THE GENETICS SOCIETY OF AUSTRALIA

17TH GENERAL MEETING

AUSTRALIAN NATIONAL UNIVERSITY

CANBERRA

MAY 21–22, 1970

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GENERAL INFORMATION

REGISTRATION. A limited amount of time will be available for registration in the morning of Thursday, May 21st, outside the entrance to the Main Physics Lecture Theatre.

SESSIONS. All sessions will be concurrent in the adjoining Main Physics Lecture Theatre and Lecture Theatre No. 8 (Building 20 of map). Due to the large number of papers, contributors are requested to observe the fifteen minute delivery time with five minutes discussion time rigorously. 35 m.m. and overhead projector facilities will be available.

SOCIETY DINNER The Society Dinner will be held at Bruce Hall at 7.30 p.m. on Friday May 22nd. Sherry will be served from 7.00 p.m.

BRUCE HALL. Meal times at Bruce Hall (Building 19 of map) are: Breakfast 8.00 to 8.30 a.m.; Lunch 12.30 to 1.15 p.m.; Dinner 6.00 to 6.45 p.m. Lunch and dinner may be purchased at Bruce Hall by non-resident members. Accounts should be settled at the Bruce Hall Office as soon as possible.

PROGRAMME

SESSION 1A - PHYSICS MAIN

Thursday Morning, 21 May.

9.30 a.m.	Hayman, D.L. & P.G. Martin	Sex-chromosome variation in marsupials.
9.50 a.m.	Stace, H.M.	Cytology of the genus *Calotis*.
10.10 a.m.	Nankivell, R.N.	Pericentric inversion polymorphisms and associated phenotypic effects in the grasshopper *Austroicetes interioris*.
10.30 a.m.	MORNING TEA	
11.00 a.m.	Brink, N.G.	Mosaic and complete mutations in *Drosophila*.
11.20 a.m.	Polak, C.E.	Analysis of induced sex-linked lethals in *Drosophila*.
11.40 a.m.	Lee, G.L.G.	Backmutation and suppression in *Drosophila*.
12.00 noon	Kerr, C.	X-chromosome inactivation in man: evidence from X-linked mutations.

SESSION 1B - PHYSICS NO. 8

9.30 a.m.	Winston, J.A.	Using linear branching models in population genetics.
9.50 a.m.	Winston, J.A.	Models of evolving populations practising positive assortative mating.
10.10 a.m.	Ewens, W.J.	Must most mutations be neutral?
10.30 a.m.	MORNING TEA	
11.00 a.m.	Clifford, H.T. & J.P. Craddock	Sex-ratios in higher plants.
11.20 a.m.	Brittan, N.H.	Seed coat colour inheritance in *Thysanotus tuberosus*.
11.40 a.m.	McWhirter, K.S.	Aleurone color variegation involving the R locus in maize.
12.00 noon	Eldridge, K.G.	Breeding system of *Eucalyptus regnans*.

SESSION 2A - PHYSICS MAIN

Thursday Afternoon, 21 May.

2.00 p.m.	Brock, R.D.	Mutation of active versus inactive genes in *E. coli*.
2.20 p.m.	Holloway, B.W. & Heidi Rossiter	Bacteriocin tolerant mutants of *Pseudomonas aeruginosa* - their properties, pleiotropy and relationship to DNA replication
2.40 p.m.	Pemberton, J.M. & B.W. Holloway	Sex factors in *Pseudomonas aeruginosa*.
3.00 p.m.	Stanisich, Vilma & B.W. Holloway	A mutant sex factor of *Pseudomonas aeruginosa*.
3.20 p.m.	AFTERNOON TEA	
3.50 p.m.	Martin, M.D.	Developmental changes in synthetic patterns of tissue proteins in *Calliphora*.
4.10 p.m.	Kinnear, J.F.	Effects of moulting hormone on synthesis, release and uptake of protein in developing larval tissues of *Calliphora*.
4.30 p.m.	Thompson, J.A. & M.M. Gunson	Developmental changes in the nuclear inclusion material of polytene larval tissues in *Calliphora*.
4.50 p.m.	Sin, Y.T.	Multiple haemolymph phenol-oxidases in *Calliphora*: Control of enzyme activity during development.

SESSION 2B - PHYSICS NO. 8

2.00 p.m.	Murray, N.D.	Natural selection in a variable population of *Calomela bartoni*.
2.20 p.m.	Ford, J.H.	Do chromosomes control their own fate?
2.40 p.m.	Craddock, E.	Chromosome hybrids in *Didymuria*.
3.00 p.m.	McWilliam, J.R.	The consequences of selection in an artificial allopoly-ploid.
3.20 p.m.	AFTERNOON TEA	

SESSION 2B - PHYSICS NO. 8 (cont.)

3.50 p.m.	Oram, R.N.	Inheritance of seed production and retention in *Phalaris tuberosa*.
4.10 p.m.	Blackwood, M.	Effect of temperature on crossing-over in maize.
4.30 p.m.	Mayo, G.M.E. & K.W. Shepherd	Recombination between "alleles" conferring rust resistance in flax.
	1. G.M.E. Mayo	Classical recombination at the M locus.
	2. K.W. Shepherd	Non-reciprocal events at the L locus.

Thursday Evening, 8.00 p.m.

SYMPOSIUM - RECENT ADVANCES IN HUMAN GENETICS

BECKER HALL - AUSTRALIAN ACADEMY OF SCIENCE

CHAIRMAN - Dr. R.L. Kirk

Professor R.J. Walsh, School of Human Genetics, University of New South Wales.

"The Study of Genetic Markers of Human Blood".

Dr. P.J. Morris, Department of Surgery, University of Melbourne.

"The Genetics of Human Transplantation".

Professor P.A. Parsons, Department of Genetics, La Trobe University.

"Aspects of Population Genetics of the Australian Aborigine with Special Reference to Skeletal Variants".

SESSION 3A - PHYSICS MAIN

Friday Morning, 22 May.

9.00 a.m.	Driscoll, C.J.	Variation in chromosome pairing in wheat.
9.20 a.m.	Quinn, C.J.	Aneuploids of a 5B translocation in wheat.
9.40 a.m.	Bielig, L.M.	Substitution of rye chromosome 5R for its three wheat homoeologues.
10.00 a.m.	Darvey, N.L.	Spatial relationships of chromosomes in the wheat nucleus.
10.20 a.m.	Stuckey, J.R.	Inheritance of the glaucous character in wheat.
10.40 a.m.	MORNING TEA	
11.10 a.m.	Hammond, K.	Population size and selection response in *Drosophila*.
11.30 a.m.	Rathie, K.A.	Artificial selection with differing population structures.
11.50 a.m.	Dyer, K.F.	Differential accumulation and effects of lethal genes in irradiated *Drosophila* populations of differing sizes.
12.10 p.m.	Nicholls, E.M.	Genetic interpretation of birthmarks.

SESSION 3B - PHYSICS NO. 8

Regulation of Recombination in *Neurospora crassa*

9.00 a.m.	Catcheside, D.G.	The *histidine-3* locus.
9.20 a.m.	Angel, T.G.	A *histidine-3* mutant in which the gene is broken.
9.40 a.m.	Catcheside, D.E.A.	The *nitrate-2* locus.
10.00 a.m.	Smyth, D.R.	Recombination in and near the *amination-1* locus.
10.20 a.m.	Austin, Barbara	Common regulation of the *amination-1* and *histidine-2* loci.
10.40 a.m.	MORNING TEA	

SESSION 3B - PHYSICS NO. 8 (cont.)

11.10 a.m.	Hartley, M.J. & P.G. Williams	Nuclear behaviour of *Puccinia graminis* in saprophytic culture and possible mechanism for somatic hybridisation.
11.30 a.m.	Knox, R.B.	Immunofluorescence study of incompatibility substances during pollen germination.
11.50 a.m.	Walen, Kirsten H.	Vaccinia virus induced chromosomal aberrations and its relationship to viral DNA synthesis.
12.10 p.m.	Smith-White, S. & C.R. Carter	Chromosome races and hybrids in *Brachycome lineariloba*.

SESSION 4A - PHYSICS MAIN

Friday Afternoon, 22 May

2.00 p.m.	Parsons, P.A.	Genetic heterogeneity in *Drosophila* for dessication.
2.20 p.m.	Moth, J.J.	Density and competition in interspecific *Drosophila* populations.
2.40 p.m.	Barker, J.S.F.	Natural selection for co-existence or competitive ability in competing species?
3.00 p.m.	AFTERNOON TEA	
3.30 p.m.	Sved, J.A.	Alternative theories of heterosis.
3.50 p.m.	Franklin, I.	On the non-existence of genes.
4.10 p.m.	Pederson, D.G.	The estimation of heritability.

