular interest.

There are intriguing similarities between lines, both within and across Groups, in the results of chromosome analysis, such as the absence of a simple chromosome I effect, and a tendency for the chromosome II effect to be larger than the chromosome III effect, when taken as isolated effects. However, the most outstanding feature is the prevalence of chromosome interaction effects, sometimes very large. Interactions are mainly I x II and II x III, but include some small and one very large I x II x III effect. The lethal analyses show even more specific similarities. The four main (highest) lines in Group 1 and the highest line in Group 2 all carry the same two lethal 2nd chromosomes at virtually maximum frequency in a balanced lethal situation. This phenomenon cannot be related simply to their presence in the common Oregon RC base population and the relaxed selection line from which three of the Group 1 lines were derived, since they were not detected in those two populations. However, they have occurred, but only briefly, in the latest re-selection line derived from the relaxed line (i.e. the lowest line in Group 1). These results and those of other selection experiments tend to support the notion that some of the "events" leading to accelerated responses, occurrence of lethals, etc., are

a function of both a specific potentiality in the base population genotype and the nature of the background genotype or level of phenotype developed by selection.

SESSION 4A

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

THE HIGHLY REPEATED DNA SEQUENCES NEAR RIBOSOMAL GENES OF DROSOPHILA MELANOGASTER

Three satellite DNA species of density 1.686 g/cc, 1.688 g/cc and 1.697 g/cc are located near the ribosomal genes on both the X and Y chromosomes. *In situ* hybridization of cRNA complementary to these satellites showed them all to be localized in the nucleoli of polytene nuclei from normal female flies and males carrying the sc^{4} sc^{8} chromosome. Thus on both the X and Y chromosomes these satellite sequences are sufficiently close to the ribosomal genes to be drawn out into the nucleolus. Buoyant density analysis was used to determine which of the satellites was more closely linked to ribosomal genes by assaying DNA-RNA hybrids formed in the presence of excess rRNA (and thus have a greater density than DNA-DNA hybrids) for the respective sequences. Only the 1.697 g/cc satellite had sequences intimately associated with the ribosomal genes. The relationship of simple, repeated sequences in the 1.697 g/cc satellite to ribosomal genes is being further defined using cloned fragments of various parts of the ribosomal gene/spacer system. These experiments are being carried out in collaboration with Dr D. Glover (Imperial College, London) and suggest that untranscribed spacer is the location of 1.697 g/cc satellite sequences.

A.R. LOHE
CSIRO Division of Plant Industry and Department of Genetics, R.S.B.S, Australian National University, Canberra, A.C.T.

EVOLUTIONARY STABILITY OF HIGHLY REPEATED DNA LOCATIONS IN THE HETEROCHROMATIN OF DROSOPHILA

The highly repeated DNAs in the sibling species *D. simulans* and *D. melanogaster* were compared. Almost all of the highly repeated DNAs, as detected by optical techniques, are different in these two species, confirming other reports of species specificity in satellite DNA arrays. However, the sequences of four *D. simulans* highly repeated DNAs were detected in *D. melanogaster* DNA by filter hybridization, although two of the sequences were present in a greatly reduced amount. A comparison of the thermal dissociation profiles of homologous and heterologous cRNA-DNA molecules indicated that for all four highly repeated DNAs, the sequences in the sibling species are identical. The major event in evolution has been modulation in the number of repeats of the basic sequence; the sequence itself has been rigidly conserved.

The chromosomal locations of the four highly repeated DNAs were mapped in mitotic chromosomes of *D. simulans* and *D. melanogaster* by *in situ* hybridization. Many of the locations are in corresponding positions in the heterochromatin of the two species' chromosomes, suggesting that the chromosomal sites of highly repeated sequences are also conserved during evolution.

The data show that when a highly repeated sequence undergoes a modulation event, this occurs at many sites located on different chromosomes. The direction of modulation at the different sites is not independent, but appears to

be coordinated; for example, the amount of 1.707 sequence has been reduced in *D. simulans* (or increased in *D. melanogaster*) at eight of the nine chromosomal locations. All the highly repeated DNAs are present on the Y chromosomes of both species, and for two sequences at least, the degree of modulation of Y-chromosome sites is not as marked as in most autosomal sites.

M. YAMAMOTO
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STUDIES ON THE FUNCTIONS OF HETEROCHROMATIN IN DROSOPHILA MELANOGASTER

There is an extremely large literature on the biochemical properties of satellite DNA, as well as many speculations on its functions. However, of the various postulates, such as chromosome pairing, housekeeping roles, centromere strengths, speciation, "bodyguard hypothesis", recombination etc... few have been tested or indeed testable in their present form.

One direct approach is to examine chromosomes which have additions or deletions of their heterochromatin, and this is most satisfactorily attempted in *Drosophila melanogaster*, where the heterochromatin is known to consist almost exclusively of specific satellite sequences.

In the first group of experiments, I have utilized a series of X chromosomes with identical euchromatic contents but having varying sized deletions of the basal heterochromatin (in one case 80 per cent of the heterochromatin has been deleted). It is found that in females homozygous for these satellite DNA deletions, chromosome segregation at meiosis is normal. However, the amount of recombination decreases as the X becomes more and more deleted in its heterochromatin. These results strongly implicate satellite DNA as having a function in the female meiotic recombination system. They also place limits on the amount of satellite DNA which can be eliminated from homologous chromosomes and yet still allow for example, chromocentral formation, and reasonable nuclear integrity.

In the second series of experiments, utilizing *Drosophila* males, I have tested the hypothesis that centromeric satellite DNA is an absolute prerequisite for homologue recognition. This has been done by constructing males carrying two extra mini heterochromatic chromosomes (of either autosomal or sex chromosomal origin) so that they are of the form 2/2 3/3 4/4 x/y mini/mini.

Cytological and genetical analyses show that the mini chromosomes (consisting almost entirely of just a centromere and associated heterochromatin) segregate at random from each other.

The results from both males and females together indicate that a substantial proportion of the sex chromosomal and autosomal heterochromatin is not absolutely necessary for certain meiotic processes such as homologue recognition.

Reference: Yamamoto, M. and Miklos, G.L.G. Chromosoma 60, 283-296 (1977).

K. KONGSUWAN
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DNA LOSS DURING C-BANDING OF LILIUM *CHROMOSOMES*

The underlying molecular basis of C-banding is not completely understood. One current hypothesis is that preferential loss of DNA occurs from the non-C-banded regions during pretreatment. The DNA remaining at the heterochromatic regions is thus thought to be responsible for the dark staining of C-bands.

This is supported by both biochemical and autoradiographic studies on mammalian chromosomes.

