Genetics Society of Australia

# 23rd General Meeting

# PROGRAMME & ABSTRACTS

*University of New South Wales*

*26-27th August, 1976*

## DETAILS OF MEETING

### PAPERS

Papers will be presented in Lecture Theatres B and D of the Biological Sciences Building.

### DEMONSTRATIONS

These will be on display in Laboratory C, ground floor, eastern end of the Biological Sciences Building (around the corner from the lecture theatres).

### MORNING AND AFTERNOON TEA

Tea, coffee and biscuits will be available in the foyer of the Lecture Theatre Block.

### ACCOMMODATION

Accommodation has been arranged at Basser, Goldstein and Baxter Colleges, due west of the Biological Sciences Building on High Street. Full board is $16.50 per day, bed and breadkfast is $9.50 per day. Meals can be provided for non-residents if 24 hours notice is given. Charges are $3.00 per head for lunch, $4.00 per head for dinner. All meals are served in the Philip Goldstein Dining Hall. Meal times are as follows:

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| Breakfast | 7.20 - 8.30 a.m. |
| Lunch | 12.30 - 1.30 p.m. |
| Dinner | 5.30 - 7.00 p.m. |

Incoming mail and messages for residents are placed in the alphabetical mail boxes in the foyer of Basser College.

The College Shop beneath the Dining Hall is open from 11 a.m. to 7 p.m. weekdays, and 5 p.m. to 7 p.m. Saturday and Sunday.

Parking in College grounds is very limited, and must be arranged through the University (663.0351 ext. 2920).

Buses 396 to Circular Quay, and 337 and 338 to Macquarie Street pass along Anzac Parade at the western end of High Street.

Please make sure to return your room key to the College Office before departure.

Payment for accommodation should be made to the Treasurer, Chris Gillies, before Friday evening. Cheques should be made out to the Genetics Society of Australia.

LUNCH

Lunch may be obtained at the University Union (E5 on map). Visitors may also avail themselves of the Senior Common Room (Floor 4, Electrical Engineering Building - G17 on map) if introduced by a UNSW member.

BANKING & POSTAL FACILITIES

The Rural Bank and the Commonwealth Bank have branches behind the library (E22) and within the shopping centre at the Blockhouse (F6/7). Stamp machines and postboxes are located on the ground floor of the Blockhouse.

PARKING ON CAMPUS

Essentially none unless you are a good talker.

BUSINESS MEETING

This will be held in Lecture Theatre D at 5.00 p.m. on Thursday 26th August. The remainder of Thursday evening is free.

SOCIAL EVENTS

Mixer - An informal gathering of members will be held in the Basser Undercroft on Wednesday 25th August, commencing at approximately 7.00 p.m.

Dinner - This will be held in the Common Room, 6th Floor, Biological Sciences Building on Friday 27th August at 7.00 p.m. for 7.30 p.m.

Opera House Concert - Thursday 26th August 8.00 p.m. Those who ordered tickets should collect them with this programme when registering.

Bus and Boat Trip, Saturday 28th August - Cancelled due to lack of starters.

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LECTURE PROGRAMME

THURSDAY, 26TH AUGUST

9.00 - 9.30 Registration

Session 1 — Lecture Theatre D

9.30 - 10.30 a.m.

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| 9.30. | D.W. Cooper | A comparison of the genetic variability at autosomal and sex-linked loci in mammals. |
| 9.50. | G.T. Lawrence<br>G.M.E. Mayo<br>K.W. Shepherd | Exceptions to the gene-for-gene relationship in flax and flax rust. |
| 10.10. | K.W. Shepherd<br>G.M.E. Mayo | Complexity of genes at the L locus in flax. |

10.30. - 11.00 Morning Tea

Session 2

11.00 - 12.40

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| 11.00. | Tony Pryor | High frequency null mutations at the glucosidase locus in maize. |
| 11.20 | P.M. Chandler<br>V. Krishnapillai | Derepressed mutants of R plasmids of Pseudomonas aeruginosa. |
| 11.40 | J.S.F. Barker<br>P.R. Widders | Selection of yeast species by Drosophil bazzatii and selection in D.buzzatii determined by yeasts. |
| 12.00 | C.J. Brackenridge | Genetic linkage and Huntington's Disease. |
| 12.20 | James J. Guinan | Increased incidence of the HLA antigens A3 and B7 in Haemochromatosis. |

12.40 - 2.00 Lunch

Session 3A — Lecture Theatre D

2.00 - 3.40 p.m.

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|---|---|---|
| 2.00 | Kristine Barlow<br>J. Gyarfas<br>C. May | Mapping of two translocations onto chromosome 4A of wheat using the isozymes of acid phosphatase and alcohol dehydrogenase. |
| 2.20 | N.C. Subrahmanyan | Genome balance in controlling chromosome stability in Hordeum interspecific hybrids. |
| 2.40 | A.J. Stocker<br>C. Pavan | Developmental puffing patterns in Rhynchosciara hollaenderi. |

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| 3.00 | Jon Martin<br>B.T.O. Lee<br>E. Connor | Apparent incipient speciation in the midge Chironomus oppositus. |
| 3.20 | Rory Hope<br>Jennifer Donald<br>Lorraine Billett | Preliminary characterization of marsupial x mouse somatic cell hybrids. |

Session 3B — Lecture Theatre B

2.00 - 3.40.

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| 2.00. | P.T. Lehrbach<br>B.T.O. Lee | Effect of a Pseudomonas R factor on U.V. - sensitivity and UV mutagenesis. |
| 2.20 | G. Zurawski | Identification by RNA-DNA hybridization of genes for 23S and 16S rRNA which map near pheA on the E. coli K12 chromosome. |
| 2.40. | J. Eadie<br>M.L. Skotnicki<br>B.G. Rolfe | The metabolic state of nitrate reductase in E.coli K12 and its biological implications. |
| 3.00 | M.L. Skotnicki<br>B.G. Rolfe | The genetic control of nitrogen fixation and nitrate reduction in E.coli. |
| 3.20 | B.G. Rolfe<br>M.L. Skotnicki<br>J. Eadie | Phage lambda lysogeny as a measure of the metabolic state of E.coli K12. |

3.40 - 5.00 Tea and Demonstrations — Laboratory C

5.00 Annual Business Meeting — Lecture Theatre D

FRIDAY, 27TH AUGUST

Session 4

9.00 - 10.15 Invited Lecture — Lecture Theatre D

Prof. B.W. Holloway, President, Genetics Society of Australia
Department of Genetics, Monash University, Clayton, Vic.

"Sex, Drug Resistance and Plasmids, or the Microbial Olympics."

10.15 - 10.45 Morning Tea

Session 5 — Lecture Theatre D

10.45 - 12.45

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| 10.45 | A.J. Godfrey<br>A.F. Morgan | Stability of group P plasmids in sub-grains of Pseudomonas aeruginosa. |
| 11.05 | R. Appels<br>W.J. Peacock | The location of polyprimidine tracts within the chromosomes of Secale cereale. |

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| 11.25. | C.B. Gillies | Can electron microscopy visualise the sites of crossover events at pachytene? |
| 11.45. | H.T. Imai<br>R.H. Crozier<br>R.W. Taylor | A model for karyotype evolution based on Australian ant data. |
| 12.05. | B.J. Richardson | The microdistribution of genetic variation in wild rabbit populations. |
| 12.25. | Peter J. Baverstock<br>B.J. Richardson<br>S. Cole | Electrophoretic data and biochemical systematics. |

12.45 - 2.00 Lunch

Session 6A — Lecture Theatre D

2.00 - 3.40

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| 2.00. | J.A. Marshall Graves | Analysis of X chromosomes inactivation in somatic cell hybrids |
| 2.20. | J.A. Donald | A method for measuring transcription applied to X-chromosome inactivation in kangaroos. |
| 2.40 | G.C. Webb<br>M.J.D. White<br>N. Contreras<br>J. Cheney | G- and C- banding studies on Warramaba virgo and its bisexual relatives. |
| 3.00. | A.R. Lohe | An analysis of satellite DNAs in Drosophila simulans. |
| 3.20. | D.R. Smyth | Locations and possible functions of heterochromatin in chromosomes of Lilium. |

Session 6B — Lecture Theatre B

2.00 - 3.40

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| 2.00 | A.E. Stark | A review of some classical theory of population genetics. |
| 2.20. | J.A. McKenzie | The effect of immigration on genetic control in populations of Drosophila melanogaster. |

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|---|---|---|
| 2.40. | Frank Nicholas | The effect of of selection on the standardised variance of gene frequency. |
| 3.00. | R.G. Beilharz | The effect of inbreeding on total reproductive potential in mice. |

3.20.

