GENETICS SOCIETY OF AUSTRALIA 16TH ANNUAL GENERAL MEETING FLINDERS UNIVERSITY, AND UNIVERSITY OF ADELAIDE 14-15 AUGUST 1969

CIRCULAR 2

PROGRAMME

AGENDA, BUSINESS MEETING

ABSTRACTS

SCANNED FROM THE ORIGINAL

### GENETICS SOCIETY OF AUSTRALIA

16th General Meeting 14-15th August, Adelaide

#### CIRCULAR 2

### Programme

A provisional programme accompanies this circular. All offers of papers have been accepted. Any member who offered to read a paper and does not appear on this programme should inform the Secretary immediately. Abstracts should be sent to the Secretary not later than July 16th if they are to be included in the final programme.

### Registration and notification of attendance

It will greatly assist the committee if all members who intend to be present at the meeting would notify the Secretary by July 16th. A form is provided. It would also be convenient if the registration fee (members including graduate students \$2, undergraduate students \$1) were paid at this time. It will be possible to register at the beginning of the meeting although there is no free time available for this purpose.

#### Genetical Society Dinner

The dinner will be held at Flinders University at 7.30 p.m. on Thursday, 14th August. The cost will be \$3 per head inclusive for the meal, sherry and table wine, members may bring guests. It is essential that those attending the dinner should notify the Secretary by July 16th.

#### Evening Lecture

A talk entitled :"General aspects of Genetic Regulation" will be given by Professor J.A. Pateman, Flinders University.

# AUSTRALIAN GENETICAL SOCIETY

# Adelaide meeting 14-15 August 1969

# Provisional programme

# Thursday 14 August, Flinders University

# Session 1A

9.00	M.J. Hynes, School of Biological Sciences, Flinders University.	Regulation of amidase in Aspergillus.
9.20	K.K. Jha, Research School of Biological Sciences,	Frameshift mutants in his-3 locus of N. crassa.
	The Australian National University	
9.40	J. Pemberton, Monash University.	Mutant of <i>Pseudomonas</i> <i>aerugonosa</i> with increased fertility.
10.00	E.M. Walker & A.J. Pittard, School of Microbiology, University of Melbourne.	Temperature sensitive conjugation defective F factor of <i>E. coli</i> K12.
10.20	R.R.B. Russell and A.J. Pittard, School of Microbiology, University of Melbourne.	Mutant strains of <i>E. coli</i> unable to synthesise protein at 42°C.
10.40	COFFEE	
11.10	K.D. Brown, Research School of Biological Sciences, The Australian National University.	Aromatic amino acid transport in E. coli.
11.30	J. Camakaris and A.J. Pittard, School of Microbiology, University of Melbourne.	The regulation of tryptophan biosynthesis in <i>Escherichia</i> <i>coli</i> K12.
11.50	S.W.K. Im and A.J. Pittard, School of Microbiology, University of Melbourne.	A mutant of <i>Escherichia coli</i> derepressed for a multi- functional enzyme concerned with phenylalanine biosynthesis.
12.10		

12.30 LUNCH

# Session 1B

9.00	S.Smith-White, C.R. Carter and H.M. Stace, School of Biological Sciences, University of Sydney.
9.20	S. Smith-White, C.R. Carter, School of Biological Sciences, University of Sydney.
9.40	H.M. Stace, School of Biological Sciences, University of Sydney.
10.00	S.H. James, Department of Botany, University of Western Australia.
10.20	C. Beltran, Department of Botany, University of Western Australia.
10.40	COFFEE
11.10	L.B. Bousefield, Department of Botany, University of Western Australia.
11.30	E. Craddock, School of Biological Sciences, University of Sydney.
11.50	N.D. Murray, School of Biological Sciences, University of Sydney.
12.10	J. Ford, Botany Department, University of Sydney.
12.30	LUNCH

Cytology of Brachycome.

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Cytology of Brachycome.

A model for the evolution of complex hybridity in Isotoma petraea.

Heterosis in interpopulational hybrids of Isotoma petraea.

B chromosome in Dampiera linearis.

Zones of overlap of chromosome races in stick insect Didymuria violescens.

Geographic variation and natural selection in the beetle Calomela bartoni.

Selective degeneration of nuclei during microsporogenesis in the Epacridaceae.

# Session 2

2.00	B. Holloway & J. Pemberton, Faculty of Science, Monash University.	A new class of recombinant deficient mutants.
2.20	B. Austin, Research School of Biological Sciences,	Specificity in rec genes in <i>N. crassa</i> .
	Australian National University.	
2.40	D.R. Smyth, Research School of Biological Sciences, Australian National University	The genetic control of recombination within the <i>am-1</i> gene of <i>Neurospora crassa</i> .
3.00	G. Grigg, C.S.I.R.O., Division of Animal Genetics, Sydney.	Excision, repair, recombination and mutation.
3.20	K.S. McWhirter, University of Sydney.	Significance of activator- dissociation system involv- ing $R$ locus in maize.
3.40	TEA	
4.10	J.A. Thomson, Department of Genetics, University of Melbourne.	Interpretation of puffing in polytene chromosomes.
4.30	H. Dady & E.H. Creaser, C.S.I.R.O. Division of Plant Industry, Canberra.	Isolation, specificity of aggregating protein and morphogenesis of avian cells in tissue culture.
4.50	N.L. Warner, Walter & Eliza Hall Institute, Melbourne.	Experimental and theoretical considerations of allelic exclusion in immunoglobulin genes in the mouse.
5.10	Business Meeting	
7.00	Sherry	
7.30	Dinner at Flinders University.	