Using quantitative autoradiography, we have attempted to test this hypothesis in root-tip chromosomes of *Lilium longiflorum*. The chromosomes were uniformly labelled with tritiated thymidine. Some were then treated for C-banding using hot saline-citrate (2 x SSC) and others used as untreated controls. Comparisons in grain numbers between untreated and C-banded chromosomes showed that the SSC treatment removed approximately 50% of the chromosomal DNA. As far as grain distribution along chromosomes is concerned, both the controls and those with C-bands show a relatively uniform pattern. Thus the DNA seems to be removed at random, with as many grains lost in proportion from the dark C-bands as the remaining pale euchromatin. Hence we conclude that, in *Lilium* at least, dark C-bands are not dark because of their relatively high content of DNA.

SESSION 4B

JON MARTIN, B.T.O. LEE, R. ANANTHAKRISHNAN and E. HARTS
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FURTHER DATA ON THE SPECIATION IN CHIRONOMUS OPPOSITUS

Previous studies have shown the existence of two cytologically distinct forms of *Chironomus oppositus* in certain Tasmanian populations, notably at Bellerive. These forms have been designated as the E_1- and E_2-types.

Work on these forms, and their relationship to other populations of *Ch. oppositus*, has proceeded along these lines of approach (cytological, biochemical and biometrical) to determine the extent to which each has been involved in the speciation process.

Data will be presented from other localities relating to the distribution of the forms; preliminary biochemical data will be discussed; and the results of breeding experiments considered. These data support the distinctness of the E_1- and E_2-types as well as suggesting the existence of at least two or three other differentiated forms in parts of the species range.

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CHROMOSOMAL POLYMORPHISM, RACIAL PARAPATRY AND INTROGRESSION IN CALEDIA CAPTIVA *(ORTHOPTERA:ACRIDINAE) IN SOUTH-EAST QUEENSLAND*

Two parapatrically distributed chromosomal races of *Caledia captiva* occur in south-east Queensland. The "Torresian race" is widely distributed from southern Papua, through Arnhem Land and Cape York Peninsula as far south as Ipswich. It is characterized by a completely acro- and telocentric chromosome complement. The "Moreton race" on the other hand has a more restricted distribution in the coastal region from about Maryborough and Fraser Island in the north, extending southwards into Northern N.S.W. Submetacentric and metacentric morphs of almost all the chromosomes exist in this race, although in parts of its distribution it is highly polymorphic, with acrocentric and telocentric chromosomal forms as well. The distribution and frequency of the alternative chromosomal morphs in the "Moreton race" have been mapped. These suggest that chromosome introgression is occurring across the contact zone from the "Torresian race" into the "Moreton race" but apparently not reciprocally.

The zone of contact between these races is at least 100 km long and in four areas has been shown to be no more than 1 km wide. At one point, a 200 metre interval transect has been taken across the tension zone. This revealed that most of the changeover between the races occurred in a 200 metre interval and that the changeover was complete over 1 km. Further, it showed that hybridization between the races is apparently occurring freely in the contact zone, although the zone is of very restricted width.

The pattern of seasonal moisture regime appears to be an important factor determining the equilibrium position of the contact zone between the races. From a map of the annual coefficient of variation around the mean weekly moisture index for this region (provided by Henry Nix, CSIRO Land Use Research), it can be seen that the iso line of 30% variation coincides within the limits of precision of both lines with the present day position of the tension zone.

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ELECTROPHORETIC VARIATION AND SIBLING SPECIES RELATIONSHIPS IN MEAT ANTS (IRIDOMYRMEX PURPUREUS)

The *Iridomyrmex purpureus* group now consists of 8 recognizable colour morphs, which vary in geographic distribution, nest architecture, and some aspects of ecology and behaviour. Continued study of the *Amy* and *Es-1* loci has confirmed that some of these colour forms are reproductively isolated in areas where they are sympatric, suggesting that they are actually sibling species. Populations of 5 colour forms have been surveyed for electrophoretic variation at 15 enzyme and protein loci, and genetic distances calculated. The result confirms what seems to be a basic distinction within the group between forms which build large compound nests and those which do not. Genetic distances between forms are unusually low for separate species, consistent with their close morphological resemblance. Superimposed on the differences between forms is a degree of variation within forms, which obscures between-form differences in some cases.

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SIBLING SPECIATION IN THE BLACKFLY SIMULIUM ORNATIPES

Fixed inversions, unique sex chromosomes and different spectra of floating inversions clearly define two sibling species within the morphospecies *Simulium ornatipes*. These have been designated as *S. ornatipes* A and B. Detailed analysis of chromosomal polymorphisms within *S. ornatipes* A reveal a widespread and consistent pattern of inversion association and deficiency of expected heterozygote genotypes in populations from central and south-east Australia. It is possible to sort these populations into two groups using linkage relationships among the polymorphisms studied. This results in both groups having essentially random inversion association and balanced genotype frequencies. This suggests that a third sibling species is present in these populations. This sibling species is homosequential having no fixed differences between it and *S. ornatipes* A.

SESSION 4C

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CONTROL OF PTERIDINE EYE PIGMENT SYNTHESIS IN D. MELANOGASTER:
EYE COLOUR MUTANTS WITH ALTERED LEVELS OF THE FIRST ENZYME OF THE PATHWAY

The eye colour of wild type *Drosophila melanogaster* is due to the presence of a brown pigment, xanthommatin, and three red pigments, called drosopterins. The drosopterins are formed by the condensation of two molecules of dihydroneopterin triphosphate. The formation of this compound from GTP is catalysed by GTP cyclohydrolase, and represents the first unique step of pteridine biosynthesis. Dihydroneopterin triphosphate is also converted to sepiapterin and isoxanthopterin, and thus represents an important branch point in the pathways of pteridine biosynthesis.

The appearance of GTP cyclohydrolase activity is found to be under strict developmental control. There is a sharp peak of enzyme activity in the body tissues at the time of pupariation, and another much larger peak at the time of emergence. The adult activity is located mainly in the head region, and is associated with the appearance of drosopterin in the eyes. Partially purified enzyme preparations are currently being used to determine whether the pupal and adult enzymes are the same. Studies are also being carried out to determine whether the two observed peaks of activity are due to the *de novo* synthesis of the enzyme.

There are approximately thirty different eye colour mutants in which the level of drosopterins is reduced relative to wild type. Of a number of mutants tested, three were found to show an altered pattern of GTP cyclohydrolase activity during development. The mutants *raspberry* and *prune* have a decreased GTP cyclohydrolase activity relative to wild type at emergence, and a markedly increased activity at pupariation. Several lines of evidence, including experiments using segmental aneuploids for the X chromosome, suggest that neither locus is the structural gene for GTP cyclohydrolase. A third mutant, *rosy* was found to show reduced GTP cyclohydrolase activity at emergence. The *rosy* locus is the structural gene for the enzyme xanthine dehydrogenase, which catalyses two reactions - pterin to isoxanthopterin, and hypoxanthine to xanthine to uric acid.

