GENETICS SOCIETY OF AUSTRALIA

21ST GENERAL MEETING

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AUSTRALIAN NATIONAL UNIVERSITY

CANBERRA

17TH - 18TH MAY 1974

A. GENERAL INFORMATION

1. ACCOMMODATION AND MEALS

For those travelling by car, A.N.U. is best reached via Northbourne Avenue and Barry Drive (see enclosed visitors guide). Accommodation for members of the Society has been arranged at John XXIII College, Daley Road (site 1 on the guide).

All meals will be in the College and meal times are as follows:

Breakfast	7.45	-	8.25	a.m.
Lunch	12.30	-	1.20	p.m.
Dinner	5.50	-	6.20	p.m.

Non-resident members of the Society may obtain lunch at the College. Tickets for lunch will be on sale at the enquiry desk at the College.

2. LECTURE PROGRAMME

All lectures will be held in the Haydon-Allen Tank, Haydon-Allen Building, Faculty of Arts (site 2 on the guide).

3. **REFRESHMENTS**

Morning coffee will be available outside the lecture theatre from 10.15 - 10.35 a.m. Afternoon tea will be served in the first year teaching laboratory in the basement of the Botany Department (site 3 on the guide), at 3.45 p.m. The demonstrations will also be on display in this laboratory.

4. SOCIAL ARRANGEMENTS

- (1) <u>A Mixer will be held in the common room of John XXIII</u> <u>College at 7.00 p.m. on May 16th.</u> The College bar will remain open after the mixer.
- (2) The Director of the Research School of Biological Sciences, Sir Rutherford Robertson, has invited the Society to be his guest at a sherry party to be held in the common room of RSBS from 5.00 - 5.45 p.m. on May 17th. RSBS is located close by the Botany Dept. (site 4 on your guide).

- (3) The Annual Society Dinner will be held in John XXIII College on May 18th at 7.00 for 7.30 p.m. The reception will be in the common room of John XXIII; the dinner will be in the dining hall of the College.
- (4) For members staying over for the Eucaryote Chromosome Conference there will be a <u>BBQ lunch</u> at the University Staff Centre (site 5 on your guide) on May 19th commencing at 11.30 a.m.
- 5. ANNUAL GENERAL BUSINESS MEETING Friday 18th

The AGM will be held at 7.15 p.m. in the common room of John XXIII. The bar of the College will open after the meeting is concluded.

B. LECTURE PROGRAMME

Friday, 17th May 1974

9.00 - 10.15 Invited Lecture

Prof. Bill Hayes - "Procaryotic Genetics in Perspective"

Chairman - David Catcheside

10.15 - 10.35 Coffee

10.35 - 12.15 Short Papers - Session 1 - Chairman, David Hayman

10.35 <u>Barry J. Richardson</u> Ecological genetics of the wild rabbit in Australia.

10.55 Greg C. Kirby

Genetic structure of different house mouse populations.

11.15	<u>Oliver Mayo</u>	Genetic and environmental influences on plasma-cholesterol level in the house mouse.		
11.35	Ian R. Franklin	Equilibria in multilocus systems.		
11.55	Stephen D. Hopper	A multivariate study of natural hybridisation in <u>Anigozanthos</u> .		
12.15 - 1.40 LUNCH				
<u>1.40 - 3.40 Short Papers - Session 2</u> - Chairman, Jim Peacock				
1.40	Bill R. Scowcroft	Somatic cell genetics with higher plants.		
2.00	Sid H. James	Variation in ovule numbers and pollination mechanism in Isotoma petraea.		
2.20	Greg J. Keighery	Genetic systems in <u>Laxmannia</u> sessiliflora.		
2.40	Kuniaki Watanabe C.R. Carter & S. Smith-White	Chromosome change and phylogeny in race A of Brachycome lineariloba $(n = 2)$.		
3.00	<u>Charlie Carter</u> K. Watanabe & S. Smith-White	Chromosome change and phylogeny in races D, E, B and C (2n = 8,10 12, 16) of <u>Brachycome lineariloba</u> .		
3.20	Christine A. Konowalow	Chromosomal duplications as a cytogenetic tool in the Australian sheep blowfly.		
3.40 - 5.00 Tea and demonstrations (see dem. programme).				

3.

Saturday, 18th May 1974

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9.00 - 10.15 Invited Lecture

Dr Noel Warner - "Genetic Control of the Immune Response". Chairman - David Catcheside

10.15 - 10.35 Coffee

- 10.35 12.15 Short Papers Session 3 Chairman, Des Cooper
- 10.35 Dan Dykhuizen The 'no-selection' lag period in chemostat populations of Escherichia coli.
- 10.55 David F. Callen The effect of mating type on the polarity of mitochondrial gene transmission in Saccharomyces cervisiae.
- 11.15John H. Campbell &Evidence for mergentB.G. Rolfeevolution in a virus.
- 11.35 <u>Barry G. Rolfe</u> & Similarity of the killing J.H. Campbell Similarity of certain bacteriocins and the control of host cell lysis by bacteriophage
- 11.55Peter Hanna &
K.F. DyerMutagenicity of organophos-
phorus compounds in bacteria
and Drosophila.

12.15 - 1.40 LUNCH

1.40 -	3.40 Short Papers - Ses	sion 4 - Chairman, Sid James
1.40	Max J. Whitten	Sex-killing systems for genetic control of sheep blowfly.
2.00	John A. McKenzie	Microdifferentiation in a natural population of D. melanogaster to alcohol in the environment.
2.20	Peter R. Baverstock	Genetic variability and environmental unpredictability.
2.40	John Mulley & J.S.F. Barker	Isozyme variation in <u>Drosophila</u> buzzattii.
3.00	Jeff T.A. Arnold	Organophosphate resistance invest- igation in <u>Lucilia</u> <u>cuprina</u> : recent developments.
3.20	Jeffrey J. Moth	Adult viability in interspecific populations of <u>Drosophila</u> at different densities.