# Friday, 15 August, University of Adelaide

# Session 3

9.00	W.J. Ewens, School of Physical Sciences, La Trobe University.	Some recent results in population genetics.
9.20	H. Daday, C.S.I.R.O., Division of Plant Industry, Canberra.	Effect environment on heritability and selection response in <i>Medicago</i> .
9.40	C.R. Leach, Department of Genetics, University of Adelaide.	Style length in Oxalis.
10.00	V. Than Aung & K.S. McWhirter, University of Sydney	Species differentiation disclosed by crossability relations in <i>Desmodium</i> .
10.20	B. Conray, School of Biological Sciences, University of Sydney.	Stability of zone of high variability in butterfly <i>Tisiphone abeona</i> .
10.40	COFFEE	
11.10	G.L. Miklos, School of Biological Sciences, University of Sydney.	Genetics of an unstable gene in Drosophila.
11.30	E.M. Nicholls, School of Human Genetics, University of New South Wales.	Melanin pigments and the genetics of pigmentation.
11.50	J. Tatchell, Department of Biological Sciences, Queensland Institute of Technology.	Inheritance of suscep- tibility to tuberculosis in human population.
12.10	D.W. Cooper, Department of Genetics, La Trobe University.	Studies on glucose-6- phosphate dehydrogenase in doves.
12.30	LUNCH	

# Session 4

2.00	Hayman, Martin & Walker, Department of Genetics, University of Adelaide.	Chromosome mosaicism in marsupials.
2.20	M. White, Department of Genetics, University of Melbourne.	Cytogenetics of laboratory hybrids in the <i>viatica</i> group of Morabine grasshoppers.
2.40	M. Andre, Department of Genetics, University of Melbourne.	Natural hybrids in the <i>viatica</i> group of Morabine grasshoppers.
3.00	G. Webb, Department of Genetics, University of Melbourne.	Patterns of late replication in the chromosomes of some Morabine grasshoppers.
3.20	J. Martin, Department of Genetics, University of Melbourne.	Inversion polymorphisms in Chironomus.
3.40	TEA	
4.10	C.J. Driscoll, Faculty of Biological Sciences, University of New South Wales.	Esterase isozymes and chromosome homoeologies in wheat and rye.
4.30	L.M. Bielig, Faculty of Biological Sciences, University of New South Wales.	Studies on the replacement of homoeologous group 5 chromosomes of wheat by chromosome 5R of rye.
4.50	R. Pettigrew, Faculty of Biological Sciences, University of New South Wales.	Studies on a group of chloroplyll mutants in hexaploid wheat.
7.30	Evening lecture.	

Adelaide University and Museum.





DR Sungth 7.8.69

### AUSTRALIAN GENETICAL SOCIETY

Adelaide meeting 14-15 August 1969

#### GENERAL BUSINESS MEETING

The business meeting of the Society will be at 5.30 p.m. Thursday, August 14 at the Flinders University.

### AGENDA

- 1. The following proposal will be put before the meeting for discussion: The Australian Genetical Society should be organised on a more formal basis, with an annual subscription and elected officers serving for at least three years.
- 2. The International Genetics Federation is a new body which is to take over the functions of the Genetics section of the International Union of Biological Sciences. The question of membership of the Federation by the Australian Genetical Society will be discussed.
- 3. It has been suggested that the Australian Genetical Society might offer an award for the best paper on a genetical topic to be presented by a predoctoral student. A predoctoral student at any Australian University would be eligible for the award.
- 4. Any other business.

Secretary.

#### Transport to Flinders University

A bus will depart at 8.50 a.m. on Thursday, 14 August from the main gate of the University of Adelaide in Victoria Avenue, opposite the University Footbridge across the River Torrens. The bus should arrive at Flinders University about 9.20 a.m. A bus will depart from Flinders University at 10 p.m. for North Terrace, Adelaide. Ample parking is available at Flinders University for those members who wish to use private cars.

#### PROGRAMME

Thursday 14 August, Flinders University

#### Session 1A

9.30 M. J. Hynes, School of Biological Sciences, Flinders University.

Regulation of amidase synthesis in Aspergillus nidulans.

Aspergillus nidulans can grow on formamide and acetamide as sole nitrogen sources utilizing a formamidase and an acetamidase respectively. A mutant at the *fmdS* locus results in inability to grow on formamide as a sole nitrogen source and to loss of formamidase activity. Similarly mutants at an unlinked locus andS leads to inability to grow on acetamide and to loss of acetamidase activity. It is suggested that these are the structural genes for the two enzymes.

Acetamide induces and ammonia represses acetamidase synthesis. Acrylamide is a substrate but not an inducer of acetamidase. Mutants that can grow on acrylamide as a nitrogen source have been isolated and these are found to be constitutive for acetamidase synthesis but are still repressible. The majority map at the amdR locus which is unlinked to amdS. One mutant maps at a second locus (amdT) unlinked to either amdR, amdSor fmdS. Constitutive mutants at either locus are semidominant to their wild type alleles in heterozygous diploids. Mutants in the amdR locus  $(amdR^-$  mutants) which grow pocrly on acetamidase and have lowered acetamidase activities have been isolated. These are recessive to both wild type and constitutive alleles. Two of these mutants may be more sensitive to repression by nitrogen metabolites than is wild type.

Formamidase is highly sensitive to repression by nitrogen metabolites and it is not clear whether it is controlled by both induction and repression, or by repression alone. The two amdR<sup>-</sup> mutants with apparent increased sensitivity of acetamidase to repression, also appear to have increased sensitivity to repression of formamidase synthesis. The mutation to constitutive synthesis of acetamidase at the amdT locus also results in poor growth on formamide and lowered levels of formamidase. This effect is recessive to wild type in heterozygous diploids.

The results suggest that two common regulator genes govern regulation of acetamidase and formamidase synthesis. In the case of acetamidase the system has properties consistent with positive control.

9.50

K.K. Jha,

Research School of Biological Sciences, The Australian National University.

Problems and prospects associated with frameshift mutagenesis in *Neurospora crassa*.

Recombination between alleles generally occurs as a consequence of the formation of hybrid DNA from two homologous molecules and subsequent excision-repair synthesis. This knowledge is derived from the use of mutants believed to be of the basesubstitution type. We would like to know the behaviour of frameshift mutants in recombination in a eucaryote and their potential use in mapping of mutated sites in the gene.

Acridine compounds with alkylating side-chains provide a convenient means of obtaining frameshift mutants. Such mutants have to be distinguished from base-substitution types and the question arises whether reversion tests with acridine compounds and other mutagenic agents are sensitive enough to permit convenient and reliable classification. Results obtained with his-3 mutants of Neurospora will be discussed.

### 10.10 J. Pemberton, Monash University.

A mutant of Pseudomonas aeruginosa with increased fertility.

A Mutant of *Pseudomonas aeruginosa* with an increased ability to form recombinants in conjugation has been isolated. The mutation is in a donor strain (FP<sup>+</sup>), which was selected as Les<sup>-</sup> (reduced ability to be lysogenised) and recombination deficient (Rec<sup>-</sup>) when used as a recipient in transduction. It is not known if the Les<sup>-</sup> Rec<sup>-</sup> phenotype is related genetically to the increased ability to form recombinants in conjugation. The mutant is like the wild type in that it is infectious for the fertility factor FP, hence it is not analogous to the Hfr forms in *Escherichia coli* which are non-infectious for sex factor.