A series of experiments will be carried out to determine whether mutations at the three loci affect the production of the GTP cyclohydrolase protein. If so, the GTP cyclohydrolase system may provide an interesting example of coordinated control at the gene level.

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EFFECTS OF U.V. IRRADIATION OF POULTRY SPERM
(i) FERTILITY, HATCHABILITY AND EGG PRODUCTION TRAITS

Results of dose response experiments will be presented on the basis of which a mutation selection experiment has been done. The U.V. dose used causes a reduction of about 33% in fertility and up to 50% in hatchability of fertile eggs compared with controls. The lower hatchability, mostly due to death of very early embryos, is interpreted as being at least partly genetic, due to the mutagenic action of the U.V. Two generations of U.V. treatment, before selection for egg production began, resulted in about 5% lower egg production than the control line. During five generations of selection for egg production, together with U.V. treatment of sperm of

selected cocks, the level of egg production did not reach or exceed that of the control line. The adult mortality of the selection line was 25-50% above the control. Chicken rearing mortality also exceeded the control slightly, though the level of fertility and hatchability in eggs from unirradiated sperm did not deteriorate. Present work with the selection line is aimed at further assessing and removing the load of deleterious mutations affecting egg production and mortality, and attempting to detect the presence of favourable mutations. Problems of design and interpretation in these areas will be discussed.

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EFFECTS OF U.V. IRRADIATION OF POULTRY SPERM
(ii) CHROMOSOME STUDY

The cytological effect of U.V. irradiation of poultry sperm on early embryonic development was investigated in the U.V. selection and control lines referred to in the abstract of Sheldon and Bobr. The U.V. treatment of sperm caused the expected marked decrease in fertility, together with a large increase in mortality of embryos less than 24 hours old in both lines. The percentage of later dead embryos (24 hrs up to 64 hrs) did not differ between lines or between treatments (irradiated versus unirradiated). Chromosome preparations were made of all dead embryos and phenotypically abnormal live embryos up to 64 hours, and a sample of normal live 64 hour embryos from each line. All dead embryos less than 24 hours old, 67% of later dead embryos and 43% of the phenotypically abnormal live embryos contained aberrant chromosomes, compared with only 2% (1 in 50) of the normal 64-hour embryos. The types and frequencies of abnormalities were: haploid and haploid-euploid mosaics, including aneuploidy, 81%; polyploid-diploid mosaics, including aneuploidy, 10%; aneuploids, 2%; and aneuploid-diploid mosaics 7%. There was a greater frequency of aneuploids and aneuploid-mosaics in the less than 24 hour deads. A higher frequency of aberrant chromosomes among later dead embryos was found in the selection line than in the control (with or without U.V.), and the selection line without U.V. had the highest frequency of phenotypically abnormal live embryos at 64 hours. Sperm from some sires were more susceptible to damage from the U.V. treatment than other sires. There was a slight decrease in sperm motility after U.V. irradiation in both lines. It is concluded that the increased frequency of chromosome abnormalities was the result of U.V. treatment of sperm.

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SOME PROBLEMS IN PARASITE RESISTANCE GENETICS

Interest in the genetics of parasite resistance in sheep has heightened in recent years due to the sharply rising costs associated with chemical control and production losses and because of the advent of strains of parasite with varying degrees of resistance to the chemicals normally used in their control.

The present management environment which protects the host population from the pathogenic effects of the parasite prevents useful adaptive genetic change by the host and encourages inconvenient genetic change in the parasite.

The difficulties of measurement of parasite resistance are described and estimates of genetic variation between and within breeds for several different

measures are presented. Evidence for genetic variation in parasite populations is summarized and possible responses of the parasite to genetic changes in the host are discussed.

A simple sheep selection programme compatible with maintaining production standards is outlined and some ideas on the requirements and direction of future research are presented.

SESSION 5A

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RESTRICTION MAP OF COLIPHAGES P_2 AND 186

The coliphages P_2 and 186 are of interest to us in our studies of prophage induction and control of genetic expression. The two phages are related and can recombine to give P_2.186 hybrid phage. P_2 and 186 DNAs, when digested with a restriction enzyme, each give a characteristic size pattern of fragments on agarose gels, and when these patterns are compared with those generated by digestion of the DNA of P_2.186 hybrids, we can, in general, order the fragments, and so deduce the physical positions along the DNA at which the restriction enzyme acts. In this way we have determined the restriction maps of P_2 and 186 for the *Eco*R1, *Hin*dIII, *Bgl*II, *Bam*H1, *Sal*1 and *Pst*1 restriction enzymes and related the restriction sites to the genetic map by marker rescue from cloned fragments.

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SUPPRESSIBLE TRANSFER DEFICIENT MUTANTS OF A PSEUDOMONAS AERUGINOSA *R PLASMID*

R (drug-resistance) plasmids isolated from strains of *Pseudomonas aeruginosa* exhibit either a narrow host range (i.e. conjugally transferable only within *Pseudomonas* species) or broad host range (i.e. transferable to genetically unrelated bacteria such as *E. coli*). We are interested in determining the genetic basis of transfer by these plasmids, with the ultimate aim of defining the genetic basis of host range. Our prototypes are R91-5, a narrow host range R plasmid, and R18, a wide host range R plasmid.

R91-5 (Inc P-10) is derepressed for conjugal transferability (100% transfer/donor cell) and is Dps^+ (sensitive to the donor-specific phages PRD1, PR3 and PR4), $Phi(Gl01)^+$ (inhibits the replication of phage Gl01), and Eex^+ (exhibits entry exclusion). Dps^+ and $Phi(Gl01)^+$ are also shared by R18, the $Phi(Gl01)^+$ phenotype being a unique property of P-1 incompatibility group plasmids such as R18. However, despite the relatedness of R18 and R91-5 in terms of properties with respect to transfer, there are differences, with perhaps the most important being the unique Dps of R18 to phages PRR1 and Pf3, and a distinct Eex.

Transfer-deficient (Tra^-) mutants of R91-5 were isolated and characterized with the intention of using complementation tests to identify Tra cistrons. Tra^- mutants of R91-5 (transfer frequency $<10^{-8}$/donor cell) have been isolated via spontaneous resistance to donor-specific phage or directly following mutagenesis. Characterization of such mutants yields various phenotypic classes, e.g. $Dps^{+/-}$; $Phi(Gl01)^{+/-}$ and $Eex^{+/-}$. An important difference between the transfer systems of R18 and R91-5 has been the demonstration of a lack of correlation between Phi(Gl01) and Eex of Tra^- mutants of R91-5, which is in contrast

to that with R18.