3.40 - 5.00 Tea and Demonstrations Laboratory C

## ABSTRACTS OF PAPERS

SESSION 1

COOPER, D.W.
School of Biological Sciences, Macquarie University,
North Ryde, N.S.W.

### A COMPARISON OF THE GENETIC VARIABILITY AT AUTOSOMAL AND SEX-LINKED LOCI IN MAMMALS

Population genetics theory leads to the expectation that X linked loci should be less variable than autosomal loci. In particular, balancing selection seems less likely at X linked loci, directional selection should lead to faster removal of the less favoured X linked allele, and the effective population size is smaller for X linked loci. Kangaroo X linked loci with their system of dosage compensation through paternal X inactivation are less likely to have balanced polymorphism than ordinary X linked loci. It is however difficult to test this expectation, principally because it is difficult to choose a sample of X linked loci without choosing the more variable loci. A method has been devised for choosing an apparently unbiased sample in kangaroos. The percent of loci polymorphic and the average heterozygosity per locus for four X linked loci in ten species of kangaroo have been compared with the same parameters for eleven autosomal loci in the same species. No significant difference was found between the two classes of loci for either parameter. An examination of the literature has revealed that, apart from the data of Prakash for Drosophila robusta, there are no convincing data which show that X linked loci are less variable than autosomal.

LAWRENCE, G.J.,[1] MAYO, G.M.E.,[1] and SHEPHERD, K.W.[2]
[1] Department of Genetics, University of Adelaide, Adelaide, South Australia.
[2] Department of Agronomy, Waite Agricultural Research Institute, Glen Osmond, South Australia.

### EXCEPTIONS TO THE GENE-FOR-GENE RELATIONSHIP IN FLAX AND FLAX-RUST

Flor's gene-for-gene hypothesis proposes that each gene determining resitance in flax interacts with a separate and specific gene controlling pathogenicity in flax rust. With one exception published data on the inheritance of resistance in the host and pathogenicity in the rust support this hypothesis: plants possessing a particular resistance gene (e.g. $_R1$) are resistant to rust strains possessing the corresponding avirulent gene ($_{A_R}1$) but susceptible to strains homozygous for the corresponding virulent gene ($_{a_R}1a_{a_R}1$). The one exception concerns the determination of pathogenicity on the host variety Williston Brown which possesses the gene for resistance where, to account for Flor's data, it has been postulated that a dominant inhibitor gene $I_M1$ interacts with the dominant gene $A_M1$ normally controlling avirulence on Williston Brown to give a virulent pathogen phenotype. Under this model rust strains of genotype

$i_M1i_M1;A_M1$ - are avirulent on Williston Brown whereas rust strains of genotype $I_M1$-;-- or--; $a_M1a_M1$ are virulent. Data will be presented which indicate that three other avirulent genes $A_L1$, $A_L7$ and $A_L10$ similarly interact with either a common inhibitor gene or closely-linked inhibitor genes and that this inhibitor gene (or genes) is closely linked to $I_M1$.

SHEPHERD, K.W., and MAYO, G.M.E.

COMPLEXITY OF GENES AT THE L LOCUS IN FLAX

At least 12 different genes conferring resistance to rust have been located at the L locus in flax. In recombination studies between pairs of these genes only one class (double-susceptible plants) of recombinants has been detected. We have argued that the failure to detect the other expected class (double resistant plants) could be due to allelic interaction between two L genes when combined in *cis* so that instead of possessing both parental specificities the recombinant plants have either no specificity or a new one. Verification of this hypothesis depends on recovering by recombination both parental specificities from putative heterozygotes exhibiting the *cis* interaction. So far we have been able to recover $L^{10}$, but not $L^2$ specificity from putative $\frac{L^2\ L^{10}}{+\ +}$ recombinants, so our hypothesis has remained unproven. However, recently we have obtained evidence that a naturally occurring specificity (conferred by gene $L^6$) may in fact be an interaction product itself, thus providing a new lead on the structure and origin of genes at the L locus.

SESSION 2

PRYOR, Tony
Division of Plant Industry, C.S.I.R.O., Canberra, A.C.T.

HIGH FREQUENCY NULL MUTATIONS AT THE GLUCOSIDASE LOCUS IN MAIZE

Three genes determining glucosidase isozyme variants are inherited as alleles of a single locus - glucosidase Mutants were detected by screening $F_1$ progeny from plants grown from EMS treated seed crossed by pollen with an electrophoretically distinguishable allele. A mutational event could be recognised as a sector in the $F_1$ ear with an altered ♀ isozyme. In the first experiment, 33 or 17.6% of the 187 $F_1$ ears tested carried apparent Null mutations. Plants from 17 of these 33 ears were selfed and in all cases the $F_2$ progeny segregated in a 3 : 1 ratio of pollen parent isozyme : no isozyme. These $F_2$ Nulls breed truely and behave genetically as homozygous for a glucosidase Null allele. There is no evidence for complementation between different Null mutants.

A second mutation experiment involving 132 $F_1$ ears gave no mutations of the glucosidase locus. There are no simple explanations for either the high frequency of occurrence of these Null mutants in the first experiment or the failure to observe them in the second experiment.

CHANDLER, P.M., and KRISHNAPILLAI, V.
Department of Genetics, Monash University, Clayton, Vic.

DEPRESSED MUTANTS OF R PLASMIDS OF PSEUDOMONAS AERUGINOSA

Mutants derepressed for conjugal transfer (Drd) have been isolated from the narrow host range R plasmide R91 and R19 by the successive mating technique of Edwards and Meynell (1968). Conjugal transfer frequencies of these mutants attained 20-100% whereas the parent plasmids transfer only at frequencies of 0.05-0.5%. A genetic analysis of transient heterozygotes designed to elucidate the nature of the plasmid mutations indicated the occurrence of both operator-constitutive and transfer-inhibitor deficient mutants because of the transdominant or transrecessive behaviour of the mutants with respect to the wild type plasmid transfer system.

The mutants, in addition to increased transfer, simultaneously manifested other characteristics such as entry exclusion (Eex), sensitivity to the donor-specific phages PRD1, PR3 or PR4 and inhibition of the replication of phage G101 (Phi). The expression of Phi is significant because this is a unique property of P group plasmids such as R18 which is characterized by promiscuous host range. This is perhaps not surprising since all these R plasmids originated from the same clinical environment and therefore are likely to be the genetic products of previous plasmid recombindational events. Consistent with this view was the fact that although R18 is uniquely sensitive to the donor-specific phages PRR1 and Pf3, confers resistance to certain aeruginocins, and is susceptible to superinfection inhibition by prophage B3 and of wide host range, the Drd mutants of R19 and R91 are distinguishable by all these criteria from R18 in addition to their distinctive Eex.

BARKER, J.S.F., and WIDDERS, P.R.
Department of Animal Husbandry, University of Sydney, Sydney, N.S.W.

SELECTION OF YEAST SPECIES BY DROSOPHILA BUZZATII AND SELECTION IN D. BUZZATII DETERMINED BY YEASTS

The cactus-breeding Drosophila of the mulleri subgroup provide particularly useful material for population genetic studies in natural populations, as the ecology, breeding site, nutritional requirements and field behaviour of some of them are reasonably well-known, and these aspects can be studied in natural populations. Thus allozyme polymorphism in Australian populations of D. buzzatii and D. aldrichi is being studied. One aspect involves yeast species distribution, and the selective influence of yeast species.

Five species of wild yeasts have been isolated from rotting Opuntia cladodes at one locality in the Hunter Valley. The relative frequency of these species appears to vary

seasonally, and they are significantly different in attractivity to D. buzzatii adults in both laboratory and field studies. Three of the yeast species differ in their ability to support larval development - in terms of larval viability and developmental time, and they impose differential selection on allozyme genotypes.

Given the variation in rot microflora available to D. buzzatii populations, preferences for different yeasts and differences in the relative fitness of genotypes when utilizing different yeasts could prove to be a potent force maintaining genetic variability.

BRACKENRIDGE, Colin J., and PROPERT, David N.
Department of Psychiatry, University of Melbourne, Vic.