When other female strains are infected with the FP<sup>+</sup> from the mutant strain to produce males, they do not show the high donor ability of the mutant, hence the fertility mutation does not involve the sex factor alone. From various crosses it has been shown that the mutant concerned in the change is located chromosomally and can be transferred during conjugation. Female and male recombinants containing the fertility lesion have respectively higher recipient and donor abilities in conjugation. If these fertile females are infected with the normal fertility factor FP, they acquire the high donor ability of the original mutant. Entry curves in interrupted matings, where the male is contraselected with phage, suggests that the mutant differs from the wild type in that the contacts formed between the mutant donor and wild type recipient are so strong as not to be broken by the ordinary techniques of interrupted mating.

10.30

E.M. Walker & A.J. Pittard, School of Microbiology, University of Melbourne.

A Temperature-sensitive conjugation-defective F factor in Escherichia coli K-12.

A mutant male strain of *Escherichia coli* K-12 has been isolated which is unable to transfer genetic material at 42°. Although transfer is inhibited, the ability to form pairs at this temperature is not affected. This strain is also resistant to infection by certain RNA-containing male-specific phages at 42°. Both temperature-sensitive phenotypes have been shown to be a result of mutation of the F factor. When a derepressed fi<sup>+</sup> R factor is introduced into the mutant strain, both F-promoted transfer and phage sensitivity at 42° return. Revertants of the mutant strain have been isolated which have regained both activities. 10.50 R.R.B. Russell and A.J. Pittard, School of Microbiology, University of Melbourne.

Mutant strains of *Escherichia coli* unable to synthesise protein at 42°C.

Amongst a collection of mutants of *E. coli* K 12 which display a rapid cessation of growth in nutrient media when placed at  $42^{\circ}$ , a number have been found which show a marked inhibition of incorporation of <sup>14</sup>C amino acid into protein at the restrictive temperature, while DNA and RNA synthesis are only secondarily affected. In seven of these mutants temperature sensitivity has been shown to be due to unstable valy1-t-RNA synthetases. In addition to temperature sensitivity the mutations cause a leaky requirement for valine at nonrestrictive temperatures, and the "switching-off" of RNA synthesis in RC<sup>Str</sup> strains. All these mutations mapped in the *val S* gene at minute 86 on the *E. coli* linkage map, and were found to be 21% co-transducible by bacteriophage Plkc with *pyr B*, and to be on the far side of it from *arg H*.

Two other mutations were found to cause temperature sensitivity of phenylalanyl-t-RNA synthetase, and to be 38% cotransducible with aro D. The temperature sensitivity of one of these phe S mutants was found to be suppressed in certain strains by the presence of a gene mapping near the gal locus. Some results on the possible mechanism of the suppression will be discussed.

# 11.10 COFFEE

11.40 K.D. Brown,

Research School of Biological Sciences, Australian National University.

Aromatic amino acid transport in E. coli.

 $C^{14}$ -labelled phenylalanine, tyrosine and tryptophan are actively taken up into *Escherichia coli* K12 by four permeases. Firstly, all three amino acids are transported by a common aromatic permease with Michaelis constants ranging from 2 to  $5 \times 10^{-7}$ M. Histidine and leucine are also transported by this permease but with much higher Michaelis constants  $(10^{-4}M)$ . Mutants lacking the common aromatic permeases are resistant to the aromatic analogues  $\beta$ -2-thienylalanine, 5-methyl-tryptophan and *p*-fluorophenylalanine. They map at a locus, designated *aro P*, which lies between *leu* and *pan* on the chromosome.

Phenylalanine, tyrosine and tryptophan are also taken up by three permeases, each highly specific for a single amino acid. Michaelis constants range from 2 to 5 x  $10^{-6}$ M. Mutants lacking the tryptophan-specific permease have been isolated. The mapping of these mutants is in progress.

Mutants lacking the phenylalanine- and tyrosine-specific permeases are also being sought.

J. Camakaris and A.J. Pittard. School of Microbiology, University of Melbourne.

The regulation of tryptophan biosynthesis in Escherichia coli K-12.

Three isoenzymes carry out the first reaction in aromatic biosynthesis in E. coli K-12. A mutant strain, AB2891, which possesses only one of these isoenzymes, DAHP synthetase (trp), is growth inhibited by tryptophan. Two classes of mutants derived from AB2891, which are able to grow in the presence of tryptophan, have been isolated : (i) those possessing a feedback resistant DAHP synthetase (trp); (ii) those with a feedback resistant DAHP synthetase (trp) which is produced constitutively. The mutation(s) in both classes is closely linked to aro H, the structural gene for DAHP synthetase (trp). As the normal repression of anthranilate synthetase (an enzyme produced by the tryptophan operon) is unaffected in class (ii) mutants, the presence of a distinct regulator locus, probably an operator, is indicated for aro H.

Trp5 mutants possess a defective tryptophanyl-t-RNA synthetase, and require tryptophan for normal growth. It has been found that both DAHP synthetase and anthranilate synthetase fail to derepress normally in trpS mutants. The simplest explanation of the observations is that free tryptophan and not charged tryptophanyl-t-RNA is the true co-repressor in tryptophan biosynthesis.

S.W.K. Im and A.J. Pittard. 12.20 School of Microbiology, University of Melbourne.

> A mutant of Escherichia coli derepressed for a multi-functional enzyme concerned with phenylalanine biosynthesis.

A mutant strain of Escherichia coli K-12 in which one of the enzymes of the phenylalanine biosynthetic pathway is derepressed has been isolated. This mutant was selected by its ability to grow on minimal agar medium supplemented with tyrosine, tryptophan, shikimic acid and a concentration of o-fluorophenylalanine (1 mM) sufficient to inhibit the growth of the wild type strain. This mutant strain excretes phenylalanine as evidenced by its ability to cross-feed phenylalanine auxotrophs. Biochemical analysis of cell free extracts prepared from this mutant showed that prephenate dehydratase is derepressed whereas 3-deoxy-D-arabino-heptulosonate-7-phosphate (DAHP) synthetase (phe) is not. By means of chromotography on DEAE cellulose it was shown that prephenate dehydratase and its associated chorismate mutase P are derepressed, whereas prephenate dehydrogenase and its associated chorismate mutase T are not derepressed. Genetic analysis showed that the mutation in question is closely linked to pheA, the structural gene for prephenate dehydratase and its associated chorismate mutase P.

