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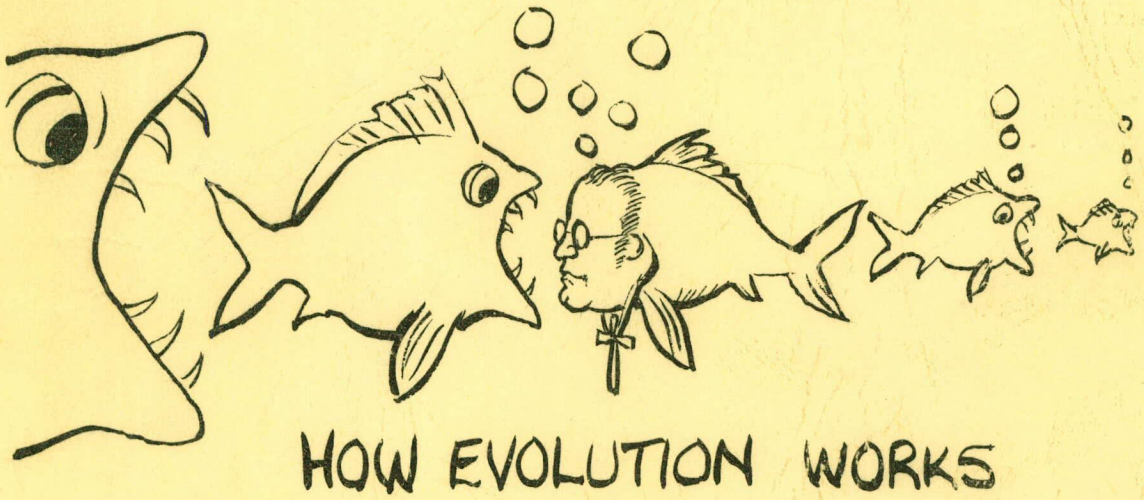
The Genetics Society of Australia

25th General Meeting

PROGRAM & ABSTRACTS



Canberra 19-20 May, 1978

General Information

1. Papers

Symposia papers will be presented in the Copland Lecture Theatre. Contributed papers will be presented at concurrent sessions in the Copland Lecture Theatre and in the adjacent lecture rooms G4 and G5.

2. Demonstrations and Posters

Demonstrations will be on display in the Bruce Hall Common Room from 4.00 pm to 5.30 pm on both Friday and Saturday.

3. Refreshments

Morning tea and coffee will be available adjacent to the Copland Theatre. Afternoon tea will be served concurrently with the demonstrations in the Bruce Hall Common Room.

4. Accommodation and Meals

Accommodation has been arranged at Bruce Hall. Fees should be paid to the Bruce Hall Fee Clerk. Rooms must be vacated by 10.00 am Sunday 21st because of the return of full time students.

Lunch for NON residents is available in Bruce Hall at $2.50. Could you please notify the conference organizers if you wish to take advantage of this. Alternatively meals may be purchased at the Union until 6.00 pm.

5. Social Arrangements

1) A Mixer will be held in the Bruce Hall Common Room from 7 - 10.30 pm on Thursday 18th May.

2) The Society Dinner will be held in Bruce Hall Dining Room on Saturday 20th May at 7.00 for 7.30 pm. Coffee and refreshments will be served upstairs in the Common Room after the dinner.

6. Annual Business Meeting

This will be held at 5.00 p.m. on Friday 20th May in the Bruce Hall Common Room.

PROGRAMME

(names of Speakers are underlined)

FRIDAY 19 MAY 1978

REGISTRATION
8.30 - 9.00 — Copland Theatre Foyer

SYMPOSIUM I
9.00 - 11.00 — Copland Theatre
Chairman: J.B. Langridge

9.00	A.	J.M. Rendel	IQas seen by a quantitative geneticist
9.40	B.	J. Gibson	Blood, sweat and tears : aids in genetic analysis of quantitative traits
10.20	C.	O. Mayo	The genetics of neurological disorders

TEA and COFFEE
11.00 - 11.30

SESSION IA
11.30 - 12.50 — Copland Theatre
Chairman: R.N. Oram

11.30	i.	A.G. Green and R.N. Oram	Genetic and environmental effects and interactions influencing seed yield of Lupinus albus (White lupin)
11.50	ii.	G. Gordon	The use of incomplete partial diallels for hybrid prediction and the estimation of additive genetic effects
12.10	iii.	K.K. Barlow and C.J. Driscoll	Mapping of 2 chromosomal male-sterility mutants in hexaploid wheat
12.30	iv.	C.E. May	Triticale X wheat hybrids

SESSION IB
11.30 - 12.50 — Copland Lecture Room G4
Chairman: J.A. Sved

11.30	i.	J.A. Mandryk	Effects of chromosome homozygosity in Drosophila melanogaster: viability, fertility, and overall fitness
11.50	ii.	J.H. Claxton and W.M. Early	Temporal patterns of radiation insensitivity among the dorsal thoracic microchaetes of Drosphila
12.10	iii.	R. Frankham and R.K. Nurthen	A fascinating polygene: its discovery, characteristics and behaviour
12.30	iv.	P. Pamilo and R.H. Crozier	Effect of haplo-diploidy on genic variation under some selection models

SESSION IC
11.30 - 12.50

Copland Lecture Room G5
Chairman: B.D.H. Latter

11.30	i.	W.P. Hall	Hybrid sinks: the paradoxical role of narrow hybrid zones as barriers to gene flow in animals of limited vagility
11.50	ii.	L.J. McDonnell, D.F. Gartside and M.J. Littlejohn	Analysis of a narrow hybrid zone between Pseudophryne bibroni and P. semimarmorata (Anura: Leptodactylidae)
12.10	iii.	L.H. Schmitt	The rate of evolution in an Australian bush-rat
12.30	iv.	I.R. Bock	Drosphila melanogaster - where did it come from?

LUNCH
12.50 - 2.00

SESSION 2A
2.00 - 4.00

Copland Theatre
Chairman: S.H. James

2.00	i.	D.E.A. Catcheside	Evidence for genes modulating local pairing in Neurospora chromosomes
2.20	ii.	D.J. Coates and S.H. James	Chromosome variation in Stylidium crossocephalum
2.40	iii.	C.R. Carter and S. Smith-White	The inheritance of B chromosomes in Brachycome dichromosomatica (syn. B. lineariloba A)
3.00	iv.	B.A. Barlow	The cytogenetic basis of dioecy in the plant genus Viscum
3.20	v.	David Jewell	Recognition of alien chromosomes and chromosome rearrangements in wheat using the N-banding technique
3.40	vi.	N.L. Darvey and S. Durvasula	Chromosome pairing in wheat-rye amphihaploids

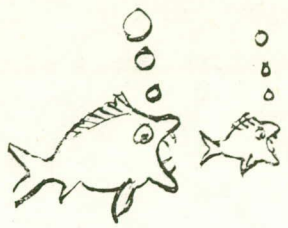
SESSION 2B
2.00 - 4.00

Copland Lecture Room G4
Chairman: J.A. Thomson

2.00	i.	A.J. Howells	The selection and some characteristics of a temperature-sensitive scarlet eye colour mutant of Drosophila melanogaster
2.20	ii.	K.M. Summers and A.J. Howells	Biochemical genetics of eye pigmentation in the Australian sheep blowfly Lucilia cuprina
2.40	iii.	P. Batterham and S.W. McKechnie	A dopa oxidase polymorphism in Drosophila melanogaster
3.00	iv.	G. Daggard	The role of alcohol dehydrogenase in the utilization of alcohol by species of Drosophila
3.20	v.	J. Gibson	Selection for alcohol tolerance in D. melanogaster.

3.40	vi.	C. Willoughby	Industrial melanism in the psocid Mesopsocus unipunctatus (Mull.) in Northern England

TEA, COFFEE - POSTERS - 4.00 - 5.00 — Bruce Hall Common Room



ANNUAL BUSINESS MEETING 5.00 - 6.00 — Bruce Hall Common Room

SATURDAY 20 MAY 1978

SYMPOSIUM II
9.00 - 11.00 — Copland Theatre

Chairman: W.J. Peacock

9.00	A.	W. Hayes	Insertion sequences: a new element in genetic variation
9.40	B.	H. Swift	DNA diminution in polytene chromosomes of Sarcophaga
10.20	C.	J. Campbell	Multigene families in genetics and evolution

TEA and COFFEE
11.00 - 11.30

SESSION 3A
11.30 - 12.50 — Copland Theatre

Chairman: B. Rolfe

11.30	i.	V. Krishnapillai	Transposon specificity in the induction of mutations in a plasmid
11.50	ii.	P. Royle and B.W. Holloway	Plasmid-chromosome hybrids of Pseudomonas aeruginosa
12.10	iii.	A.F. Morgan	Generalized transduction with the virulent Pseudomonas aeruginosa phage E79, and the use of P-2 plasmid carrying recipients to eliminate phage killing
12.30	iv.	A.J. Godfrey and A.F. Morgan	P-1 incompatibility group plasmid instability in Pseudomonas aeruginosa strain pat

SESSION 3B
11.30 - 12.50 — Copland Lecture Room G4

Chairman: D.D. Shaw

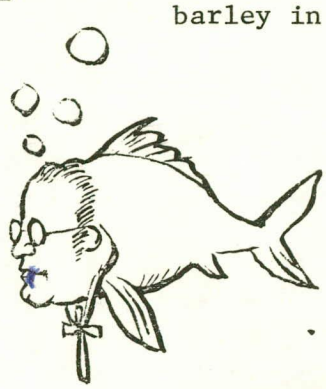
11.30	i.	D.G. Bedo	Polytene chromosome replication in Simulium ornatipes
11.50	ii.	G.B. Peters	Germ line polysomy in the grasshopper Atractomorpha similis

12.10	iii.	M. Yamamoto	Cytogenetical studies of autosomal heterochromatin in meiotic pairing in the male Drosophila melanogaster; implications for the functions of satellite DNA
12.30	iv.	D.R. Smyth and T. Shaw	Cytological location of DNA synthesized at pachytene in Lilium henryi

SESSION 3C
11.30 - 12.50

Copland Lecture Room G5
Chairman: J.M. Dearn

11.30	i.	J.C. Mulley J.W. James and J.S.F. Barker	Allozyme genotype-environment relationships in natural populations of Drosophila buzzatii
11.50	ii.	J.C. Daly	Gene flow in populations of wild rabbits
12.10	iii.	A.H.D. Brown, E. Nevo and D. Zohary	Genetic diversity in the wild progenitor of barley in Israel



LUNCH
12.50 - 2.00

SESSION 4A
2.00 - 3.40

Copland Theatre
Chairman: R. Appels

2.00	i.	W. Hayes	Breakdown of plasmid incompatbility in a tif mutant of E. coli
2.20	ii.	J. Langridge	Construction of molecular vectors for plant cells
2.40	iii.	J.G. Ellis and A. Kerr	The genetics of biological control of crown gall
3.00	iv.	M. Fischer and W.R. Scowcroft	Genetic variability of cauliflower mosaic virus DNA
3.20	v.	W.R. Scowcroft, P.R. Whitfeld and R. Frankel	Changes in chloroplast DNA of isonuclear male sterile hybrids of tobacco

SESSION 4B
2.00 - 3.40

Copland Lecture Room G5 4
Chairman: M.J. Whitten

2.00	i.	M.E. Goddard and R.G. Beilhalz	Guide dog genetics
2.20	ii.	J.T.A. Arnold and M.J. Whitten	Correlation of field organophosphorus-resistance levels and seasonal favourability for Lucilia cuprina

2.40	iii.	J.M. Dearn, J.A.McKenzie and M.J. Whitten	The genetic basis of resistance to the insecticide diazinon in Victorian populations of Lucilia cuprina
3.00	iv.	R.H. Maddern, G.G. Foster and D. Bedo	Compound chromosomes in Lucilia cuprina
3.20	v.	G.G. Foster and R.H. Maddern	Genetic manipulation of sheep blowfly populations

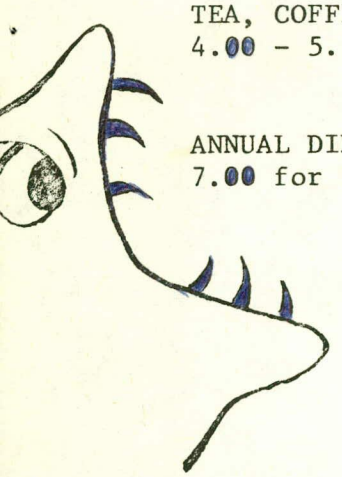
SESSION 4C
2.00 - 3.40

Copland Lecture Room G5
Chairman: D.L. Hayman

2.00	i.	D.D. Shaw and Pat Wilkinson	Homologies between non-homologous chromosomes
2.20	ii.	C.M. Bull	Further investigations of a rapid cline in B chromosome frequency in the British grasshopper Myrmeleotettrix maculatus
2.40	iii.	G. Lentzios, A.J. Stocker, and J. Martin	C-banding in some related species of Australian chironomids
3.00	iv.	G.C. Webb and H.P. Neuhaus	Extensive chromosome polymorphism in the Australian Plague Locust revealed by G- and C-banding
3.20	v.	E. Ephrati-Elizur and S. Luther-Davies	The isolation and characteristics of strains derived from T44 (λ) with an unusual complex phenotype