GENETIC LINKAGE AND HUNTINGTON'S DISEASE

Because of the usually late age of onset of Huntington's disease, many patients suffering from this dominantly inherited disorder have reproduced and passed the abnormal gene to half their offspring before they themselves have shown manifestation of clinical signs and symptoms. At present there is no means of determining which subjects at risk will later develop Huntington's disease but several recent developments in this area show some promise. Because of the nature of the disorder, the genetic linkage approach has several major drawbacks, but analysis of the linkage relationship of the Huntington's gene and eighteen polymorphic marker systems in twenty four Australian families gave positive lod scores with $P_1$, Gm and Hp.

GUINAN, J.J.
Tissue Typing Laboratory, N.S.W. Blood Transfusion Service, Sydney.

INCREASED INCIDENCE OF THE HLA ANTIGENS A3 AND B7 IN HAEMOCHROMATOSIS

Idiopathic haemochromatosis is a rare disease characterized by excessive deposits of iron in the body. Therapy of this disease involves regular removal of the excess iron by phlebotomy. Forty-seven patients were tissue typed as it was planned to make use of their platelets to selectively absorb unwanted HLA specificities from typing sera.

The frequency of each of 25 well defined HLA antigens was compared to HLA frequencies in a random control population of 713. Increased frequencies of 2 antigens were found in the haemochromatosis patients:

HLA-A3 (patients 70%, control 29%, p corrected $10^{-3}$)
HLA-B7 (patients 55%, control 28%, p corrected $10^{-2}$)

The increased frequency of HLA-A3 has recently been reported by other groups (Simon, et al., 1975, Bomford, et al., 1976 and Fauchet, et al., 1976). The increased frequency of HLA-B7 has not been reported previously but it is noteworthy that strong linkage disequilibrium exists between HLA-A3 and B7.

Fauchet et al. also reported an increased frequency of HLA-B14 but although the frequency was raised in our patients (patients 15%, controls 8%) the difference was not statistically significant.

Current concepts of the significance of increased frequencies of HLA antigens in certain diseases involve the close linkage of the HLA system, particularly the HLA-B series, with genes controlling the immune response. The association between HLA-A3 and haemochromatosis is of interest not only for its diagnostic value but also because it belongs to the HLA-A series.

SESSION 3A

BARLOW, K., GYARFAS, J., and MAY, C.
School of Botany, University of New South Wales, Kensington, N.S.W. —

MAPPING OF TWO TRANSLOCATIONS ONTO CHROMOSOME 4A OF WHEAT USING THE ISOZYMES OF ACID PHOSPHATASE AND ALCOHOL DEHYDROGENASE

Chromosome 4A in hexaploid wheat posses a gene for a sub-unit of alcohol dehydrogenase (ADH) on the α arm and two structural genes for acid phosphatase (ACPH) on the β arm. Transec, a variety which has a translocation from rye onto the β arm, is characterised by both the ACPH genes. This translocation-breakpoint has been mapped cytologically at 1 unit from the centromere (Driscoll and Bielig, 1968) and hence the genes for ACPH on 4A must lie within this distance.

Line W possesses a translocation to chromosome 4A from Triticum timopheevi, a diploid species of wheat. Pairing data suggests that the α arm is missing and the hypothesis is confirmed by the absence of the ADH marker. Also, one of the ACPH genes is missing which suggests that the translocation-breakpoint falls between these 2 genes on the β arm.

SUBRAHMANYAM, N.C.
Department of Genetics, R.S.B.S., A.N.U., Canberra, A.C.T.

GENOME BALANCE IN CONTROLLING CHROMOSOME STABILITY IN HORDEUM INTERSPECIFIC HYBRIDS

Interspecific crosses of Hordeum parodii (2n = 42) with H. bulbosum (2n = 14 or 28) and H. vulgare (2n = 14), and H. procerum (2n = 42) with H. bulbosum, H. vulgare and H. parodii were made. Crosses between parodii and diploid bulbosum resulted in haploids (2n = 21) of parodii, whilst the crosses of parodii by tetraploid bulbosum or diploid vulgare gave hybrid progeny. The procerum by diploid bulbosum cross produced invariably haploids (2n = 21) of procerum whereas, procerum by tetraploid bulbosum or diploid vulgare crosses resulted in both hybrids and haploids of procerum. The cross between procerum and parodii gave hybrid progeny which did not reach maturity.

Cytological observations on two-week old embryos obtained from reciprocal crosses revealed chromosome variability (not less than 21 in any cell) in haploid producing crosses. This shows that chromosome elimination leads to haploid formation irrespectiveof which species were used as female parent.

The results indicate that the ratio of the parental genomes in the zygote determines whether predominantly haploids or hybrids are produced in any cross combination. Furthermore, procerum appears to be not only more efficient in eliminating bulbosum chromosomes in comparison with parodii, but also capable of eliminating vulgare chromosomes. The possibility of 'stability factors' in overcoming chromosome elimination, a hierarchy of chromosome elimination and the general existence of genome balance for chromosome stability in interspecific crosses, are discussed.

STOCKER, A.J., and Pavan, C.
Department of Genetics, University of Melbourne, Parkville, Vic.

DEVELOPMENTAL PUFFING PATTERNS IN RHYNCHOSCIARA HOLLAENDERI

The larval salivary glands of Rhynchosciara hollaenderi with their highly polytene chromosomes provide a system in which correlations between biochemical and cytological aspects of gene expression can be carried out. However, detailed knowledge of the puffing changes that occur in salivary gland chromosomes during normal larval development are needed in order to establish such correlations. In order to provide such detailed information, we have undertaken a complete analysis of puff information and regression in 3 morphologically distinct regions of this organ throughout mid-larval to pupal development. In carrying out this investigation we have obtained the following results:

1) Puffing differences among the 3 gland regions have been distinguished and analysed.

   The presence of these differences suggests that the gland regions may be functionally differentiated in the secretory products they produce and also possibly, in the pathways they utilize during differentiation.

2) Specific puffing sequences have been found and correlated with morphological and physiological events which occur in the development of Rhynchosciara (i.e. changes in body form and hormone titres).

3) Developmental events in Rhynchosciara, a primitive Diptera, have been correlated with similar events in Drosophila, a higher Diptera. Recognition of these similarities in developmental processes between members of 2 suborders of Diptera have allowed us to make specific comparisons between the puffing sequences of these 2 organisms.
   Such comparisons, particularly with respect to the ecdysone-induced late larval puffing changes, have suggested that both similarities and differences in the control of gene activity may exist between Rhynchosciara and Drosophila.

MARTIN, Jon, LEE, B.T.O., and CONNOR, E.
Department of Genetics, University of Melbourne, Parkville, Vic.

## APPARENT INCIPIENT SPECIATION IN THE MIDGE CHIRONOMUS OPPOSITUS

Chironomus oppositus is quite polymorphic throughout its distribution area in south eastern Australia. In certain Tasmanian populations, most notably at Bellerive, there is an unusual distribution of inversions. All arms are polymorphic although arm G was not included in the study. Only arm F appears to fit Hardy-Weinberg expected values when the total population is studied; all other arms show highly significant deviations. Further investigation reveals that the population can be split into two subgroups, one having the sequence combination $B_1$,$D_4$,$C_1$ or $C_3$,$E_1$, and $A_1$ or $A_2$ (the $E_1$-group), the other having the combination $B_2$,$D_1$ or $D_2$, $C_2$,$E_2$ and $A_2$ or $A_5$ (the $E_2$-group). Within each of these groups the inversion polymorphisms fit Hardy-Weinberg values quite well. Genetic distance calculations indicate that the two groups differ from each other to a much greater extent than either differs from other Tasmanian or mainland populations. It is further shown that larvae of the two groups differ in metrical characters when subjected to multiple discriminant function analysis; the basic difference appears to be that $E_1$ group larvae are larger than $E_2$-group larvae.

We would postulate that the two groups are therefore undergoing a speciation process which appears to be unique to certain Tasmanian populations.

HOPE, Rory, DONALD, Jennifer, and BILLETT, Lorraine
Department of Genetics, University of Adelaide, Adelaide, S.A.

## PRELIMINARY CHARACTERIZATION OF MARSUPIAL X MOUSE SOMATIC CELL HYBRIDS

Marsupial lymphocytes from Pseudocheirus peregrinus (ring-tailed possum) and Megaleia rufa (red kangaroo) have been fused with cells from 6-thioguanine resistant, HGPRT deficient permanent mouse cell lines (PG-19 and 1-R). Selection in HAT medium has enabled the isolation, for the first time, of a number of proliferating hybrid clones that contain readily identifiable marsupial and mouse chromosomes. There is a rapid and preferential loss of marsupial chromosomes from these hybrids. In several of the hybrid clones, mouse and marsupial biochemical markers have been identified. A number of 6-thioguanine resistant sub-clones have been selected from the hybrids with a view to investigating the X-linkage of certain marsupial biochemical markers. In this paper the result- of our preliminary cytogenetic and biochemical characterization of the hybrid clones and sub-clones are presented. Marsupial x eutherian somatic cell hybrids provide particularly useful material for investigating genetic regulatory mechanisms and for chromosome mapping in marsupials.