12.40

1.00 LUNCH

#### Session 1B

9.30

S.Smith-White, C.R. Carter and H.M. Stace, School of Biological Sciences, University of Sydney.

The Cytology of Brachycome. Chromosome numbers and polyploidy.

The 50-odd taxonomically recognised species of *Brachycome* have a wide range of chromosome numbers. Haploid numbers of n = 2, 3, 4, 5, 6, 7, 9, 10, and 13 are reported. The haploid numbers of the various species do not conform with the subgeneric "phylogenies" which have been proposed on the basis of morphological studies.

A number of species include B-chromosomes in their complements, and in several of the recognised species, different base numbers have been found in different localities.

A number of species show different levels of polyploidy with different patterns of geographical distribution. In this respect the taxonomic species *B. aculeata* is the most complex, having diploid, tetraploid, octaploid, 10-ploid and 12-ploid levels. This species is mainly distributed in montane and alpine habitats, and the geographical patterns of the ploid levels are very complex.

> It is clear that the genus has been a very pliable one with respect to chromosomal evolution, in the past, and it is probable that many species are subject to *de novo* chromosomal change at the present time. It is anticipated that a detailed study of the geographical patterns of ploidy and other "intra specific" chromosome differences will allow an interpretation of the historical evolution of the group, in a way which has been done with *Themeda* and with *Goodenia bellidifolia*. The total story, however, will be much more complex.

> Similar differences in base numbers and in ploid levels are found in a number of species of the genus *Calotis*.

9.50 S. Smith-White, C.R. Carter, School of Biological Sciences, University of Sydney.

The cytology of Brachycome lineariloba.

As a taxonomic species, *B. lineariloba* is distinctive, and readily recognised by its leaf form, stemless habit, and fruitlet characteristics. It shows considerable variation in the size of capitula, and especially in the length of the "petals" or ligulate florets, which vary from 1 mm to 10 mm or more in length. Flower colour is blue or white. This variation was noted by taxonomists, but was not considered to justify specific rank for the variants.

Cytologically the species contains a number of distinct forms. The larger flowered forms have 2 pairs of chromosomes, and will be referred to as "species 'A'". These forms had been collected from Pt. Augusta to Pimba from the western parts of the Flinders Ranges, and from the Wilcannia district of N.S.W. In the three areas mentioned, the chromosome morphology of the species is different. These chromosome morphologies are described and illustrated.

The small flowered forms in the Pt. Augusta and Flinders range districts (Species B) have 2n = 12. The quantity of chromosome material is much greater than the species A, but species B is not a hexaploid in relation to A. One amphihaploid plant was discovered in Pt. Augusta locality where species A and B were growing together.

Most of the chromosomes of species A and B could be recognised in this amphihaploid.

The small flowered form in western N.S.W. (Species C) has 2n = 16. It is assumed to be of amphidiploid origin from forms like species "A" and "B".

10.10 H.M. Stace, KCMINZ School of Biological Sciences, University of Sydney.

B-chromosomes in Brachycome lineariloba.

B-chromosomes are found in a number of species of Brachycome, but those found in the *B. lineariloba* species with n = 2 are of particular interest.

Two kinds of accessory chromosome are found in this species. One kind is referred to as a B-chromosome. It is about 4 microns long, with a median centromere, and is probably an isochromosome. There may be one, two, or three such B chromosomes in different plants.

The paper reports the meiotic behaviour of the B-chromosomes when present in single, double and triple dose. A survey has been made of the frequency of the B in several different populations of the species, and the paper discusses the characteristics of these frequency distributions.

The other kind of accessory chromosome is much smaller, of the order of 1 micron. It is referred to here as a "gamma" chromosome. There may be up to 20 or more such gamma chromosomes in a nucleus. Gamma chromosomes are mitotically unstable. Different cells in the same tissue of some plants have been found to contain from 0 to 22 such chromosomes. Feulgen staining, with or without DNA-ase treatment proves them to be chromosomal bodies. 10.30 S.H. James,

8.

Botany Department, University of Western Australia.

A model for the evolution of complex hybridity in Isotoma petraea.

Complex hybridity in *Isotoma petraea* has evolved via the sequential fixation of interchanges in a heterozygous condition upon a primitive chromosome end sequence and amongst populations of inbreeders. Certain aspects and consequences of the biology of *Isotoma* render the evolutionary hypotheses proposed by Cleland and Darlington untenable for *Isotoma petraea*.

A model exploiting interchange mutation, self pollination with infrequent interpopulational hybridization and the adaptive superiority of genetic heterozygotes is described. The model suggests that once chance associates the requisite interchange mutations in a suitably preadapted population system, natural selection will elicit the evolutionary perfection of complex hybridity.

10.50 I.C. Beltran,

### Botany Department,

University of Western Australia.

Heterosis and epistasis in interpopulational hybrids of Isotoma petraea

- 1. A model based on the pursuit of genetic heterozygosity and the exploitation of relatively translocated internal chromosome segments has been proposed to account for the evolution of complex hybridity in *Isotoma petraea*.
- 2. Breeding experiments involving four of the primitive structurally homozygous populations demonstrate a marked heterosis for plant size in the interpopulational heterozygotes.
- 3. Synthetic hybrids heterozygous for one complex and for the primitive "axillaris" genome exhibit seed abortion patterns explicable in terms of parental behaviour and epistasis.
- 4. The relevance of these observations to the evolutionary model proposed and the possibility of subjecting the model to further tests is discussed.

# 11.10 COFFEE

11.40 L.R. Bousfield, Botany Department, University of Western Australia.

B chromosomes in Dampiera linearis R.Br.

A survey of chromosome numbers in *Dampiera linearis* R.Br. has allowed the identification of several cytological races including diploids of restricted occurrence, a tetraploid race of predominantly coastal distribution, and a widespread hexaploid race. In addition, plants with B chromosomes are of frequent occurrence in the ecotonal region at the junction of the diploid and tetraploid races. The behaviour of B chromosomes in the pollen mother cell meiosis of plants from this area is described. Variation between plants has been observed with respect to aspects of B chromosome movement and division, and also with respect to the effect they may have upon the A chromosome complement. An hypothesis is presented to account for the meiotic behaviour of B chromosomes in D. *linearis*, in terms of their role in restricting recombination in interpopulational hybrids.