For the purposes of complementation tests, we have screened R91-5 Tra^- mutants for suppressible mutations. Such mutants were identified by the use of three suppressors: *sup-1*, an informational suppressor, *supB*, an amber suppressor, and *sup-2*, perhaps also an amber suppressor since it was isolated in a manner similar to *supB*. Each mutant was transduced into isogenic su^+ and su^- hosts, and subsequent transfer to an R^- was tested. The majority of R91-5 Tra^- mutants detected as suppressible could be categorized as inefficiently suppressed (<100x↑ transfer frequency). However, of 12 mutants determined to be efficiently suppressed, transfer frequencies from su^+ hosts ranged from 10^{-3}-10^{-4}/donor cell compared to $<10^{-8}$ from su^- hosts.

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ANALYSIS OF HIGH PETITE FREQUENCY MUTANTS IN THE YEAST SACCHAROMYCES CEREVISIAE

In the yeast *Saccharomyces cerevisiae* the *petite* mutation is cytoplasmically inherited and results in loss of respiratory competence. Suitable spontaneous *petites* have been crossed and shown to give rise to respiratory competent diploids. It has been observed that some of these diploids form abnormal sectored colonies on selective medium, suggesting that *petites* arise from these strains at a higher than normal frequency.

Abnormal sectoring has been found to be due to high frequency *petite* formation and this can range up to 80% per generation. High frequency *petite* formation has been shown to be a stable characteristic which is inherited in a non-Mendelian fashion. These results suggest that abnormal forms of mitochondrial DNA have been formed during the restoration of respiratory competence observed upon crossing spontaneous *petites*.

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ISOLATION OF AUXOTROPHS OF THE BLUE-GREEN ALGA, ANACYSTIS NIDULANS

Initial attempts to isolate auxotrophs of *Anacystis nidulans*, by nitrosoguanidine mutagenesis, penicillin enrichment and screening on supplemented minimal medium, resulted in the recovery of only six phenotypic classes: $Nit\ A^-$, Bio^-, Met^-, Phe^-, Cys^-, Ace^-. The use of a complete medium [*J. Gen. Microbiol.* 79, 233 (1973)], additional mutagens (ethyl methanesulphonate and UV light), variation of the starvation period prior to penicillin enrichment and multiple cycles of enrichment extended this range of phenotypic classes to include $Nit\ B^-$, Thi^-, Pab^-, Glu^-, Ser^-, Ade^-, and Mad^-. These classes could be divided into two groups; $Nit\ A^-$, $Nit\ B^-$, Bio^-, Thi^- which occurred frequently and the remainder which arose as rare mutational events.

The range of phenotypic classes was considered to be narrow compared with all possible auxotrophic phenotypes and a number of likely causes of this were examined. *A. nidulans* was found to be no more resistant to mutagens than heterotrophic bacteria (e.g. *Escherichia coli*), implying that repair processes were no more potent than usual. Neither extensive gene reiteration nor genome multiplicity could explain the lack of some phenotypic classes. Cross-feeding which could prevent the identification of auxotrophs was excluded as were inefficiencies in the methods used. Examination of the uptake of some metabolites showed that most (e.g. uracil, guanine, threonine, glycine, cysteine, leucine, arginine, tyrosine and phenylalanine) were not incorporated into the wild type in quantities sufficient to satisfy a nutritional require-

ment, although others (e.g. methionine) could be. This suggested that many auxotrophs were double mutants having an increased permeability to, as well as requiring, a specific supplement. The necessity for double mutations would account for the rare occurrence of some auxotrophs and the absence of others. The frequent occurrence of mutants defective in nitrate assimilation (Nit A$^-$, Nit B$^-$) or vitamin biosynthesis (Bio$^-$, Thi$^-$) could be due to a single mutational event since reduced nitrogen sources (e.g. ammonium ions) are efficiently assimilated by the wild type while vitamin requirements are sufficiently small to be satisfied by wild type permease systems.

SESSION 5B

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WHEAT-BARLEY HYBRIDS AND ISOLATION OF ADDITION LINES

Wheat and barley have been hybridized with the aim of producing a set of seven addition lines having individual pairs of barley chromosomes added to the chromosome complement of wheat. Such lines would provide novel material suitable for (1) determining the gene content of barley chromosomes (2) determining the evolutionary relationship between wheat and barley chromosomes and (3) transferring desirable characters from barley to wheat.

Initially barley (2x=14) was used as the female parent in crosses with wheat (6x=42) and 28-chromosome F_1 hybrids were obtained. Although these hybrids were self sterile, some 49-chromosome progeny (heptaploids) were obtained after backcrossing with wheat pollen. These heptaploids containing 21 wheat pairs plus 7 barley univalents were again backcrossed with wheat pollen and a few 43 - chromosome addition lines were isolated from their progeny. However, they were all sterile and exhibited pistillody due to unfavourable interactions between barley cytoplasm and the wheat nucleus.

To overcome pistillody the more difficult reciprocal wheat x barley cross was made and 18 F_1 plants were obtained from more than 5,000 pollinations. However, only one of these F_1 plants appeared to be a true hybrid possessing the requisite 28 somatic chromosomes which form 28 univalents at meiosis; the remaining plants possessed a wide variety of chromosome numbers ranging from 21 to 36. These unexpected chromosome constitutions have been ascribed to abnormal mitoses during early zygotic divisions of the F_1 hybrids, resulting in elimination of some barley chromosomes and duplication of others. We have observed also that one of the barley chromosomes when present in a wheat background, results in abnormal pre-meiotic mitoses in archeospore cells. Despite these difficulties the true hybrid has been backcrossed to wheat two times, similar to the earlier programme using barley as female parent, and many 43-chromosome monosomic addition lines possessing wheat cytoplasm have been isolated.

In most cases these plants were self fertile and 44-chromosome plants have now been isolated in low frequency from their progeny. These form the raw material for establishing a set of wheat-barley addition lines and our progress in identifying such lines is described in the companion paper below.

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ISOZYME EXPRESSION IN WHEAT-BARLEY ADDITION LINES

The isolation and characterization of addition lines involving wheat and an alien species is greatly facilitated when characters from the alien species can be detected in the putative addition lines. The 44-chromosome plants isolated from wheat x barley hybrids, described in the preceding paper, were morphologically different from the wheat parent but did not exhibit any obvious morphological characteristics of barley. In contrast, we have found that many biochemical characters of barley, principally isozymes, are expressed in the putative addition lines. These are proving much more valuable than morphological characters for identifying the individual addition lines and establishing the gene content of barley chromosomes.