SESSION 4B - PHYSICS NO. 8

2.00 p.m.	Woods, W. & B. Egan	Induction of the non-UV inducible coliphage 186.
2.20 p.m.	Pilarski, L. & B. Egan	Genetic evidence for the involvement of DNA circularity in gene function.
2.40 p.m.	Kretschmer, P. & B. Egan	Isolation of a suppressor-host in *Staphylococcus aureus*.
3.00 p.m.	AFTERNOON TEA	
3.30 p.m.	Jha, K.K.	The mutants of *Neurospora* resistant to 8-aza-adenine and the genetic regulation of purine metabolism.
3.50 p.m.	Krishnapillai, V.	Differential transductional behaviour of closely related *Pseudomonas* phages.
4.10 p.m.	White, M.J.D.	A Lyon like hypothesis in grasshoppers.

4.30 p.m. BUSINESS MEETING - PHYSICS MAIN

7.00 p.m. SOCIETY DINNER, BRUCE HALL, A.N.U.

ABSTRACTS OF

CONTRIBUTED PAPERS

SECTION 1A

HAYMAN, D.L. and P.G. MARTIN, Dept. of Genetics and Botany, Univ. of Adelaide, Adelaide. -- *Sex-chromosome variation in marsupials* -- The size of the X-chromosome and the Y-chromosome in marsupial species has been found to vary between different species. The nature of this variation has been examined and the present state of knowledge about it will be reported to the meeting.

STACE, H.M., Dept. of Biological Sciences, Univ. of Sydney, Sydney. -- *Cytology of the genus* Calotis -- Initial studies concerning chromosomal variation within the genus *Calotis* reveal a base number n = 8. Species derived from the base number show affinities with either ecological or geographical regions in south-eastern Australia. Areas of particular interest are the Darling River Basin and the montane regions of south-eastern Australia. Possible implications of the available data will be discussed with respect to theories of breeding systems and environmental adaptation.

NANKIVELL, R.N., Dept. of Genetics, Univ. of Melbourne, Melbourne. -- *Pericentric inversion polymorphisms and associated phenotypic effects in the grasshopper* Austroicetes interioris -- In *A. interioris* the X-chromosome and three of the autosomes show pericentric inversion polymorphism. Some gross morphological characters such as testis follicle number, tibial spine number or colour pattern polymorphism have not been found to be markedly affected by the inversion polymorphisms but body weight is influenced by the fourth autosome with Standard-4 homozygotes being heavier, on the average, and Quorn homozygotes lighter than the heterozygotes.

Non-distal chiasmata provide most of the useful long term genetic recombination in this species and, in nearly all bivalents, such chiasmata are more frequent in a heterozygote than in the corresponding homozygotes and more frequent if the individual has a Buronga X-chromosome rather than a Standard X-chromosome. Buronga X individuals also show better regulation in the formation of these chiasmata.

The polymorphisms (especially the Flinders-Standard 6 and the Buronga-Standard X polymorphisms) influence the response of individuals to the environment so that, for example, individuals with certain karyotypes are found more readily during the hot part of the day, others in habitats where the sibling species, *A. pusilla*, is common.

BRINK, N.G., School of Biological Sciences, Flinders Univ., Adelaide. -- *Mosaic and complete mutations in* Drosophila -- Since most chemical mutagens and UV appear to only primarily affect one strand of the DNA double helix, it is of interest to determine how complete mutations are derived following mutagen treatment. Extensive analyses in fungi have tended to indicate that completes are derived from mosaics by two main mechanisms: (a) the occurrence of a lethal hit in the complementary DNA strand to that which carries the mutant hit, or (b) excision-repair of hetero-duplex regions of DNA, caused by mutation in one strand. This could either result in a mutant base pair, or wild type base pair depending in which strand was excised. An alternative hypothesis to these two, is that complete and mosaic mutations are produced independently by different mechanisms.

This paper reports on an attempt to determine which of these alternatives may apply in *Drosophila* sperm following E.M.S. treatment. Initial studies indicated that most of the mosaics produced by this mutagen possessed about 50% somatic mutant tissue, suggesting that only one of the two chromatids had been mutated. It was further found that mosaic frequency (but not complete) declined with storage of treated sperm in inseminated females. However, the transmission of treated chromosomes to the next generation was not affected by storage, but decreased with increasing dose of the mutagen. These results are discussed in relation to the problem of whether complete mutations are derived from potential mosaics.

POLAK, C.E., Dept. of Genetics, La Trobe Univ., Melbourne. -- *Analysis of induced sex-linked lethals in* Drosophila -- Fifteen sex-linked lethals have been induced by the alkalating agents ethane methane sulphonate, N-methyl-N'nitrosoguanidine and N-nitrosomethyl urea and the acridine half-mustard ICR-170 in the region delimited by the deficiency $Df(1)w^{258-11}$. This region lies between the mutants *zeste* and *white*, a distance of 0.67 map units, and in which there are 12 identifiable salivary gland bands.

All lethals were each tested for complementarity with each other, resulting in the identification of 11 complementation groups. This strongly suggests therefore, that each salivary gland band represents a functional unit of genetic organization.

With one exception each given lethal was recombinationally distinct from every other lethal with which it complemented. The exchange of flanking markers plus the derived distances permitted the construction of a genetic map. Since deficiencies, at least in *Drosophila*, reduce the frequency of recombination on either side of the deficiency it can be concluded that all these lethals are point mutations suggesting that these alkalating agents result in single nucleotide changes. In general, the degree of additivity of map distances decreased as the distance between any pair of mutants decreased.

LEE, G.L.G., Hawkesbury Agricultural College, Richmond -- *Backmutation and suppression in* Drosophila -- Previous work has established that the allele-specific, locus non-specific super suppressor *su* $(Hw)^2$ is without effect on a series of distinguishable backmutations of the suppressible mutant sc^1 in *Drosophila melanogaster*. This finding is equally applicable to both X-ray induced and spontaneous back-mutations. The testing of many alleles over many loci revealed that only the loci *sc* and *ct* have more than one suppressible allele. This poses the question of whether these alleles are merely identical reoccurences of one another or result from distinct events in different areas of the same cistron. A phenotypic study of a number of suppressible *sc* alleles in the same genetic background was found to support the latter possibility. Further evidence for this non-identy comes from the cut locus where only one suppressible allele, ct^K is responsive to a single dose of the suppressor. The picture of *su*$(Hw)^2$ as a suppressor of a number of distinguishable alleles in a single cistron is quite compatible with a translational interpretation of suppression.

The mutant *Bar* is reported in both Bridges & Brehme (1944) and Lindsley & Grell (1968) as $su^2(Hw)$ suppressible. I have been unable to confirm this and extensive tests of *B* and three other alleles at this locus in various combinations have also failed to detect suppression. From a survey of the early literature and from an investigation of the *Bar* locus itself a theory of how this erroneous report persisted in the literature is presented.

KERR, C., Dept of Preventive & Social Medicine, Univ. of Sydney -- *X-Chromosome inactivation in man : evidence from X-linked mutations* -- Evidence of cell-mosaicism with respect to a specific gene-product is a valuable adjunct to carrier-detection in females heterozygotic at an x-linked locus. Such findings fulfill the predictions of the inactive x-chromosome theory of dosage compensation in mammals (Lyon hypothesis; LH). While direct proof of an LH effect has been confirmed for only a few x-linked mutations in man there are numerous indirect data to support theoretical predictions. However there are also many problems of interpretation allied to ignorance of the specific nature of biochemical lesions, inaccessibility of some human tissues, complex patterns of tissue differentiation and a mosaic-effect of certain mutations in the hemizygotic male. Findings relevant to LH predictions will be discussed with especial reference to the loci for glucose-6-phosphate dehydrogenase deficiency, factor VIII deficiency, ocular and dermatological mutations, Duchenne pseudohypertrophic muscular dystrophy and agammaglobulinaemia.