SESSION 3B

LEHRBACH, P.R., and LEE, B.T.O.
Department of Genetics, University of Melbourne, Parkville, Vic.

## EFFECT OF PSEUDOMONAS R FACTOR ON UV-SENSITIVITY AND UV-MUTAGENESIS

The R factor pMG2 confers multiple drug resistance to gentamicin, sulphonamides and streptomycin. pMG2 also increases the resistance of host cells to ultraviolet light. The UV-protecting property of pMG2 has been examined in a variety of radiation and chemical-mutagen sensitive mutant of Pseudononas aeruginosa. Enhanced survival occurs in strains of $uvr^{+}rec^{+}$ (wild type) genotype and a variety of $uvr^{-}rec^{+}$ type mutants. No protection occurs in a recA-type mutant. pMG2 also enhances UV-induced mutagenesis.

These effects appear to be due to host-cell controlled plasmid-determined DNA repair function(s).

Studies on cells deficient in a DNA polymerase 1 function in P. aeruginosa suggest that a plasmid-determined repair resynthesis function may be responsible for increased UV-survival and enhanced UV-mutability in pMG2-containing cells.

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

## IDENTIFICATION BY RNA-DNA HYBRIDIZATION OF GENES FOR 23S and 16S RRNA WHICH MAP NEAR PHEA ON THE E. COLI K12 CHROMOSOME

Transducing phage carrying various portions of the 56 min (new map units) region of the Escherichia coli K12 chromosome have been isolated (Zurawski, G. and Brown, K.D. (1976). J.Mol. Biol. 102, 311-324). These phage provide convenient sources of defined regions of E.coli DNA on which the only known genes are those of the phenylalanine (pheO,pheA) and tyrosine (aroK,aroF,tyrA) operons.

In DNA-RNA hybridization experiments, using uniformly $^{3}H$-uridine labelled RNA from E.coli K12, DNA's prepared from the transducing phage λ phe10 and λtyr2 were able to hybridize at least 30% of the RNA. The magnitude of this hybridization, with a region which represents only 0.3-0.6% of the total E.coli chromosome, shows that the 56 min region is directing the synthesis of a major component of the RNA pool. Competition hybridization experiments identified this component as ribosomal RNA (rRNA). Similar experiments using purified 23S and 16S rRNA as competitors demonstrated that a gene for 23S and a part of a 16S RNA gene were present on λphe10 and λtyr2 DNA.

The phage λphe10 carries pheA, pheO and the rRNA genes but no genes of the tyrosine operon. Two other phage,λ tyr25 and λtyr38, which carry the tyrosine operon and the part of the phenylalanine operon proximal to tyrA, were found not to carry rRNA genes. This data suggests that these previously

unidentified rRNA genes (named rrnD)map between 56 and 55.5 min on the E.coli K12 chromosome. This map location places rrnD in a region containing two other genes concerned with RNA metabolism (ranA and trmC).

EADIE, J., SKOTNICKI, M.L., and ROLFE, B.G.
Department of Genetics, R.S.B.S., A.N.U., Canberra, A.C.T.

THE METABOLIC STATE OF NITRATE REDUCTASE IN E. COLI K12 AND ITS BIOLOGICAL IMPLICATIONS

SKOTNICKI, M.L., and ROLFE, B.G.

THE GENETIC CONTROL OF NITROGEN FIXATION AND NITRATE REDUCTION IN E. COLI

ROLFE, B.G., SKOTNICKI, M.L. and EADIE, J.

PHAGE LAMBDA LYSOGENY AS A MEASURE OF THE METABOLIC STATE OF E. COLI K12

SESSION 5

GODFREY, A.J., and MORGAN, A.F.
Department of Genetics, Monash University, Clayton, Vic.

STABILITY OF GROUP P PLASMIDS IN SUB-STRAINS OF PSEUDOMONAS AERUGINOSA

The stability of the P incompatibility group plasmid R68, is very different in two sub-strains of P. aeruginosa, strain one (PAO) and strain two (PAT). In PAO, the plasmid is normally stable and capable of mediating chromosomal transfer at low frequency. In PAT, on the other hand, the plasmid is unstable and capable of chromosome donor ability at a relatively high frequency.

Phenotypically the plasmid confers resistance to the antibiotics, carbenicillin, tetracycline and kanamycin/ neomycin; resistance to the aeruginocin AR41; and mediates its own transfer and promotes chromosomal donor ability. In PAT and mutants of PAO, the plasmid loses these markers at high frequency. The loss in PAT appears to be dependent upon a functional recA-like recombination system.

Breakdown patterns of R68 and a variant of R68 (R68.45) in unstable lines are used to produce a phenotypic map of the plasmid. Possible mechanisms for the instability are discussed.

APPELS, R., and PEACOCK, W.J.
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## THE LOCATION OF POLYPYRIMIDINE TRACTS WITHIN THE CHROMOSOMES OF SECALE CEREALE

Polypyrimidine tracts (single stranded lengths of DNA containing only the pyrimidine bases) were isolated from Secale cereale DNA using a standard chemical degradation procedure. Labelled cRNA was synthesised from the polypyrimidine tracts with E. coli RNA polymerase. The sequences recovered in the cRNA probe represented approximately 0.05% of the genome and consisted of sequences repeated many times over. The sequences however were not part of a single "satellite" as judged from a rather broad melting profile of RNA-DNA hybrids and terminal TI-RNAase digests of the cRNA. Although not homogeneous, the cRNA was found at major sites on only three of the seven chromosome pairs. In contrast to the majority of highly repeated DNA sequences (isolated using hydroxylapatite chromatography) which are principally localised in terminal heterchromatin, the poly-pyrimidine tracts were interstitial. Cross-hybridisation of cRNA from a defined polypyrimidine tract .... TCTTC .... (a satellite from Drosophila melanogaster) presented an in situ hybridisation pattern similar to that obtained with the Secale cereale cRNA probe, with 20% mismatching of base pairs.

The Secale cereale cRNA probe cross-hybridised with Triticum aestivum DNA to yield RNA-DNA hybrids identical (by $T_m$ criteria) to those formed in the homologous hybridisation reaction. The complementary sequences were four times more abundant in T. aestivum and were also specifically distributed among chromosomes.

The observations will be discussed in terms of the usefulness of hybridisation reaction for identifying chromosomes and the possibility that the sequences identified represent "spacer" DNA normally part of a gene complex.

GILLIES, C.B.
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## CAN ELECTRON MICROSCOPY VISUALISE THE SITES OF CROSSOVER EVENTS AT PACHYTENE?

The synaptonemal complex (SC) has been shown conclusively to be the basis of homologous chromosome pairing in meiotic prophase I. Absence of SC formation almost universally leads to absence of meiotic crossing over. This, together with the few cases in which SCs are present without the occurrence of crossing over, has led to the idea that the SC is a necessary but not sufficient condition for genetic recombination during eukaryotic meiosis.

It has been suggested that remnants of the SC which persist during diplotene are the sites of crossover events which eventually become chiasmata. Recently, Carpenter (PNAS 72: 3186, 1975) has suggested that the dense SC associated "nodules" she found at pachytene in Drosophila are directly involved in the process of genetic recombination. Somewhat

similar bodies, termed "nodes", have been found in the central component of the SCs of Ascomycetes by myself and other workers. This report will consider the evidence from serially sectioned Neurospora asci that such "nodes" correspond in number and position with expected crossover sites.

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[1]National Institute of Genetics, Japan
[2]School of Zoology, University of New South Wales, Kensington, N.S.W.
[3]Division of Entomology, C.S.I.R.O.