C. ABSTRACTS

RICHARDSON, Barry J. Dept. Genetics, RSBS, ANU, Canberra Ecological genetics of the wild rabbit in Australia

Since its first release in Australia a century ago, the rabbit has established itself in a wide range of habitats. This paper summarises results obtained in the first year of a study of enzyme variation in this species. The geographical and temporal distribution of variants in 6-phosphogluconate dehydrogenase will be described. The Km (6PG), Km (NADP), energy of activation, pH curves and temperature stability of the three isoenzymes have been determined but no differences were found. The distribution of variation in other enzymes will also be described and the distribution of alleles in animals from marginal and good habitats compared. The results will be discussed in terms of the social structure and evolution of the rabbit in Australia.

5.

KIRBY, Greg C. Dept. Genetics, University of Adelaide, S.A. Genetic structure of different house-mouse populations.

House mice (Mus musculus) modify their population structure as a response to different environmental conditions. An F-statistics analysis and a genetic distances analysis carried out on four mouse populations shows how differences in ecological conditions can change the genetic structure of mouse populations.

MAYO, Oliver¹, J.R. SABINE¹ and G.C. KIRBY² Waite Agric. Res. Inst.(1) and Genetics Dept.(2) Univ. of Adelaide Genetical and environmental influences on plasma-cholesterol level in the house mouse.

The heritability of plasma-cholesterol level in man and mouse is 30-60%, and some limited progress has been made in determining the loci involved in the genetical component of variability in cholesterol level in man. This report describes a preliminary investigation of cholesterol level in mice, with a view to determining the sources of genetical variation. Eight inbred lines (C57BL, CBA, BALB/c, A^WB, A^EB, DBA, Sed, Swiss-Albino) and some local feral mice have been examined for plasma cholesterol level on diets containing either no cholesterol or added crystalline cholesterol. Dietary cholesterol lowers cholesterol level in some strains but no in others. A start is being made on the genetical analysis of these responses.

FRANKLIN, Ian R. C.S.I.R.O. Div. Animal Genetics, Epping, NSW Equilibria in Multilocus systems.

As a result of recent advances in the equilibrium theory of selection at two and three loci, some patterns have emerged which allow predictions for more complex models. Theorems, and assertions concerning the number of equilibria which may exist, and be stable, for arbitrary multilocus models will be presented.

HOPPER, Stephen D. Botany Dept. Univ. Western Australia, Perth A Multivariate study of Natural Hybridization in Anigozanthos.

The genus Anigozanthos consists of nine predominantly-outbreeding perennial species which occur only in the Southwestern Province of Western Australia. Natural hybrids derived from all six biparental combinations of A. humilis, A. manglesii, A. viridis and A. bicolor have been located in a detailed survey of areas of sympatry. The hybrids appear in bispecific and trispecific assemblages on cleared farmland, roadside and railway verges, and seminatural areas maintained by annual slashing. A number of these assemblages have been selected for detailed multivariate investigations using the techniques of discriminant functions and canonical analysis.

The population structures encountered varied from simple bispecific parental combinations associated with distinct sterile F_1 hybrids to complex biparental and triparental hybrid swarms containing F_1 and later generation derivatives. Although most populations were locally restricted, some extended continuously for up to 15 miles along railway and road verges. When set against a background of parental entities which in themselves vary geographically, natural hybridization within this <u>Anigozanthos</u> syngamon poses challenging problems for evolutionary interpretation. An outline of the significance and probable dynamics of the situation will be presented for discussion.

SCOWCROFT, Bill

Div. Plant Industry, C.S.I.R.O., Canberra Somatic Cell Genetics with High Plants

The essential feature of plant improvement is a recurrent cycle of hybridisation and selection. Somatic cell genetics offers the potential of increasing the efficiency of selection and the range of available genetic variability through somatic hybridisation.

Since plant cells are totipotent it is possible to regenerate a fully fertile plant from a single cell. Further it is a relatively routine procedure to culture large numbers of plant cells under defined conditions such that biochemical mutants can be isolated. Not only can such techniques be utilised to understand the biosynthetic pathways of higher plants, but, perhaps more importantly, to provide valuable techniques for plant breeding programs. For example, biochemical mutants are essential for isolating ovbrid genotypes following somatic hybridisation of species which, because of reproductive barriers, cannot be sexually hybridised. Preliminary work also indicates that in vitro culture of plant cells will yield genotypes which are resistant to those plant diseases where the pathogenicity is due to a toxin.

JAMES, Sid H.

Dept. Botany, University of Western Australia, Perth Variation in ovule numbers and pollination mechanism in Isotoma petraea.

Pollination behaviour in <u>Isotoma petraea</u> is subject to environmental and genetic circumstances. It would appear that the assembly of the original complex hybrid occurred on Pigeon Rock, as a stablized entity in the F₂ of an interpopulation heterozygote which combined hybrid vigour and a highly penetrant dominant factor for selfing. The donor population was probably that of an iron-ore outcrop about 6 miles away in the South Wyndarling Ranges. KLIGHERY, Greg J. Dept. Botany, University of Western Australia, Perth Genetic Systems in Laxmannia sessiliflora Dene. (Liliaceae).

Laxmannia sessiliflora, as presently defined, is a small perennial herb, distributed throughout southern temperate Australia. The species contains several clearly defined forms, which differ markedly in their genetic systems.

In Eastern Australia, there is a uniformly tetraploid (n = 8) form, which shows little variation in morphology or breeding behaviour. Since all populations flower in September - November compared to May - July for W.A., and none are found on the Nullabor Plain, this form is both seasonally and spatially isolated and constitutes a distinct biological species.

In Southwestern Australia some five forms can be recognised. These are all allopatric, diploid, morphologically distinct and often differ in their breeding systems (i.e. ability to self, possession of post zygotic lethals); yet they can be easily crossed in the glasshouse. If these hybrid progeny are fertile, it would appear that L. sessiliflora in W.A., is composed of a series of locally adapted forms, and contains the majority of variations in genetic systems found between the other species of the genus.