SESSION 1B

WINSTON, J.A., Dept of Mathematics, La Trobe Univ., Melbourne -- *Using linear branching models in population genetics* -- Genotypic frequency models are often used to describe evolving populations. Predictions based upon these models are usually given in terms of relative genotypic fitnesses. In contrast, describing these populations by linear branching models (i) avoids the use of relative measures of "fitness", (ii) allows for a clear definition of fitness, when one is available, (iii) enables predictions to be made regarding survival of mutations without referring to the viability of non-mutant genotypes, providing selection is not density dependent and providing the mutant allele is rare when introduced, and (iv) enables us to predict not only whether a mutation has a chance of persisting, but also how this chance varies with changes in population parameters. Methods are given for determining whether a particular population can be represented by one of these linear branching models. A range of examples is cited

WINSTON, J.A., Dept of Mathematics, La Trobe Univ., Melbourne -- *Models of evolving populations practising positive assortative mating* -- The theory referred to in the previous paper has been employed to analyze linear branching models of populations practising positive assortative mating when two alleles, one "wild" and one rare (mutant), segregate at an autosomal locus. These are "genotypic number" models and are contrasted with the "genotypic frequency" models developed by Parson (1962) to describe the same populations. We have obtained both conditions that ensure there is some chance that a mutation persists and, when survival is possible, the magnitude of the "survival probability". We observe how this probability varies with the degree of positive assortative mating, the degree of "fitness" exhibited by each genotype, and the degree of dominance exhibited by the mutant allele. In the absence of density-dependent selection the fate of a mutation is shown to be independent of the viability of the wild genotype. For a large class of populations the probability that a mutation is independent, or nearly so, of the degree of positive assortative mating practised.

EWENS, W.J., Dept. of Mathematics, La Trobe Univ., Melbourne. -- *Must most mutations be neutral?* -- The proposition has recently been advanced by Kimura and others that the large majority of gene substitution processes refer to selectively neutral alleles replacing each other by random drift, with replacements of inferior by superior alleles by natural selection forming only a small minority of gene substitutions. This argument derived originally from the concept of "genetic loads" (although it is also claimed by Kimura now to have substantial experimental support). The "genetic load" argument is questioned (in detail rather than in principle) and it is claimed that a revised analysis reveals that there is effectively no load-imposed ceiling on the rate of selectively controlled substitutions. It is therefore claimed that it is not proper to claim, as a result of mathematical "load" arguments, that most substitutions refer to selectively neutral genes.

CLIFFORD, H.T. and J.P. CRADDOCK, Botany Dept., Univ. of Queensland, Brisbane. -- *Sex-ratios in higher plants* -- Reports of sex-ratios in natural populations of dioecious species of higher plants often differ from the expected equal proportions of the sexes. Similar deviations were observed for several angiosperm and gymnosperm species growing wild in South-East Queensland. However, further investigations showed that when certain precautions were taken with collection of data, the sex-ratios of many populations initially regarded as anomalous, approached unity.

BRITTAN, N.H., Dept. of Botany, Univ. of Western Australia, Perth. -- *Seed coat colour inheritance in* Thysanotus tuberosus -- The testa of seeds developed after artificial self-pollination of *T. tuberosus* plants collected from various localities between Melbourne and Brisbane was uniformly black. Cross-pollinations using plants from different localities also resulted in black seeds. Selfing some of the F1 plants produced only black seeds, other plants upon selfing showed a proportion of brown seeds. The relationship between the production of brown seeds, the proportion of black and brown seeds produced and the parental plants will be discussed. A tentative hypothesis will be advanced to account for the observations.

McWHIRTER, K.S., The Univ. of Sydney, Sydney. -- *Aleurone color variegation involving the* R *locus in maize* -- A heritable system producing variegated aleurone (colorless areas on a colored background) arose during study of a mutant R^g allele. The sudden appearance of phenotypic instability has been observed repeatedly in maize. As with preceding cases, the analysis of the present system has given evidence for production of the variegated aleurone phenotype by interaction of two genetic elements. A "regulator" element, located at or near the R^g allele, appears to interact with a second (activator) element, inherited independently of the *R* locus. Sub lines of the R^g mutant stock carry the postulated "regulator" element, and the sudden origin of the postulated "activator" element was the critical event in origin of the new system.

The mechanism producing aleurone tissue variegation is unknown. Cell lethality and mutability of a previously unknown inhibitor locus are unlikely, since the extent of variegation is related to dosage of the R^g gene. Induced chromosome breakage, or somatic mutation of R^g to *r* are possible mechanisms. However, germinal mutation of R^g has not been observed in variegated stocks. The variegated phenotype closely resembles that produced by chromosome breakage in McClintocks Ac-Ds system. Direct evidence for chromosome breakage in the present system has not yet been obtained.

The significance of a variegation system involving *R* alleles may be that it provides evidence for a regulatory element which potentially could be implicated in such genetic phenomena as mutability of stippled, paramutation, metastability of *R* alleles and allelic difference in spontaneous mutation rate of R^r alleles.

ELDRIDGE, K.G., Forest Research Institute, Canberra. -- *Breeding system of* Eucalyptus regnans -- *Eucalyptus regnans* is sexually reproduced and monoecious. Its flowers are bisexual, protandrous, and open. The flowers are not specifically adapted to pollination by any one vector. Pollination is probably by many species of insects, and to a smaller extent by birds and wind. The mean free path of genes of *E. regnans* is probably of the order of 60 to 300 metres and effective population size 200 to 3000 trees.

A successful technique of self-pollination was developed using unwoven terylene sleeves and blowflies. Of 16 trees examined, 15 were self-fertile to some extent, and the self-fertility of the other tree was uncertain. It appears that selfing is possible in most individuals of this species.

Breeding system of Eucalyptus regnans (contd) --

Observations on the degree of selfing from the study of a marker gene on one tree suggest a small proportion of self-pollination in natural populations. The large proportion of small seedlings found in the nursery, and the presence of runts in the field experiments could also result partly from self-pollination.

During natural selection homozygous progeny from selfing are likely to be eliminated due to the effect of inbreeding depression. As a result the remaining trees which reproduce the forest would be heterozygous.

McWhorter. R^c Gene sent to phytochrome.

Blackwood Maize

Lee MCG. 1968-9. Reproduct-
Depression — E. coli.

H.A. Inst of Rad Biol. { S.S / DS Phage

SESSION 2A

BROCK, R.D., Div. of Plant Industry, CSIRO, Canberra. -- *Mutation of active versus inactive genes in* E. coli. -- A range of mutagenic agents have been tested using the β-galactosidase locus of *E. coli* where the gene can be held in the active (induced) or inactive (non-induced) state while replication is inhibited. Treatment with alkylating agents (DES, EMS and NG) induced a higher frequency of mutation when applied to the active gene than when applied to the inactive gene. Gamma rays and base analogues had the same mutagenic efficiency for both active and inactive genes.

These results support the view that alkylating agents act directly upon the nucleotide bases which become available to the mutagen when the DNA helix is opened for the synthesis of messenger RNA.

HOLLOWAY, B.W. and HEIDI ROSSITER, Dept. of Genetics, Monash University, Melbourne. -- *Bacteriocin tolerant mutants of* Pseudomonas aeruginosa - *their properties, pleiotropy and relationship to DNA replication.* -- It seems very likely that in bacteria there is close physical association between the bacterial cell membrane, the chromosome, and certain enzymes including DNA polymerase. One way of studying such relationships is to obtain bacterial mutants in which the properties of the membrane have been altered. While direct proof of a membrane mutant is difficult to obtain, it appears likely that mutants which are tolerant (as distinct from resistant) to the action of bacteriocins may include mutants of the cell membrane. Such mutants are very easy to isolate in *Pseudomonas aeruginosa*. Many appear to be deletion mutants even though they have been isolated from unmutated populations. They are pleiotropic for a wide range of properties including radiation sensitivity, host cell reactivation, ability to be lysogenized, recombination ability, permeability, activity of nitrate reductase, and sensitivity to mitomycin and ethyl methane sulphonate. The results support the working hypothesis that such bacteriocin tolerant mutants may provide an experimental approach to a further understanding of DNA replication and its relationship to the architecture of the cell.

PEMBERTON, J.M. and B.W. HOLLOWAY, Dept. of Genetics, Monash Univ., Melbourne. -- *Sex factors in* Pseudomonas aeruginosa. -- New sex factors have been isolated from naturally occurring strains of *Pseudomonas aeruginosa.* These sex factors have been transferred into strain 1, a naturally occurring, genetically characterized, female strain. Strain 1 males harboring these sex factors fall into two classes: those which transfer the chromosome from the same origin as the previously characterized strain 2 sex factor and those which transfer the chromosome from another origin forty-eight minutes from the first origin. The second type of sex factor is capable of acting in the same manner as an F-prime.

The use of this second type of sex factor provides a means of mapping that region of the chromosome which was previously inaccessible to mapping by interrupted mating with the strain 2 sex factor. By employing both types of sex factors it has been possible to provide evidence for the genetic circularity of the chromosome of *Pseudomonas aeruginosa.*

STANISICH, VILMA and B.W. HOLLOWAY, Dept. of Genetics, Monash Univ., Melbourne. -- *A mutant sex factor of* Pseudomonas aeruginosa. -- A strain of *Pseudomonas aeruginosa* carrying a mutant sex factor has been isolated from a naturally occurring male strain. The mutant is characterized by its ability to produce recombinants when mated to males while still retaining its ability to act as genetic donor to females. This former property, not possessed by the parent male, has been termed 'Extended Fertility'.