TEA, COFFEE AND POSTERS
4.00 - 5.30

Bruce Hall Common Room



ANNUAL DINNER
7.00 for 7.30

Bruce Hall Dining Room

POSTERS

1.	D.F. Callen, C. Roland Wolf and Richard M. Philpot	Cytochrome P-450 and the Activation of Promutagens in *Saccharomyces cerevisiae*.
2.	G. Lentzios, A.J. Stocker, and J. Martin	Silver Banding in Polytene and other Chromosomes of related Australian Chironomid Species.
3.	Cedric E. May and Rudi Appels	The Detection of Rye Chromosome 2R Substitutions in Wheat and of a Reciprocal Translocation between Chromosome 2R and a Wheat Chromosome.
4.	Barry G. Rolfe and Peter M. Gresshoff	Genetic Studies of the Nodulation Process in White Clover.
5.	A. Sampson, G.C. Webb, and M.J.D. White	C-Banding Polymorphism in Keyacris scurra.
6.	M. Hani Soliman and J.H. Claxton	A Laboratory Exercise in Theory and Practice of Selection against Specific Genes.
7.	J.M. Szymura, J.B. Mitton, and W.P. Hall	Population Genetic Analysis of a Narrow Hybrid Zone Between the Discoglossid Anurans, *Bombina bombina* and *B. variegata* in Poland.
8.	J.A. Thomson, H.E. Schroeder and A.M. Tassie	Genetics of Cotyledonary Storage Proteins in *Pisum*.
9.	M. Kaye Trembath and Alexander Tzagoloff	The Genetic Identification of Loci on Mitochondrial DNA.
10.	Dennis L. Welker	Genetic Analysis of Radiation-sensitive Mutants of *Dictyostelium discoideum*.
11.	K. Kongsuwan and D.R. Smyth	Chiasma Distribution and its Relationship to C-Bands in Chromosomes of *Lilium*.
12.	J. Mulley and K. Shearer	Three genetically distinct populations of European carp in Australia.

I.Q. as seen by a quantitative geneticist.

J.M. Rendel
Division of Animal Production, CSIRO, Epping. N.S.W. 2121.

Heritability is usually expressed as a ratio estimating the fraction of the variance of some metric in a population that is due to genetic differences between individuals. Ideally it is estimated in a population which is not subdivided, which is mating at random and living in an environment in which genetic differences between individuals do not interact with environmental ones. This fraction can be estimated because relatives are genetically more like each other than unrelated people and the correlations expected between relatives can be stated. The human species is divided into subpopulations and does not mate at random even within subpopulations so that the variance with respect to a trait is made up not only of the simple genetic components and the simple environmental ones but also components resulting from interactions and correlations. Care has to be taken when estimating H2 and E2. Care must also be taken when formulating one's concept of these entities. One may consider H2 as the fraction of variance one expects to be genetic in a population which is not subdivided and which is mating at random and then add in other contributions to variance as consequences of departure from ideal conditions. Various approaches to the I.Q. data leads to estimates of H2 in the narrow sense between 0.5 and 0.6 in ideal populations. The subdivision of the human population poses further problems of estimation. Correlations which will inflate correlations between relatives, will be introduced if groups with different means which have not been recognised as separate groups are included in one population and groups which are recognised as separate groups will demand the collection of appropriate evidence before differences between groups can be analysed. The extent to which subdivisions affect are effected by genetic differences are of interest when considering long term evolutionary changes and also current social structure. I.Q. is one metric which has been applied to the human personality. It is a satisfactory one in so far as it is repeatable. On its own it is inadequate to take us very far in the analysis of either population structure or evolutionary change.

Progress in the genetic analysis of quantitative traits in human populations

John Gibson

Department of Population Biology
Research School of Biological Sciences
Australian National University, Canberra

The vast majority of traits of medical and social significance are quantitative and their genetic analysis has lagged well behind advances in other branches of human genetics. The successes of the classic biometrical approach have not matched the increased sophistication of the mathematical techniques.

Results of studies in experimentally amenable organisms have encouraged the use of segregating genetic markers to dissect quantitative variation in human populations. The practical value of this approach is controversial although some small scale studies have produced intriguing results and in one case indicated linkage between a marker locus and factors affecting a quantitative trait.

Another strategy has been to focus attention on the enzyme systems involved in a particular trait and to explore these in vitro with cultured fibroblasts or leucocytes. The immediate value of this work for quantitative genetic analysis has been to show how complex phenotypic characters can be subdivided into biologically relevant components which are more likely to yield to the available modes of analysis.

THE GENETICS OF NEUROLOGICAL DISORDERS

O. Mayo
Biometry Section,
Waite Agricultural Research Institute,
University of Adelaide,
GLEN OSMOND,
South Australia, 5064.

These disorders will be considered under three convenient but not necessarily profound headings: first, the multifarious single-gene disorders, now numbering several hundred, gradually being classified, "solved" biochemically, counselled with various degrees of adequacy, and in some cases treated satisfactorily; secondly, the chromosomally determined disorders, where similar but slower progress is being achieved; and thirdly, multifactorially determined disorders, where progress is very varied (recent advances in the prevention of neural tube defects may be contrasted with the partly successful maintenance but rare "cure" of schizophrenia and epilepsy).

It will be emphasised that a few disorders in any particular population will contribute a major part of the morbidity and suffering in that population, e.g. Huntington's chorea (incidence of about 1 in 10,000 in the U.K. and Australia), microcephaly (where Qazi and Reed (1975) have claimed that 1 in 300 of the U.S. general population is mentally retarded on account of heterozygosity for a gene for microcephaly), or schizophrenia, with a frequency of 1 in 100 to 3 in 100 (depending on definition) in Australia, the U.K. or the U.S.A. The implications of this fact will be discussed.

Improvements in diagnosis and heterozygote detection and the ethical problems thereof (e.g. in Huntington's chorea) will be discussed. The possible importance of pharmacogenetics will be treated in some details.

Reference

Qazi, Q.H. and Reed, T.E. 1975 *Clinical Genetics* 7, 85-90.

GENETIC AND ENVIRONMENTAL EFFECTS AND INTERACTIONS INFLUENCING SEED YIELD OF *LUPINUS ALBUS* (WHITE LUPIN)

A.G. Green* and R.N. Oram
CSIRO Division of Plant Industry, P.O. Box 1600, Canberra City, A.C.T. 2601.

Families generated by crosses among 14 parental lines have been tested and selected over the past 3 years to develop cultivars of this new, high-protein leguminous crop, which yield well enough to make its' cultivation profitable in south-eastern Australia. The yields of F3 families grown at Wagga in 1974 ranged widely (850 - 2400 kg ha^{-1}), and broad-sense heritability was quite high (h^2 = 0.57). However, the responses to selection achieved in F4 at Wagga and Canberra were much lower than expected (realized h^2 = 0.25 and 0.09), because the ranking of the families differed markedly in these 3 environments.

Twenty lines have now been tested for 3 years at both sites. The mean yields for the 6 environments ranged from 600 to 1880 kg ha^{-1}. The 5 high-alkaloid (toxic) parents had the highest yields, particularly in the most favourable environments; most of the low-alkaloid selections yielded more than the low-alkaloid parents. The yield of the lines was positively correlated with their height at maturity, and with their rates of yield increase with environmental improvement. Three selections will be tested throughout Australia as potential new cultivars.

THE USE OF INCOMPLETE PARTIAL DIALLELS FOR HYBRID PREDICTION AND THE ESTIMATION OF ADDITIVE GENETIC EFFECTS

Geoff Gordon*
Department of Agronomy, Waite Agricultural Research Institute,
The University of Adelaide, Glen Osmond, South Australia 5064.

The additive and non-additive components of quantitative genetic characters can be statistically approximated by the use of diallel analysis. These are termed general combining ability and specific combining ability respectively.

When general combining ability estimates account for 50% or more of the variation due to the genetic effect in a sampled population, individual variations of general combining ability can be discerned. Use of an incomplete partial diallel, consisting of 20% of the partial diallel, enables an accurate estimate of the ranks of the general combining abilities relative to one another.

The probability of correctly detecting the parents in a diallel with the largest non-additive effect is high and thus the genotypes with the highest additive genetic effects can be confidently isolated.

As the general combining ability (gca) ranks remain stable when the diallel has been reduced, the missing hybrids in the diallel (the remaining 80%) can be estimated by the equation:

phenotype = mean effect + gca female parent+gca male parent

These estimated hybrids can then be used by the breeder to determine promising genotypes. The procedure can also be used to estimate the amount of non-additive genetic effect in the sampled population by calculating the differences between the observed hybrids and the predicted values for these hybrids.

MAPPING OF 2 CHROMOSOMAL MALE-STERILITY MUTANTS IN HEXAPLOID WHEAT

IAiii

K.K. Barlow* and C.J. Driscoll
School of Botany, University of N.S.W., Kensington, Sydney.

Two chromosomal male-sterility mutants in hexaploid wheat, Probus *(ms1b)* and Cornerstone *(ms1c)* were located on the α are of chromosome 4A, approximately 50 map units from the centromere. The mutants failed to complement one another.

Full pairing at meiosis was low in the F_1's of crosses between each mutant and 3 varieties of wheat which had markers on 4A. The 3 varieties were Transfed, Hairy Neck and Line W. Each involves a translocation to chromosome 4A: Transfed and Hairy Neck from 2R and 5R of rye respectively and Line W from *T. timopheevi*.

The translocation point in Transfed has been mapped to 1 map unit from the centromere on the β arm of chromosome 4A (Driscoll & Bielig, 1968). In Hairy Neck, the translocation point was mapped to 30 map units from the centromere on the β arm of 4A (Driscoll & Sears, 1965). The 4A chromosome in Line W is proposed to have an interstitial segment of *T. timopheevi* chromatin which includes the centromere, a large part of the α arm and only a small part of the β arm. (based partially on unpublished data of J. Gyarfas).

Since alien chromatin is involved in each case, the observed pairing at metaphase I in the F_1's of each cross is proposed to involve synapsis (S), desynapsis (D) and asynapsis (A). Values were calculated for S, A & D and these used to calculate the percentage of PMC's with an exchange as $\frac{S+D}{S+A+D} \times \frac{100}{1}$. The map distance between the loci involved can then be calculated as $\frac{S+D}{S+A+D} \times \frac{100}{1} \div 2$.

The observed pairing at metaphase I and the recombination values between *ms1b*, *ms1c* and the Transfed translocation were lower than expected. The map distance between ms^{1b}, ms^{1c} and Lr were 38 m.u. and 20 m.u. respectively. One possible explanation is active repulsion occurring between the wheat and the alien chromatin which results in reduced recombination between the loci.

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TRITICALE X WHEAT HYBRIDS

Cedric E. May
Agricultural Research Institute, Wagga Wagga

A number of hexaploid triticales (AABBRR, 2n = 42) appear to be completely resistant to *Septoria tritici*, the pathogen causing septoria leaf blotch of wheat. In an attempt to transfer this resistance into hexaploid wheat (AABBDD, 2n = 42), triticales were crossed as the female parent to a set of wheat varieties. Successful crosses were of the order of 65% and about 66% of the seed germinated and grew.

Meiotic chromosome counts of these plants showed that nearly all were the expected 14" + 14', the A and B genome chromosomes of the hexaploids pairing well and the chromosomes from the wheat D genome and the triticale R genome of cereal rye not at all. Occasional multivalents were present. Only one line set F_2 seed and could be further backcrossed. All others were completely sterile indicating that unequal separation of the univalents was common and their subsequent incorporation into the nuclei of pollen and egg cells was rare.

The proteins and isozymes of this material have been analysed by acrylamide gel isoelectric focussing to investigate their inheritance and their use as chromosomal markers. The chromosomes which carry the genes conferring resistance to *S. tritici* may then be detected by the methods of biochemical genetics.

EFFECTS OF CHROMOSOME HOMOZYGOSITY IN DROSOPHILA MELANOGASTER: VIABILITY, FERTILITY, AND OVERALL FITNESS.

Mandryk, J.A.*

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

Several studies of cage populations of D.melanogaster, which compared the fitness of chromosome homozygotes with that of chromosome heterozygotes, have indicated that viability forms an unexpectedly small part of overall fitness (Sperlich and Karlik, 1970, Genetica 41:265; Sved, 1971, 1975, Genetic Res. 18:97, 25:197; Tracey and Ayala, 1974, Genetics 77:569). Other studies have shown that fertility differences in Drosophila are often of significant magnitude, and it was the aim of this study to see whether or not in this type of experiment, fertility fitness components could account for the observed difference between viability estimates and overall fitness estimates. Overall fitness estimates were obtained from the cage populations, while fitness component estimates were obtained from auxiliary experiments. The component estimates were reasonable predictors of population equilibria in homozygous populations ($Cy/+_i$ and $+_i/+_i$ flies). However, the rate of elimination of Cy/+ from heterozygous populations ($Cy/+_{mix}$ and $+_{mix}/+_{mix}$ flies), could not be explained by the components measured. A major difficulty in interpreting results from fitness component experiments comes from the large standard errors associated with the fitness estimates.