Within two of these forms, and in at least 3 populations, an aneuploid change to give 2n = 7 has occurred, persisted and spread. Detailed mapping of the chromosomal forms has been carried out in these populations. Since aneuploidy is unknown in any other species of the genus, though common in the Liliaceae, an understanding of these cytological forms may provide evidence of the evolutionary significance of such a change.

On the Perth coastal plain, L. <u>sessiliflora</u> and a probable derivative L. <u>ramosa</u> are frequently associated, yet on the older Darling peneplain they are almost invariably allopatric. This sympatry appears to be a function of the recent colonization of the area. The species when in sympatry are often found to be genetically more distinctive than their surrounding neighbours in allopatry. Studies are being undertaken on the nature of the barriers which keep these closely related species separate, despite the fact that they flower together and can be easily crossed in the glasshouse. WATANABE, Kuniaki, C.R. CARTER and S. SMITH-WHITE School of Biological Sciences, Univ. of Sydney, NSW Chromosome change and phylogeny in the races of Brachycome lineariloba A (n = 2).

Striking differences occur in prophase chromosome condensation pattern and in metaphase karyotype in the several races of B. lineariloba A (n = 2).

These differences in karyotype involve changes in centromere position, relative arm length, presence and position of secondary constrictions, trabants and satellites and appear to result from translocation.

Differences in condensation pattern are also in part due to the consequences of translocation. This is established from meiotic pairing analysis in hybrids. The proximity of certain segments to heterochromatin appear to cause their conversion to, or from, early or late condensation.

CARTER, Charlie R., K. WATANABE and S. SMITH-WHITE School of Biological Sciences, Univ. of Sydney, NSW. Chromosome change and phylogeny in races D,E,B and C (2n = 8, 10, 12, 16) of Brachycome lineariloba.

Detailed analysis of karyotype and condensation patterns in the various races of <u>B</u>. <u>lineariloba</u> and related species enables further interpretations of phyletic evolution within the group.

The concept of a basic set of four chromosomes throughout this group is maintained although some changes can be identified. Chromosome I (large, metacentric) appears uniform in all races. Chromosome II (large, subacrocentric) shows a small, probably interstitial deficiency in the short arm in races E, B and C. Chromosome III appears uniform throughout, but chromosome IV shows some changes.

Chromosomes I and II show early condensation in mitotic prophase in all races. The karyotypes of E x A hybrids (somatic number 6) verifies the sexual system of race E and meiotic analysis demonstrates considerable duplication in race E.

The phyletic implications of these data will be discussed.

KONOWALOW, Christine A. Dept. Fntomelogy, C.S.I.R.O., Canberra Chromosomal Duplications as a Cytogenetic Tool in the Australian Sheep Blowfly.

By adjacent-1 segregation, Y-autosome translocations in the Australian Sheep Blowfly often generate viable individuals which are deficient for part of the Y-chromosome and carry a duplication for a segment of the translocated autosome. The extent of the duplication can be observed cytologically through meiotic and mitotic studies and more accurately through the analysis of polytene chromosomes. Sex limited inheritance of markers indicates the extent of the genetic map covered by the duplicated segment. The effect of the duplications on fertility, viability and problems of gene dosage have been studied. The isolation of a family of deficiencies in the duplicated segment following irradiation and the analysis of their genetical and cytological content offers a powerful tool in fine structure mapping. The system should permit the transfer of small interstitial regions from the autosome to the Y chromosome which would be useful in genetic control.

DYKHUIZEN, Dan Dept. Genetics, RSBS, ANU, Canberra The 'no-selection' lag period in chemostat populations of Escherichia coli.

In the selection experiments I have been running between tryptophanrequiring and wild-type <u>E</u>. coli in glucose limited chemostats, a period of no selection is observed before selective changes start. This period, which I call the lag period, will be discussed in this talk. The number of generations of the lag is constant for generation times between one and three hours. The length of the lag period is influenced by the size of the chemostat but not by the initial ratio of the genotypes and not usually by the concentration of tryptophan. The cessation of the lag is not caused by build-up of a component in the media. Some possible interpretations of why this lag exists and their meaning for ideas on how natural selection acts, will also be discussed.

CALLEN, David F.

Dept. Genetics, University of Adelaide, S.A. The effect of Mating Type on the Polarity of Mitochondrial Gene Transmission in Saccharomyces cerevisiae.

The effect of mating type on the transmission of a mitochondrially inherited spiramycin resistant gene was investigated in crosses between resistant strains derived from two complete tetrads and sensitive strains which shared a common nuclear genetic background. The phenotype of the α mating type, irrespective of whether antibiotic resistant or sensitive, was always the more frequent class in the diploid progeny of a cross. A spiramycin resistant strain in which the mating type had been mutated from a to α showed a corresponding change in transmission frequency from that characteristic of the a strain to that characteristic of the α strain. A variety of other antibiotic resistant markers, selected in the same genetic background, all showed a similar effect of mating type. CAMPBELL, John H. and B.G. ROLFE Dept. Genetics, RSBS, ANU, Canberra Evidence for Mergent Evolution in a Virus.

It is proposed that bacteriophage λ has evolved from a simpler ancestral phage by fusion with small col factor episomes. In particular, the segment of λ chromosome extending from genes P to S appears to be a recently intercalated colK-like chromosome. The colicin gene of this col factor has become the S gene of λ and the transcriptional control elements have been developed into a system for a more precise delaying of the transcription of the "late genes" of λ . Eight characteristics of the P-S segment are consistent with, and explained by, a col factor origin. At least two other segments, b₂ and int-gamma region may also have originated as intercalated col factors. A theory of Mergent Evolution as a characteristically viral mode of evolution will be discussed.