The property of 'Extended Fertility' is transmissible to both male and female cells under conditions where concomitant transfer of chromosome is unlikely, and hence it is concluded that the mutation is associated with the sex factor FP, or another transmissible plasmid.

Although individual clones of the mutant line are homogeneous with respect to the property of 'Extended Fertility', it appears that these cells still possess the wild type sex factor FP. Hence if 'Extended Fertility' is the result of an alteration of FP it would suggest that more than one copy of the sex factor normally exists in *P. aeruginosa* male bacteria.

MARTIN, M.D., Dept. of Genetics, Univ. of Melbourne, Melbourne. -- *Developmental changes in synthetic patterns of tissue proteins in* Calliphora. -- Developmental changes in the patterns of synthesis of proteins in the larval fat body, haemolymph, salivary gland and body wall of *Calliphora* will be discussed. Autoradiography of dried acylamide gels proved to be the most sensitive technique available for quantitative comparisons of protein synthesis within and between tissues. This work has defined the times at which co-ordinated gene switching appears to take place during development. It provides a basis for the study of hormonal control of gene activity and, in addition, has yielded considerable information on the relation between particular proteins from different tissues.

KINNEAR, J.F., Dept. of Genetics, Univ. of Melbourne, Melbourne. -- *Effect of moulting hormone on synthesis, release and uptake of protein during larval development in* Calliphora. -- An important question relating to the mechanism of action of the ecdysones involves the nature of the stimulus to protein synthesis. Is it specific, affecting only one or a few protein species, or is it non-specific? Evidence has been obtained in the present work that the short-term effect of the hormone is not protein specific in fat body and salivary gland. Further, exogenous crustecdysone has no significant influence either on the release of fat-body proteins into haemolymph during early larval development, or on uptake of protein from the haemolymph later in larval life. Two levels of steroid hormone action during larval-prepupal development thus appear to exist in *Calliphora*: a non-specific effect, probably on translation and a specific effect on transcription of particular loci.

THOMSON, J.A. and M.M. GUNSON, Dept. of Genetics, Univ. of Melbourne, Melbourne. -- *Developmental changes in the nuclear inclusion material of polytene larval tissues in* Calliphora. -- The major ribonucleoprotein inclusion bodies of the polytene nuclei from larval ventral nephrocytes, Malpighian tubules, pericardial cells, fat body and salivary glands of *Calliphora stygia* show characteristic developmental patterns at the light microscope level. Three morphologically and developmentally distinct classes of nuclear inclusions occur in these tissues. In fat body and salivary gland nuclei, morphological changes in the inclusion material can be correlated with the pattern of protein synthesis during the third larval instar, and with conspicuous changes in chromosome morphology. The appearance of cytologically diverse nuclear inclusions, in an ordered tissue-specific sequence, may thus reflect differential activation of the genome. These findings appear to have an important bearing on present concepts of nucleolar function.

SIN, Y.T., Dept. of Genetics, Univ. of Melbourne, Melbourne. -- *Multiple haemolymph phenoloxidases in* Calliphora: *Control of enzyme activity during development.* -- It has been suggested that activation of the prophenoloxidase of larval *Drosophila* is controlled by production of an activator protein synthesized in the salivary gland, and by inhibitors in the haemolymph. The present study shows that, in both *Calliphora* and *Drosophila*, the source of the activator is in cuticle secreting cells in general, whether of the body surface, dermal glands or tracheal lining. Salivary glands without attached duct liberate an inhibitor of prophenoloxidase activity *in vitro*, and not an activator. Developmental changes in pro-enzyme, activator and inhibitor will be discussed in relation to control of enzyme activity. Some of the pro-enzyme components of haemolymph differ in their potential substrate specificity but are inter-related in their sub-unit composition and these are to some extent interconvertible.

SESSION 2B

MURRAY, N.D., School of Biological Sciences, Sydney Univ., Sydney. -- *Natural selection in a variable population of* Calomela bartoni -- The native Chrysomelid beetle *Calomela bartoni* provides opportunities for the study of natural selection under field conditions. Two of its races, *bartoni* and *juncta*, meet to form a narrow hybrid zone five miles west of Wombeyan Caves, N.S.W.. Changes in genotype frequencies both within and between collecting seasons have been studied in this area, as well as certain aspects of reproductive success. These data reveal the existence of strong selective differences between some genotypes and point towards a possible instance of frequency-dependent selection in a natural population.

FORD, J.H., School of Biological Sciences, Sydney Univ., Sydney -- *Do chromosomes control their own fate?* -- In the tribe Styphelieae of the Epacridaceae, 3 of the 4 nuclei produced from anther meiosis regularly degenerate and only one nucleus is functional. The purpose of this mechanism is not obvious in diploid species but it enables the maintenance of permanent triploidy in at least one species of the tribe.

At late prophase in the first meiotic division, the chromosomes are aligned at the nuclear membrane in a non random manner. The positions of the chromosomes seem to be related to the structure of the spindle at metaphase and this, in turn, controls the segregation of chromosomes and to some extent the selective degeneration of the 3 nuclei after meiosis.

The chromosomes may then, by some specific interaction with the nuclear membrane at prophase, control their own fate.

CRADDOCK, E., School of Biological Sciences, Sydney Univ., Sydney. -- *Chromosome hybrids in* Didymuria -- The Australian stick insect *Didymuria violescens* consists of an array of distinct chromosome races, showing variation in both chromosome number and sex-chromosome mechanism. Hybridisation between races does occur in at least some of the zones of overlap in the field.

Cytological studies of experimentally produced hybrids and hybrid derivatives reveal the nature of the chromosomal rearrangements involved in the evolution of this species group. The observed reduction in fertility of chromosome hybrids must provide a degree of genetic isolation between races. Chromosomal rearrangements may thus be highly significant in the initiation of speciation.

McWILLIAM, J.R., Div. of Plant Industry, CSIRO, Canberra. -- *The consequences of selection in an artificial allopolyploid* -- Allopolyploids produced by colchicine treatment of sterile interspecific hybrids derived from crosses between a range of distinct ecotypes of *Phalaris tuberosa* (2n=28) and *Phalaris arundinacea* (2n=28) were recombined and exposed to repeated cycles of artificial selection in two contrasting field environments. The consequences of this selection on a number of developmental and reproductive characters, and on the cytological behaviour of the populations are described, and the evolutionary consequences discussed.

ORAM, R.N., Division of Plant Industry, CSIRO, Canberra -- *Genetics of seed production and retention in* Phalaris tuberosa -- Australian phalaris, being an essentially wild ecotype, matures its seeds over a period of several weeks, and sheds them soon after they ripen. The proportion retained has been increased markedly by selection (McWilliam and Schroeder, 1965, J. Aust. Inst. agric. Sci. 31: 313). It is now shown that total seed yield also can be improved in an advanced breeding population.

Fifty five half-sib families were grown in duplicated 4-plant plots at 100 x 40 cm spacings. Panicle compactness and glume stiffness were rated jointly before flowering. When the earliest seeds were ripening, two tillers were removed per plant for seed retention measurement, and the remainder were enclosed in a calico bag, so that total seed yield could be measured.

Seed production and retention were both moderately heritable, but highly variable phenotypically, so that each would respond markedly to selection. The population means should increase by 45-50% following one generation of selection of the upper 10% of plants. The two characters were genetically independent, and each was closely correlated genetically with a character which could be rapidly scored before anthesis. Thus selection of the upper 10% of plants on either estimated floret number per plant, or panicle compactness and glume stiffness, should result in increases of 33% in total seed production, or of 41% in the proportion of ripe seed retained, respectively. Selected plants then could be interpollinated in isolation, allowing one generation of selection to be completed annually.

BLACKWOOD, Margaret, School of Botany, Univ. of Melbourne, Melbourne -- *Effect of temperature on crossing-over in maize* -- Experiments carried out in the Phytotron at the Plant Industry Division of CSIRO under controlled conditions indicated that temperature had an effect on the rate of crossing-over in maize. The loci of C and Sh were used in the study and the general effect was a reduction in percentage recombination with rise in temperature.

Recombination between 'alleles' conferring rust resistance in flax

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

MAYO, G.M.E., Dept of Genetics, Univ. of Adelaide, Adelaide -- *Classical recombination at the M locus* -- Among test-cross progeny of repulsion heterozygotes of two 'alleles' at the M locus, reciprocal products of recombination have been recovered; viz. double-immune (double dominant) and double susceptible (double recessive) plants. We have extended this analysis to a three point test based on segregants among F_2 progeny of coupling heterozygotes. Again reciprocal products were recovered in equal numbers and, from this, a tentative map of the locus has been constructed.