So far we have determined the chromosomal location of barley structural genes for alcohol dehydrogenase, a glutamate oxaloacetate transaminase, four esterase isozymes and an endopeptidase. Together these isozymes characterize four separate addition lines and a fifth is distinguished by the presence of a barley storage protein in its endosperm. We are currently analysing other isozymes to extend our mapping of barley chromosomes and to find suitable markers to characterize the remaining two addition lines.

Several complete or partial disomic addition series have been produced in the Triticeae, which includes the cereals wheat, rye, and barley and numerous wild grasses. This work on the genetic control of barley isozymes is part of a wider study of the genetic control of isozyme expression and of gene and chromosome evolution in this tribe. The current findings with barley isozymes will be compared with the results that have been obtained with other species.

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C-BANDING IN THE EVALUATION OF CHROMOSOME PAIRING IN A 5B-MUTANT WHEAT-RYE POLYHAPLOID

A high pairing 5B-mutant of wheat produced by Sears (1975) in the wheat variety Chinese Spring was crossed with a self-compatible cereal rye. Resulting haploids with 28 chromosomes were studied at meiosis with regards to the pairing behaviour of the chromosomes.

The mean chiasma frequency per cell was 1.43. Both ring and rod bivalents as well as trivalents were observed. C-banding revealed that the majority of bivalents were between wheat chromosomes. However, pairing between wheat and rye chromosomes also occurred in approximately ten per cent of cells. It was noted that the majority of such associations were rod bivalents involving the weak or non-heterochromatic arm of the rye chromosome.

Thomas and Kaltsikes (1974, 1976) noted that terminal heterochromatin interfered with the pairing of homologous rye chromosomes. The present study indicates that this is also true for homoeologous pairing between wheat and rye chromosomes. Wheat chromosomes would probably require a moderate degree of sequence specificity for homoeologous pairing to occur. The strong terminal C-bands on rye chromosomes are somewhat lacking in sequence specificity and hence would have little in common with their wheat homoeologues. This level of specificity among rye chromosome ends is so inadequate that even non homologous rye chromosomes could pair. These were observed as both ring and rod bivalents.

Non-homologous pairing of rye chromosomes was also observed by Bowan and

Rajhathy (1977) in diploid rye which showed some pairing failure as a result of colchicine treatment prior to meiosis. Heterochromatin in rye is seen as condensed DNA at interphase and colchicine would enhance this effect by further condensing the DNA. This would result in a further loss of specificity for pairing and account for the low frequency of multivalents observed in diploid rye cells.

Hence colchicine mimics the effect of terminal heterochromatin by condensing the chromosomes and thereby reducing the specificity for chromosome pairing. Whether the homoeologous group 5 system in wheat has a similar mode of operation remains to be seen.

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GENETIC CONTROL OF CHROMOSOME PAIRING IN HORDEUM

Meiotic chromosome behaviour was studied in the hexaploid *Hordeum parodii* (2n = 6x = 42), six haploids (2n = 3x = 21) obtained from a cross between *H. parodii* and *H. bulbosum* (2n = 2x = 14) through selective elimination of *bulbosum* chromosomes and four hybrids (2n = 28) between *H. parodii* and *H. vulgare*.

The alloploid nature of *H. parodii* was evident from the exclusive bivalent formation at the hexaploid level. In haploids both non-homologous and homeologous chromosomes paired at prophase. Foldback pairing of single chromosomes, bivalents and trivalents were observed at prophase and metaphase I. At diakinesis, the pairing involved a maximum of 20 chromosomes which decreased to 12 by metaphase I. This decrease was used in partitioning the non-homologous associations from homoeologous pairing. The significance of chiasmate associations as to their possible origin from crossing over is discussed. A "hemizygous-ineffective" control for the diploid-like behaviour of the hexaploid *parodii* is proposed to explain the homoeologous chromosome pairing in its haploid derivatives.

A decrease in the proportion of chromosomes paired at metaphase I in the *parodii-vulgare* hybrids compared to *parodii* haploids was observed. Such decrease is likely due to the suppression of homoeologous chromosome pairing by the factor(s) present on the *vulgare* genome.

DEMONSTRATIONS

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APPROACHES TO SOMATIC CELL GENETICS USING LOW CHROMOSOME NUMBER COMPOSITES

The fate of foreign genetic material, when introduced into plant protoplasts, has been investigated with various experimental systems (1). It has also been possible to describe the interactions between nuclei of different plant species, brought together by spontaneous, or induced fusion of protoplasts (2). Within animal cells, *in vitro*, the uptake of isolated chromosomes (3), and the co-ordination of nuclei within heterokaryons (4), have both been studied.

Three members of the Compositae *Crepis capillaris* (n=3). *Haplopappus gracilis* (n=2), and *Brachycome lineariloba* (n=2), are under investigation. In all three species, the chromosomes are few in number, large, and easily distinguishable from one another thus allowing cytogenetic studies at the level of single chromosomes.

Using these three species, the uptake and fate of exogenous genetic material into protoplasts will be examined. This foreign genetic material will be in the form of isolated nuclei (5), isolated chromosomes (3), chromosome fragments, and naked DNA (6). Encapsulation of chromatin fragments and DNA, within lipid vesicles, should facilitate the passage of this material into protoplasts. Such a system has been successful with animal cells (7).

The effect of various drugs on these species will be assessed with a view to using the HAT, or similar selective system for isolation of heterokaryons (8).

Preliminary characterization of tissue cultures derived from the three species has been geared to defining problems, and developing techniques involved in cell fusion and chromosome isolation. Results, so far, fall into five categories.

1. Analysis of karyotypic instability.
2. Measurement of the efficiency of mitotic arrest, induced by various agents, as a prerequisite for bulk chromosome isolations (3).
3. Development of protoplast isolation techniques.
4. Estimation of nuclear fusion rates in caffeine induced binucleates (9).
5. Demonstration of morphogenic potential in *B. lineariloba* tissue cultures.

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RODENTS OF PAPUA NEW GUINEA

Rodents comprise about half the mammalian fauna of Papua New Guinea (excluding bats). There are more than 50 species of rodents in 20 genera; but they all belong to a single family the *Muridae* (rat and mouse like rodents). There are no other Eutherian mammals (excluding bats) present in the region and, in the absence of competition, there has been a great deal of evolutionary radiation and these Murid rodents occupy niches normally filled by other animals, e.g. there are aquatic rodents and arboreal rodents with prehensile tails.

We have karyotyped as many animals as possible, hoping to establish evolutionary relationships. Using our karyotypes and the karyotypes obtained by Baverstock *et al.* (1977a,b) of the related Australian rodents it is possible to make several conclusions.