ROLFE, Barry G. and J.H. CAMPBELL Dept. Genetics, RSBS, ANU, Canberra Similarity of the Killing Action of Certain Bacteriocins and the Control of Host Cell Lysis by Bacteriophage λ .

Two phage genes are necessary for the lysis of E. coli cells infected with coliphage λ . Gene R codes for an endolysin which hydrolyzes the cell wall. Gene S is thought to disrupt the cell membrane at the scheduled time of lysis. We report on additional components in this phage control of host cell lysis. A third protein which is continuously synthesized is involved as a lysis regulator. In addition, λ phage has an alternative pathway for triggering endolysin activity which is independent of the S gene.

Genetic and biochemical studies will be presented which indicate a similarity between the action of the S protein of λ and the action of certain bacteriocins on the membrane of E. coli.

It is proposed that colicins which kill by interfering with energy metabolism and the S function of phage λ act by draining the energy reserves of a cell by "short circuiting" specific energy pathways of the cell. Colicin tolerance and colicin "immunity" result from mutations and proteins which specifically block energy flows along particular pathways and thereby prevent colicins (and in some cases S function) from dissipating the energy reserves of the cell through that pathway. HANNA, Peter & K.F. DYER Dept. Genetics, Monash University, Victoria. Mutagenicity of Organophosphorus Compounds in Bacteria and Drosophila.

Organophosphorus compounds are well known for their insecticidal activity. However many are commonly used in industry and some also used as pharmaceuticals. Over 130 organophosphorus compounds have so far been tested for mutagenic properties in our laboratory using various bacterial strains of <u>Salmonella</u> and <u>E. coli</u>. Approximately 15% of these show mutagenic activity and it appears that the mutational event is similar in each case. Base pair substitutions rather than frame shift mutations were found.

Difficulties arise in testing many of these compounds in <u>Drosophila</u> because of their high insecticidal activity. In order to overcome this difficulty, and to test for the development of resistance, <u>Drosophila</u> populations were established to which the compounds could be administered in the food medium. Evidence for the accumulation of resistance and the induction of mutations will be presented in the case of a number of both simple and complex organophosphorus compounds.

WHITTEN, Max J. Dept. Entomology, C.S.I.R.O., Canberra Sex-killing Systems for Genetic Control of Sheep Blowfly.

Where a pest species is utilised for its own control either by the release of sterilised or genetically incompatible individuals there is often a need for a practical means of separating the sexes or for eliminating one or other sex. This paper discusses the systems that have been developed for separating both sexes and for eliminating females. The most promising sex-killing system which lends itself to mass-rearing conditions utilises Yautosome translocations involving autosomes which carry high order resistance genes to dieldrin or diazinon. Susceptible females are eliminated as first instar larvae with a discriminating dose of insecticide, leaving males for use in genetic control. Improvements are made to the system by using Y-autosome translocations with high alternate segregation or by developing special duplication strains.

McKENZIE, John A.

Dept. Genetics & Human Variation, La Trobe University, Vic. Microdifferentiation in a Natural Population of D. <u>melanogaster</u> to Alcohol in the Environment.

Strains of D. <u>melanogaster</u> derived from a vineyard population were more resistant to alcohol in the environment than strains from a population derived from an area removed from the vineyard. Within the vineyard population those strains most closely associated with alcohol in the environment of the cellar, were more resistant than those collected outside the cellar. There was evidence of gene flow between the inside and outside cellar components of this population but microdifferentiation has occurred within the cellar despite this. The adaptation appears to be independent of the ADH system and involves both additive and dominance genetic effects.

BAVERSTOCK, Peter R.

Institute of Medical & Veterinary Science, Adelaide, S.A. Genetic Variability and Environmental Unpredictability.

It has been accepted as dogma that a temporally unpredictable environment favours genetic variability according to the 'nichevariation hypothesis'. However, selection between populations (i.e. group selection) is an implicit or explicit assumption in all models describing the system. A model is presented based on natural selection and predicts a decline in genetic variability. Experimental data from Drosophila support this prediction. Other workers have found that genetic variability increases in Drosophila populations subjected to fluctuating temperature, which they interpret in terms of the 'niche-variation hypothesis'. However their experimental method is inappropriate and cannot possibly be explained by the hypothesis. The present paper interprets their results in terms of 'extreme-environment heterosis' which implies that in many cases, heterosis (and hence maintenance of high levels of genetic variability) may be manifest only in unfavourable Since a fluctuating environment is also likely to environments. be a harsh environment, genetic variability increases not because of niche-variation but rather because of heterosis.

MULLEY, John and J.S.F. BARKER Dept. of Animal Husbandry, University of Sydney, NSW Isozyme Variation in Drosophila buzzatii.

Drosophila buzzatii lives in association with cactus plants of the genus <u>Opuntia</u>. The distribution of these introduced species is discontinuous.

Initially 29 loci were analysed from 8 localities in Queensland and New South Wales. The 6 variable loci were then investigated further following north-south and east-west transects increasing the number of localities to 31 (some localities being resampled several times).

Levels of variation were measured and the relationship between variability, population position and environmental conditions investigated. The level of detectable variation was exceedingly low compared with other Drosophila species. ARNOLD, Jeff T.A. Dept. Entomology, C.S.I.R.O., Canberra Organophosphate resistance investigation in Lucilia cuprina: recent developments.

With the advent of a sufficiently sensitive and reliable larval resistance test for L. cuprina, OP-resistance investigations were extended to this more appropriate stage. They have revealed that there is little correlation between levels of adult and larval resistance, though as yet there is found no case where larval OP-resistance is not expressed in the adult. The implications for resistance-gene frequencies in the field are discussed.