SHEPHERD, K.W., Agronomy Dept, Waite Agricultural Res. Inst., Univ. of Adelaide, Adelaide -- *Non-reciprocal events at the L locus* -- In contrast, test-cross progeny of repulsion heterozygotes involving L 'alleles' have yielded only one of the two recombinant classes expected; viz. double-susceptible plants. For example, with alleles L^2 and L^{10} Flor detected 12 double-susceptible plants in 3,858 test-cross progeny and we have detected 7 in 3,222. The failure to detect double-immune plants may be due to the non-reciprocal nature of the event (e.g. mutation or conversion) producing the double-susceptible plants. Alternatively, it is possible that both double-dominant $\{\frac{L^2L^{10}}{+\ +}\}$ and double-recessive $\{\frac{+\ +}{+\ +}\}$ recombinants are produced by reciprocal crossing over, but the former are not recognized because of interaction between the two dominant alleles in cis position leading to loss of detectable function at this locus. On this hypothesis, the double-susceptible plants would consist of genotypes $\frac{L^2L^{10}}{+\ +}$ and $\frac{+\ +}{+\ +}$ in equal numbers and it should be possible to recover by recombination functional L^2 and L^{10} alleles from the former genotype but not from the latter one. The results of tests designed to distinguish between these alternative explanations will be presented and discussed.

SESSION 3A

DRISCOLL, C.J., School of Botany, Univ. of N.S.W., Sydney -- *Variation in chromosome pairing in wheat* -- A number of chromosomes are known to carry genes which affect chromosome pairing in wheat. The long arm of chromosome 5B carries a gene which prevents homoeologous but allows homologous pairing.

Naturally-occurring variation, includes a translocation involving 5B and minor genetic variation that affects pairing in intergeneric hybrids. Induced variation includes aneuploidy, substitution of related chromosomes for 5B, point mutations and chromosome 5B translocations.

The first experiment to be described involves detection of naturally-occurring variation among varieties of hexaploid wheat. This variation does not affect pairing in the varieties themselves, but it does affect the amount of pairing obtained in intergeneric hybrids.

The second experiment to be described involves an irradiation project designed firstly, to isolate point mutations which would permit increased homoeologous pairing and secondly, to isolate translocations involving $5B^L$. Ditelocentric $5B^L$ was treated with γ-rays and later pollinated onto *Aegilops variabilis* and hexaploid wheat. Selfed seed was also obtained from the same (X_1) tillers.

Hybrids involving *variabilis* are being screened to detect mutations for high pairing. From the hybrids involving hexaploid wheat, four different translocations involving $5B^L$ have been isolated. These show different quadrivalent characteristics. They are expected to be useful in obtaining high pairing intergeneric hybrids.

QUINN, C.J., School of Botany, Univ. of N.S.W., Sydney -- *Aneuploids of a 5B translocation in wheat* -- 'Poso', a compactoid variety of hexaploid wheat, differs from variety 'Chinese Spring' by a reciprocal translocation involving chromosomes 5B and 7B. This is of interest since it involves the chromosome that bears the pairing inhibitor gene(s). The translocation heterozygote, when crossed with alien species, does not usually produce hybrids deficient for the pairing inhibitor.

The translocation chromosome carrying the pairing inhibitor has been isolated in a homozygous aneuploid stock (19" + T_1"). The translocation chromosome deficient for the pairing inhibitor has been isolated in a heterozygous aneuploid with 5B (19" + T_2/5B). This last stock has been tested as a method of producing wheat x alien hybrids with a high level of homoeologous pairing. The results indicate that normally there is a strong selection against

Aneuploids of a 5B translocation in wheat (contd) --
20 chromosome eggs carrying the translocation chromosome. However, a high transmission of this chromosome occurred in a family segregating for the yellow chlorophyll mutant on 7A. The Poso translocation breakpoints are in the short arm of 5B and the long arm of 7B. It is suggested that translocations involving breakpoints in the long arm of 5B may be more useful in eliminating the pairing inhibitor from intergeneric hybrids.

BIELIG, L.M., School of Botany, Univ. of N.S.W., Sydney --
Substitution of rye chromosome 5R for its three wheat homoeologues --
Chromosome 5R of rye, which bears the gene for pubescent peduncle (*Hp*), is homoeologously related to the three group 5 chromosomes of hexaploid wheat and has been substituted for each of them.

The vegetative vigour and high fertility of the $5R^{L}$(5A) and 5R(5D) substitutions indicate that the long arm is the more essential arm of the chromosome 5R.

The gene which controls the diploid pairing behaviour of *Triticum aestivum* is located on the long arm of chromosome 5B. If chromosome 5R is to substitute satisfactorily for 5B, it too, must restrict pairing to homologous chromosomes.

Chromosome $5R^{L}$ and 5R entire have been substituted for chromosome 5B. The irregular meiotic behaviour of both these substitution lines was comparable to that of a nullisomic 5B individual isolated simultaneously. This demonstrated that neither $5R^{L}$ nor 5R can regulate meiotic synapsis as does $5B^{L}$. In the $5R^{L}$(5B) substitution, individual, wheat-rye pairing was observed, for the first time. This pairing has been substantiated by pertinent testcrossing.

The $5R^{L}$(5B) and 5R(5B) substitution lines were poorly fertile. Thus, in terms of fertility, 5R can satisfactorily replace 5A and 5D but not 5B, even though 5A and 5D can replace 5B.

An individual has been isolated which appears to have resulted from an exchange between 5R and 5B. This plant had a chromosome complement of 20" + 1' , possessed the *Hp* character and was meiotically regular and fully fertile. As both 5R and 5B were present as monosomes in its parental plant, it is thought that an exchange occurred between these two monosomes, even though they are not observed to pair in the presence of the $5B^{L}$ gene.

DARVEY, N.L., School of Botany, Univ. of N.S.W., Sydney --
Spacial relationships of chromosomes in the wheat nucleus --
Hexaploid wheat has two pairs of sub-terminal satellited chromosomes (1B, 6B) which give rise to a range of one to four macronucleoli in metabolic cells of meristematic tissue. (Micronucleoli are sometimes also present, for example, as produced by chromosome 5D). The degree of fusion of macronucleoli is determined in part by the spacial proximity of nucleolar organizing regions.

Homologous N.O.Rs are no closer to each other than non-homologous N.O.Rs as indicated by a comparison of the degree of fusion of macronucleoli in a stock possessing two homologous N.O.Rs and a stock possessing two non-homologous N.O.Rs. Actually, the amount of fusion is more than expected on the basis of randomness - a result of anaphase orientation of chromosomes.

These studies and our measurements of the distances between marked metaphase chromosomes throw doubt on the concept of some association in hexaploid wheat.

However, at the last pre-meiotic interphase, a single nucleolus invariably occurs. Colchicine has been shown to suppress this fusion. Colchicine also results in marked asynapsis at metaphase I. As colchicine does not affect pairing of an isochromosome it must be affecting an earlier component of pairing which involves association of homologues.

Thus homologues associate before synapsis is initiated; however, this association may be peculiar to the last interphase before meiosis.

STUCKEY, J.R., School of Botany, Univ. of N.S.W., Sydney --
Inheritance of the glaucous character in wheat -- Chromosomes 2B, 4B and 6B had been implicated as possessing genes affecting the glaucous character. These chromosomes and others have been analysed for their effect on glaucousness. The presence of a gene on the short arm of chromosome 2B has been confirmed. The other two chromosomes have been shown to be not involved in this character; the earlier results stemmed from the presence of recessive background mutations on chromosome 2B in the particular aneuploid lines studied.

From observations on the group 2 nullisomic-tetrosomic lines it has been determined that chromosome 2D bears a weak promoter of glaucousness. Chromosome 2A has a null effect.

From observations on 19 of the 21 chromosomes (1A and 5D excluded) only chromosome 2B has been shown to bear a major gene for entire plant glaucousness.

This is confirmed by the fact that the following additional mutations have been located on $2B^{s}$: a dominant inhibitor, a terminal deletion, and a recessive mutation.

It has also been determined that group 3 chromosomes bear genes affecting the distribution of glaucousness. Chromosome 3A has a gene necessary for glaucousness of the peduncle. Chromosome 3B has a minor gene with the same effect, however chromosome 3D has a null effect.

From varietal intercrosses and backcrossing of major genes into different backgrounds it has been demonstrated that the phenotype results from an interaction of genes for promotion and inhibition of glaucousness.