1. *Rattus* species have very different karyotypes from all other Papuan and Australian rodents. This suggests the *Rattus* group is not closely related to the *Uromys/Melomys* group as was previously thought on the basis of dental morphology. The New Guinea *Rattus* species fall into two distinct groups - the *R. leucopus* group (5 species) closely related to each other and the *R. sordidus* group (at least 2 species) related to other *sordidus* species in Australia.

2. All other species examined have karyotypes which can be derived from one another and from the Australian rodents (excluding *Rattus* species). There has been extreme conservation of karyotype despite wide morphological changes.

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ECOLOGICAL STUDIES ON THE POLYMORPHISM OF CYANOGENESIS IN POPULATIONS OF LOTUS CORNICULATUS *IN ANGLESEY, WALES*

The environmental factors influencing a steep morph-ratio cline in a maritime population of *Lotus corniculatus* have been studied in detail. The frequency distribution of cyanogenic plants in the cline has remained stable for 16 years, plants very near the sea being predominantly acyanogenic, whereas 200 m inland 70 per cent of the plants were cyanogenic. Analyses of the biotic, edaphic and microclimate environment of this population showed that an exposure gradient (wind and windborne salt) and the distribution of known selective herbivores were the only factors which were consistently associated with the cline.

On the basis of these results and the hypothesis that cyanogenesis is a protection against herbivores it was predicted that other sites along the coast, which showed similar environmental variation should also show a similar distribution of selective herbivores and of cyanogenic plants. It was confirmed that at sites exposed to wind and windborne salt the selective

herbivores were rare and the frequency of cyanogenic plants was low. At sites which were less exposed, the numbers of selective herbivores and the frequency of cyanogenic plants were both higher.

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PACHYTENE CHROMOSOMES OF ANNUAL MEDICAGOS

There are approximately 34 annual species of *Medicago*, and over a dozen of these "medics" occur as naturalized self-sown legumes in pastures of southern and south-western Australia. Studies of mitotic metaphase chromosomes have revealed that all but five species have 2n=16 chromosomes. The somatic chromosomes range from 1.8 to 5.0 µm in length, with most being metacentrics or submetacentrics shorter than 3.5 µm. Four species - *M. constricta*, *M. polymorpha*, *M. praecox* and *M. rigidula* have 2n=14, and one species - *M. murex* has both 2n=14 and 2n=16 strains. The uniformity of the somatic karyotypes has generally precluded their use in determining species relationships and evolution.

The pachytene chromosomes of annual medics range from 20 to 60 µm in length, with the main chromatic knobs arranged around the centromeres. Nucleolus organizers are usually located near the centromeres. The more distinctive pachytene karyotypes which can be compiled have allowed study of cytological relationships of species. Thus the probable derivation of the 2n=14 *M. murex* from the 2n=16 *M. murex* has been determined, and the four 2n=14 species have been found to have distinctly different idiograms. Pachytene karyotypes of the 2n=16 species are now being prepared. *M. tornata*, *M. truncatula* and *M. arabica* show karyotypic features which are different from 2n=16 *M. murex*. Relationships inferred from pachytene idiograms will be contrasted with taxonomic relationships, which are based primarily on pod morphology.

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SERIAL SECTION RECONSTRUCTION OF MEIOTIC CHROMOSOMES AT THE ULTRASTRUCTURAL LEVEL

The basic techniques in preparation and reconstruction of serial electron micrographs will be illustrated. Results from reconstruction of zygotene and pachytene stages in wild type and rearranged *Neurospora* and maize will be shown. These allow preparation of ultrastructural karyotypes, and study of the three-dimensional aspects of meiotic chromosome pairing and recombination.

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A 'THOUGHT' EXPERIMENT: ISOLATION OF MAMMALIAN STRUCTURAL GENES BY MOLECULAR CLONING

The induction of steroid hormones of specific gene products in selected target organs offers attractive possibilities for molecular analysis of the control of vertebrate gene expression. This has been capitalized on particularly by O'Malley and Schimke with regard to the induction of hen oviduct ovalbumin synthesis by estrogen and progesterone, to the extent that ovalbumin gene fragments have been purified and amplified by molecular cloning,

paving the way for isolation, identification, and characterization of the ovalbumin 'regulon'. However, this system has not been genetically analyzed; neither have most similar systems in mammals.

A notable exception is the induction of ß-glucuronidase in mouse kidney by testosterone. Paigen and coworkers have mapped both the structural gene (*Gus*) and an adjacent regulatory locus (*Gur*) which controls the extent and kinetics of androgen inducibility. Coupled with the availability of a testosterone receptor(-) mutant (*Tfm*), this system theoretically offers great potential for unequivocal molecular analysis. However, all attempts to identify ß-glucuronidase mRNA by immunoidentification of heterologous translation products have been unsuccessful, probably reflecting extensive post-translational modification required in synthesis of the active enzyme.

This demonstration suggests approaches to the isolation and identification of ß-glucuronidase gene fragments which rely on the genetic information available for the enzyme, by-passing the necessity for mRNA identification.

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CHROMOSOME STUDIES IN MARSUPIAL GLIDERS (GENUS PETAURUS)

Sixteen *Petaurus breviceps* from South Australia, Victoria, New South Wales, Australian Capital Territory, Northern Territory and New Guinea were karyotyped using leukocyte culture.

The X-chromosome was found to be not, as previously thought, a medium sized chromosome, but the smallest of the complement apart from the dot-like Y chromosome. Over half the X chromosome C-bands with the barium hydroxide technique, the nonstaining portion being 2 per cent of the total haploid chromosome length.

A striking dimorphism of one of the smaller pairs of autosomes was revealed with C-banding. One chromosome had almost the entire short arm C-band positive, while its apparent homologue had the usual small amount of procentromeric C-banding. This dimorphism cannot be explained simply by the addition or loss of the extra C-banding material from the other "homologue", there being no chromosome present in the karyotype with the required complementary size and arm ratio.

The karyotypes of thirteen *P. breviceps* were successfully C-banded. Surprisingly nine of these were heterozygous for this C-band 'variant', including animals from New South Wales, Australian Capital Territory and South Australia. Both predicted homozygotes were also found.

A single male *Petaurus norfolkensis* was also studied. The chromosome complement, (reported here for the first time) appear essentially the same as that of *P. breviceps*, the single animal of *P. norfolkensis* studied having more procentromeric C-banding than *P. breviceps*. Again the same chromosome pair showed dimorphic C-banding.