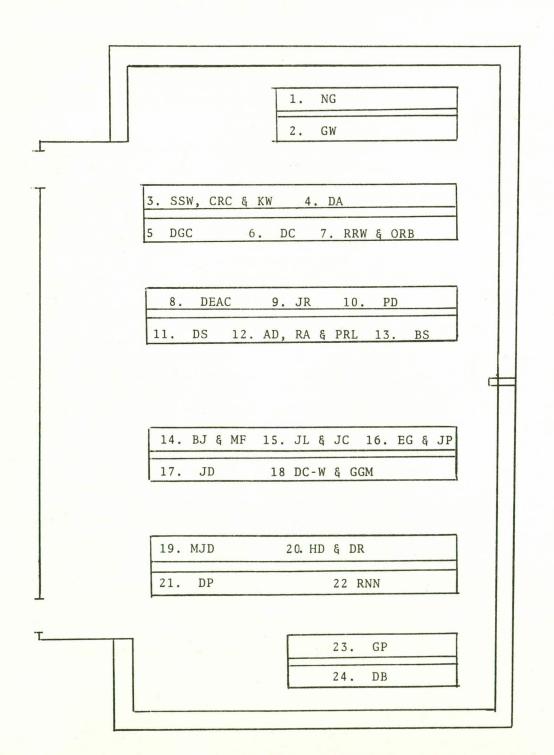
MOTH, Jeffrey J. Dept. Animal Husbandry, University of Sydney, NSW Adult Viability in Interspecific Populations of Drosophila at different densities.

Survival of newly eclosed adults of D. simulans st and D. melanogaster Or-k-C, fed excess quantities of dead yeast throughout life, was followed daily for 7 days in an experiment where adult density (6 levels), species frequency (6 levels) and 32P tissue content (2 levels) were varied factorially. A separate experiment to compare surivival in different types of experimental unit was also done. Similar experiments to those described above were completed for D. simulans st competing against D. melanogaster yw. The entire data was subjected to a least-squares (unbalanced, missing-plot) analysis of variance.

D. <u>melanogaster Or-R-C</u> had highest survival, with D. <u>melanogaster</u> <u>yw and D. simulans st lower</u>, but equal, in survival. The competing stock of D. <u>melanogaster</u> influenced D. <u>simulans</u> survival survival being highest when yw was the competitor. As populations aged, survival fell. Increasing density reduced viability for all three stocks, but species frequency effects, although significant, were not consistent. The female sex achieved higher survival than did the male in both D. <u>melanogaster</u> stocks, but the reverse was true in D. <u>simulans st</u>. <u>32P</u> lowered viability. Experimental unit type altered survival - highest survival being obtained in the cardboard unit. Numerous interactions were significant and these are discussed.

Adult density was shown to have a delayed effect on viability the delay before the appearance of the effect (an increase in death rate) being decreased as density rose. The term variably delayed density dependent has been adopted to describe the fitness component adult viability. Some high density populations showed a second re-adjustment (a decrease) in their death rate - this being a reaction to the effect of reduced density caused by high early mortality. D. DEMONSTRATIONS

(1) Laboratory Layout



(2) Demonstration Abstracts

GROVER, Nerinda S. (Dem.1) Dept. of Botany, ANU, Canberra Isoenzyme Variations in Arabidopsis thaliana.

Several pure-breeding geographical races of <u>Arabidopsis thaliana</u> have been screened for electrophoretic variations, and from a study of appropriate F₂ progenies, genetic variants at eleven isozyme loci (viz., three esterases, three peroxidases, two leucine amino-peptidases, one acid phosphatase and two glutamate oxalacetate transaminases) have been detected.

The results obtained from the analysis of gene frequency changes in the segregation generations in response to selection for high seedling weight in a population composed of a mixture of a number of artificially synthesised double-cross progenies will be demonstrated.

WEBB, Graham C. (Dem.2) Dept. Population Biology, RSBS, ANU, Canberra Late replicating Y-chromosomes in the earwig Forficula auricularia.

The most commonly occurring male sex-chromosome system in Forficula auricularia is of the XY-type. Here the Y is small and mitotically stable and will be referred to as the Y_1 . This Y_1 -element is the last to complete replication but has relatively few grains in most late-labelled spermatogonial metaphases. The X-chromosome is also moderately late replicating in spermatogonial divisions but is not so in follicle cell mitoses.

Two other types of Y-chromosomes are represented in Australian populations of this european species. One of them, known as the Y_2 , is large and mitotically unstable. Cells with one or two Y_2 's predominate but three or four Y_2 -elements can occur. This Y_2 is very heavily labelled in late-labelled spermatogonial metaphases. Finally a Y_3 -chromosome has been recognised which is larger than the Y_2 but shows a similar replication pattern to it.

Different populations appear to have different frequencies of Y_1 , Y_2 and Y_3 types.

SMITH-WHITE, Spencer, C.R. CARTER, K. WATANABE (Dem.3) School of Biological Sciences, University of Sydney, NSW The Biology of Brachycome lineariloba

The demonstration will deal with a number of aspects of the biology of <u>Brachycome lineariloba</u> including chromosome change, meiotic behaviour in the quasidiploid and various hybrids, condensation pattern analysis, population polymorphisms, ecogeology and phylogeny.

ANGUS, Don (Dem.4) Salisbury College of Advanced Education, S.A. Morphological Variation in Clianthus formosus.

The demonstration will present photographs of both normal and an erect variant of Sturt Pea, <u>Clianthus</u> formosus found at Kingoonya, South Australia.

CATCHESIDE David G. (Dem.5) Dept. Genetics, RSBS, ANU, Canberra Regulation of Genetic Recombination in Neurospora crassa

Genes known to be concerned with recombination are of three phenotypic kinds; there should be a fourth. Those of general effect (nuc) presumably determining endonucleases, exonucleases, polymerases and ligases specific to DNA, are detected by production of recessive mutants which result in a general failure of recombination, abortion of meiosis and so infertility. In natural populations virtually only the dominant genes are present. The other two classes of gene regulate the frequency and some other properties of recombination in quite local regions of the chromosomes. Natural populations appear to be polymorphic in respect of these genes. One class consists of genes (cog) located within the individual regions subject to control. Dominant alleles result in higher frequencies of recombination. These genes are probably the targets for endonuclease and nicks in them start a local event of recombination. The third class of genes (rec) of local control are situated away from the regions controlled and their dominant alleles reduce recombination. They are each specific to a number of regions, at which there must be a fourth class of gene, comprising recognition sites (con) for the products of the rec genes.