HAMMOND, K., Dept of Animal Husbandry, Univ. of Sydney, Sydney -- *Population size and selection response in* Drosophila -- The effects of founder and parent population sizes on short term unidirectional response to mass selection and on replicate variation have been examined. *Drosophila melanogaster* were selected for abdominal bristle number at 33% and 100% for 10 generations. Founder sample sizes of 1, 10 and 50 pair all replicated over time and parent populations of 1, 10, 20, 50 and 100 pair replicated within time were utilised in an unbalanced design. A preliminary analysis of the data from 3 replicates over time is presented.

Generally the selection applied was less than that expected. The effect on mean response of reduction in founder population size was marginally greater than that expected over the 10 generations but mean response in the smaller sample lines tended to slight curvilinearity. The observed relationships between parent population size and mean response agreed with the expected in all but the one pair parent populations where the response was less than expected relative to the 10 and 20 pair populations. Trends in response of the control lines were random and more extreme at the smaller population sizes. Variances and coefficients of variation of original observations increased slightly with increasing population size. Between replicate variation of responses generally markedly decreased as population size increased. This variation was usually slightly greater in the control lines.

RATHIE, K.A., Dept. of Animal Husbandry, Univ. of Sydney, Sydney -- *Artificial selection with differing population structures* -- Mass selection for increased abdominal bristle number in *Drosophila melanogaster* was done in six lines, all derived from the same 50 initial families, and using 50 pairs of selected parents in each generation of each line. The reference lines were undivided (U) populations. The other two treatments each consisted of lines with ten sublines, each of five pairs, which were intermingled every six generations. In treatment CR there was crossing with retention of all sublines, while in treatment CC crossing was preceded by culling the poorer 50% of sublines. The selection intensity was 20%, each treatment had two replicates, with three cycles (18 generations) of selection and full pedigree recording. Residual treatment effects were noted during 14 further generations of mass selection.

Selection responses of U and CC were similar, while CR was inferior in total response after generation 12. The largest and smallest increases in phenotypic variance were in the lines with highest and lowest rates of selection response respectively. James and McBride's "spread of genes" technique revealed large differences between lines both within and between treatments, while the between-lines relationship was not necessarily greatest between replicates.

DYER, K.F., Dept. of Genetics, Monash University, Melbourne -- *Differential accumulation and effects of lethal genes in irradiated* Drosophila *populations of differing sizes* -- A number of populations of *Drosophila melanogaster*, varying in size from approximately 50 individuals to more than 5,000, have been chronically irradiated with 4,000R γ rays per generation and studied over a period of 50 generations to determine whether and to what extent the accumulation and equilibrium frequency of lethal chromosomes differ from one to the other.

For partially recessive lethal genes the equilibrium mean gene frequency is independent ofpopulation size (Nei, Proc. Natl. Acad. Sci. 60:517 1968). The rate of accumulation and equilibrium frequency of completely recessive or overdominant lethals both vary with population size.

The results of the present experiments are as follows: (1) Lethals accumulate more rapidly and to a greater extent in larger populations. (2) Productivity varies systematically with population size. (3) Elimination of lethals varies with population size.

The conclusions from these results including estimates of the proportion of partially recessive, recessive and over-dominant lethals present in the populations will be discussed.

NICHOLLS, E.M., School of Human Genetics, Univ. of N.S.W., Sydney -- *Genetic interpretation of birthmarks* -- Mention is made of variegation in plants which has been investigated for many years by a number of workers. Genetic and chromosomal mechanisms have been proposed and generally accepted. In mammals coat colour variegation has been observed and reported to a lesser extent. Observations on pigmentary mosaicism in man are reported in this paper and it is believed that these observations are best explained on a gene or point somatic mutation theory. This theory is not intended to preclude the possibility of other genetic mechanisms as causative factors in some cases. A number of dominant conditions and two recessive conditions (albinism and xeroderma pigmentosum) are discussed.

SESSION 3B

Regulation of recombination in *Neurospora crassa*

CATCHESIDE, D.G., Research School of Biological Sciences, A.N.U., Canberra. -- *The* histidine-3 *locus* -- The frequency of prototrophic recombination between pairs of *his-3* alleles is increased in the absence of the dominant gene *rec-w*$^{+}$, which may be the same as Jha's *rec-4*$^{+}$. The locus of *rec-w* is in linkage group V. The degree of increase is determined by genes at the *recognition* locus, situated 0.25 units distally to the *his-3* locus. In the presence of *cog*$^{+}$, derived from Y8743 which has Lindegren wild stocks as ancestors, the increase is about thirty fold. When *cog*, derived from Emerson a, is present in both parents of a cross the degree of increase is not greater than about five fold. There are also characteristic differences in the distribution of flanking markers.

ANGEL, T.G., Research School of Biological Sciences, A.N.U., Canberra. -- *A* histidine-3 *mutant in which the gene is broken* -- The *his-3* mutant TM429 involves a reciprocal translocation (interchange) in which one break is in the *his-3* locus. It arose from a *cog*$^{+}$ strain. The removal of *cog*$^{+}$ from the main part of *his-3* renders crosses between TM429 and *his-3* mutants carrying *cog* quite insensitive to the absence of *rec-w*$^{+}$. The regions flanking TM429 are rarely represented by the parental class among prototrophs, conversion being effectively excluded from TM429.

CATCHESIDE, D.E.A., Research School of Biological Sciences, A.N.U. Canberra. -- *The* nitrate-2 *locus* -- The frequency of prototrophic recombinants in crosses between all tested pairs of *nit-2* alleles is reduced about eight fold by the dominant gene *rec-z*$^+$. *Rec-z* and *nit-2* are unlinked. There is evidence of another *rec* gene, *rec-t*$^+$ closely linked to *nit-2*, which is also effective in reducing recombination frequency between *nit-2* alleles.

SMYTH, D.R., Research School of Biological Sciences, A.N.U., Canberra. -- *Recombination in and near the* amination-1 *locus* -- *Rec-3* reduces allelic recombination in the *am-1* locus by an order of magnitude. The regions nearby are apparently unaffected. Nevertheless, variation in the characteristics of non-allelic recombination between *am-1* and *gul-1*, a locus less than 0.4 map units away, is associated with the *rec-3* constitution. However, the difference is probably due solely to the effect of *rec-3* on *am-1* itself. This result is consistent with the suggestion that allelic and non-allelic recombination occur by the same basic process, and that observed differences between them are due to differences in the method of detection.

AUSTIN, Barbara, Research School of Biological Sciences, A.N.U., Canberra. -- *Common regulation at the* amination-1 *and* histidine-2 *loci* -- Recombination between alleles is reduced by *rec-3*$^+$ at the *am-1* locus and by *rec-x*$^+$ at the *his-2* locus. The two recombination genes are both in the same region of the left arm of linkage group I between *acr-3* and *arg-3*. All known stocks are either *rec-3 rec-x* or *rec-3*$^+$ *rec-x*$^+$. Recombination between *rec-3* and *rec-x* is less than 0.5%, with 95% probability. The evidence suggests that the two *rec* genes are the same, although they act on unrelated loci.

HARTLEY, M.J. and P.G. WILLIAMS, Dept. of Agricultural Botany, Univ. of Sydney, Sydney. -- *Nuclear behaviour of* Puccinia graminis *in saprophytic culture and a possible mechanism for somatic hybridisation.* -- The successful culture of *Puccinia graminis* on artificial medium has simplified the examination of nuclear behaviour in this dicaryon. It has shown that the infection structures produced by germinating urediospores, apart from their function of host penetration, are essential for the re-establishment of the dicaryotic condition. Differentiation in the vesicle appears to organize the conjugate nuclei division. When dividing the two nuclei are arranged in adjacent positions across the cell with division axies parallel to the longitudinal axis of the cell and each pair of non-sister nuclei move towards opposite ends of the cell.

It is postulated that exchange of spindle fibres between adjacent poles could alter the genotype of the rust without altering the phenotype. Subsequent nuclear exchange between two such mixed genotype races would give the race variants that have been obtained from mixing races of rust.

KNOX, R.B., Dept. of Botany, Australian National Univ., Canberra. -- *Immunofluorescence study of incompatibility substances during pollen germination.* -- Pollen grains bear proteins which are rapidly leached out in aqueous media. These proteins have been localized in the inner cellulosic intine of the pollen grain wall[1,2], and to a lesser extent in other wall layers. A number of cytochemical methods were used: (a) reaction with stains for proteins, and UV absorption at 280 nm[2]; (b) enzymic activity - for ribonuclease, esterase, acid phosphatase, amylase and protease[1,2]; (c) antigenic activity[3] when antisera were prepared against pollen leachates in rabbits, using immunofluorescence techniques. All these methods show proteins are concentrated in the cellulosic intine especially at apertures or pores, the sites of pollen germination.