TEMPORAL PATTERNS OF RADIATION INSENSITIVITY AMONG THE DORSAL THORACIC MICROCHAETES OF DROSOPHILA

Claxton, J.H. and Early, W.M.*

Department of Microbiology and Genetics
University of New England
Armidale. N.S.W. 2351

A large dose of X-irradiation (≃ 10,000 R) given to young Drosophila pupae prevents the appearance of bristles. Bristle development becomes progressively less sensitive to radiation when the dose is given to older pupae.

This technique has been utilized to establish regional variation in the age when bristle-forming cells on the dorsal thorax begin to show radiation insensitivity.

The results are discussed in relation to the likelihood that X-rays only prevent bristle development if the dose is given prior to the final divisions in epidermal cells that are committed to form bristles. Thus the regional/temporal patterns in the beginning of radiation insensitivity probably reflect comparable patterns in cell division and possibly also in bristle cell determination. In turn this focuses attention on time as an important component in the function of bristle pattern determining mechanisms.

A FASCINATING POLYGENE: ITS DISCOVERY, CHARACTERISTICS AND BEHAVIOUR

R. Frankham and R.K. Nurthen
School of Biological Sciences, Macquarie University, North Ryde, N.S.W. 2113.

An allele which greatly reduces abdominal bristle number, alters the bristle pattern and reverses the sex-dimorphism for this character has been discovered. This allele is also temperature sensitive with a T.S.P. during the pupal period. It has been mapped to 2-91.95 and is a new allele at the smooth locus.

This allele was at a frequency of 1/120 in the base population from which replicate high and low abdominal bristle selection lines were founded. We have been able to follow the fate of this allele in these selection lines and to confirm a number of predicted effects of an initially rare allele of large effect under artificial selection, viz. asymmetrical response to selection, chance loss of a favourable allele and changes in heritability under selection.

EFFECT OF HAPLO-DIPLOIDY ON GENIC VARIATION UNDER SOME SELECTION MODELS

Pamilo, P.*, R. H. Crozier

School of Zoology, University of New South Wales, Kensington, N. S. W. 2033

We compare the probabilities of balanced polymorphism and the expected heterozygosity levels in haplo-diploid and diploid populations under some deterministic selection models. Computer-generated random numbers are used in analysing situations in which fitnesses are the same in the two sexes, and in which they differ. In both cases, the potential for balanced polymorphism is less in haplo-diploids than in complete diploids. Heterozygosity differences are more marked again, because of a greater bias, in haplo-diploids, for equilibrium allele frequencies to depart from 0.5. The magnitude of these differences depends on the intensity of selection: when the range of possible fitness values is reduced, the difference between the two genetic systems is also reduced.

HYBRID SINKS: THE PARADOXICAL ROLE OF NARROW HYBRID ZONES AS BARRIERS TO GENE FLOW IN ANIMALS OF LIMITED VAGILITY

William P. Hall
Department of Genetics, University of Melbourne, Parkville, Victoria, 3052

Some morphospecies are subdivided into mosaics of genetically distinctive populations which meet parapatrically in narrow zones of hybridization, a situation which may be fairly common in animals of limited vagility. Where adequate markers are available, e.g. in *Sceloporus* lizards, *Bombina* frogs, and *Spalax* rodents, analyses show: 1. F_1 hybrids are fertile enough to backcross to both pure parental stocks. 2. Despite F_1 fertility, markers do not introgress beyond the narrow geographic limits of the hybrid zones. 3. Each marker shows the same microgeographic distribution in the zone, indicating that each is responding similarly to a common factor, rather than to individually unique selection coefficients. Despite the apparent antiquities of the hybrid zones, there is no evidence for the evolution of effective premating isolation between the hybridizing forms.

These somewhat paradoxical observations may be explained by the assumptions: 1. hybrid and backcross genotypes are less fit than parental genotypes and compete less for limiting factors in the environment. In each generation there will be a net influx of pure parental types from each side into the less effectively exploited area of the hybrid zone. The influx will function to prevent upstream migration of introgressed genes out of the hybrid zone and will also prevent any gene from surviving for long enough within the limits of the zone to have a chance of being incorporated with others to form a multigenic premating isolation mechanism.

ANALYSIS OF A NARROW HYBRID ZONE BETWEEN PSEUDOPHRYNE BIBRONI AND P.SEMIMARMORATA (ANURA: LEPTODACTYLIDAE).

L.J. McDonnell, D.F. Gartside[1] and M.J. Littlejohn
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The morphologically distinguishable toadlets, Pseudophryne bibroni and P.semimarmorata, hybridize in a narrow zone about 40 km north of Melbourne. They have similar breeding call structures, utilize similar breeding sites, and have overlapping breeding seasons. Studies of morphological and protein variation show that a wide range of recombinant individuals occurs at localities within the zone of interaction. All these factors suggest that there is random mating within the hybrid zone. Despite the potential for introgression however, the taxa remain distinct outside the area of interaction, and so are considered to be species.

Variation in adult morphology (pigmentation) in population samples from the area of interaction have been studied over a 15-year period (1960 - 1974). Change in morphological composition of samples during this time indicates that P.bibroni has moved southwards. Two additional sets of observations are consistent with this hypothesis: (1) the pattern of geographic variation in lactate dehydrogenase is asymmetric; and (2) the southern limits of hybridization based on morphology, Ldh and embryonic mortality, coincide; whereas these characters show different widths, and borders of replacement to the north. The hybrid zone however, does not appear to be correlated with any major environmental factor.

THE RATE OF EVOLUTION IN AN AUSTRALIAN BUSH-RAT

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Nei (1975) and Sarich (1977) have calibrated "electrophoretic clocks", which relate the time of separation of populations to the genetic distance between them. Both authors have presented population data which support their calibrations, although the calibrations differ by a factor of about four. A genetic study of populations of the Australian bush-rat, *Rattus fuscipes greyii*, provides a unique opportunity to test these calibrations.

R. f. greyii populations occur on a series of offshore islands of South Australia and on three separate areas on the mainland. From data on recent changes in sea level and other biogeographic information it is likely that all populations were isolated within the last 14,000 years. A study of electrophoretically detectable genetic variation gave a mean genetic distance (using Nei's metric) between populations of 0.17. Using the electrophoretic clocks of Nei and Sarich, this distance corresponds to 0.85 and 2 million years separation, respectively .

Most of the genetic differences between *R. f. greyii* populations are attributable to the fixation of alternate genes which are presumed to have been present in a common ancestral population, while some genetic differences are due to the accumulation of new mutants after bifurcation. The former mechanism of genetic divergence (due to genetic drift and/or directional selection) can occur rapidly, especially in small isolated populations, and may account for the unusually rapid rate of evolution.

DROSOPHILA MELANOGASTER - WHERE DID IT COME FROM?

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Popular misconception notwithstanding, *Drosophila melanogaster* is not endemic to the half-pint milk bottle. *D. melanogaster* is one of over 1,400 described species in the genus *Drosophila*; its closest taxonomic affinities lie within the *melanogaster* species group, a cluster of almost 100 species distributed from the South Pacific through northern Australia, New Guinea and Asia to Africa. While *D. melanogaster* and its sibling species *D. simulans* are cosmopolitan, the two species are almost invariably only found in and about cities and farms (*i.e.*, in "domestic" situations) except in Africa and, apparently to some extent, in India. In Africa, both *melanogaster* and *simulans* are widespread in natural habitats removed from human activities, and four other sibling species also occur in Africa and Mauritius. It therefore appears that these six very closely related species (the *melanogaster* subgroup) evolved in the Ethiopian Biogeographic Zone, *melanogaster* and *simulans* having subsequently adapted to domestic conditions and become cosmopolitan within historical times.

Since most of the *melanogaster* group species occur in south-east Asia, it appears most likely that, although *melanogaster* itself and its siblings evolved in Africa, the ultimate origin of the ancestors of the *melanogaster* subgroup is to be found in the Oriental Biogeographic Zone. No information concerning the phylogenetic age of the species is available.

EVIDENCE FOR GENES MODULATING LOCAL PAIRING IN *NEUROSPORA* CHROMOSOMES

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Genetic maps of the *nitrate-2* locus made with sets of mutants isolated in different wild-types are not all of the same size. Maps constructed by crossing mutants induced in two different wild-types are, in some instances, drastically shorter than either of the maps derived from crosses within the two sets of mutants involved. The effect is independent of $rec\text{-}1^{+}$ which is dominant in reducing recombination between *nit-2* alleles.

Possible explanations for low yields of prototrophic recombinants from heterozygotes include chromosomal rearrangements, non identity of the amino acid sequence coded by $nit\text{-}2^{+}$ in different wild-types and failure of a step in recombination such as chromosome synapsis. The finding that spore abortion is normal and low and flanking marker recombination is normal and high in heterozygous crosses is inconsistent with a substantial chromosomal rearrangement but consistent with the other hypotheses. The suggestion that the phenomenon is caused by variation in genes concerned with synapsis of small regions of a chromosome has the merit of providing an explanation for the disparity in the size of maps made with sets of mutants isolated from different wild-types.

CHROMOSOME VARIATION IN *Stylidium crossocephalum*

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84 different karyotypes were identified from 228 plants of *S. crossocephalum*. 11 different "stable genomes" identified as homokaryotypes in more than a single locality, occurred over substantial areas, sometimes limited by distinct geographical or ecological boundaries and in one case overlapping, forming a zone in which stable genome heterokaryotypes were found. Some of the unique or locally restricted karyotypes could be attributed to recombination within stable genome heterokaryotypes but many were quite distinct from any nearby stable genome. Native heterokaryotypes exhibit multiple chromosome associations, unequal bivalents and univalents, and may be up to 50% pollen sterile. Synthetic heterokaryotypes involving geographically more widely separated parents exhibit similar, but more extensive meiotic irregularities resulting in nearly complete sterility. Differences between genomes can range from single centromere shifts, additions or deletions, to multiple translocations involving all chromosomes.

The fine scale of the mosaic, the population structure and the intensity of the repatterning process strongly supports an interpretation involving the origin and establishment of new chromosomal races within the single, continuous native population; that is, sympatric divergence.

THE INHERITANCE OF B CHROMOSOMES IN BRACHYCOME DICHROMOSOMATICA (SYN. B. LINEARILOBA A).

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In over 1000 plants studied, plants with 1, 2 or 3 B chromosomes constitute 10% of plants. Plants with odd numbers of B's tend to lose them in meiosis.

This loss is balanced by non-disjunction and preferential distribution to the generation nucleus in the 1st P.G. division. Transmission through the embryo sac does not involve preferential segregation.

Evidence will be presented to show a higher frequency of B's in marginal populations as compared with central populations. Additionally, plants with one B appear less fit than plants with 2 B's. On these bases, a reasonable fit between observed and theoretical frequencies of 0B, 1B and 2B plants is evident.

THE CYTOGENETIC BASIS OF DIOECY IN THE PLANT GENUS *VISCUM*

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Initial studies in *Viscum fischeri* (2n = 23) in Kenya showed that male plants were constantly heterozygous for a series of reciprocal translocations, producing 7 bivalents and an open chain of 9 chromosomes at meiosis. Female plants were constantly homozygous, producing 11 bivalents. Since *V. fischeri* consistently has a female-biased sex ratio of 0.34, it was concluded that the translocation heterozygosity was associated with maintenance of the sex ratio.

Further studies on another 21 dioecious species from Africa, Europe and Asia have shown that all have translocation heterozygosity. Most species have sex-associated translocations with male plants heterozygous and female plants homozygous. Some species have floating translocations which occur in both male and female plants. In some populations of *V. album* in Japan sex-associated rings of different sizes occur in male and female plants. Biased sex ratios occur in some but not all species.

Extensive translocation heterozygosity has not been found in monoecious species of *Viscum*. It is now concluded that translocations are associated with the establishment of dioecy in the genus, probably through their effects on linkage relationships of non-allelic genes for unisexuality.

RECOGNITION OF ALIEN CHROMOSOMES AND CHROMOSOME REARRANGEMENTS IN WHEAT USING THE N-BANDING TECHNIQUE

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N-banding has been used to identify each of the fourteen chromosomes of the tetraploid *Aegilops variabilis* Eig. These patterns differ from the patterns of the nine wheat chromosomes that band with this technique.

C-banding (Gill & Kimber, 1974) and N-banding (Gerlach, 1977) have been used for identifying specific wheat chromosomes at mitosis. The C and G banding patterns of *Secale cereale* L. chromosomes have been extensively studied. However the techniques used with rye usually give faint bands or no bands with wheat chromosomes.