Although *Petaurus* leukocyte cultures generally grew only moderately well, G-banding studies were possible on the *P. norfolkensis* male. On the basis of G-banding patterns, the first seven pairs of autosomes could be paired without difficulty, but the remaining 6 autosomes including, the dimorphic chromosomes each had an apparently unique G-banding pattern. The G-banding pattern of any of the individual six chromosomes was consistent between different cells.

The C- and G-banding patterns may both be indicative of an inter-relationship of one chromosome with more than one other. Meiotic studies to elucidate

chromosome homologies within the six autosomes have so far been unsuccessful.

Silver N-banding revealed that none of these six autosomes bears a major nucleolus organizer.

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AN IMPROVED IN SITU *HYBRIDIZATION METHOD*

Previously reported *in situ* hybridization techniques have employed a time consuming series of manipulations to effect the denaturation of chromosomal DNA and subsequent reannealing of DNA-RNA hybrids. This demonstration presents a new protocol which combines the denaturation and reannealing process. DNA is heated in a solution of 50% formamide - 50% 4 x SSC containing the RNA to be hybridized. After 1 hour at 70^{o} the preparation is slowly cooled to 37^{o} over a period of 6 hours and incubated at 37^{o} for a further 10 hours. The technique eliminates the possibility of premature reannealing of the DNA while employing hybridization conditions which, *in vitro*, lead to accurate base pairing. DNA-RNA hybrids are detected by immunological techniques including the indirect immunofluorescence technique of Rudkin and Stollar (1977). Such techniques may provide potential for the precise chromosomal location of sites of RNA synthesis. Some examples of progress to date are given.

Rudkin, G.T. and Stollar, B.D. (1977). Nature 265, 472.

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GENETIC VARIATION AND SOCIAL BEHAVIOUR IN A SPECIES COMPLEX OF PONERINE ANTS

Patterns of allozyme variation have been studied in the *Rhytidoponera impressa* group, a species complex of ponerine ants inhabiting mesic habitats along the east coast of Australia. Of the 22 loci examined, 15 are monomorphic and identical in all populations. Mean heterozygosity estimates tend to be quite low (averaging 3%), and yet exhibit considerable interpopulation variation, as do gene frequencies. These findings support the theoretical contention that haplodiploid species should have low intrapopulation genetic diversity coupled with considerable interpopulation differentiation. The electrophoretic analysis reveals the existence of t least four, partially sympatric, phenotypically similar species, distinguished by markedly different gene frequencies. Reproduction isolation between these species appears to be complete, except possibly in one area of southern Queensland. The geographical distribution of these species in northern New South Wales and southern Queensland is remarkably coincident with the distribution of other sibling species of rainforest ants and suggests that rainforest habitat was even more severely restricted during some period(s) in the past, with the Clarence River Valley acting as an important geographical barrier to many species. Finally, patterns of genotypic diversity within single ant nests indicate a dimorphism of colony types: monogynous, queen-reproductive colonies and polygynous colonies where worker-like individuals have replaced queens as reproductives. These results are discussed in relation to recent kin-selectionist explanations for the evolution of altruistic social behaviour in insects.

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GENETIC SYSTEMS OF THE PARTHENOGENETIC GRASSHOPPERS WARRAMABA VIRGO *and* XIPHIDIOPSIS LITA

The all-female Australian grasshopper *Warramaba virgo* arose in W.A. an uncertain number of millenia B.P. by hybridization between two bisexual species whose modern representatives are the species 'P169' and 'P196'. The hybrid constitution of *W. virgo* is maintained by a genetic system involving (1) premeiotic doubling of the chromosome set (2n→4n), followed by (2) synapsis restricted to sister chromosomes and (3) normal two-division meiosis. P196 and P169 can be crossed in the laboratory (in either direction) to produce 'synthetic *virgo*' individuals. In the case of the cross P196♀ x P169 ♂ , male hybrids are also viable. The fecundity of synthetic *virgo* is very low, but females can produce more females by parthenogenesis. Triploid hybrids have also been obtained between *W. virgo* and males of P196 and P169. Male triploids are totally sterile, but a few offspring have been obtained from female triploids, by parthenogenesis. The triploid oocytes exhibit the *virgo* type of premeiotic chromosome doubling, the P196 or P169 chromosome set undergoing the extra replication synchronously with the *virgo* chromosomes. cRNA prepared from the highly repetitive DNA of P196 hybridizes *in situ* specifically to the centromeric C-bands of the X_1 and X_2 chromosomes of *W. virgo*. The C-banding pattern of *W. virgo* varies from one geographic clone to another and some differences in DNA late replication exist between geographic populations. *W. virgo* and P196 come into parapatric geographic contact near Kalgoorlie, W.A., without forming mixed colonies. Presumably, there is mutual exclusion from one another's territories because hybridization leads to effectively sterile triploids. P196 exhibits an extraordinary cline in fecundity, and *W. virgo* has been able to extend a salient into its territory where its fecundity is minimal. The parthenogenetic Tettigoniid grasshopper *Xiphidiopsis lita*, from Hawaii and other Pacific islands, is also a diploid but its karyotype does not suggest a hybrid origin. Meiosis has not been studied so the genetic system is essentially unknown. One remarkable feature is the huge pair of metacentric X-chromosomes, which include considerably more than 50% of the total DNA. C-banding studies indicate that the size increase is not due to heterochromatin. Presumably *X. lita* evolved from a bisexual species of the genus in which one or more autosomes have been incorporated in the X-chromosome (i.e. a neo-XY or X_1X_2Y species).

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THE AUSTRALIAN SHEEP BLOWFLY, LUCILIA CUPRINA, *FOR ILLUSTRATING THE BASIC CONCEPTS IN GENETICS*

For many years *Drosophila melanogaster* has been the preferred organism for illustrating many of the important concepts in genetics. It is not the object of this demonstration to dislodge *Drosophila* from its well-earned pedestal but rather to provide an alternative organism, closer to home, to elucidate some of these basic concepts.

L. cuprina comes with its advantages and disadvantages. On the negative side, it is more labour intensive to maintain and it requires certain facilities (e.g. fume cabinet for larval development) to render it an accept-

able addition to one's laboratory. On the positive side it is larger and therefore some mutants can be handled without a microscope (e.g. eye colour and body colour mutations). Further, a female lays 200-300 eggs during a brief interval of time (10-20 minutes), and therefore egg hatch can be readily used to measure dominant lethality, whether irradiation -induced or because of chromosomal rearrangements. *L. cuprina* may also have some novelty value as it has not yet been institutionalized to the same degree as *Drosophila*.