Thus there are two types of interaction controlling the initiation of genetic recombination, (i) the nicking of cog genes with diverse efficiencies by endonuclease determination by a nuc-d gene and (ii) control of access of endonuclease to cog genes by the products of rec genes which associate with con genes situated near to cog genes and possibly identical to them. COOPER, Des W. (Dem.6) Biological Sciences, Macquarie University, NSW Typing of a transferrin polymorphism in the Echidna (Tachyglossus aculeatus) using Gradipore electrophoresis.

Gradipore electrophoresis is a form of acrylamide slab electrophoresis in which the protein mixture being resolved moves through graded series of pores of decreasing size. At the point of application the acrylamide concentration is about 4% while at the other end of the slab it is 25-30%. As electrophoresis proceeds large molecules are progressively more hindered than small ones. At the limit the molecules are arranged along the slab in order of their size, with each molecule having stopped at a particular point beyond which it cannot go because the pore sizes are too small. The technique allows rapid high resolution separation of serum and other protein mixtures. As with other gel electrophoresis, histochemical stains for enzymes and other proteins can be applied to its surface. The demonstration illustrates the typing of a transferrin polymorphism in the Echidna. It is hoped to use this polymorphism in an analysis of the population structure of this unusual animal.

WILLING, Rudolf R. and O.R. BYRNE (Dem.7) Dept. of Botany, ANU, Canberra Hybridisation in Poplars

Techniques which we have found successful in manipulation of interspecies crosses in poplars are briefly outlined. Resultant hybrids between some species previously regarded as "incompatible" are illustrated. Applications of this technique in poplar breeding, particularly with respect to rust resistance, are considered.

CATCHESIDE, David E.A. (Dem.8) School of Biological Sciences, Flinders University, S.A. Control of recombination in the <u>nitrate-2</u> locus of Neurospora crassa.

A dominant gene $\underline{rec-z}^+$ repressing recombination between $\underline{nit-2}$ alleles has been described (Catcheside, 1970). More recently, $\underline{rec-z}$ has been mapped and found to be located on linkage group V close to the $\underline{rec-1}$ locus. Rec-1, the first rec locus discovered in Neurospora affects recombination between his-1 alleles. Analysis of progeny from crosses segregating at both rec-1 and rec-z show that the rec loci, if different, are less than 0.7 map units, apart (95% confidence limit). Thus it is probable that the rec-1 gene product not only represses recombination between <u>his-1</u> alleles, but also between alleles of the <u>nit-2</u> gene which is located on a different chromosome. However, rec-1 does not control recombination in general since it does not affect I9 other chromosomal segments. A general pattern of recombination control is emerging with each of the three known rec loci, rec-1, rec-2 and rec-3, having been shown to affect more than one but not all chromosomal segments. Theoretical considerations predict that there may be two sorts of recognition site adjacent to or within the segment of chromosome where control is exercised. One type, a binding site for the recombination enzymes has probably been identified already (Angel, Austin & Catcheside 1970). A genetic factor very close to the nit-2 locus has now been found which shows some of the characteristics expected of the second type; the binding site for the rec-1⁺ gene product.

RENDEL, James M (Dem.9)

Division of Animal Genetics, C.S.I.R.O., Epping, NSW. DNA Replication in Abnormal Chick Neuroblasts.

This demonstration consists of a series of photographs illustrating the pattern of incorporation of tritiated thymidine during the differentiation of abnormal chick neuroblasts.

DUNSMUIR, Pam (Dem.10) Dept. Genetics, RSBS, ANU, Canberra The Satellite DNA sequences of Macropus rufogriseus.

DNA, isolated from the red-necked wallaby <u>Macropus rufogriseus</u>, has been analysed in CsCl density gradients. In neutral CsCl gradients a single satellite species, representing about 24% of the total nuclear DNA, was observed. In actinomycin D-CsCl gradients two satellite species were seen - one, Act-1, corresponding to the 24% satellite seen in neutral CsCl, and the second, Act-2, a cryptic satellite representing about 4% of the total DNA. The resolution of these satellite species from the mainband DNA was found to vary quite widely according to the ratio of actinomycin D to DNA in the density gradient.

The Act-1 satellite DNA has been purified. Evidence from denaturation studies indicates that it comprises a fairly homogeneous group of DNA molecules with a base composition of 49% (G+C). The renaturation rate suggests that the repeat length is quite long -1000 nucleotides. Cytological hybridization results suggest that this satellite DNA is localized at the centromeres of each of the autosomes and the X chromosome (2n = 14A + XY, d). There appears to be differences in the amount of satellite DNA present on different chromosome pairs. SHAW, David D. (Dem.11) Dept. Population Biology, RSBS, ANU, Canberra The Genetics of chiasma frequency variation in the Desert Locust, (Schistocerca gregaria).

A disruptive selection programme for high and low chiasma frequency over five generations has produced two lines of <u>Schistocerca</u> <u>gregaria</u> with mean cell values of 21.66 and 17.68. Selection was facilitated by the use of a testis sampling technique which allowed direct meiotic assay of the individual without hindering its reproductive capacity and use for selective breeding after chiasma analysis.

Realised heritability estimates for the high and low line were 0.25 and 9.40 respectively. The low value in the high line is thought to be due to the genes responsible for high values undergoing a higher recombination in high frequency individuals; alternatively the line may have reached its "upper cell limit".

Genetic analysis of high x low lines and all their derived backcross and F_2 generations, reveal that the major genetic component is additive with a small unidirectional dominance component toward high frequency types.