12.00

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E. Craddock, School of Biological Sciences, University of Sydney.

Zones of overlap of chromosome races in stick insect Didymuria violescens.

The stick insect *Didymuria violescens* shows considerable chromosomal variation, having several chromosome races, each of which is karyotypically distinct. Areas where such chromosome races meet are of vital importance in a consideration of possible modes of speciation. An interpretation of events in some of the zones of overlap in *Didymuria* will be presented and discussed.

12.20 N. D. Murray, School of Biological Sciences, University of Sydney.

Geographic variation and natural selection in the beetle Calomela bartoni.

A remarkable case of intraspecific variation has been discovered in the native Chrysomelid beetle *Calomela bartoni*. The geographic details of the pattern of variation reveal some interesting evolutionary situations, especially in regions where very different forms meet. Special methods of approaching some of the general problems will be discussed in relation to the field biology of *Calomela*.

12.40 J. Ford, Botany Department, University of Sydney.

Selective degeneration of nuclei during microsporogenesis in the Epacridaceae.

The family Epacridaceae is subdivided into two tribes the Epacrideae and the Styphelieae. In a series of papers on microsporogenesis in the Epacridaceae, Smith-White (1955-59) observed that while in the Epacrideae pollen regularly developed in tetrads, the Styphelieae exhibited a diversity of pollen types. He termed this phenomenon the formation of "variable tetrad pollen". In the genus Styphelia (of the Styphelieae), following an "apparently" normal meiosis in the pollen mother cell 3 nuclei regularly migrate to one end of the cell and proceed to degenerate. Only one microspore nucleus is functional. Further to this, Smith-White established that in the triploid species, *Leucopogon juniperinus*, the functional microspore has a regular chromosomal complement; there is some mechanism which selects which nuclei degenerate.

Electron and light microscope studies have given some insight into this problem and I shall discuss some of the possible controlling mechanisms.

1.00 LUNCH

# Session 2

2.20 B.W. Holloway and J. Pemberton, Department of Genetics, Monash University.

A new class of recombination - deficient mutant in Pseudomonas aeruginosa.

Mutants of Pseudomonas aeruginosa with a reduced ability to be lysogenized (Les ) are often found to be deficient in recombination ability (Rec<sup>-</sup>) as measured by their inability to produce recombinants in both transduction and conjugation. Not only is the altered recombinational ability reflected in an overall reduction of recombination frequency but also by changes in the quality of recombination, as demonstrated by altered frequencies of cotransduction or cotransfer of markers known to be linked. This occurs not only when Rec strains are used as recipients (with Rec<sup>+</sup> donors in both transduction and conjugation) but also in the reverse situation with Rec- donors and Rec<sup>+</sup> recipients. The lack of recombinants and the altered linkage relationships of genes in the recombinants that are formed in this latter situation cannot be due to the absence of recombination enzymes in the recipient. The normal plating on the Rec<sup>+</sup> recipients of phages grown on the Rec donors suggests that the results are not due to Host Controlled Modification in the usual sense. It is concluded that in this type of Rec mutant, the DNA has acquired a different specificity such that it is no longer a normal substrate for the wild type recombination enzymes.

2.40 B. Austin and D.G. Catcheside, Research School of Biological Sciences, Australian National University.

The specificity of rec genes in Neurospora crassa.

Genes (rec) affecting allelic recombination have been found for five different loci (his-1, his-2, his-2, am and nit-2) in Neurospora crassa. At least five or six different rec genes are involved and each is highly specific. Thus rec-1 affects only his-1 and none of at least eight other loci. Rec-3, which affects am, is very closely linked to rec-x, which affects his-2; they may be identical.

Allelic recombination has been studied at ten different loci; rec genes have been found for five of them, without exhaustive search.

In every case the dominant *rec* gene reduces recombination at the locus controlled and usually also changes the distribution of the flanking markers among prototrophic recombinants.

3.00

D.R. Smyth.

Research School of Biological Sciences, Australian National University.

The genetic control of recombination within the *am-1* gene of *Neurospora crassa*.

Results of crosses between amination-1 alleles of Neurospora crassa are affected by a gene difference at an unlinked locus, recombination-3. Crosses involving the  $rec-3^{+}$  allele differ from those in which the rec-3 allele is homozygous in at least two ways:

- 1. The frequency of prototrophs (a selected type of recombinant) is from about 5 to 20 times smaller.
- 2. Amongst these prototrophs, the difference between the frequencies of the two parental combinations of flanking chromosome markers is usually reduced.

Possible roles for the *rec-3* gene product can be considered using schemes of recombination which involve hybrid DNA molecules.

G. Grigg, C.S.I.R.O., Division of Animal Genetics, Sydney.

Excision, repair, recombination and mutation.

No abstract.

3.40 M.J. Hartley,

3.20

Department of Agricultural Botany, University of Sydney.

Frequency of reverse mutation in Aspergillus nidulans. The ability of mutants of Aspergillus nidulans to revert by chemical mutagenesis was examined. The mutants which were at separate loci concerned with nitrogen metabolism were induced by nitrous acid, N-methyl-N<sup>1</sup>-nitro-N-nitro-soguanidine and diepoxybutane and reverted by these mutagens and diethylsulphate.

The ability of mutants to revert was affected by the inducing mutagen, the bifunctional diepoxybutane giving a much higher percentage of nonrevertible mutants than nitrous acid and nitrosoguanidine. 45% of these non-revertible mutants were associated with translocations and

hrinus. there is evidence that the bifunctional agent substantially increases the frequency of translocations over that given by the monofunctional agents.

The frequency of reversion among the individual revertible mutants varied by a factor of more than 100 but even so inducing mutagen and locus had a detectible influence on revertability. There was an inverse relationship between the effectiveness of these agents as forward mutagens and the overall frequency of reversion of the mutants they induce. Those mutants induced by diepoxy-butane, that did revert, were reverted most frequently by diepoxy-butane itself, though this agent was least effective at reverting mutants induced by nitrous acid and nitrosoguanidine. This specificity was not observed among the other agents. It is suggested that diepoxybutane can induce revertible mutants by a process other than a transitional type change or a frame shift, possibly by a transversional type change.

#### 4.00 TEA

4.30 J.A. Thomson, Department of Genetics, University of Melbourne.

Interpretation of puffing in polytene chromosomes.