## A MODEL FOR KARYOTYPE EVOLUTION BASED ON AUSTRALIAN ANT POPULATIONS

We surveyed the karyotypes of over 100 Australian ant species for C-banding patterns using an air-drying technique. The primitive genus Myrmecia had the lowest number (2n = 9) in our sample, as well as by far the highest in Hymenoptera (2n = 84). Although a variety of other types were found, the most important detectable rearrangements in ant karyotype evolution appear to be, in diminishing order of significance, Robertsonian rearrangements, pericentric inversions, and "growth" of constitutive heterochromatin. Chromosome measurement analysis contraindicates polyploidy having played a significant role, if any at all, in ant karyotype evolution. Our C-banding and other data are more consistent with a model of chromosomal change in which numbers generally increase through centric fission than decrease through centric fusion. This model is supported by theoretical considerations on the likely effects of pericentric inversions because if, as seems likely, these occur and are fixed at random with respect to the centromere, then most chromosomes at any time will not have terminal or nearly terminal centromeres and hence will be unavailable for centric fusion. To the extent that centromere size is being continually augmented by gene duplication mechanisms, however, such chromosomes will be constantly available for fission. This model has fewer assumptions than the usual generalized selectionist one, is consistent with the ant data to hand, has wide potential applicability, and could serve at least as the null hypothesis against which claims of directional selection effects in karyotype evolution can be measured.

RICHARDSON, B.J.
Department of Population Biology, R.S.B.S., Canberra, A.C.T.

## THE MICRODISTRIBUTION OF GENETIC VARIATION IN WILD RABBIT POPULATIONS

The temporal and spatial distribution of alleles in rabbit populations in different environments will be described. The processes that give rise to these distri-

butions will be considered by relating data on changes in phenotype proportions from age class to age class in several cohorts of kittens to various mortality events in each environment. Mortality factors include predation, myxomatosis and various types of physiological stress. A computor model is used to examine alternative explanations of the field data.

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[1]Institute of Medical and Veterinary Sciences, Adelaide, S.A.
[2]Department of Population Biology, R.S.B.S., A.N.U., Canberra, A.C.T.

ELECTROPHORETIC DATA AND BIOCHEMICAL SYSTEMATICS

Constancy of rates of evolution of proteins is an explicit or implicit assumption in most biochemical approaches to cladistic taxonomy. By applying the concepts of symplesiomorphy and synapomorphy to electrophoretic data it may be possible to avoid this assumption and hence improve the resolving power of electrophoretic data as a systematic tool.

SESSION 6A

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

ANALYSIS OF X CHROMOSOME INACTIVATION IN SOMATIC CELL HYBRIDS

I am using somatic cell genetic methods to search for factors which control the differential expression of X chromosomes in the somatic cells of female mammals. In the experiments reported here, I have tested the hypothesis that the active or inactive state of an X chromosome depends on the continued presence of a controlling factor on its homolog, or on one of the autosomes.

Mouse x hamster cell hybrids have been obtained which have full sets of mouse chromosomes, but different partial sets of hamster chromosomes. The states of the X chromosomes (as indicated by their morphology and DNA replication times) in these hybrids has been examined, and it has been found that the properties of each X chromosome remain unchanged, despite loss of any combination of autosomes, or of the other X. There is no evidence, therefore, that factors on other chromosomes control the activity of X chromosomes

DONALD, Jennifer A.
Department of Genetics, University of Adelaide, Adelaide, S.A.

A METHOD FOR MEASURING TRANSCRIPTION APPLIED TO X-CHROMOSOME INACTIVATION IN KANGAROOS

It is possible to differentiate between active and inactive portions of the DNA by using tritiated uridine-induced chromosomal aberrations as an index of transcriptional activity. The technique rests on the assumption that such aberrations occur principally when the DNA and labelled RNA are in apposition, during transcription.

This method was applied to the paternal X-inactivation system of kangaroos to investigate the effects of X-chromosome inactivation on RNA synthesis. The results of a comparison between the paternal X-chromosome of a hybrid kangaroo and the two X-chromosomes of a normal female supported the conclusion that dosage compensation operates by paternal X-inactivation in kangaroo lymphocytes. However, there was significantly greater transcriptional activity of the paternal X in fibroblasts than in lymphocytes of the same animal, which agrees with recent biochemical findings suggesting activation of the paternal X in fibroblasts.

WEBB, G.C., WHITE, M.J.D., CONTRERAS, N., and CHENEY, J.
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## G- AND C-BANDING STUDIES ON WARRAMABA VIRGO AND ITS BISEXUAL RELATIVES

G- and C-banding patterns have been investigated in the parthenogenetic morabine grasshopper Warramaba virgo (Key) from localities in Western Australia and from western N.S.W. There is considerable variation in the pattern of C-banding between different localities, some variation within localities, and some technical variation.

The suggestion of Hewitt (1975) that W. virgo was the product of hybridization of two bisexual species P196 and P169 will be discussed in the light of findings to date including comparisons of G- and C-banding of the ancestors and the related species P151 and P125. P169 shows a high level of variation of G- and C-bands which are polymorphic in the two populations investigated; P196, P151 and P129 are also variable. In general the G- and C-banding results and some autoradiographic data give support to the Hewitt hybrid-origin hypothesis.

A few female diploid hybrids between P169 females and P196 males have been bred and these appear to undergo the same meiotic processes as in W. virgo; i.e. premeiotic tetraploidization with pairing between identical chromosomes during meiosis leading to a diploid egg with the same genome as the female parent. When W. virgo is fertilized by P196 or P169 males the male haploid genome is added to the diploid genome in the egg yielding triploid males and females. Triploid males are sterile but the females are able to produce triploid eggs by the W. virgo meiotic mechanism.

LOHE, A.R.
Genetics Department, R.S.B.S., A.N.U., Canberra, A.C.T.

## AN ANALYSIS OF SATELLITE DNAS IN DROSOPHILA SIMULANS

Drosophila simulans total DNA was centrifuged in an actinomycin D-CsCl gradient, and fractions of the gradient examined in five different ways to detect the highly repeated, or satellite DNAs. This analysis reveals seven distinct byoyant density satellites present in the species.

The sequences of satellites are not lost during evolution but are rigidly maintained as is demonstrated by positive filter hybridization assays of four satellites from the sibling species D. melanogaster to D. simulans DNA. However, the absolute amount of a given satellite is different between the two species. The chromosomal locations of the satellites are being compared in the two species by in situ hybridization to ascertain whether the sites are also maintained within the heterochromatin. In this way, information regarding the rate of evolution of the heterochromatic regions of the chromosomes compared with the evolution of the euchromatin can be obtained.

SMYTH, D.R.
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LOCATIONS AND POSSIBLE FUNCTIONS OF HETEROCHROMATIN IN CHROMOSOMES OF LILIUM

To date no one has described much, if any, heterochromatin in true lilies. Following C-banding treatments of root-tip cells, we have revealed three categories - at every centromeric region, adjacent to all nucleolar constrictions, and in several intercalary regions. By varying the time of pretreatment, each of the classes appear and disapppear in a set, overlapping order.

As far as function is concerned, the apparent universality of centromeric bands suggest a role in chromosome movement. The nucleolar bands are adjacent to secondary constrictions, and probably fit McClintock's original definition of "nucleolar organizing body" better than thecommon usage, which ascribes organization to the constriction itself. Finally, the function of intercalary heterochromatin, which shows extreme inter-specific variation imposed on an apparently stable karyotype, is enigmatic.

SESSION 6 B

STARK, A.E.
School of Community Medicine, University of New South Wales.

A REVIEW OF SOME CLASSICAL THEORY OF POPULATION GENETICS

The genotypic distribution of a population at generation $t$ is given by the array $f_0(t)aa + f_1(t)aA + f_2(t)AA$.

The frequencies of mating pairs at generation $t$, denoted $(f_{xy}(t))$ in a model of non-random mating are assumed to be given by

$$f_{xy}(t) = f_x(t)f_y(t)\,[1 + \mu d_x(t)d_y(t)/S(t) + \nu \ell_x(t)\ell_y(t)/T(t)], \quad (1)$$

$$(x = 0,1,2;\ \ y = o,1,2),$$

where the elements of $[d_x(t)]$ etc. are functions of $[f_x(t)]$ which make $(1)$ a canonical form.

If $\mu$ is held constant, gene frequencies remain constant and the genotypic distribution tends at a geometric rate to

the array $(q^2+\lambda pq)\ aa + (2pq - 2\lambda pq)\ aA + (p^2+\lambda pq)AA$, where $q$ and $p$ are the respective frequencies of genes $a$ and $A$ and $\lambda$ is related to $\mu$ by the formula $\lambda = \mu/(2-\mu)$.