The effects of such readily induced changes in the pattern of recombination on the evolution of linkage and the release of variation at the genome level are as yet unknown. Further studies are being performed to determine the relative roles of both chiasma frequency and chiasma position in the evolutionary dynamics of the genetic system.

DANIAL, Arthur, R. ANGELL, P.R.L.C. LAM-PO-TANG (Dem.12) Cytogenetics Unit, Prince of Wales Hospital, Randwick, NSW Banding Techniques in Human Chromosomes.

A demonstration of several different techniques of chromosome banding (G, Q, C, T, R, Gll Bands) will be presented. The chromosome complement is from a boy with an autosomal (chrom. no. 9) ring chromosome. The child who has gross somatic defects and mental retardation was originally described by Turner et al (1962).

SHINEBERG, Barry (Dem.13) Cold Spring Harbor Laboratory, U.S.A. The degradation of amino-terminal β -galactosidase fragments of Escherichia coli.

Prematurely terminated fragments of β -galactosidase are rapidly degraded in growing cells of Escherichia coli, though the wild type polypeptide is stable. The processes involved in the degradation of the incomplete chains are complex. Mutants in which the stability of the fragments is greatly enhanced have been obtained. The mutations of these strains are located in the lon gene, which affects a wide range of activities in E. coli cells including the over-production of capsular polysaccharide, sensitivity to UV irradiation and the lytic activity of bacteriophages. The degradation is greatly reduced by substances which inhibit electron transport and uncouple oxidative phosphorylation. The degradation is dependent on an oxygen supply to the cells. The targets of the mutations and the inhibitors of respiration are different. Attempts to detect the degradation in cell extracts have been unsuccessful.

JOHN, Bernard and M. FREEMAN (Dem.14) Dept. Population Biology, RSBS, ANU, Canberra Supernumerary chromosome systems in natural populations of two Australian grasshoppers.

Heterochromatic supernumerary chromosomes are not an uncommon feature of the population structure of many grasshoppers. These so-called B-chromosomes are of interest because it has been claimed that they are retained in natural populations by virtue of inherent mechanisms of accumulation rather than by positive selection. The demonstration illustrates two such supernumerary systems currently under investigation.

Buforania crassa is an arid species. The two populations so far studied, one in Woolantana and the other in Alice Springs, both have from 1-5 mini-supernumeraries in 50% of the males examined. Their behaviour in the female has not yet been analysed.

By contrast the B-chromosome of Phaulacridium vittatum is larger than any of the conventional members of the chromosome set and is present in far fewer individuals in the natural populations sampled to date. The highest frequency recorded (11-15%) is from populations in the vicinity of Hobart (Jackson and Cheung 1967). Even here, however, males with two B-elements are rare. In the Hobart material it has been claimed that the single B and the X elements of the male segregate preferentially following association at first prophase of meiosis. As the demonstration shows we have been unable to confirm this behaviour in an analysis of 1250 males taken as a single sample from a population in Crookwell N.S.W. where 0.8% of the males carried a B-element.

LANGRIDGE, John and J.H. CAMPBELL (Dem.15) Dept. Genetics, Div. Plant Industry, C.S.I.R.O., Canberra and Dept. Genetics, RSBS, ANU, Canberra The experimental evolution of new gene functions in bacteria.

Some evolutionary changes which allow bacteria to metabolise novel compounds will be demonstrated using Escherichia coli and a series of β -galactoside compounds. These changes include:

- (1) constitutive enzyme production
- (2) mutations of multiple copies of a gene
- (3) alterations in the kinetic characteristics of an enzyme
- (4) activation and modification of a previously undetected gene
- (5) increased permeability of the bacterium for the new compound
- (6) elimination of the toxic effects of the compound or its metabolic products

As will be shown, the response to selection depends on the compound used and, in particular, to how 'foreign' the compound is to that species.

GOLDRING, Elizabeth S. and W.J. PEACOCK (Dem.16) Dept. Genetics, Div. Plant Industry, C.S.I.R.O., Canberra Partial Denaturation of Drosophila melanogaster Mitochondrial DNA

Drosophila melanogaster mitochondrial DNA can be isolated as supercoiled molecules using ethidium bromide gradients. Open circles, which presumably arise from breaks in the naturally occurring supercoils, have a contour length of about 6μ measured using the phage ϕ X174 as an internal standard.

Partial denaturation of the mitochondrial DNA has revealed a single large region (about 20% of the molecule) which melts at a lower temperature than the rest of the genome. Melting profiles of the mitochondrial DNA are triphasic, and the low melting regions of the molecule must be nearly pure AT. This suggests that much of the mitochondrial DNA in D. melanogaster is not translated and restricts its informational content.

DEARN, John M. (Dem.17) Dept. Population Biology, RSBS, ANU, Canberra Speciation and Chromosomal Variation within the Genus Kosciuscola (Orthoptera : Acrididae).

The genus Kosciuscola comprises five species of grasshoppers four of which are found only in the higher regions of S.E. Australia while the fifth is endemic to Tasmania. The animals are all wingless and exist in small isolated populations between which there is little, if any, gene flow. Preliminary studies carried out in the Snowy Mountains have shown that the species are distributed altitudinally and that within species there is considerable phenotypic variation associated broadly with altitude.

Both K. usitatus and K. cognatus, which have contiguous and nonoverlapping ranges, are polymorphic for a large supernumerary block of heterochromatin on the smallest chromosome of the complement. The role of this segment is being investigated by the study of both temporal and spatial variation in segment frequency in natural populations.

The demonstration will present the results of three detailed transects in terms of the species distributions and show the range of chromosomal variation both between and within species. CLARK-WALKER, G. Desmond and G.L.G. MIKLOS (Dem.18) Dept. of Genetics, RSBS, ANU, Canberra Circular DNA molecules from Yeast.

This demonstration will illustrate the methods of extracting and characterising circular DNA molecules in the yeast <u>Saccharomyces</u> <u>cereviseae</u>. The main theme is the cellular localisation of a <u>class of covalently closed circular DNA of nuclear buoyant</u> density and contour length 1.9 um. The methods will also illustrate the use of circular mitochrondrial molecules as markers of cytoplasmic contamination in nuclear extraction procedures.