In slurries of pollen in gelatin media prepared for freeze-sectioning, diffusion of the antigenic substances occurs extremely rapidly through the exine, activity appearing as halos around the grains within 30 seconds - the time between initial contact with the medium and freezing. There is some evidence that incompatibility substances diffuse in this fashion from pollen grains. In *Phalaris* and other grasses, the antigenic substances are exclusively localized in the poral intine. These species have a gametophytically-determined incompatibility system. However in Composites with a sporophytically-determined system, antigenic substances have been detected both in the intine and the superficial pollenkitt (of tapetal origin)[3]. Preliminary results from immunological studies, using immunofluorescence techniques to

Immunofluorescence study of incompatibility substances during pollen germination (contd.) --

specifically localize the incompatibility substances during pollen germination and pollen tube growth in the stigma will be presented.

[1] R.B. Knox & J. Heslop-Harrison (1969) Nature 223: 92-94.
[2] R.B. Knox & J. Heslop-Harrison (1970) J.Cell.Sci. 6: 1-27.
[3] R.B. Knox, J. Heslop-Harrison & C. Reed (1970) Nature 225: 1066-7.

WALEN, Kirsten H., School of Biological Sciences, Sydney Univ. Sydney. -- *Vaccinia virus induced chromosomal aberrations and its relationship to viral DNA synthesis.* -- Tritiated thymidine labelled and unlabelled cells in G_2 period were infected with vaccinia virus. As these cells proceeded into mitosis they were arrested in metaphase by colchicine treatment. Examination of such cells at various times after infection revealed increasing numbers of cells with damaged chromosomes, ranging from simple breaks to stickiness and uncoiling. Most frequently these chromosome abnormalities were associated with damage to the cell membrane. Labelled chromosomes lost the label as the abnormalities became increasingly severe.

Exposure of these virus damaged mitotic cells to tritiated thymidine immediately before harvest showed typical vaccinia viral foci of DNA synthesis in these cells. However, contrary to observations on cells in interphase, where viral DNA synthesis occurs in the cytoplasm, the latter viral DNA foci were associated with the "digested" chromosomal material. These observations are discussed in terms of (i) mechanisms for virus induced chromosomal aberrations, and (ii) host nuclear contribution to viral DNA synthesis.

SMITH-WHITE, S. and C.R. CARTER, School of Biological Sciences, Sydney University, Sydney. -- *Chromosome Races and Hybrids in* Brachycome lineariloba. -- Five biological species differing in chromosome number have been found in this species complex. They have been designated A (n=2), B (n=6), C (n=8), D (n=4) and E (n=5). Species A has three racial forms which differ in Karyotype. These are denoted A_1, A_2 and A_3. Overlap zones between species and races occur and several hybrids have been found. A_1 and A_2 differ by an unequal interchange. C is of amphidiploid origin. B, E and D probably represent a reducing series. Overall relationships and distributions are discussed.

SESSION 4A

PARSONS, P.A., Dept. of Genetics, La Trobe Univ., Melbourne. -- *Genetic heterogeneity in* Drosophila *for dessication* -- Strains set up from single inseminated females of *D. melanogaster* derived from two wild populations have been shown to differ in their ability to withstand dessication, as measured by mortalities after 16 hours in a dry environment, thus there are genes segregating in wild populations for ability to withstand dessication. A more detailed study on strains from one of the wild populations, showed that strains with high wet and dry weights lose water by dessication relatively less rapidly and have lower mortalities, than strains with lower wet and dry weights.

Variability within and between five inbred strains was studied with results as above. Heritabilities for wet weight, dry weight, and mortality were 0.40, 0.41 and 0.60 respectively, showing the likelihood that the traits would be amenable to further genetic analysis.

The relevance of the results will be discussed in relation to stress to high temperatures, and the ecology of the species in general.

MOTH, J.J., Dept. of Animal Husbandry, Univ. of Sydney, Sydney. -- *Density and competition in interspecific* Drosophila *populations* -- Fitness, or the adaptedness of an individual to a particular environment, is a complex concept in population genetics. It is for this reason that we have found it necessary to divide fitness into components and to make analytical measurements of the effect of density and species proportion on these.

We enclosed different numbers and proportions of optimally reared, newly eclosed (less than 8 hours old) adults of *D. simulans* vermilion and *D. melanogaster* Or-R-C in standard volume containers according to a

6 (Density: 10, 20, 40, 80, 160, 320 pairs)

x 6 (Species proportion: 0, 20, 40, 60, 80, 100 percent *D. simulans*)

x 2 (P32: Adults reared on media containing or not containing P32)

factorial design. These seventy-two treatment combinations were replicated three times.

For the first seven days of adult life we have determined the effects of density and species proportion on three components of adult fitness (i.e. on viability, fecundity, and hatchability of eggs laid).

BARKER, J.S.F., Dept. of Animal Husbandry, Univ. of Sydney, Sydney. -- *Natural selection for coexistence or competitive ability in competing species?* -- Numerous studies with laboratory populations of *Drosophila*, *Tribolium* and other genera have shown that when two species are placed in competition in a closed environment, one species is eliminated. The time to elimination may be rapid or quite prolonged, depending on the particular genetic strains of the two species and the environment provided.

Yet in natural populations, any one species is normally associated with many other species, at least some of which could be potential, if not actual, competitors. To what extent then has natural selection acted either to increase ecological displacement thus allowing the observed coexistence or to increase competitive ability of some species resulting in elimination of other actually competing species?

A beginning has been made to experimental analysis of this question. By using discrete generations and setting up each generation with equal numbers of the two species, natural selection may operate in either direction in either species. Mutant strains of *D. melanogaster* and *D. simulans* that were initially similar in competitive ability were used, and four replicate populations maintained together with single - species populations of each strain. Over some 30 generations, there have been no apparent changes in the competitive ability of either strain or in the degree of ecological displacement.

SVED, J.A., School of Biological Sciences, Sydney Univ., Sydney. -- *Alternative theories of heterosis* -- Two hypotheses have traditionally been put forward to explain the nature of heterosis: (1) overdominance per se at individual loci, and (2) dominance or just partial dominance at individual loci. Arguments based on the expected equilibrium frequency determined by the balance between mutation and selection have cast doubt on the adequacy of the second hypothesis. It will be argued that if there is a high level of linkage disequilibrium, such as now seems likely in populations of small size, genes which are dominant rather than overdominant might be present with frequencies higher than predicted by the mutation-selection balance. Thus it might not be possible to rule out with any certainty the second hypothesis.

FRANKLIN, I.R., Div, of Animal Genetics, CSIRO, Sydney. -- *On the non-existence of genes* -- Theoretical evidence is presented which challenges the premise, implicit in much of classical population genetics theory, that correlations in gene frequency (linkage disequilibrium) are not important in natural populations. It is shown that non-random mating, and selection, can produce stable correlations in gene frequency, and that in particular two locus theory seriously underestimates the intensity of linkage disequilibrium between loci in a multilocus system. As a result of these findings it is necessary to reexamine the concept of the gene (or more exactly gene frequency) as the unit of evolutionary change.

PEDERSON, D.G., Dept. of Agricultural Botany, Univ. of Sydney, Sydney -- *The estimation of heritability* -- The genetic parameters of a breeding population may be estimated by choosing a random sample of parents, constructing all possible crosses (excluding reciprocals) and carrying out a diallel analysis. The mean squares in the analysis are functions of χ^2 - variables and have known distributions in terms of (i) the number of parents (ii) the number of individuals per full-sib family (iii) the number of replicates in the experimental design (iv) the degree of inbreeding of the parents relative to the population of interest, and (v) the additive genetic, dominance, and error variances. Each of these variables has been set at a fixed value and a series of "analyses" carried out by generating random χ^2 - variables. An estimate of heritability is obtained from each analysis and the sampling distribution is therefore built up. The aim is to determine the values of (i), (ii), and (iii) above which give an unbiased estimate of heritability with minimum sampling variance.

A substantial bias is found to occur when few parents are used. Although the sampling variance of the heritability is inversely related to the number of individuals in the analysis, a single analysis involving more than 20 parents is found to be a most inefficient procedure and alternatives are suggested.