If systematic mating occurs at rate $\alpha$ and random mating at rate $1-\alpha$, three standard systems of partial inbreeding can be identified as follows:

| | Partial selfing | Partial sib mating | Partial parent-offspring mating |
|---|---|---|---|
| $\lambda$ | $\alpha/(2-\alpha)$ | $\alpha/(4-3\alpha)$ | $\alpha/(4-3\alpha)$ |
| $\nu$ | $\alpha$ | $2\alpha/[(2-\alpha)(4-\alpha)]$ | $\frac{1}{2}\alpha/(2-\alpha)$ |

MCKENZIE, J.A.
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## THE EFFECT OF IMMIGRATION ON GENETIC CONTROL IN POPULATIONS OF DROSOPHILA MELANOGASTER

Immigration by wild type flies into an established compound chromosome control zone was studied in the laboratory using discrete generation population cages. Immigration rates of less than 10% per generation by virgin migrants were unlikely to disrupt the zone. The zone could be disrupted by immigration rates of 0.5% if the migrants had mated, although there was some indication of a possible equilibrium between immigration rate and the maintenance of the control zone.

These results will be discussed in relation to the results of a release of a compound chromosome stock into a natural population.

NICHOLAS, Frank
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## THE EFFECT OF SELECTION ON THE STANDARDIZED VARIANCE OF GENE FREQUENCY

The standardized variance of gene frequency $[f = \frac{\sigma^2_q}{q(1-q)}]$ is one of the many parameters studied by workers attempting to examine the relative importance of selection and random drift in determining the observed pattern of evolution. In studies involving f, selection has been implicated if observed f values are heterogeneous, and the type of selection has been inferred from the relative magnitude of f values. However, the conclusionsas to the type of selection acting have been made without a proper understanding of the way in which various models of selection affect f.

In this study, the theoretical effect of directional and heterotic selection on the standardized variance of gene frequency has been examined. It has been found that heterotic selection always results in f values lower than

those expected due to drift alone. Additive directional selection can result in low f values, but values larger than those expected due to drift will be observed under additive selection with low initial gene frequency, or when the populations have been separated for a relatively long period of time in which case f expected due to drift is quite high (around 0.7 or greater).

The effect of selection on f is unlikely to be detected if the observed value of f is less than 0.1.

BEILHARZ, R.G.
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THE EFFECT OF INBREEDING ON TOTAL REPRODUCTIVE POTENTIAL IN MICE

A control population of mice has been propagated for 26 generations by 20 pairs (families) of mice each leaving 1 son and 1 daughter selected at random from the litter. The daughter has continued the family number. The son has moved systematically to family n + 1, N + 2, n + 4, n + 8, n + 16, n + 1, .... in generations 1, 2, 3, 4, 5, 6, .... to produce generations 2, 3, 4, 5, 6, 7, .... respectively. This breeding plan has avoided any possibility of inbreeding for 5 generations. Thereafter the theoretical inbreeding coefficient has risen irregularly, but with major peaks at generations 6, 11, 16, 21, and 26, and with minor peaks at generations 9, 14, 19, and 24. Actual inbreeding coefficient must be higher than the theoretical inbreeding coefficient as not all families have produced a son and daughter in each generation.

Data are presented to show that Total Reproductive Potential (Total weight of progeny produced at 9 weeks of age per female mated) is very sensitive to changes in inbreeding coefficient. Eight of the nine peaks of theoretical F were associated with a drop in reproduction. In only 2 of the remaining 17 generations did reproduction show a decrease from the previous generation.

ABSTRACTS OF DEMONSTRATIONS

1. BARTHEL, Sylvia, and GRESSHOFF, Peter
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CHLAMYDOMONAS REINHARDI: MOLECULAR GENETICS AND ITS APPLICATIONS

The heterothallic green unicellular alga Chlamydomonas reinhardi has served as an experimental material in investigations concerned with:

(i) DNA repair and replication
(ii) cytoplasmic inheritance and chloroplast autonomy
(iii) mutation-ultrastructural correlations
(iv) cell wall assembly
(v) photosynthesis
(vi) genetics of recombination
and (vii) cell cycle analysis.

This demonstration aims to emphasise the past involvement of C. reinhardi in research concerned with the molecular biology, genetics and physiology of eukaryotes, as well as pointing towards recent interests in this alga in our laboratory.

These recent interests centre on the molecular genetics of gene transfers either by transformation or protoplast fusion. The research programme takes particular advantage of genetic lesions resulting in the loss of the cell wall. Additionally an expanded spectrum of mutants are utilised.

2. BEDO, D.G.
Department of Population Biology, R.S.B.S., A.N.U., Canberra, A.C.T.

## POLYTENE CHROMOSOMES IN PUPAL AND ADULT BLACKFLIES

Eight Australian blackfly species representing three genera, Simulium, Austrosimulium and Cnephia, were examined for the presence of good quality polytene chromosomes. Banded polytene chromosomes were found in malpighian tubules, hind gut, fat body and ovary, but only those in the malpighian tubules of female adults and pupae proved to be cytologically favourable. Detailed comparison of larval salivary gland and adult malpighian chromosomes were made in Simulium ornatipes and, to a limited extent, in S. melatum. The banding patterns of chromosomes from both tissues are identical with minor differences in puffing and chromocenter expression. A survey of the remaining six species shows five of them to have malpighian chromosomes suitable for analysis. This work offers the novel approach of simultaneous cytological study of larval, pupal and adult populations in the Simuliidae. The ability to recognise sibling species in adults also has potential practical significance in efforts to control vectors of onchocerciasis.

3. DARVEY, N.L.
Plant Breeding Institute, University of Sydney, N.S.W.

## RESTITUTION IN WHEAT-RYE HYBRIDS

Part of a novel breeding method for the rapid production of triticales depends on the phenomenon of genome restitution on the embryo side of a wheat-rye (4x) polyhaploid. Theoretically, restituted embryos are then fertilized by triticale pollen to give rise to a vast genotypic array of secondary triticales.

The breeding method involves two basic steps

(1) Male sterile wheat x rye, and
(2) Wheat-rye polyhaploid x triticale

Both steps are carried out in the field by planting the parents in alternating rows. Resulting triticales would then be subjected to selfing and selection.

During 1975, 63 seed were obtained on 87 wheat-rye polyhaploids grown adjacent to 6x and 8x triticales. In one cross involving 27 plants, 33 seed were obtained from thirteen of the 27 plants; however no seed was obtained from 9 plants of the same genotype which were isolated from the triticale pollen.

Cytological examination of root tips from the resulting seed by use of heterochromatin banding and standard Feulgen techniques confirmed the phenomenon of female genome restitution. There was also good evidence to suggest that polyhaploids containing an extra dose of chromosome 1R and particularly of chromosome 5R gave higher frequencies of restitution than polyhaploid plants containing an extra dose of other rye chromosomes.

4. DONNELLAN, S., DANIEL, A., and LAI, L.Y.C.
Cytogenetics & Cell Biology Unit, Prince of Wales Hospital, Randwick.

## SOME RELATIONSHIPS BETWEEN MEMBERS OF THE LIZARD FAMILY - SCINCIDAE

The lizard family Scincidae is well represented in Australia with approximately 19 genera and 150 species.

The species, Egernia cunninghami (Cunningham's Skink)
Tiliqua scincoides (Blue tongue Skink)
Sphenomorphus quoyii (Eastern water Skink)
Leiolopisma delicata (Garden Skink)

were selected to investigate phylogenetic relationships as represented in chromosome morphology by the application of the chromosome banding techniques: Q,C,G and N developed in human cytogenetics.

Initial results in Egernia cunninghami reveal a diploid number of 32 with 22 macrochromosomes (18 meta and sub-metacentrics, 4 acrocentrics) and 10 micro-chromosomes. The microchromosomes in this species are G and C band negative indicating that they represent a significant proportion of the genome. This result is discussed in relation to the other species.

5. GERLACH, W.L.
Division of Plant Industry, C.S.I.R.O., Canberra, A.C.T.

## LOCATION OF HIGHLY REPEATED DNA SEQUENCES IN THE WHEAT GENOME

A rapidly renaturing DNA fraction from hexploid wheat (var. Chinese Spring) has been isolated and a number of its biochemical properties characterized. In situ hybridization shows that this DNA is located at a number of specific sites on the chromosomes. Ditelocentric stocks are being used for individual chromosome identification.

The results are compared with those of a chromosome banding technique which also permits identification of some chromosomes. These procedures should be of value in monitoring individual wheat chromosomes in cereal breeding programmes and in investigating the origin of the B genome in wheat.