The banding patterns of certain chromosomes allow a high degree of precision in the identification of particular chromosome rearrangements. Gill & Kimber, (1977) have used a C-banding technique to identify a wheat-rye 1R/1D translocation, a reciprocal 4A/6B translocation and two translocations from *Aegilops umbellulata* chromosome 6 to chromosome 6B.

In this work N-banding has been used to identify the translocation present in Aurora (1B/1R), Poso (5B/7B) and for the identification of some addition lines of *Ae. umbellulata* and *Ae. variabilis* to wheat.

N-banding analysis can be carried out on both mitotic and meiotic chromosomes. Wheat chromosomes have not previously been identified at meiosis using a banding technique.

CHROMOSOME PAIRING IN WHEAT-RYE AMPHIHAPLOIDS

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Chromosome pairing in wheat-rye amphihaploids is evaluated statistically on the basis of a two-stage process of chromosome pairing. The first stage is association (a) among potential pairing partners and the second stage is chiasma formation (p) among associated chromosomes. The p values are generally close to zero in most wheat-rye amphihaploids but may be as high as 50%. On the absence of the Ph locus (Sears' ph mutant) p values are regularly high and around 60%. Association (a) is also low in wheat-rye amphihaploids and generally in the range 3-21%. The a values are not influenced by the absence of the Ph locus. However the a values are considerably higher when there is an additional dose of any of the rye chromosomes in the wheat-rye polyhaploids. This is independent of the highest paired association (presumably the pair of rye homologues) being removed from each cell before statistical analysis. The significance of these observations will be discussed.

THE SELECTION AND SOME CHARACTERISTICS OF A TEMPERATURE-SENSITIVE *SCARLET* EYE COLOUR MUTANT OF *DROSOPHILA MELANOGASTER*

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Temperature-sensitive mutants are particularly useful in developmental studies, since they can be used to determine the times at which genes act. The *scarlet* gene in *D.melanogaster* is active in the pigment cells of the eyes, probably facilitating the uptake and storage of xanthommatin (brown pigment) precursors. In order to obtain information about the active period for this gene during development, attempts were made to induce and select a temperature sensitive *scarlet* mutant.

EMS-treated males (e^{11}; bw) were mated to st Ki ry^{2};bw females and the progeny raised at 29°C. From approx. 23,000 F1 progeny, six new *scarlet* mutant stocks were established, one of which (st^{754ts}) had a temperature-sensitive eye colour phenotype. Temperature-shift and temperature-pulse experiments have been carried out with st^{754ts}. These have shown that accumulation of xanthommatin becomes critically sensitive to temperature early in pupal life and a temperature-sensitive period then extends almost up to adult emergence. This major temperature-sensitive period commences before the synthesis of xanthommatin is initiated, showing that the *scarlet* gene does not control the onset of pigment accumulation. A minor period of temperature-sensitivity also occurs at pupariation. Since the eye disk becomes determined during this developmental period, it is possible that the *scarlet* protein plays some role in the determination process.

BIOCHEMICAL GENETICS OF EYE PIGMENTATION IN THE AUSTRALIAN SHEEP BLOWFLY *LUCILIA CUPRINA*

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Six genetic loci are involved in the production of screening pigments in the eyes of *Lucilia cuprina*. Of these at least two are involved in the production of enzymes of the xanthommatin biosynthetic pathway. *Yellowish* is probably the structural gene for tryptophan oxygenase and *yellow* is concerned in the production of kynurenine hydroxylase. *Tangerine* mutants are blocked in the final step of the pathway and this locus appears to be involved in the production of phenoxazinone synthase.

Larvae of the *white* and *topaz* strains fail to accumulate ^{3}H-3-hydroxykynurenine normally in their malpighian tubules, unlike the other mutants. It is suggested that cells in *white* and *topaz* strains are unable to retain xanthommatin precursors, reducing the amount of substrate available for xanthommatin synthesis. The *white* and *topaz* loci may therefore code either for membrane proteins involved in precursor uptake by cells or intracellular proteins involved in storage of these compounds.

Two known genes, *white* and *grape*, affect the production of a yellow pteridine pigment, and studies of pteridine biosynthesis in wild type and mutants are in progress.

A DOPA OXIDASE POLYMORPHISM IN *DROSOPHILA MELANOGASTER*

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In 1961, Lewis and Lewis mapped a locus regulating dopa oxidase activity to chromosome II - 52.4, about 2.3 cM from the structural locus for alcohol dehydrogenase. In keeping with the interest of our laboratory, in selective mechanisms maintaining gene-enzyme variation (including the importance of linkage), a study of the dopa oxidase system has been undertaken.

Initially two major problems needed to be overcome. Firstly, since dopa oxidase exists as an inactive proenzyme which must be activated *in vitro* (and on electrophoretic gels), a tedious preparative procedure is necessary to purify the activator protein from gram quantities of 48 hr old pupae. Secondly, there are no known electrophoretic variants of dopa oxidase.

Both of these obstacles have been overcome. A simple 'synthetic' activator has been discovered which allows rapid staining of a dopa oxidase enzyme, and two new electrophoretic variants of this protein have been detected at polymorphic frequencies in the Chateau Tahbilk Winery population. A structural locus for this dopa oxidase maps to chromosome II - 80. Electrophoretic mobility comparison demonstrated that this new enzyme is distinct from the protein-activated proenzyme reported by others. Continuing laboratory and field studies should give some insight into the crucial selective forces on this region of chromosome II.

THE ROLE OF ALCOHOL DEHYDROGENASE IN THE UTILIZATION OF ALCOHOL BY SPECIES OF DROSOPHILA

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The measurement of the kinetics of Alcohol dehydrogenase (ADH, E.C. 1.1.1.1) in three species of Drosophila; D.melanogaster, D.simulans and D.busckii, indicates the presence of species differences in their ability to metabolise alcohols. Evidence presented indicates that alcohol, particularly ethanol, can be used as a source of energy by these species of Drosophila, in proportion to their relative levels of ADH activity.

The ability of Drosophila to utilize a higher order alcohol (ie, 1-propanol) as an energy source appears to reflect not only ADH activity but also aldehyde toxicity such that lower levels of ADH activity could be advantagous in certain environmental conditions. This is used as a possible mechanism to explain the maintenance of Adh polymorphism in D.melanogaster and as a method of niche seperation in the other species of Drosophila examined.

SELECTION FOR ALCOHOL TOLERANCE IN D. MELANOGASTER

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Alcohol dehydrogenase activity accounts for some 40% of the variation in alcohol tolerance in strains of D. melanogaster isolated from two wineries in New South Wales. Successful selection for increased alcohol tolerance in a population segregating for fast and slow allozymes at the alcohol dehydrogenase structural gene locus was not always accompanied by an increase in the allozyme with most enzyme activity. The results underline the biochemical flexibility that can be exploited under selection pressure and suggest caution in accepting evolutionary arguments which rely heavily on intuitive knowledge of the biochemistry of an organism.

INDUSTRIAL MELANISM IN THE PSOCID MESOPSOCUS UNIPUNCTATUS (MULL.) IN NORTHERN ENGLAND.

Dr. C. Willoughby
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Mesopsocus unipunctatus in northern England displays an obvious colour dimorphism such that the light form is common and highly cryptic in rural areas on lichen - covered bark, while the dark, industrial melanic, form is common and highly cryptic in urban areas on dark bark without epiphytic growth.

Genetic crosses indicate that the melanic character is inherited as a Mendelian dominant and that separate alleles, linked on the same chromosome, control the respective melanisms of the head-thorax and of the abdomen.

Multivariate analysis of eleven environmental variables point to the importance particularily of visual selection by predators for crypsis but also of climate.

A computer model is devised to simulate the decrease in melanic frequency between the industrial south and the rural north of Yorkshire, from the start of the industrial revolution to the present day, using four ecological variables.

Symposium talk: W. Hayes

"Insertion sequences: a new element in genetic variation"

About 10 years ago a new class of revertable, highly polar mutations was found in bacteria, plasmids and phages. When present in transducing phages, these mutations were found to increase the buoyant density of the phage particles and were assumed to be due to insertions of extraneous DNA fragments. This was later confirmed by DNA heteroduplex analysis which visualised the insertion as a single-stranded DNA loop or 'bubble' when the mutant strand was annealed to an homologous wild type strand. These insertion elements comprise many diverse DNA sequences, ranging from 800 to many thousand base-pairs long, but in bacteria four distinct sequences, IS 1-4, are common. They may insert into many different chromosomal sites, even in the same gene, in either orientation and can transpose from one site to another, and from chromosomal to plasmid or prophage DNA and vice versa, in the absence of the bacterial recombination system. When inserted in one orientation IS2 is mutagenic, but acts as a strong promoter in the other, converting an inducible system into a constitutive one. If several copies of the same IS are present in the chromosome, normal recombination between them can lead to deletion, transposition or inversion of the intervening chromosome segment. Similarly, homologous ISs in chromosome and prophages or plasmids may result in insertion of chromosome segments into, say, the plasmid, or of the plasmid into the chromosome. The genetic determinants of resistance to many antibiotics, normally carried in and transmitted by conjugative plasmids, are bounded by ISs and are freely transposable; they are termed "transposons". In addition some ISs, while remaining in situ, can induce repeated deletions of DNA adjacent to one of their extremities, so that genes located at the other extremity may be brought under the control of new promoters. The structure and mode of replication of ISs, and their possible applicability to phenomena in higher organisms, will be discussed.

DNA diminution in polytene chromosomes of *Sarcophaga*

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Selective loss of DNA-containing material from chromosomes (diminution) is known to occur in a wide variety of invertebrate embryos during early cleavage. A differential increase of DNA (amplification), particularly of ribosomal DNA cistrons, is known from numerous invertebrates and amphibians. Small DNA containing granules are extruded from polytene chromosomes in several species of diptera. This phenomenon is particularly prominent in the pulvillus cells of the flesh-fly *Sarcophaga*, as studied by Roberts (1968, J. Cell Biol. 39: 112a). We were interested to determine whether or not this process involved rDNA cistrons, or unique sequences of the *Sarcophaga* genome. The extruded granules were found to contain a highly repetitive and AT-rich DNA. Similar sequences were located in two large heterochromatic blocks at the centromeres of two of the five autosomes. We have concluded that the granules are formed at these centromeric sites, and are lost into the nucleoplasm during polytenization. Studies with cytological hybridization indicate that this highly repetitive DNA is under-replicated in these polytene nuclei. The extrusion process thus appears to involve diminution of two specific areas of the genome and not amplification. Implifications for chromosome structure of this and other cases of diminution are briefly considered.

Multigene families in genetics and evolution

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One of the conspicuous specializations of eukaryotic genetic systems is the presence of multiple copies of genes organized into multigene families. Typically these gene copies are (i) tandomly linked, (ii) homologous in base sequence and (iii) related or overlapping in function. The families genes may all be identical in sequence (e.g. for histones and γRNA) or divergent (e.g. for antibodies β-like haemoglobins). Multigene families exhibit a variety of genetic and evolutionary properties not shared by single copy genes. A crucial problem for eukaryote genetics is to ascertain the prevalence of multigene family units. Information from four sources, DNA chemistry, protein chemistry, evolution and genetics suggest that they are both numerous and important.

1) A sizable percentage of eukaryotic DNA sequences are reiterated hundreds of times (middle repetitious) to millions of times (highly repetitious). Moreover even the "single copy" DNA fractions contains multigene families with non-identical copies.

2) Most important proteins of higher animals occur in several isozymic forms. Their genes may be organized into multigene families since such units can be very small. The several tandomly linked genes for haemoglobin chains show most of the essential properties of a multigene family: variation in gene copy members phylogenetically and within a species, homology between functionally related, unlinked multigene families, coincidental evolution of gene members, preservation of identical sequences within a family, microheterogeneity in protein structure, cryptic gene members and fusion alleles (Lepore haemoglobins).

3) Multigene families give rise to new complete families by duplication during evolution. Genes related to immune functions are beginning to show a rich history of repeated duplication and divergence of multigene families related to cell recognition.

4) Multigene families develop two sorts of "complex alleles" widely observed in eukaryotes, polymorphisms with many alleles and alleles which differ from one another by multiple mutational alterations. Both sorts of "alleles" can result from differences in expression, or even simply the absence, of individual member genes in a multigene family.

TRANSPOSON SPECIFICITY IN THE INDUCTION OF MUTATIONS IN A PLASMID

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Two transposons TN501 (coding for mercury resistance) and TnC (coding for trimethoprim and streptomycin resistance) have been used to obtain insertion mutations affecting plasmid transfer (Tra^+) and carbenicillin resistance (Cb^R) in the narrow host range R plasmid R91-5 of *Pseudomonas aeruginosa*. Tn501 induced Tra^- mutations occur at 0.1%-0.5% whereas TnC induced them at 20-50%. Both transposons induced Cb^S at 0.05%-0.1%. Unexpectedly 42% of the Tn501 induced Tra^- mutants became simultaneously Tra^-Cb^S whereas only 0.2% were so with TnC. 70% of the double mutants induced by Tn501 failed to revert to Cb^R presumably because they were due to deletions. Surprisingly amongst those that reverted to Cb^R about 50% simultaneously regained Tra^+. The Tra^- mutants induced by both transposons were tested for resistance/sensitivity to the donor-specific phage PRD1, inhibition of phage $G101^R$ = $Phi(G101)^+$ and entry exclusion = Eex^+. With Tn501 14% of Tra^- became $PRD1^R$ whereas it was 70% with TnC. $Phi(G101)^-$ occurred at 21% and 9% respectively with Tn501 and TnC induced Tra^-. And although 32% of Tn501 induced Tra^- were Eex^-, 0% were so with TnC. All these data indicate considerable differences in the specificity of mutations induced by the two transposons and even more importantly suggest that Tn501 influences expression of unrelated gene functions in a novel way.