Criticisn of the use of chromosomal puffing in dipteran polytene nuclei as an indicator of gene activity is examined in relation to the selection of experimental systems and the presumed range of synthetic activities carried out by each type of cell. In the past, a major criterion of selection has been the favourability of chromosome morphology for cytological analysis. As a consequence, the proportion of the genome which may become activated in a range of functionally diverse cells appears to have been under-estimated. Comparative aspects of polytene chromosome behaviour in different tissues and at different stages of development are illustrated with reference to footpad and trichogen cells from pupae, and to salivary gland and fat body cells from larvae, of the Brown Blowfly, *Calliphora stygia*. Other problems of interpretation arising in studies of chromosomal puffing are briefly reviewed.

4.50

O. H. Dady and E.H. Creaser, C.S.I.R.O., Division of Plant Industry, Canberra.

Research School of Biological Sciences, Australian National University, Canberra.

Isolation, specificity of aggregating protein and morphogenesis of avian cells in tissue culture.

The genetic control of the surface properties of mammalian and avian cells and its significance in morphogenesis is an unresolved problem of modern biology. There are numerous theories concerning cell adhesions and aggregations. All vertabrae cells so far examined carry a net negative surface change, and contact interaction between them have been considered in terms of lyophobic colloid theory as developed by Derjagin, Landau, Verwey and Overbeek, and known as DLVO theory. In essence this theory considers contact processes as regulated by a balance between potential energies of electrostatic repulsion ( $V_R$ ) and potential energies of attraction ( $V_A$ ) due to London Van der Wall's interaction.

Curtis treated the aggregation as a flocculation process. The flocculation is the adhesion of particles due to their collision brought about by Brownion motion, sedimentation or by flow of medium. Flocculation due to agitation of two medium is termed arithmetic flocculation and in this process there is a certain probability that a collision produces an adhesion. Although Moscana suggested the biochemical basis of cell aggregation, he did not present conclusive evidence. Finally Curtis concluded:

"From what is known about the chemistry of cell adhesion there appears to be no reason for predicting the existence of some cementing material, specific or otherwise, in the adhesions of normal or tumorous tissue cells".

The paper to be presented gives evidence about isolation of a protein responsible for the aggregation of avian cells. Additional information will be presented about the specificity of this aggregation. This investigation suggests that the major forces in cell aggregation are determined by specific protein molecules.

5.10 N.L. Warner & M.A.S. Moore, Walter & Eliza Hall Institute Melbourne.

Experimental and theoretical considerations of allelic exclusion in immunoglobulin genes in the mouse.

Mouse immunoglobulins can be divided into classes on the basis of physico-chemical, biological and antigenic properties. Each class represents the expression of a distinct and separate immunoglobulin heavy (H) polypeptide chain gene, and five classes have so far been recognised. Genetically controlled iso-antigenic differences (allotypes) of four of the H-chain genes have been detected and these loci are termed Ig-1 to Ig-4 with 8 alleles recognised for the Ig-1 locus. These loci are extremely closely linked.

Plasma cell tumors were induced in BALB/c, NZB, and (BALB/c x NZB)F1 hybrid mice and the myeloma proteins produced by the tumors were typed for immunoglobulin class and allotype. In all cases, the myeloma proteins produced by tumors arising in heterozygous mice represented only one of the parental Ig alleles present in the tumor bearing animal. This constitutes a demonstration of autosomal allelic exclusion.

Morphological and karyotypic studies on the murine plasma cell tumors have shown that the tumor population contains a high frequency of binucleate cells, and often of a cycling population with near diploid and near tetraploid stem lines.

These results will be discussed in terms of two possible approaches to allelic exclusion:

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- (i) random repression of one parental allele,
  - (ii) development of homozygosity for the chromosome carrying the Ig H-chain genes.
- 5.30 Business Meeting
- 7.00 Sherry
- 7.30 Dinner at Flinders University.

# Friday, 15 August, University of Adelaide

#### Session 3

9.00 W.J. Ewens School of Physical Sciences, La Trobe University.

Some recent results in population genetics.

A classical result of Fisher is that if the fitness of the heterozygote at any locus exceeds that of both homozygotes, then there is a stable internal equilibrium gene frequency. Two generalizations of this result are discussed: one to the case of finite populations, the other to the case where fitness depends on more than two loci. It is found in both these generalizations that results are found which are in a sense contrary to those of Fisher.

9.20

D.W. Cooper, M.R. Irwin and W.H. Stone, Department of Genetics, La Trobe University.

Studies on glucose-6-phosphate dehydrogenase (G6PD) in doves.

Starch-gel electrophoresis has been used to characterize the G6PD of three species of doves of the genus *Streptopelia*, *risoria*, *senegalensis*, and *humilis*. An autosomally controlled polymorphism in electrophoretic mobility was discovered in each species. The electrophoretic pattern of the *humilis* heterozygote suggests that the enzyme is a tetramer. The evolutionary relationship between G6PD of dove and of mammalian red cells will be discussed.

9.40

H. Daday, C.S.I.R.O., Division of Plant Industry, Canberra.

The effect of environment on heritability and predicted selection response in *Medicago sativa*.

The effect of environment on selection response of metric characters is still a controversial topic of quantitative genetics, represented by two opposing views. Hammond stated ng the

that an unfavourable environmental condition can be a limiting factor in the response to animal selection. In contrast, Falconer found no effect of high and low planes of nutrition on heritabilities of body weights of mice, and improvement of the genotype for growth on a low plane did carry with it a considerable improvement for growth on a high plane.

The conclusion of Falconer has been examined in an outbreeding population of *Medicago sativa* under favourable environments and under stress conditions, and the results were found to be inconsistent with those of Falconer.

This investigation concerns the effect of environments on mean plant growth, heritability and predicted response of plant parameters in *M. sativa* at three localities. The three environmental treatments (high, medium and low) caused significant changes in the mean values. The heritability of plant growth varied between 0.55 and 0.95 under high and medium treatments, but it was reduced to zero by the low treatment. The expected direct response to selection was superior with the high treatment than with the low. The indirect selection was found to be advantageous if a particular locality was exposed to frequent environmental stress, provided family x locality interaction was absent. It is concluded from these investigations that unfavourable environmental conditions may severely limit response to selection in *M. sativa* populations for such conditions.

10.00

C.R. Leach, Department of Genetics, University of Adelaide.

Style length in Oxalis.