The demonstration provides information on the following experiments:

- marker genes and genetic mapping
- gene action, e.g. epistasis
- insecticidal resistance genetics
- descriptive and experimental cytogenetics
- irradiation induced dominant lethality

Some of these experiments can be performed without the need to maintain cultures of *L. cuprina*. Given sufficient notice I envisage that suitable stocks could be provided from the Genetics Department at the University of Melbourne (e.g. pupae of F_2 or a backcross). It would remain for the receiving laboratory to allow the adults to emerge and then to provide these directly to students for analysis. Where egg hatch studies were contemplated, the flies would simply require protein feeding for several days prior to the practical class.

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GENETIC ANALYSIS OF DICTYOSTELIUM DISCOIDEUM *USING THE PARASEXUAL AND SEXUAL CYCLES*

Dictyostelium discoideum is a simple eukaryote which is useful for studies on differentiation and development. One advantage of the system is that developmental mutants are readily isolated.

We are continuing to formalize genetic analysis in this organism using the parasexual cycle. Comment will be made on each aspect of this cycle. The major classes of mutations isolated and mapped will be described. Studies have been commenced on the sexual system. Aspects of formation of the sexual structure and reactions between amoebae of opposite mating will be discussed.

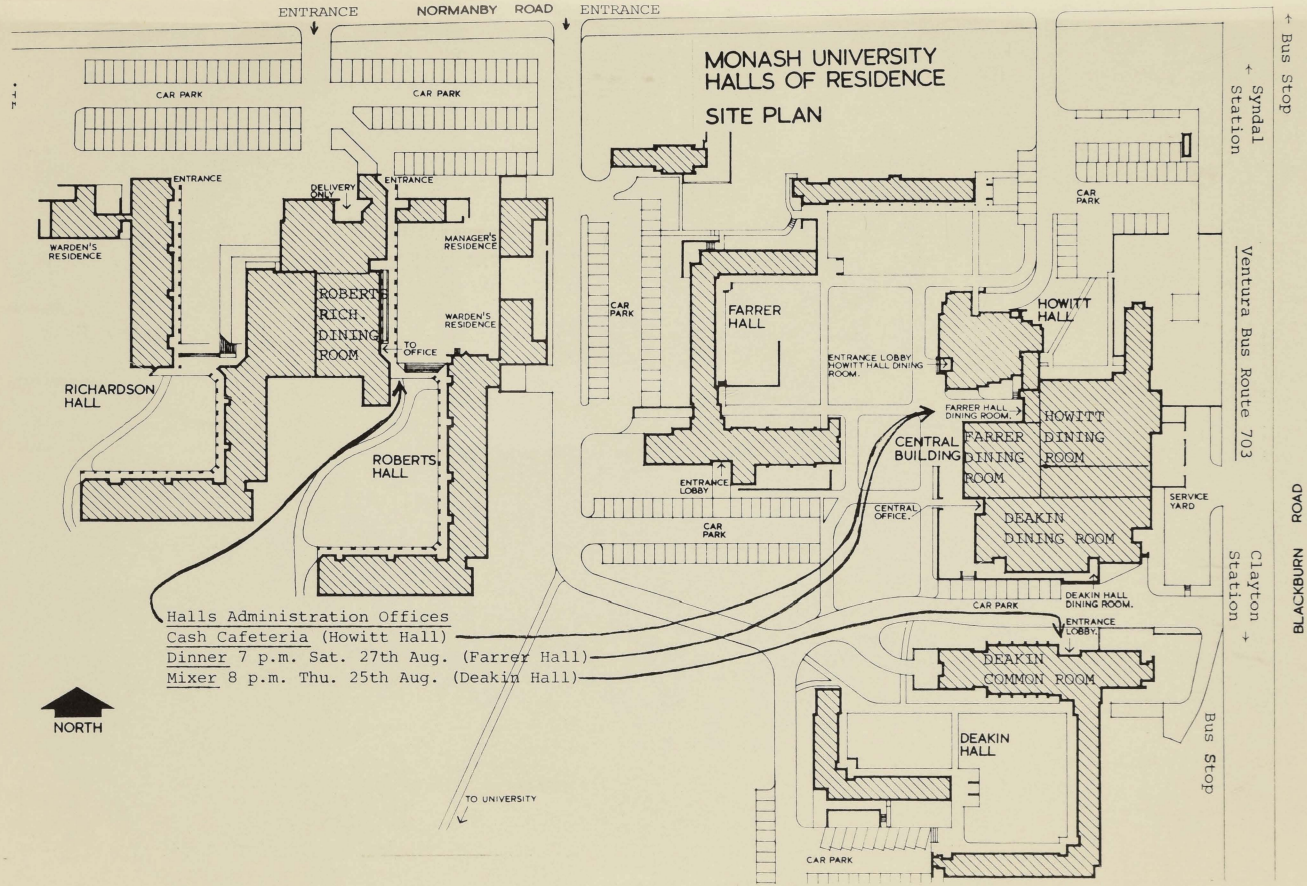
JOINT SYMPOSIUM WITH SECTION 11 (Zoology) OF ANZAAS

This will be held on Monday 29th August in the Rivett Theatre, Barry Building, University of Melbourne.

THE GENETICAL CONSEQUENCES OF ENVIRONMENTAL HAZARDS

Professor P.A. Parsons - Convener

Session 1	Chairman: Professor A.M. Clark
9.30 - 10.15	Dr D.G. MacPhee
Chemicals in our environment: Genetic risk versus benefits	
10.15 - 11.00	Dr Ken Dyer
Ionizing radiation	
Session 2	Chairman: Dr B.T.O. Lee
11.30 - 12.15	Professor M.J. Whitten
Genetical consequences of pesticides - is there a biological solution?	
12.15 - 1.00	Mr J.E. Cummins
Genotype and drug responses in rodents and man	


MONASH UNIVERSITY
HALLS OF RESIDENCE
SITE PLAN
ENTRANCE
NORMANBY ROAD
ENTRANCE
CAR PARK
CAR PARK
ENTRANCE
DELIVERY ONLY
ENTRANCE
WARDEN'S RESIDENCE
MANAGER'S RESIDENCE
ROBERT RICH DINING ROOM
WARDEN'S RESIDENCE
TO OFFICE
RICHARDSON HALL
ROBERTS HALL
CAR PARK
FARRER HALL
ENTRANCE LOBBY HOWITT HALL DINING ROOM
CAR PARK
HOWITT HALL
FARRER HALL DINING ROOM
CENTRAL BUILDING
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DEAKIN HALL DINING ROOM
CAR PARK
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CAR PARK
TO UNIVERSITY
Halls Administration Offices
Cash Cafeteria (Howitt Hall)
Dinner 7 p.m. Sat. 27th Aug. (Farrer Hall)
Mixer 8 p.m. Thu. 25th Aug. (Deakin Hall)
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Clayton Station →
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