PLASMID-CHROMOSOME HYBRIDS OF *PSEUDOMONAS AERUGINOSA*

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Hybrid FP' plasmids have been isolated containing both FP plasmid and *Pseudomonas aeruginosa* chromosome. Selection for such plasmids is provided by using a *recA* bacterial host and the plasmid FP110. FP' plasmids have been obtained for two bacterial chromosome regions, the *pro-73* region and the *argH lys-12* region. Both FP' plasmids are stable in a *recA* background, and initially unstable when transferred into a rec^+ background. Unexpectedly, derivatives can be selected for the *pro-73* containing FP' plasmid which are stable in both *recA* and rec^+ backgrounds. These have a very low ability to integrate into the *P. aeruginosa* chromosome, and can act as sex factors transferring chromosome from a novel origin.

GENERALIZED TRANSDUCTION WITH THE VIRULENT *PSEUDOMONAS AERUGINOSA* PHAGE E79, AND THE USE OF P-2 PLASMID CARRYING RECIPIENTS TO ELIMINATE PHAGE KILLING

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A mutant of phage E79 has been isolated that, when combined with a temperature-sensitive mutation and the use of E79 antiserum, is capable of generalized transduction at frequencies of between 2×10^{-6} and 2×10^{-5} per pfu. However, linkage analysis has shown that the transducing particles are not capable of transducing the 3-5 minutes of chromosome that the reported molecular weight of the phage, 120 Megadaltons, would suggest. If the recipient carries a P-2 incompatibility group plasmid, then phage killing of the recipients is totally eliminated, even at high multiplicities of infection. Using such strains it has been possible to show that E79 itself is capable of transduction at a frequency of about 10^{-7} per pfu. The implications for the evolution of *Pseudomonas* spp will be discussed.

P-1 INCOMPATIBILITY GROUP PLASMID INSTABILITY IN *PSEUDOMONAS AERUGINOSA* STRAIN PAT

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The P-1 plasmid, R68, is unstable in PAT. The instability results in apparent fragmentation of the plasmid and is accompanied by chromosomal mobilization ability (Cma). R68 is stable in Rec-A$^-$ hosts and in >1% of cells surviving treatment with mitomycin C or EMS. Cma is abolished in stable clones.

R68 is also stable in cells already harbouring the P-2 plasmid R38. Curing of R38 by amino-acid starvation, does not revert the host to instability.

Instability can be reintroduced into stable lines by transduction of a carbenicillin resistant element from an unstable PAT donor. This element was derived from rare clones of PAT/R68 in which Cb^r was found to be stable, although all other plasmid markers had been lost. We propose that P-1 instability in strain PAT is mediated by a cryptic plasmid, which can act as a recipient for the Cb^r transposon carried by R68.

POLYTENE CHROMOSOME REPLICATION IN SIMULIUM ORNATIPES

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In general polytene chromosomes show a three phase H^3-thymidine labelling pattern during replication. These are:

(1) A precontinuous stage of short duration at the beginning of the S phase in which puffs and interband regions are labelled.

(2) A continuous labelling of the entire chromosome.

(3) A discontinuous labelling phase in which bands of high DNA content show replication for later periods

Polytene chromosome replication in Simulium ornatipes was studied both in vivo and in vitro using double labelling with H^3thymidine and C^{14} thymidine. The overall pattern of replication was found to conform to that outlined above.

Heterochromatic regions clearly displayed late replication patterns, thus showing different behaviour to that in Drosophila. Preliminary results also indicate that C-banded regions display considerable variability in their replication time.

GERM LINE POLYSOMY IN THE GRASSHOPPER *ATRACTOMORPHA SIMILIS*

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In seven populations of *A. similis* from North Queensland, 23% of males sampled were found to be polysomic for the megameric chromosome nine. There was no significant between-site difference in the frequency of polysomy among these populations. This polysomy was observed only in the germ line and, within that tissue, there was much intra-individual mosaicism.

Laboratory selection for germ line polysomy raised the frequency of polysomic males from 23% to 71%, while selection against polysomy reduced this frequency to 5%. The mode of transmission of these extra chromosomes is unlike that by which stable B chromosomes are transmitted in both this and other grasshopper species.

CYTOGENETICAL STUDIES OF AUTOSOMAL HETEROCHROMATIN IN MEIOTIC PAIRING IN THE MALE DROSOPHILA MELANOGASTER; IMPLICATIONS FOR THE FUNCTIONS OF SATELLITE DNA

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The hypothesis that satellite DNA is of fundamental importance in homolog recognition and subsequent chromosome pairing is a widely accepted hypothesis. The evidence in support of it is however circumstantial. Without any critical experiments, several workers have further inferred the importance of satellite DNA in speciation by providing "fertility barriers" with the failure of chromosome pairing.

Genetical and cytological examinations of sex chromosome heterochromatin in both males and females of D. melanogaster have indicated that the pairing hypothesis is highly improbable, pairing being mediated in the male by "pairing sites". I have examined the meiotic behaviour of heterochromatically and/or euchromatically rearranged autosomes in the male. In every case, the heterochromatin of chromosomes, II, III and IV does not play a role in homologous chromosome pairing, but rather euchromatic homology is important for the process. Neither massive autosomal heterochromatic deficiencies nor radical rearrangements of the heterochromatin cause any pairing failure and there is no evidence for heterochromatic autosomal pairing sites. These results on autosomes indicate that satellite DNA per se is not crucial for male meiotic pairing of any member of the D. melanogaster genome.

CYTOLOGICAL LOCATION OF DNA SYNTHESIZED AT PACHYTENE IN *LILIUM HENRYI*

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Chromosomal DNA replication is essentially complete before meiosis begins in *Lilium* anthers. However, a small amount of DNA synthesis (about 0.1%) occurs later in pachytene nuclei. This synthesis may be directly related to crossing over, which is thought to occur at pachytene (H. Stern and Y. Hotta 1977 Phil. Trans. R. Soc. Lond. 277, 277-294).

As a test of such a relationship, we have attempted to locate the exact cellular sites of DNA synthesized at pachytene. Meiotic cells were extruded from anthers and cultured *in vitro* in ^{3}H-thymidine. They were then fixed, embedded, sectioned, and autoradiographed for light microscopy. Grains were taken to reflect DNA synthesis only if (i) they were removed by DNase but not RNase or Pronase, and (ii) they were leached out by hot HCl of the same strength as that which removed label in control S-phase nuclei.

A small amount of DNA synthesis was detected in pachytene nuclei. The few grains were scattered evenly over chromosomes. If the synthesis were confined to the few sites of crossing over in each cell, clusters of grains might have been expected. Unexpectedly, at least ten times more DNA synthesis occurred in the cytoplasm. Here grains occurred in definite clusters in a limited number of sites scattered in each cell. These cytoplasmic grains may reflect mitochondrial DNA synthesis, plastid replication or ribosomal DNA amplification. Further biochemical data could help choose between these and other possibilities.

ALLOZYME GENOTYPE-ENVIRONMENT RELATIONSHIPS IN NATURAL POPULATIONS OF DROSOPHILA BUZZATII

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Allozyme gene frequency data from natural populations of Drosophila buzzatii were analysed for genotype-environment relationships. Allele frequency and heterozygosity from six loci polymorphic throughout eastern Australia and a number of potentially key environmental levels and fluctuations were examined by a variety of multivariate techniques. Significant genotype-environment associations were found for five of the six loci investigated, and after correcting for geographical location, significant associations remained for Est-2 and Adh-1 gene frequencies and heterozygosities, and for Pgm gene frequency. These results will be discussed in relation to selection and gene flow, and provide the basis for subsequent laboratory studies to disentangle confounding effects of (a) environmental levels and environmental fluctuations and (b) allele frequency and heterozygosity, and to subsequently verify and determine the nature of natural selection at allozyme loci.

GENE FLOW IN POPULATIONS OF WILD RABBITS

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The population structure of the wild rabbit, Orytolagus cuniculus, leads to a measure of inbreeding and to microgeographical differences in gene frequencies within a population. This is because a population is subdivided into discrete breeding groups and these groups occupy one to three adjacent warrens. Within each group a social hierarchy is established where the dominant animals breed more frequently than do the subordinates. Adults are sedentary and will normally remain in the same breeding group throughout their reproductive life.

Two possible processes, diffusion and dispersal, which could lead to gene flow within the population, were investigated. Despite the tendency of sub-adults to disperse throughout the population at the end of each breeding season diffusion appears to be the more important mechanism of gene flow. Diffusion arises from 1) aggregation of a number of adjacent warrens into warren groups, 2) shared paternity between dominant and subordinate animals within these groups, 3) occasional infidelity between warren groups, 4) recruitment of sub-adults into the breeding population from adjacent warrens.

GENETIC DIVERSITY IN THE WILD PROGENITOR OF BARLEY IN ISRAEL

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Genetic variation stored in the wild progenitors of cultivated crops could represent a major resource for future plant breeding. From an electrophoretic survey of 28 loci, we determined the level and patterns of allozyme variation in several natural populations of Hordeum spontaneum, the wild self-fertilising progenitor of diploid, cultivated barley. Considering all the samples from Israel as a whole, 25 loci were variable with an average of 3.8 alleles per locus. In the average populations, about 30% of loci were polymorphic, the number of detected alleles per locus was 1.48, and the heterozygosity was 0.3%. Diversity measured as the per locus probability that two random gametes drawn from the population would differ is 0.10, whereas this probability in a bulk of the sampled populations is 0.19. Thus extensive diversity is to be found both between and within populations of this species.

The allozyme variation shows the following properties: (1) It exists predominantly as homozygous lines (from 1 to 33 in a sample of 50 plants per site), between which there is little outcrossing (estimated at 1.6%). (ii) It is sharply differentiated between sites. (iii) Associations occur between environmental parameters and the level or the kind of variation. (iv) There are correlations in allelic state over loci. We conclude that natural populations of the species deserve further exploration and use in plant breeding.

BREAKDOWN OF PLASMID INCOMPATIBILITY IN A *tif* MUTANT OF *E. COLI*

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Plasmids of the same group (e.g. F-prime factors) cannot, by definition, co-exist in the same cell. The *E. coli* K12 strain T44 (*thr. leu. lac*) carries a highly pleiotropic *ts* mutation, *tif-1*, the expression of which leads to induction of DNA repair and other functions. To assess the dominance or recessiveness of *tif-1*, a large F-prime factor (F' 143:thy^+tif^+) was introduced into T44. As part of a study of the genetic interactions between this factor and the bacterial chromosome, an attempt was made to eliminate F'143 by superinfecting the merozygotes with another F-prime factor (F' lac^+). Half (10/20) of the resulting lac^+ recombinants were found to carry both F-prime factors simultaneously, as judged by back-crossing to tester strains. T44 was then compared with its parental tif^+ strain, C600, with respect to another pair of F-prime factors. After 40-50 generations without selection, 30/30 C600 recombinants had lost the phenotype of the initial plasmid while 13/30 (43%) of T44 recombinants had retained the phenotypes of both plasmids. A third F-prime factor (F' lac^+) was subsequently introduced into, and retained under selection by, one of these "doubles". Experiments are in hand to show whether these F-prime factors are replicated and transferred independently, or as a co-integrated unit.