0. corniculata as found in South Australia possesses only two (long and short) of the three possible tristylic forms but it also has a homostyle form. Cytological studies show that heterostyle plants have 2n = 24 and homostyle plants a much larger number; probably 2n = 48. Two types of homostyle were found:- one which crossed readily with longs and shorts and another which was a pseudogamous apomict.

Two plants were produced with the apomictic homostyle as pollen parent. These had two new floral arrangements and one was highly sterile. The other spontaneously produced a number of capsules and a cytological study of plants from this seed revealed a variable chromosome number and a chromosomal rearrangement.

Crosses indicate that short is dominant to long and homostyle; and homostyle crossed with long produces plants with an intermediate phenotype. Crosses have been made to establish whether disomic or tetrasomic behaviour is present in longs and shorts. 10.20 U. Than Aung and K.S. McWhirter, Department of Agricultural Botany, The University of Sydney.

Levels of species differentiation in the genus Desmodium.

This study was of the nature and extent of biological barriers to gene transfer among a group of seven related, but morphologically distinct, forms in the genus *Desmodium*. These forms of the tropical legume *Desmodium* were introduced from Hawaii and Latin America, and include the commercial pasture species *D. intortum* (Green leaf) and *D. uncinatum* (Silver leaf).

The 42 hybrid combinations produced by crossing the 7 forms in diallel series were studied, and observations on crossability, hybrid seed development, growth and development of F1 hybrid plants, and pollen and ovule fertility of F1 hybrid plants were obtained.

These studies disclose various levels of differentiation among the 7 forms of Desmodium. Only one, CPI 38722 ("Big Stipule"), appears to be reproductively isolated from the remaining forms. Each of the remaining 6 forms is involved in at least one of the 14 apparently fully fertile F1 hybrids obtained. However, the pattern of results shows all 7 forms to be distinguishable on the basis of hybridization results. Various barriers to gene transfer occur, including failure to cross (6 combinations), reduced crossability, abortion of hybrid seeds (6 combinations), lethality of F1 hybrid plants (10 hybrids), and pollen and ovule sterility of F1 hybrid plants (6 hybrids). Certain of these barriers to gene transfer appear to be under simple genetic control. The results suggest a level of incipient speciation that may be reversed in the synthesis of a complex germ plasm source for use in a breeding programme.

10.40 COFFEE 11.10 B.A. Co

B.A. Conroy, School of Biological Sciences, The University of Sydney.

The stability of the zone of high variability in the butterfly *Tisiphone abeona*.

The range of the highly variable race T.a. joanna has been constant at least since the beginning of the century. The various characters contributing to the variability show smooth clines when population means are plotted against latitude. However, the correlations between the characters within populations are very low. Evidence will be presented to show that the variable zone is the result of past hybridization among the three races - the southern orange form T.a. aurelia, the yellow northern form T.a. morrisi and the mountain race T.a. regalis. The present rate of dispersal is very low. Some clines in quantitative and qualitative characters are restricted to a thirty mile area while others spread over two hundred miles further south. The importance of selection against the hybrids per se will be discussed. 11.30 G.L. Miklos, School of Biological Sciences, The University of Sydney.

Genetics of an unstable gene in Drosophila.

The general problem of the production of abnormal segregation ratios has been investigated using two irregular systems: the second chromosome complex carrying the Segregation - Distorter (SD) gene and the sc<sup>4</sup>sc<sup>8</sup> chromosome.

A new hypothesis has been advanced to account for the behaviour of the  $sc^4sc^8 X$ .

Combination of the SD and the sc<sup>4</sup>sc<sup>8</sup> systems caused meiotic chaos, and any explanation not involving divine intervention seemed extremely improbable.

11.50 J. Tatchell,

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Department of Biological Sciences, Queensland Institute of Technology.

Inheritance of susceptibility to tuberculosis in human population.

No abstract.

12.10 E.M. Nicholls, School of Human Genetics, University of New South Wales.

Melanin pigments and the genetics of pigmentation.

Hair and skin pigmentation is subject to complex genetic control. A knowledge of the biology and biochemistry of the melanocyte is a necessary adjunct to understanding the genetics of normal and anomalous pigmentation. The following aspects are discussed (1) the structure of the melanocyte and its relation to the epidermal cells (2) the cellular milieu in which the melanocyte functions (3) the ultrastructure of the melanocyte; the melanosome (4) the classical biochemical pathway for the production of melanin involving tyrosine and tyrosinase (5) a model system which, if operative in vivo, (a) limits the role of tyrosinase to the conversion of tyrosine into dopa; (b) provides for colour variation in mammals and domestic poultry by non enzymic reactions between dopa, cysteine and ferric ions. In the model system pH variation is the determinant of colour variation. If colour variation is in fact to be explained in this manner, some pigmentary genes must have the role of providing the necessary pH variation in the melanosome.

18.

12.30 LUNCH

Session 4

2.00 D.L. Hayman, P.G. Martin and P. Walker, Department of Genetics, The University of Adelaide.



Parallel mosaicisms of supernumerary and sex chromosomes in *Echymipera kalabu* (Marsupialia).

Echymipera kalabu (Peramelidae : Marsupialia) does not have the full chromosome complement in all its adult somatic tissues. The chromosomes missing are the Y-chromosome in the male and an X-chromosome in the female. The full complement is present in the corneal epithelium and the reproductive tissue. A parallel mosaicism to this exists with respect to small supernumerary chromosomes which are found in certain animals of this species. These supernumeraries must be subject to the same control system as that which is responsible for the elimination of the sex chromosomes.

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

Cytogenetics of laboratory hybrids in the *viatica* group of Morabine grasshoppers.

Speciation appears to have occurred in the *viatica* group in association with chromosomal rearrangements (mostly fusions and a pericentric inversion). It seems highly probable that these rearrangements have played a primary role as genetic isolating mechanisms since they diminish the fecundity of the hybrids. In some hybrid combinations there is a general breakdown of spermatogenesis which is not directly related to the chromosomal rearrangements. Inhibition of male development occurs in several hybrid combinations.

2.40 M. Andre.

Department of Genetics, University of Melbourne.

Natural hybrids in the viatica group of Morabine grasshoppers.

The zones of geographic overlap between one member of the *viatica* group ("P24XY") and two races of *viatica* (with 17 and 19 chromosomes respectively) have been studied on Kangaroo Island. Natural hybrids between P24XY and *viatica*<sub>17</sub> were found and some degree of introgressive hybridization is occurring. In the case of the overlap zone between P24XY and *viatica*<sub>19</sub> only a single female hybrid has been found. Laboratory studies have been carried out on the cytogenetics of these hybrids and on backcrosses.