6. LANGRIDGE, J.
Division of Plant Industry, C.S.I.R.O., Canberra, A.C.T.

A MOLECULAR VECTOR FOR PLANT AND BACTERIAL CELLS

The diagrams show:

(a) the preparation of a hybrid molecule composed of the replication sequence and coat protein gene of cauliflower mosaic virus combined with the replication sequence and kanamycin resistance gene of the bacterial plasmid RP1;

(b) the method of isolation of the replication sequences of chloroplast DNAs and the linking of such sequences to plasmid DNA.

7. LATTER, B.D.H.
School of Biological Sciences, University of Sydney, Sydney, N.S.W.

GENE FREQUENCY DISTRIBUTIONS IN SPECIES OF DROSOPHILA

One way of testing the applicability of Kimura's neutrality hypothesis to genetic polymorphisms in natural populations, involves the pooling of data from large scale surveys to determine the shape of the overall gene frequency distribution. Provided the gene frequency data are homogeneous over the species examined, and the loci concerned are subject to similar mutation rates, comparisons may readily be made of observed distributions with those predicted for electrophoretic variants under the hypothesis of selective neutrality.

The equilibrium gene frequency distribution for the charge class model of electrophoretic variation has not yet been determined for populations with geographic structure. Computer simulation has therefore been used to determine the equilibrium distribution of mean gene frequency for both neutral models and those involving natural selection. Comparisons with data from natural populations of Drosophila indicate that the neutral model sensu stricta is inappropriate, but the selection coefficients involved appear to be of an extremely low order. From an evolutionary point of view, much of the electrophoretic variation may justifiably be considered to be effectively neutral.

8. McWHIRTER, K.S.
Department of Agricultural Botany, University of Sydney.

CANALIZATION OF ENDOSPERM DEVELOPMENT IN OPAQUE-7 MAIZE

The opaque-7 mutant in maize is associated with a high lysine content of the endosperm protein and a range of other phenotypic effects.

Segregation of opaque endosperm vs normal endosperm phenotypes was studied in a range of genetically heterogeneous maize crosses, also heterozygous at the opaque-7 locus. Widely varying but reproducible frequencies of opaque endosperm kernels were observed in F2 and reciprocal backcross matings. Also, there was marked but not complete discontinuity of endosperm phenotypes. These observations conform to expectation for a threshold character, and provide evidence for segregation of alleles in a polygene complex which may substitute for the major gene in determining texture of the triploid endosperm. The control of endosperm development is interpreted to involve 3 components,

1) a major gene - the dominant 07 allele,

2) a polygene complex,

and 3) a threshold of endosperm developmental activity resulting in discrete levels of phenotype expression.

This genetic system for canalization of endosperm development is disrupted by mutation of the 07 locus.

9. MORAN, C., and SHAW, D.
Department of Population Biology, R.S.B.S., A.N.U., Canberra, A.C.T.

CHROMOSOMAL RACES IN CALEDIA CAPTIVA WITH A NARROW ZONE OF HYBRIDIZATION IN S.E. QUEENSLAND

Two chromosomal races of the grasshopper Caledia captiva show contiguous non overlapping distributions in S.E. Queensland. The "Torresian" race, which occurs widely throughout Eastern Queensland, the Northern Territory and South-western Papua, is fixed for easily recognisable acro- and telocentric chromosomes. The "Moreton" race is restricted to the coastal regions of S.E. Queensland and Northern New South Wales and its chromosomes are characterised by a series of large polymorphic pericentric inversions. The geographical distribution and the frequency variation of these inversions have been mapped over most of the range of the race.

Several transects have been made across the zones of contact between the two races. The region of transition between these two chromosomal races is extremely narrow and abrupt. Only minimal levels of hybridisation between contiguous populations has been detected.

The observed frequency of hybrid karotypes along the contact zone is correlated with the structural arrangement of the X chromosome found in the "Moreton" race.

10. MULLEY, J.C., and LATTER, B.D.H.
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## GENETIC VARIATION IN PRAWNS

Genetic variation is being studied in 12 species of Australian prawns from the genera Penaeus and Metapenaeus. Abnormally low levels of genetic variation are emerging with average heterozygosity estimates between 2 and 4 per cent. A large number of loci have been examined, and the level of variation is consistent between species. In some species sample sizes are large and taken from widely separated localities. It appears that the amount of variation in some groups of species may be lower than many previous electrophoretic studies suggest.

At those loci where genetic variation was found the degree of geographical differentiation is small. Furthermore, much of the variation is restricted to the same loci over species. Finally genetic distances will be estimated and compared with morphological taxonomy.

11. NICHOLLS, E.M., LAZER, C., MITCHELL, N., GILBETT, D., and THERIN, G.
School of Community Medicine, University of New South Wales.

## LEUCOAGGLUTINATION

Genetic studies of agglutination of blood cells began with Landsteiner in 1900. The cells agglutinated were the erythrocytes. The first leucocyte agglutination was described in 1926. The method has not played a great part in defining polymorphic systems in leucocytes: current procedures for recognizing leucocyte antigens most often involve a lymphocytotoxicity test. The first agglutination of leucocytes by the technique on display was carried out (Nicholls 1974) using bacterial antigens. It was believed that T lymphocytes, recognizing antigen, produced leukotactic factors which clumped other leucocytes. This procedure also recognized histocompatibility antigens. The sera of patients with cancer and autoimmune diseases, and of multiparous women, also cause agglutination similar in appearance to that caused by antigen. However, the appearance of the agglutination in these cases may be quite different, more in character with a weak red cell agglutination. Perhaps the first type of agglutination is due to antibody activation of lymphocytes as proposed for antigen, while the other is a passive agglutination as in a red cell agglutination. The theory being considered to explain the production of the antibodies in cancer and autoimmune diseases is briefly as follows. In cancer the clonal growth of the tumour cells is paralleled by a similar growth of clones of lymphocytes,

which by the time the tumour contains say $10^{10}$ cells, should be very large. In autoimmune disease large clones of lymphocytes also arise with activity against self antigens. Antibodies against these large numbers of lymphocytes may arise as a negative feedback control within these systems. These antibodies may be anti-allotypic or anti-idiotypic.

12. SAVILLE, T., DANIEL, A., GRAS, L., STEWART, L., SILVER, M. and LAM-PO-TANG, P.R.L.C.
Cytogenetics and Cell Biology Unit, Prince of Wales Hospital, Randwick/

THE STRUCTURE OF ISOCHROMOSOMES OF X AND Y IN MAN

Mixoploidy is only found in about 35% of the cases of ovarian dysgenesis in man. Most of the mixoploids have a 46 cell line with an "isochromosome" derived from the X or Y. The true nature of these isochromosomes has yet to be determined although the generally accepted model is of centromere misdivision. The other cell line is hypodiploid with monosomy for the X. It is a logical hypothesis that the proportion of 45 cells in vivo reflects the level of stability of these isochromosomes. Data on isochromosomes of the q(long) and p(short) arms of the X and Y are compared with that of i(17q) found in human myeloid leukaemias and i(18p) found in small metacentric syndrome. These results are discussed with reference to the concept of centromeric suppression (Sears & Camera, 1952., Niebuhr, 1972 and Daniel & Lam-Po-Tang, 1976)

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Sears, E.R., Camara, A., (1952). A transmissable dicentric chromosome. Genetics 37, 125.
Niebuhr, E. (1972). Dicentric and Monocentric Robertsonian translocations in Man. Humangenetik 16, 216-226.

13. SCHMITT, L.H., and WHITE, R.J.
Department of Genetics, University of Adelaide, Adelaide, S.A.

A COMPARISON OF GENETIC AND METRIC VARIATION IN RATTUS FUSCIPES GREYII.

In South Australia, the southern bush-rat (Rattus fuscipes greyii) inhabits many off-shore islands as well as three separate areas on the mainland. These populations have been reproductively isolated for 6,000-14,000 years. A study has been made of genetic variation using sixteen electrophoretically detected loci and metric variation using fourteen skull and four external measurements. The metric data have been analysed by canonical discriminant analysis and the genetic distance metric of Nei and by correspondence analysis (a modification of principal components for contingency tables). These analyses are summarised by means of dendrograms and scatter diagrams. The patterns in genetic and metric variation show many similarities.