CONSTRUCTION OF MOLECULAR VECTORS FOR PLANT CELLS

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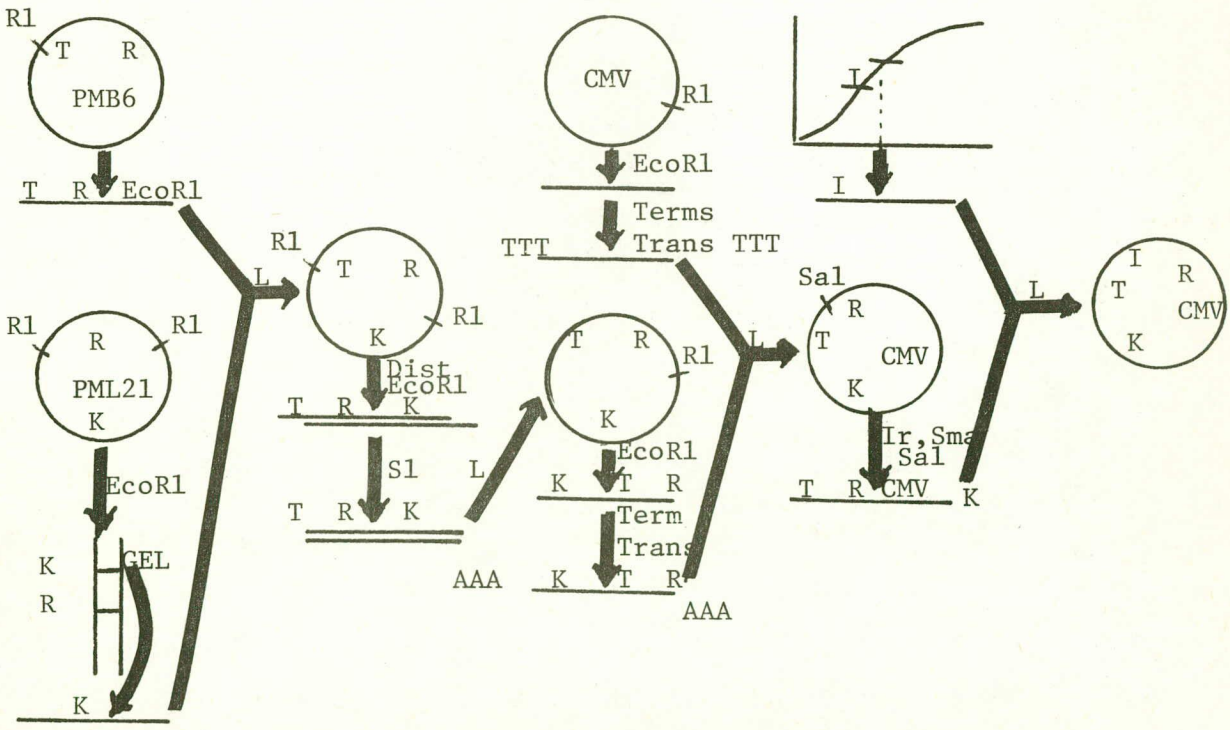

AAA = polyadenine; CMV = cauliflower mosaic virus; dist = distamycin A; I = intermediate repeated plant DNA; Ir = $(NH_4)_2$ $IrCl_6$; K = gene for kanamycin resistance; L = ligase; PMB9 & PML21 = plasmid vectors; R = plasmid replicon; R1 = EcoR1 site; S1 = S1 nuclease; Sma, Sal, EcoR1 = restriction nucleases; T = gene for tetracycline resistance; term trans = terminal transferase; TTT = polythymine.

THE GENETICS OF BIOLOGICAL CONTROL OF CROWN GALL

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Crown gall is a plant cancer induced by the soil borne pathogen *Agrobacterium radiobacter* var. *tumefaciens*. The genes for tumour induction are located on a large bacterial plasmid, the Ti plasmid, part of which becomes stably incorporated and transcribed in tumorous plant cells. This is an example of a naturally occurring feat of biological engineering.

Crown gall is now controlled in the field by an antagonistic organism, *A. radiobacter* var. *radiobacter* strain 84 which produces a highly specific antibiotic, agrocin 84. The involvement of plasmids in biological control has been elucidated. Sensitivity of the pathogen to agrocin 84 is linked to tumour induction on the Ti plasmid and production of agrocin 84 is also determined by a plasmid, the agrocin 84 plasmid.

Agrocin 84 production has been transferred by conjugation to two recipient strains of *Agrobacterium*. Surprisingly, only one of the two transconjugants is effective in biological control. Our research now indicates that two requirements must be met by an effective biological control agent - (1) production of an effective antibiotic
(2) growth and antibiotic production at the site of disease control.

In searching for new biological control organisms it is envisaged that both requirements may not be met by a singly organism. Combining both requirements by genetic manipulation is now a possibility for "manufacturing" new biological control agents for soil borne diseases.

GENETIC VARIABILITY OF CAULIFLOWER MOSAIC VIRUS DNA

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A restriction endonuclease map of Cauliflower Mosaic Virus (Ca MV) DNA, strain Campbell has been constructed. Circular molecules of Ca MV DNI digested with EcoR$_1$ endonucleases give rise to 3 fragments, with Hind III 7 fragments. Sal I, Bam I, Xho I each have one site per molecule giving rise to linear molecules.

The restriction sites have been oriented by means of a) intermediate fragments obtained in partial digests and b) by recovery of individual fragments from agarose gels and their subsequent digestion by a second restriction enzyme.

The DNA of other 2 strains of Ca MV - New York and A.C.T. - have been compared with Campbell DNA. The three DNAs differ as shown by restriction enzyme analysis. The New York strain contains only 2 EcoR$_1$ sites, and the A.C.T. strain has different positioning of Hind III sites within the molecule.

CHANGES IN CHLOROPLAST DNA OF ISONUCLEAR MALE STERILE HYBRIDS OF TOBACCO

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Isonuclear male sterile lines (plasmatypes) of tobacco were produced by successive backcrosses of each of six different species of Nicotiana to a single variety of N. tabacum as the recurrent male parent.

Chloroplast DNA (ct-DNA) from each of the plasmatypes, the respective maternal species and the recurrent male parent was compared by $EcoR_1$ restriction endonuclease analysis.

Four of the plasmatypes had a restriction fragmentation pattern which was identical to that of the respective maternal parent. In the remaining two plasmatypes, the fragmentation pattern of the ct-DNA was different to that of the respective maternal parent (N. glutinosa and N. bigelovii). None of the fragmentation patterns were like that of the recurrent male parent.

The results indicate that nucleotide substitutions can occur in ct-DNA, presumably as a consequence of interaction with a foreign nucleus.

GUIDE DOG GENETICS

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and

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Many dogs reared as potential guides for the blind are found to be unsuitable for training. The records of the Royal Guide-dogs for the Blind Association show that the major reason for rejection is fearfulness then dog distraction, excitability and hip dysplasia. Using these records the heritability of rejection was estimated to be 0.44 and of rejection for fearfulness to be 0.46. Variation due to maternal environment and common environment within litters was found to be unimportant which is in contrast to other studies.

A crossbreeding experiment found heterosis for most traits to be non-significant but there appears to be some heterosis for traits involving social behaviour.

In this crossbred population there is significant additive variation for excitability and dog distraction as well as fearfulness. The genetic correlations between scores at 6 and 12 months (important because dogs are castrated at 6 months) are approximately 1.0.

Multivariate genetic analysis and the implications of these results for a practical breeding program are discussed.

CORRELATION OF FIELD ORGANIPHOSPHORUS-RESISTANCE LEVELS AND SEASONAL FAVOURABILITY FOR *Lucilia cuprina*

J.T.A. Arnold and M.J. Whitten

Assays for field OP-resistance levels in the Australian Sheep Blowfly have now been made for 9 consecutive seasons at 6 locations along a transect through N.S.W. They have shown fluctuations which could reflect changes in seasonal favourability; i.e. the effect of varying and opposing pressures of insecticide usage and natural selection.

We attempt to gain evidence to support this hypothesis by correlating larval and adult end-of-season field resistance levels with the respective seasonal "favourability index" derived from local meteorological records.

THE GENETIC BASIS OF RESISTANCE TO THE INSECTICIDE DIAZINON IN VICTORIAN POPULATIONS OF *LUCILIA CUPRINA*

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The resistance of the sheep blowfly, Lucilia cuprina, to the organophosphorus insectivide diazinon has been examined in four separate localities in Victoria. Results indicate that resistance is determined by a single locus on chromosome 4. The frequency of the resistance allele appears to have reached a very high frequency in all four populations despite the different blowfly management practices that are employed in these localities. The theoretical and practical implications of this finding will be discussed.

COMPOUND CHROMOSOMES IN *LUCILIA CUPRINA*

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Lucilia cuprina (the Australian sheep blowfly) causes economic losses of the order of fifty million dollars per annum. For this, and biological reasons *Lucilia* has been selected for a study of the feasible use of genetically contrived sterility and/or load to reduce or control the field population. A strain carrying a pair of compound autosomes is almost completely sterile when mated with the structurally normal (metacentric) form, and this type of sterility has been proposed as one method of population control.

Though compound chromosomes had been produced in *Lucilia*, they had not been obtained readily enough to develop vigorous strains for field release. By applying the methodology of radiation genetics gained from *Drosophila melanogaster* it has been possible to regularly produce such compounds. When males are irradiated as pupae the induction of compounds is comparable to that found in *Drosophila*.

Genetic manipulation of sheep blowfly populations

G.G. Foster and R.H. Maddern

A field trial of a translocation male/eye colour strain has been underway since September 1976. Results from 1976-7 were described at the 1977 GSA meeting, and will be briefly reviewed. Results for the early part of 1977-8 indicate a level of genetic load in excess of 50% in the release area; trap catch indices suggest significant suppression in the release area compared to a nearby non-release area. These, and results for the late part of 1977-8 will be discussed.

HOMOLOGIES BETWEEN NON-HOMOLOGOUS CHROMOSOMES

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Cytological studies of hybrids between two chromosomal forms of the grasshopper, Caledia captiva have revealed a clear case of pairing and exchange between non-homologous chromosomes. The genomes of each of the two chromosomal forms are readily identifiable by their marked differences in morphology and in the pattern of C-heterochromatin distribution.

Multiple chromosome associations are a regular feature of all diploid cells. In many cases, these multiples involve two or more non-homologous chromosomes from within the same haploid genome (i.e. Daintree/Daintree or Moreton/Moreton). Such associations are clearly identifiable by the heterochromatin markers on the chromosomes and reveal unambiguous evidence of meiotic exchange and chiasmata. The X chromosome frequently associates with an autosome and Anaphase I cells present evidence of X/Autosome exchanges. A correlation exists between the position of the exchange event in non-homologous pairs and the location of heterochromatin (proximal heterochromatin = proximal exchange; interstitial heterochromatin = interstitial exchange).

The relevance of these observations to both claims in the literature of interchange heterozygosity in hybrids and to patterns of pairing and exchange in monohaploid plants will be discussed.

FURTHER INVESTIGATIONS OF A RAPID CLINE IN B CHROMOSOME FREQUENCY IN THE BRITISH GRASSHOPPER *MYRMELEOTETTRIX MACULATUS*

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Studies initiated by John & Hewitt showed the British grasshopper *M. maculatus* was polymorphic for the presence of one or more supernumerary (B) chromosomes in populations restricted to south central England. At the edge of this range they found rapid clines from B containing populations to those without B's. Hewitt & Ruscoe proposed these were selective clines with cooler wetter microclimates selecting against individuals with B's. Subsequent attempts to support this by showing phenotypic differences between individuals with and without B's have been largely unrewarded.

This paper reports the investigation of an alternative hypothesis for the rapid cline in East Anglia, that it represents the contact of two groups of populations which, in isolation, have developed different co-adapted gene complexes, and the cline is a zone where less fit hybrids are produced. A prediction of this hypothesis is that some pre-mating or post-mating isolation may exist between populations on either side of the cline. An extensive series of mating trials gave only slender evidence for assortative mating, and no evidence of inviability in crosses across the cline.

In common with many other examples of rapid geographical change in the composition of populations, substantial evidence to support major hypotheses remains elusive.

C-BANDING IN SOME RELATED SPECIES OF AUTRALIAN CHIRONOMIDS

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Department of Genetics, University of Melbourne

The C-banding technique has been carried out on polytene and other chromosomes of 10 related species of Australian chironomids. In general, little C-banded heterochromatin was found in the group of species examined. Polytene chromosomes provided the best type of material in which to study the distribution of this heterochromatin and indicated that it is not significantly underreplicated during polytenization in the genus Chironomus. C-bands mainly occurred at and in the vicinity of centromeres, at telomeres, within some nucleoli, and at a few interstitial regions including sex-linked loci. Not all of these regions were C-banded in each of the species considered Some closely related species were similar in the position and amount of C-bande material, but others were quite different. Thus, the amount and distribution of C-bands is not always in accord with other taxonomic criteria. Within this group of 10 species, the primary event appears to have been a gain in C+ heterochromatin from the presumed central species, Ch. oppositus. Secondary loss has then occurred in several lines. For most chromosomes, the amount of C+heterochromatin is balanced over the karyotype. The telocentric fourth chromosome is often an exception and this is the chromosome that has been involved in the tandem fusions which have occurred in some species. Increases in the amount of C+heterochromatin seem to be restricted in most members of the genus Chironomus and perhaps other Chironominae as well. Possible implications of this on the direction of karyotype evolution are discussed.