3.00 G. Webb.

Department of Genetics, University of Melbourne.

Patterns of late replication in the chromosomes of some Morabine grasshoppers.

The *cultrata* group of morabine grasshoppers (Acridoidea, family Eumastacidae) contains species with XO, XY and  $X_1X_2Y$  sex chromosome mechanisms. The identity of the chromosomes involved in the formation of the multiple sex chromosome systems can be traced by the pattern of late replication in mitotic cells.

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Department of Genetics, University of Melbourne.

J. Martin,

Evolution of the genus Chironomus in Australia and New Zealand.

The cytology of eight Australian and one New Zealand species of Chironomus has been studied in detail and material of several others have recently become available. All but one of these species apparently belong to the *Pseudothummi* group which occurs also in North America, Europe and on the Pacific islands. The other species would appear to belong to the similarly widely distributed thummi group.

A diagram of the phylogenetic relationships of the members of the *Pseudothummi* group has been constructed. The common Victorian species *Ch. oppositus* appears to be central to this scheme with many of the intraspecific polymorphisms of this species occurring as interspecific differences between other species.

#### 3.40 TEA

4.10

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C.J. Driscoll, Faculty of Biological Sciences, University of New South Wales.

Esterase isozymes and chromosome homoeologies in wheat and rye.

Electrophoretic separation on starch gel allows detection of a number of esterases in hexaploid wheat. Three esterase bands are present in the area of fast mobility. Diploid rye has one, slightly slower, band in this area. Wheat-rye hybrids possess these four bands and a fifth band, considered to be of hybrid origin. The slowest wheat band and the rye band are governed by genes on homo-eologous chromosomes 3A and 3R. The five bands are considered to result from four homogeneous and six heterogeneous dimers derived from four protomers produced by genes on chromosomes 3A, 3R and presumably 3B and 3D. The 3A gene  $(3A^{2})$  is located on the left arm of 3A and the 3R gene (3R) on the short arm of 3R, the arm that bears a stem rust resistance gene.

Two further bands, governed by 3A and 3D, are located on the lower portion of the zymogram. This 3A gene,  $(3A^{l})$ , is located on the opposite arm to  $3A^{u}$ .

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Three X-ray-induced translocation lines possess the resistance gene but lack  $3A^{\prime}$ . Two of these lack  $3A^{\prime}$ , whereas the third lacks 3R. On the basis of one break per chromosome, the first two translocation chromosomes, and perhaps the third, possess the rye centromere.

4.30 *L.M. Bielig*,

Faculty of Biological Sciences, University of New South Wales.

Studies on the replacement of homoeologous group 5 chromosomes of wheat by chromosome 5R of rye.

The diploid meiotic behaviour of *Triticum aestivum* is regulated by a gene located on the long arm of chromosome 5B.

An individual simultaneously monosomic for chromosomes 5B and the long arm of rye chromosome 5R was pollinated by *Aegilops peregrina*, a species that has been used for detecting the activity of  $5B^{L}$ . Analysis of pairing behaviour of the F<sub>1</sub> demonstrated that  $5R^{L}$  is unable to regulate meiotic pairing as does  $5B^{L}$ . The rye telocentric, which is cytologically recognisable was observed to pair in a few cells. This was either rye-wheat or rye-peregrina pairing.

By use of aneuploids, an individual was obtained in which chromosome 5B was replaced by 5R<sup>L</sup>. In this individual, which was irregular meiotically, the rye telocentric was observed to pair in 3.5% of cells. This is thought to be wheat-rye chromosome pairing, a phenomenon previously considered not to occur. The authenticity of this apparent wheat-rye pairing is now being investigated.

Chromosomes  $5R^{L}$  and 5R entire have been substituted for chromosomes 5A and 5D respectively. The 5R(5D),  $5R^{L}$  (5A) and  $5R^{L}(5B)$  substitutions are all vegetatively vigorous, hence the long arm of 5R is the more important arm. Whereas the  $5R^{L}(5A)$  substitution is highly fertile, the  $5R^{L}(5B)$  substitution is almost male sterile.

4.50 R. Pettigrew,

Faculty of Biological Sciences, University of New South Wales.

Studies on a group of chlorophyll mutants in hexaploid wheat.

A spontaneously-occurring yellow mutant of hexaploid wheat involves a single partially dominant gene. This mutation cannot be a deletion because all deletions are observed in the 21 nullisomics of hexaploid wheat and all of these are green.

The homozygous yellow mutant has a pigment content approximately 1/5 that of normal green. It has a higher chlorophyll a:b ratio and a lower chlorophylls : carotenoids ratio. However, it

grows fairly vigorously and is fully fertile.

The mutant gene has been located on chromosome 7A by monosomic analysis. Also chromosomes 7B and 7D each possess a gene that interacts with the mutant gene. The homoeologous genes on these chromosomes compete with the mutant gene giving rise to different degrees of yellowness according to the ratio of the number of mutant genes : normal genes.

Of three other EMS-induced yellow mutants of hexaploid wheat, one has been shown to involve an allele of the above mentioned gene. The other two involve mutations on one of the homoeologous group 7 chromosomes and may also be allelic.

Electron microscopy has revealed a variety of structural abnormalities in the chloroplasts of these mutants.

7.30 EVENING LECTURE.

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The attention of members is drawn to the following papers to be given before the Australian Mammal Society in the No. 2 Theatre Napier Building on Friday 15 August.

10.00-10.30	P. Shaughnessy. Transferrin polymorphism in Southern Fur Seals.
11.00-11.30	R. Hope. Genetical polymorphisms in populations of Trichosulfus vulpecula.
11.30-12.00	P. Martin. Cytological evidence on Evolution in the Macropodiae.
12.00-12.30	D. Pye. Rattus fuscipes assimilis in Victoria. An unusually high level of non-diploid animals.
Groups of macropoles divided by kenyctype resemblence. yle (1 Peterous 2 Bettingia 3598. 2 Bettingia 3598. 3 Aepyprymnus (20) 4 Dendrologus 4598 5 Lagochestes Hypsiprymnodon Repregale thylogale Dorcops Setorix Anychogalea Lagostophys 22, 18 22 20 24	
6	Manopus, Megalina, Wallaba