14. SHAW, D., and KNOWLES, G.R.
Department of Population Biology, R.S.B.S., A.N.U.
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THE ANALYSIS OF CHIASMA DISTRIBUTION IN TWO SPECIES OF THE GENUS CALEDIA (ORTHOPTERA : ACRIDINAE) USING A COMPUTERISED OPTICAL DIGITISER

A new computerised system of analysing the distribution and frequency of chiasmata along the diplotene bivalent has been devised. This involved the projection of a fine light spot via a drawing tube into the field of view of the microscope. The width of the light spot is similar to that of each chromatid and the spot can be moved along the chromosome of each bivalent in a standardised manner. The light cursor is mounted on a drawing board and is attached to two take-up drums by inextensible strings. Changes in the length of these strings after movement of the cursor are converted into voltage charges by mounting the drums on the shafts of potentiometres. The string lengths are converted into X and Y co-ordinates and the digitiser is connected to a PDP 12 digital computer.

The data, recorded on tape, include the following:- for each bivalent, a mean value of the distances of each chiasma from the centromere is recorded, together with bivalent and cellular chiasma frequencies. Frequency distributions of chiasmata per unit chromosome length are printed out for each bivalent. Frequency distributions of the interference distance variation within chiasma frequency classes are also provided.

As an example, the technique has been used to analyse the chiasma patterns in two species of the genus Caledia and in two of the chromosomal races within the species C. captiva. Statistical comparisons have been made of the frequency of chiasmata at the bivalent and cellular levels and of the positions of these chiasmata along the bivalents at diplotene.

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

MAPSIM - A TEACHING PROGRAM FOR COMPUTER SIMULATION OF GENE MAPPING IN DROSOPHILA

MAPSIM is a computer program which simulates the mapping of an unknown recessive visible or lethal mutation to a particular position on a model chromosome II of D. melanogaster. A set of 11 recessive and 3 dominant markers is provided for the mapping, together with the mutant whose position on the chromosome is generated at random. Only single marker stocks are provided, so that any multiple marker stocks required for the analysis must be synthesised. The building-up of stocks and gradual narrowing down of the area of interest are aspects of gene mapping which are too time-consuming to be attempted in normal practical classes, but in many respects this part of the procedure is more instructive than the actual

analysis of the final testcross data to determine the map position, and constitutes the main value of the program.

The basic principle of the program is that all input and output are in terms of phenotypes, rather than genotypes. The program of course keeps track of and manipulates genotypes, but these are not displayed. Two levels of uncertainty are built into the program - normal chance variation, and an additional small random variation in recombination along the chromosome, so that only information from 3-point crosses using reasonably closely linked markers can give accurate map positions.

16. WILLIAMS, Keith, STENHOUSE, Fay, and ROBSON, Gill
Genetics Department, R.S.B.S., A.N.U., Canberra, A.C.T.

## DIFFERENTIATION AND GENETIC ANALYSIS IN THE CELLULAR SLIME MOULD DICTYOSTELIUM DISCOIDEUM

Dictyostelium discoideum occupies the border between unicellular and multicellular organisms. It lives as a solitary amoeba in the soil litter layer and eats bacteria; when starved, up to $10^5$ amoebae aggregate together by chemotaxis and form a 'slug' which migrates to the surface of the soil (towards heat and light). Final differentiation occurs with the formation of the asexual fruiting body consisting of 3 cell types - spore, stalk, basal disc. Spores are dispersed and each releases a single amoeba on germination.

This life cycle is readily reproduced in the laboratory with large numbers of amoebae, sufficient for biochemical analysis. Of particular interest is the asexual fruiting body which shows relatively constant proportioning of the 3 cell types and hence represents a simple model for embryogenesis.

Present studies emphasise the development of genetic analysis in D. discoideum. Genetic analysis using the parasexual cycle is proving to be successful and most of the linkage groups have been marked. The haploid chromosome number is 7 and, although the chromosomes are very small, each chromosome has been identified using Giesma banding techniques.

48TH ANZAAS CONGRESS - "Science for Society"
Melbourne : August 29 - September 2, 1977.

We are writing to all the professional societies that have been asked to contribute symposia to our section programme in order to draw attention to our need for information.

The Congress is a long way off but we have a deadline early in December for the submission of material for the First Congress Circular. We have to provide programme details: titles of symposia, the session at which each will be given and lists of speakers. A complicating factor is that our programme has to be integrated with those of other sections.

All this will take a great deal of time and to make any real progress we need to know how many professional societies will be presenting symposia.

We would then appreciate an early decision from the Genetics Society of Australia. If a symposium is to be arranged, and we very much hope it will, a broad provisional title that will indicate the scope would be very helpful. We will then be able to allocate it to an appropriate session.

Over recent years there has been a marked increase in the number of societies of professional biologists which meet independently of ANZAAS Congresses. For this reason, and others, fewer and fewer of us attend these Congresses which, as far as biologists are concerned, no longer fulfil the objective "of bringing together scientists of all types and occupations so that they may interchange information and ideas".

From several sources we have received suggestions that this important objective could be achieved by an association of specialist societies on the lines of the American Institute of Biological Sciences. The major function of such an association would be to organise annual scientific meetings involving all the member societies.

If there is sufficient interest in this proposal, the Committee of Section 11 (Zoology) would arrange for a discussion to be held at the ANZAAS Congress in Melbourne next year.

We would be pleased to hear, at your earliest convenience, whether representatives of your Society would take part.

F.H. Drummond A.A. Martin
Joint Secretaries of Section 11

The opinions of the membership on these matters will be solicited at the Business Meeting on Thursday.

## POSITION VACANT

GRIFFITH UNIVERSITY
Brisbane

School of Science

## LECTURER IN GENETICS

Griffith University admitted its first undergraduates in 1975. The educational philosophy is to encourage a multi-disciplinary approach wherever appropriate. The School at present has 26 faculty staff across the areas of mathematics, physics, chemistry, biochemistry, physiology and science, technology and society.

It is anticipated that the appointee will have interests in molecular genetics and its interactions with biochemistry. The main teaching duties will be responsibility for the second year general genetics course and laboratory, but there will also be participation in the integrated first year and a third year course in molecular genetics.

As well as pursuing individual research interests, the appointee will be encouraged to initiate or participate in collaborative research. Some research interests presently in the School include: biochemistry of growth and differentiation; isozyme genetics and evolution; membrane proteins and energetics; contractile systems; electron microscopy; reproductive physiology.

The appointment will be from July 1st. 1977 and will probably, but not necessarily, be in the lower half of the lecturer salary scale, which is at present $13,033 - $17,427. Further details of the post and of the method of application may be obtained from the School Administrator, School of Science, Griffith University, Nathan, Qld. 4111. The closing date for applications is October 16th.

GENETICS SOCIETY OF AUSTRALIA 23RD GENERAL MEETING
UNIVERSITY OF NEW SOUTH WALES 26-27 AUGUST 1976

ADDITIONAL ABSTRACTS

B.G. Rolfe, M.L. Skotnicki, J. Eadie, D. Dykhuizen and J.H. Campbell

## PHAGE LAMBDA LYSOGENY AS A MEASURE OF THE METABOLIC STATE OF E. COLI K12

The biological function of the lambda rex gene is to aid in the establishment of lysogney under aerobic and anaerobic growth conditions in most E.coli K12 strains. Anaerobically in E. coli K12 strains, the rex function is necessary for the stable maintenance of established lambda lysogens by helping to maintain repression during anaerobic growth. Bacterial mutants which show a marked increase in λ lysogeny also have the capacity to fix nitrogen. This provides us with a simple bioassay for bacterial mutants defective in regulation of their metabolic state.

J. Eadie, M.L. Skotnicki and B.G. Rolfe.

## THE METABOLIC STATE OF NITRATE REDUCTASE IN E. COLI K12 AND ITS BIOLOGICAL IMPLICATIONS

Factors affecting the physiological state of a mutant of E. coli which appears to be defective in its ability to switch from aerobic to anaerobic conditions, will be reported. Adenine, Molybdenum, Iron, carbon source, temperature and oxygen play an important part in the aerobic/anaerobic switch mechanisms.

M.L. Skotnicki and B.G. Rolfe

## THE GENETIC CONTROL OF NITROGEN FIXATION AND NITRATE REDUCTION IN E. COLI

Using a mutant of E. coli defective in its ability to switch from aerobic to anaerobic conditions, nitrogen-fixing strains were isolated. These strains now exhibit a range of pleiotropic changes, such as ability to use histidine as sole carbon/nitrogen source, non-fermentation of glucose, and inability to use succinate, acetate and glycerol. Other mutants of E. coli defective in nitrate reductase or uncoupled in oxidative phosphorylation showed similar pleiotropic changes.

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