Extensive chromosome polymorphism in the Australian Plague Locust revealed by G- and C-banding

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The large supernumerary B-chromosome present in some individuals of the locust Chortoicetes terminifera shows unique patterns of G- and C-banding which will be compared in detail. The heritability of these banding patterns has been demonstrated both by laboratory crosses and by the fact that in individual egg pods collected from the field carrying a single B-chromosome the B always shows a common pattern of banding. Individuals from different egg pods however, usually show different banding patterns in their B-chromosomes and over 30 variants have so far been identified using scanning procedures and a simple computerised editor. The variation of the B-chromosomes contrasts with the evolutionary conservatism of G-banding illustrated in vertebrates. There is a strong meiotic drive in single-B females with 87% of eggs receiving the B-chromosome. Despite this, the frequency of B-chromosomes in natural populations rarely exceeds 15%. The B is the last chromosome to begin and end DNA replication and shows close chromatid apposition which along with its almost complete C-banding indicate that it is genetically almost inert. It may in fact have a negative effect on viability to counter the strong meiotic drive in females. Considerable variation also occurs in the terminal and interstitial C-bands present on the standard chromosomes and a particularly notable variant of chromosome 4 will be dealt with in detail.

THE ISOLATION AND CHARACTERISTICS OF STRAINS DERIVED FROM T44(λ) WITH AN UNUSUAL COMPLEX PHENOTYPE

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A number of mutants with an unusual phenotype have been isolated from cultures of T44(λ). Common to all these strains is the ability to modify the phenotype of the parent strain. This characteristic is transducible. An auxotroph which requires five amino acids and is resistant to SM, was transduced to become a prototroph and SM sensitive. Genetic experiments have shown that the original auxotropic mutations have not reverted and can be rescued.

Another characteristic of some strains is the ability to tolerate high concentrations of several antibiotic drugs. In vitro studies have shown that this resistance is not due to alterations in ribosomal proteins which may hinder drug binding. The drug resistant strains are not amenable to genetic studies as they resist phage infections and conjugation. In these strains the modifying or suppressing character is much more pronounced than in the non-resistant variants. In addition, it was found that protein synthesis in these strains is probably faulty, since β-galactosidase is very themolabile.

POSTER 1

CYTOCHROME P-450 AND THE ACTIVATION OF PROMUTAGENS IN *SACCHAROMYCES CEREVISIAE*.

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In *Saccharomyces cerevisiae* the cellular content of cytochrome P-450 was investigated and shown to be dependent on the growth phase of aerobic cultures, the carbon source of the medium and the strain genotype. Yeast cells harvested from log phase cultures grown on glucose were capable of metabolising many promutagens to products active genetically in the same cells. Data will be presented showing the induction of mitotic gene conversion or recombination in the diploid strains D4, D5 or D7 by the promutagens dimethylnitrosamine, ethyl carbonate, aflatoxin B_1, carbon tetrachloride and chloroform.

Growth of a particular strain on medium containing galactose resulted in lower cellular concentrations of cytochrome P-450 and a reduced genetic activity of all promutagens (except aflatoxin B_1) compared with cells grown on glucose medium. Cumene hydroperoxide is known to support cytochrome P-450 mediated reactions and when this compound was incubated with a promutagen in the yeast activation system there was an increase in genetic activity. In some cases, the addition of promutagens to whole cell suspensions was investigated and a stable complex with cytochrome P-450 could be observed. These experiments all suggest that the metabolism of these promutagens by yeast cells is attributed to the cytochrome P-450-dependent monooxygenase system.

POSTER 2

SILVER BANDING IN POLYTENE AND OTHER CHROMOSOMES OF RELATED AUSTRALIAN CHIRONOMID SPECIES

G. Lentzios*, A.J. Stocker, J. Martin

Although silver banding techniques have been extensively used in cytogenetics, particularly to localize nucleolar organizers of mammalian chromosomes, little has been done using these techniques in polytene chromosomes. Since polytene chromosomes provide higher resolution than other types of chromosomes they are excellent systems in which to study the mechanisms of the various banding techniques. Many questions still remain on the mechanism and specificity of silver banding. We are examining some of these questions utilizing chironomid polytene chromosomes. We are also examining the number, location, and evolution of nucleolar-producing regions in these related species. When used under stringent conditions, the technique was specific for sites which are active in nucleoli production. Different types of staining can be shown, corresponding to the degree of expansion of the nucleolus.

The technique should also prove useful in examining certain stages of meiosis and in identifying chromosomes having low levels of polyteny.

POSTER 3

THE DETECTION OF RYE CHROMOSOME 2R SUBSTITUTIONS IN WHEAT AND OF A RECIPROCAL TRANSLOCATION BETWEEN CHROMOSOME 2R AND A WHEAT CHROMOSOME

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In an attempt to introduce chromosome 2R of rye into a commercial Australian wheat, a backcrossing program was initiated utilising a Sears Chinese Spring 2R(2B) substitution line. On analysing the supposedly BC_1F_3 progeny of one of these crosses, it was found that the 2R chromosome was present but that the short and long arms of this chromosome had apparently undergone translocations. From a check of the pedigree of these plants, it is reasoned that there must have been a reciprocal centromeric translocation between a chromatid of 2R and a chromatid of a wheat chromosome (possibly 2B) and that this must have occurred in one of the original F_1 plants. The present generation is consequently F_4 rather than BC_1F_3. From this material, we are isolating homozygous lines of the short and long arm translocations and of the 2R substitution.

The chromosomes are being identified and checked by an *in situ* labelling technique of root tip mitoses and pollen mother cell meioses. The probe being used is a highly repeated DNA fraction from rye which is specifically located in the telomeric heterochromatin of rye and is present to only a very limited degree in wheat.

POSTER 4

GENETIC STUDIES OF THE NODULATION PROCESS IN WHITE CLOVER

Barry G. Rolfe and Peter M. Gresshoff

The symbiotic relation between *Trifolium repens* (white clover) and *Rhizobium trifolii* strains was studied.

It was found that bacteroids isolated from nodule protoplasts of white and subterranean clover as well as soybean retained their viability and other genetic properties. High viability was obtained only when bacteroids were protected by the appropriate osmotic conditions. This colony forming ability of bacteroids enabled an investigation of the various compartments composing a nodule.

Interactions between genetically marked strains of *R. trifolii* were studied to investigate the complementation of processes required for the establishment of effective nodulation. It was found that mixed infections with two effective (nitrogen-fixing) strains showed cloning, i.e. any one plant protoplast contained only on bacterial type, although both were present in the same nodule.

Various ineffective (non-nitrogen-fixing) strains gave different complementation responses with effective strains. Some strains were not aided but in fact impeded the effectiveness of the nodule and often the total plant response. Our findings suggest that complementation between ineffective strains of *Rhizobium* for effective nodulation will only be observed between certain mutants.

POSTER 5

C-banding polymorphism in Keyacris scurra

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The morabine grasshopper Keyacris scurra is well known for its interacting inversion polymorphism systems (see White et al. 1963 and earlier) and is now being investigated using modern techniques. We have found extensive C-band polymorphism at some localities and used the bands to characterise the Standard and inverted chromosomes Blundell and Tidbinbilla. Generally it appears that the race with 2n = 17 in the males has more interstitial C-bands than the race with 2n = 15 in the males. In particular we have studied this in hybrids between the two races.

POSTER 6

A LABORATORY EXERCISE IN THEORY AND PRACTICE OF SELECTION AGAINST SPECIFIC GENES

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There are relatively few laboratory exercises in Population Genetics where the theory and its application can be illustrated to students in introductory courses. While it is practical to demonstrate gene frequency changes with natural and artificial selection, the unification of these results with algebraic equations derived and discussed in lectures is often unsatisfactory. Student disinterest and disappointment often follows.

The laboratory exercise described here allows students to follow changes in gene frequency when complete selection is practiced on autosomal and sex-linked genes. Students then derive the formulae presented in the lectures. This is followed by experimentation with the same type of genes in *Drosophila melanogaster* - the observed and the calculated changes in frequency are compared. This approach has increased the students' understanding of the concept of gene frequency change with selection. Another, secondary, benefit of the exercise, is to observe the effects of random sampling by comparing class with indidivual results.

POSTER 7

POPULATION GENETIC ANALYSIS OF A NARROW HYBRID ZONE BETWEEN THE DISCOGLOSSID ANURANS, *BOMBINA BOMBINA* AND *B. VARIEGATA* IN POLAND

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Contact hybrid zones between *Bombina bombina* L., a lowland frog, and *B. variegata* L., a highland form, can be traced along the foothills of the Balkan and Carpathian Mts. Electrophoretic studies in Poland show that the species away from the contact zone are fixed for different alleles at 6 of 15 loci examined. 5 of the 6 loci were scored from 20 to 100+ individuals from each of 19+ populations samples in a 40 km wide transect across the hybrid zone west of Krakow. These data show: 1. Gene frequencies at the 5 loci correlate over space to 0.972 or higher. 2. 99% of the variance is summarized by the first principle component of a PC analysis of the correlation matrix. 3. The average proportion of individuals heterozygous per locus in each population is within 1-2% of that predicted for a population in Hardy-Weinberg equilibrium. 4. Most populations are also in Hardy-Weinberg equilibrium for each of the 5 loci taken independently. 5. Heterozygotes for the marker loci are found out to 20 km from the center of the hybrid zone, but 50% of the gene frequency change occurs over 5 km. 6. Some genetically homozygous individuals of one species migrate 15 km or more into essentially pure populations of the other species. 7. Populations within the 5 km central strip show significant gametic disequilibrium in pairwise comparisons, and the most central population also shows a significant excess of 5 locus parental genotypes. 8. The data fit Hall's hybrid sink model for parapatric hybridization.

POSTER 8

GENETICS OF COTYLEDONARY STORAGE PROTEINS IN *PISUM*

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Cotyledonary storage proteins of legumes are here defined as organ-specific proteins sequestered in the membrane-bound protein bodies of mature cotyledons. Genetic, developmental and physiological (nutritional) evidence supports recognition of two quantitatively major families of storage holoproteins comprising the legumin and vicilin fractions. Holoprotein patterns are inherited additively without formation of new interaction products; qualitatively the patterns are unaffected by the direction of the cross.

Genetic loci specifying the major acidic [40 kilodalton (kd)] and major basic (20kd) polypeptides of the legumin fraction have been identified using electrophoretic variants as markers for the structural and/or processing genes involved. Loci affecting minor legumin components involving 25,27 and 37 kd polypeptides, and vicilin polypeptides of about 75,70,55,50,30 and 12-14 kd are also being studied. Linkage analyses currently in progress will establish the chromosomal distribution of these loci as a preliminary to investigation of their multiplicity and functional interrelationships. This work should provide information on the origin and evolution of genes governing the storage proteins, and on their susceptibility to manipulation through artificial selection.

POSTER 9

THE GENETIC IDENTIFICATION OF LOCI ON MITOCHONDRIAL DNA

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Yeast mitochondrial DNA, although of a size comparable to that of bacteriophage, has limited information sequences. The genes present are of two types denoted *mit* and *syn* genes. *Mit* genes are responsible for the synthesis of protein subunits of the mitochondrial inner membrane. Seven clearly distinct *mit* loci have been identified and mapped as the result of the analysis of a large number of mitochondrial mutants with specific enzymatic defects; 3 loci are involved in the synthesis of cytochrome oxidase, 2 for coenzyme QH_2 -cytochrome c reductase and 2 for mitochondrial ATPase. *Syn* genes are transcribed to form mitochondrial ribosomal and transfer RNAs. Mutants deficient in mitochondrial protein synthesis have been used to identify and map a number of specific transfer RNA genes. Both *mit*$^-$ and *syn*$^-$ mutations were assigned to loci on the bases of two genetic criteria; a lack or very low frequency of recombination between mutations, and the restoration of respiratory competence in a number of mutants by the same set of ρ^- clones. Although the number of genes represented has not yet been resolved, our results suggest that all the major *mit* loci have been identified. The mapping of loci relative to known antibiotic resistance markers was achieved by recombination analysis and by the analysis of the loss or retention of the *mit* and *syn* alleles in ρ^- clones with characterized deletions.

POSTER 10

GENETIC ANALYSIS OF RADIATION-SENSITIVE MUTANTS OF *DICTYOSTELIUM DISCOIDEUM*

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The cellular slime mould *Dictyostelium discoideum*, a simple eukaryotic micro-organism which has been used as a model developmental system, also has properties which make it a useful system in which to study DNA repair. Mutants that are defective in the repair of DNA can be readily isolated on the basis of increased sensitivity to either ^{60}Co gamma rays or 254 nm ultraviolet light. Genetic characterizations based on the para-sexual cycle of *D. discoideum* indicate that the radiation-sensitive mutations affect at least nine loci. Mutations of the radC gene lead to increased sensitivity to UV but do not affect gamma ray sensitivity. The radC mutants make fewer single strand breaks in their DNA following UV irradiation than do their parental strains. Thus the radC mutants appear to be defective in the incision step of a UV-specific excision repair system. Double mutant haploids bearing the radA and radC mutations are more sensitive to UV than either single mutant haploid, indicating that these genes are involved with separate repair pathways.

POSTER 11

CHIASMA DISTRIBUTION AND ITS RELATIONSHIP TO C-BANDS IN CHROMOSOMES OF *LILIUM*

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There has been much speculation concerning the biological role of repetitive DNA and of constitutive heterochromatin. One hypothesis suggests that repeated DNA sequences, frequently localized in C-banded heterochromatin, may function in regulating the frequency and position of recombination.