WHITE, Michael J.D. (Dem.19)

Dept. of Genetics, University of Melbourne, Vic.

- (1) Triploid grasshopper hybrids
- (2) The anomalous karyotype and male meiosis of roaches belonging to the Genus Polyzosteria.

(1) The demonstration will include photographs and (it is hoped) living triploid male and female hybrids between the all-female parthenogenetic species Moraba virgo and various related bisexual species. Photographs of the karyotypes of these hybrids will also be shown.

(2) Species of this genus possess, in both sexes, large numbers of accessory chromosomes, in addition to the normal autosomes and X-chromosomes. The accessory chromosomes are closely associated with the X during the prophase of male meiosis. They orientate very irregularly on the first metaphase spindle and pass undivided to the poles. At the second meiotic division they divide normally. The term supernumerary chromosomes is inappropriate for these elements, since they seem to be invariably present in all individuals and are presumably essential for viability.

DADAY, Hunor and D. ROBERTSON (Dem.20) Dept. Genetics, Div. Plant Industry, C.S.I.R.O., Canberra A biochemical subunit of morphogenesis.

The process of "self" and "not-self" recognition seems to be a widespread phenomenon in immunology; it occurs in the reaggregation in vitro of dispersed cells of sponges and vertebrates and in incompatibility systems in plants which involve the acceptance and rejection of pollen. Dissociated cells of avian and mammalian embryos can reaggregate to form histoformative structures, in vitro. Cell-to-cell recognition and subsequent aggregation appear to depend upon receptor sites on the cell surface which accept certain intercellular adhesive molecules. The present investigation is the first report on purification and characterization of the bioactive subunit of intercellular adhesive protein, isolated from vertebrates.

Bioactive proteins were extracted by EDTA from 10-day-old chick embryos and fractionated by Bio-gel P-10. Both large and small molecular fractions were eluted, and the small molecular fraction showed a 33-fold greater bio-activity in terms of cell aggregation. The small molecular fraction was further separated after SDS treatment by high voltage electrophoresis and five ninhydrin positive bands were obtained. After the removal of SDS from the eluted peptides, only one of the peptides showed bioactivity. The MW of the active peptide was estimated by Bio-gel P-2 as 750, and aggregating activity was 100-fold greater than that of the original large molecular fraction. Bioactivity of the activefraction was not affected by treatment with heat, DNase, RNase, collagenase, neuraminidase or hyaluronidase. No carbohydrates or lipids were identifiable in the active peptide, which appears to contain only amino acids. Investigation of composition, structure and cell surface specificity is in progress.

PORTER, David L. and J. MARTIN (Dem.21) Dept. of Botany, ANU, Canberra & Genetics Dept. Melbourne Univ. Vic. Chromosomal Polymorphism in Polypedilum nubifer.

Polypedilum nubifer (Diptera, Chironomidae), 2n = 8, is widespread throughout Australia and is also known from the Middle East, North Africa, Sri Lanka and Taiwan. There are three large metacentric chromosomes, numbered 1 to 3 in order of length, with arms designated A/B, C/D and E/F, and a small acrocentric chromosome 4, arm G. So far there are about 30 alternative sequences known, some of which are strongly sex-linked. The species is female heterogametic, females being heterozygous for a heterochromatic end on the small fourth chromosome, whilst males are homozygous for its absence. Three main areas are to be figured in the demonstration:

- (i) A description of the alternative sequences and their possible phylogenetic relationships.
- (ii) The two levels of cytological sexual differentiation.
- (iii) An arm by arm analysis of geographic variation in southern and eastern Australia using genetic distance and genetic uniqueness estimates.

NANKIVELL, R. Neil (Dem.22) Dept. Population Biology, RSBS, ANU, Canberra Chromosomal differences in closely related species of Atractomorpha Saussure.

The three known Australian species of Atractomorpha, A. similis (Bolivar), A. australia Rehn and an unnamed species, recently discovered in Arnhem Land by Dr K.H.L. Key, have 2n(d) = 18 + XO, all members of the complement being rod chromosomes. The two named species are known to have supernumerary (B) chromosomes in some of their populations. There is an indication that they have, in some individuals, additional A chromosomes in the germ line, a peculiarity observed in other Pyrgomorphine grasshoppers by a number of workers (see dem. 23). The chromosome differences include:

the number of autosomes with heterochromatic knobs in the centromere region, and the size of these knobs,

the presence of long heterochromatic segments at the distal ends of some autosomes,

the relative size of the megameric chromosome, and

the presence of a lightly staining band on the X chromosome near the centromere end.

The three species also show marked differences in chiasma frequency and localization and one species has polymorphism for supernumerary segments.

PETERS, Greg B. (Dem.23) Dept. of Botany, ANU, Canberra Extensive germ-line polysomy in the pyrgomorphid grasshopper Attractomorpha similis.

Extra chromosomes occur in 10-20% of the male individuals in six central Queensland populations of A. similis. Tri-, tetra- and hex-asomic states have been found but the tetrasomic state is the most common. Multivalent configurations are rare on account of the low chiasma frequency ($\bar{x} = 1.1$ per bivalent) found in this species.

The extra chromosomes appear to be confined to the germ line and presumably arise de novo in each generation.

BERMAN, David L. (Dem.24) Dept. of Botany, ANU, Canberra Genetic analysis of isozyme variants in the sheep blowfly, Lucilia cuprina.

Esterase and alpha-amylase variants at isozyme loci of adults of the sheep blowfly, Lucilia cuprina are demonstrated.

At the Est-5 locus, six alleles have been studied among both laboratory reared and field collected populations; in addition, polymorphisms for three variants at the Est-3 locus are being investigated. These isozyme loci are currently being mapped with respect to previously located morphological markers.