SESSION 4B

WOODS, W.H., and EGAN, J.B., Dept of Biochemistry, University of Adelaide, Adelaide. -- *Induction of the "non-ultraviolet-inducible" coliphage 186* -- The temperate coliphages have been divided into two groups (Jacob and Wollman, 1956): those which recombine readily with lambda phage and are inducible by ultraviolet irradiation (the "lambda-related" phages) and a second group (the "non-ultraviolet-inducible" phages) the members of which have neither of these properties. Further, the latter group is not subject to zygotic induction, in contrast to the "lambda-related" phages. The different behaviour in these properties between the two groups suggests some variation in the repressor-genome relationship.

Coliphage 186 had been classified into the "non-ultraviolet-inducible" group since it neither recombined with lambda nor exhibited zygotic induction. However, we found that phage 186 was induced by ultraviolet irradiation and that the other "non-ultraviolet-inducible" phages W, 18 and 299, were not induced by the same dose of radiation.

The non-zygotic induction of coliphage 186 has been confirmed. It is not due to an inability of the female to support a phage 186 induction process since lysogenic recombinants are inducible by ultraviolet irradiation. Experiments involving potentially zygotically inducible mutants of 186 are in progress in an attempt to characterize this behaviour of 186.

Jacob, F. and Wollman, E.L. (1956). Ann. inst. Pasteur, 91: 486.

PILARSKI, Linda, and EGAN, Barry, Dept of Biochemistry, University of Adelaide, Adelaide. -- *Genetic evidence for the involvement of DNA circularity in gene N function* -- when coliphage λ infects a cell the N gene is one of the first genes expressed, and N production appears to act as a positive control on at least two promoter sites. In the absence of the N product mRNA transcription is minimal or absent, and infection aborts. In a Kaiser-Hogness Transformation assay system we have shown that while other genes can be transcribed from either whole or fragmented DNA, the N gene can only be transcribed from an intact λ chromosome and not from a fragment. However, N product can act at its appropriate targets on fragmented as well as intact DNA. This would suggest that circularity, as the unique potential of whole DNA, plays an important role in the transcription of gene N.

KRETSCHMER, P., and EGAN, J. Barry, Dept of Biochemistry, University of Adelaide, Adelaide. -- *Isolation of a suppressor host in* Staphylococcus aureus -- The method of isolation involved two unlinked markers affecting lactose fermentation.

$Z^+ \rightarrow Z^-$ - mutation of the structural gene for the β-phosphogalactosidase in the lac operon.

$car^+ \rightarrow car^-$ - mutation in either the E_I or HP_r gene of the phosphotransferase system involved in the uptake of carbohydrates. Such mutation are pleiotrophic, affecting the fermentation of most carbohydrates.

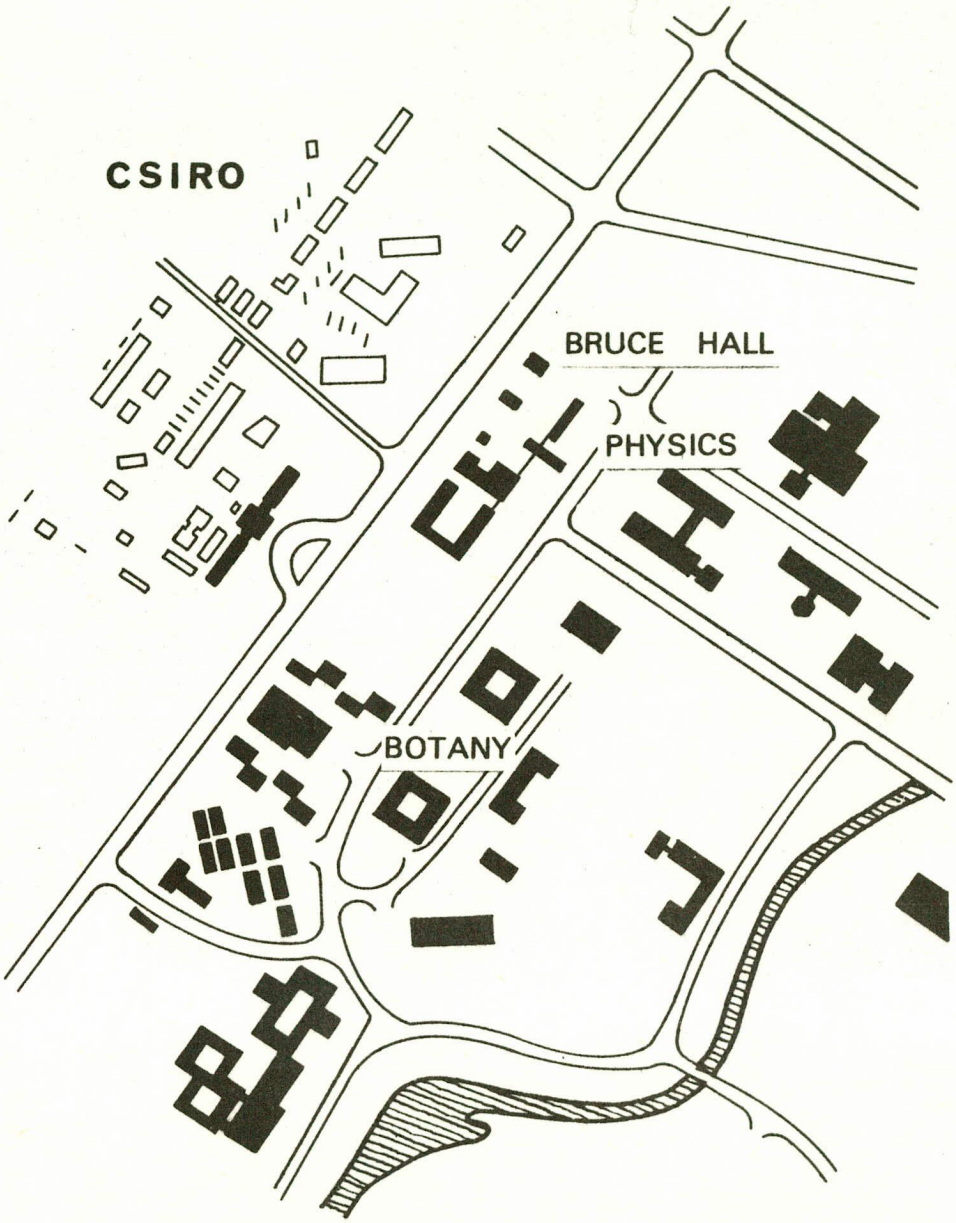
A number of Z^- mutants (lac^-) were first isolated, and from each of these a number of car^- (suc^- mal^-) mutants isolated. Reversion of these double mutants Z^- car^- to lac^+ would require either the double mutation to Z^+ car^+ or, if the original mutations are suppressible, a mutation to Su^+. The single mutation to Su^+ would be much more probable than the double mutation to Z^+ car^+.

A number of revertants have been isolated at a frequency of 10^{-8}, and used to isolate suppressor-sensitive mutants of a staphylococcus phage, which essentially proves the suppressor nature of the revertant.

JHA, K.K., Research School of Biological Sciences, A.N.U. Canberra. -- *The mutants of* Neurospora *resistant to 8-aza-adenine and the genetic regulation of purine metabolism* -- There are at least two different mechanisms known for resistance to purine analogues, such as 8-aza-adenine and 8-azaguanine. Elimination of one mechanism through mutation has permitted isolation and identification of the other. The relationship of the second mechanism to purine metabolism and the purine auxotrophs is being studied. The genetics and physiology of 8-aza-adenine-resistant mutants leads to the hypothesis that the *aza* locus specifies a product involved in the regulation of purine biosynthesis. These mutants should assist the study of the sub-unit structure and allosteric sites of the first enzyme of purine biosynthesis.

KRISHNAPILLAI, V., Dept of Genetics, Monash University, Melbourne. -- *Differential transductional behaviour of closely related* Pseudomonas *phages* -- *Pseudomonas* transducing phage F116 is unique since it protects bacterial DNA or partially protects phage DNA against restriction by the host controlled modification (HCM) system.

Two new phages (126 and 130) have been isolated which are extremely similar to F116 by serology, prophage immunity, and HCM characteristic vis-a-vis phage DNA. But although the new phages are capable of transduction there are quantitative differences in transduction frequency, in linkage of co-transducible genes and in transductions into lysogenic recipients when compared with F116. But significantly, phage 126, unlike F116 or 130, is unable to protect bacterial DNA during transduction. These results will be discussed in terms of HCM.


CSIRO
BRUCE HALL
PHYSICS
BOTANY

Sorghum

	Dark	Red	FR	Low	High
Hybrid { A3197	No	NO	No	Faint	Nil
R7078	No	+ intense	Faint	Intense	Mod

Wheatland Milo

(Bd Eng)

Discussion

4g -

Cytoplasm — Plastids also

T° switch ~ 20°.

Once screen