Our aim was to test this by describing the influence (if any) of C-heterochromatin in the distribution of chiasmata in *Lilium* chromosomes. Two distantly-related species were used, *L. henryi* and *L. pardalinum*. The sites of intercalary and nucleolar C-bands differ in these two species. C-banding patterns enable the unambiguous recognition of five of the twelve bivalents of *henryi* and of seven of twelve in *pardalinum*. We mapped the distribution of chiasmata along these bivalents and the following was observed: (i) No terminalization of chiasmata was detected, at least between diakinesis and metaphase I, as the distribution of chiasmata at the two stages was similar. (ii) Very few if any chiasmata could be localized to the C-bands themselves. (iii) Within species, the pattern of chiasmata distribution was similar in heterologous but morphologically similar bivalents, irrespective of the presence or location of C-bands. (iv) Comparing the two species, the localization of chiasmata was quite different. In *pardalinum*, relatively more of the chiasmata were located proximally. Once again there was no clear correlation with C-band location. Therefore while chiasmata probably do not occur in C-bands in these *Lilium* species, we have no evidence for any other correlation between C-band location and chiasmata distribution.

POSTER 12

THREE GENETICALLY DISTINCT POPULATIONS OF EUROPEAN CARP IN AUSTRALIA.

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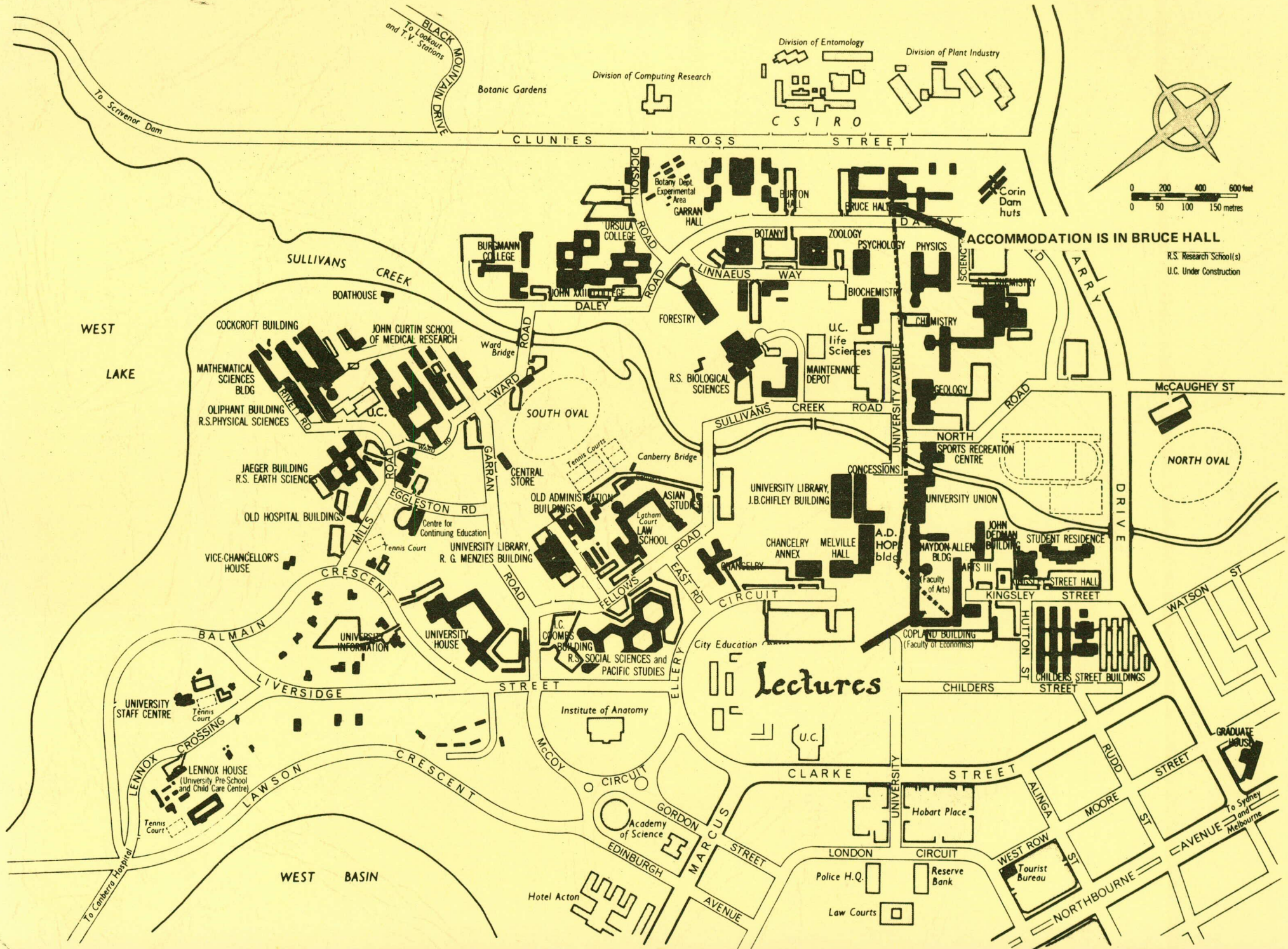
An electrophoretic investigation has shown that three genetically distinct populations of the carp, Cyprinus carpio, are present in Australia as a result of three separate introductions. Apparently, only the latest introduction is responsible for the recent rapid increase in numbers and extension in range which began about 1964. Interspecific hybrids were demonstrated electrophoretically between one of the carp populations, and the goldfish Carassius auratus.


ACCOMMODATION IS IN BRUCE HALL
R.S. Research School(s)
U.C. Under Construction
0 200 400 600 feet
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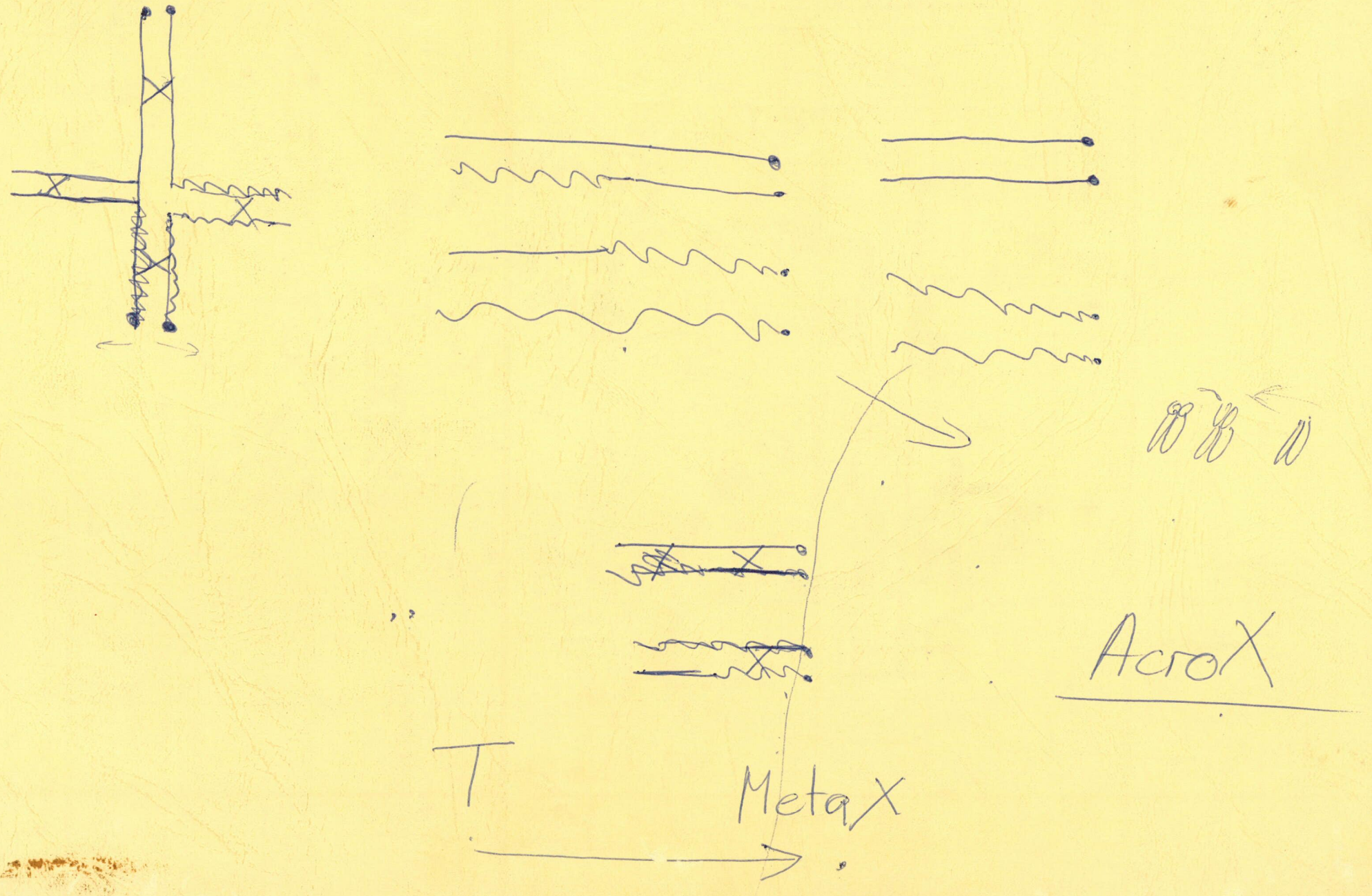
BLACK MOUNTAIN DRIVE
To Lookout and T.V. Stations
To Scrivenor Dam
Botanic Gardens
Division of Computing Research
Division of Entomology
Division of Plant Industry
C S I R O
CLUNIES ROSS STREET
DICKSON ROAD
Botany Dept. Experimental Area
GARRAN HALL
BURTON HALL
BRUCE HALL
Corin Dam huts
URSULA COLLEGE
BURGMANN COLLEGE
JOHN XXIII COLLEGE
DALEY
SULLIVANS CREEK
BOATHOUSE
WEST LAKE
COCKCROFT BUILDING
JOHN CURTIN SCHOOL OF MEDICAL RESEARCH
Ward Bridge
WARD ROAD
MATHEMATICAL SCIENCES BLDG
TRIVETT RD
OLIPHANT BUILDING R.S.PHYSICAL SCIENCES
U.C.
JAEGER BUILDING R.S. EARTH SCIENCES
OLD HOSPITAL BUILDINGS
VICE-CHANCELLOR'S HOUSE
MILLS ROAD
EGGLESTON RD
Centre for Continuing Education
Tennis Court
UNIVERSITY LIBRARY, R. G. MENZIES BUILDING
GARRAN ROAD
CENTRAL STORE
SOUTH OVAL
Tennis Courts
Canberry Bridge
OLD ADMINISTRATION BUILDINGS
ASIAN STUDIES
Lgtham Court LAW SCHOOL
FELLOWS ROAD
CRESCENT
BALMAIN
UNIVERSITY INFORMATION
UNIVERSITY HOUSE
J.C. COOMBS BUILDING R.S. SOCIAL SCIENCES and PACIFIC STUDIES
EAST RD CIRCUIT
ELLERY
LIVERSIDGE STREET
UNIVERSITY STAFF CENTRE
Tennis Court
LENNOX CROSSING
LENNOX HOUSE (University Pre-School and Child Care Centre)
Tennis Court
LAWSON CRESCENT
To Canberra Hospital
WEST BASIN
Institute of Anatomy
McCOY CIRCUIT
GORDON
Academy of Science
EDINBURGH AVENUE
MARCUS STREET
Hotel Acton
FORESTRY
BOTANY
ZOOLOGY
PSYCHOLOGY
PHYSICS
LINNAEUS WAY
BIOCHEMISTRY
R.S. BIOLOGICAL SCIENCES
MAINTENANCE DEPOT
U.C. life Sciences
CHEMISTRY
UNIVERSITY AVENUE
GEOLOGY
SULLIVANS CREEK ROAD
McCAUGHEY ST
NORTH SPORTS RECREATION CENTRE
NORTH OVAL
CONCESSIONS
UNIVERSITY LIBRARY, J.B.CHIFLEY BUILDING
UNIVERSITY UNION
CHANCELRY ANNEX
MELVILLE HALL
A.D. HOPE bldg
CHANCELRY
HAYDON-ALLEN BLDG (Faculty of Arts)
JOHN DEDMAN BUILDING
STUDENT RESIDENCE
ARTS III
STREET HALL
KINGSLEY STREET
HUTTON ST
COPLAND BUILDING (Faculty of Economics)
CHILDERS STREET BUILDINGS
CHILDERS STREET
City Education
Lectures
U.C.
CLARKE STREET
UNIVERSITY
Hobart Place
LONDON CIRCUIT
Police H.Q.
Reserve Bank
Law Courts
Tourist Bureau
WEST ROW ST
NORTHBOURNE AVENUE
To Sydney and Melbourne
ALINGA
RUDD STREET
MOORE ST
GRADUATE HOUSE
WATSON ST
DRIVE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