GENETICS SOCIETY OF AUSTRALIA

7TH ANNUAL GENERAL MEETING

UNIVERSITY OF MELBOURNE

11-12 DECEMBER 1958

PROGRAMME

ABSTRACTS

SCANNED FROM THE ORIGINAL

GENETICS SOCIETY OF AUSTRALIA

MELBOURNE MEETING 11th - 12th DECEMBER, 1958

All daytime sessions will be held in the Zoology Department.

PROGRAMME

Thursday, 11th December:

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| 9.30 a.m. | I.I.Oster (Bloomington, Indiana) |
| 10.00 a.m. | G.S.Christie - General effects of heliotrope alkaloids |
| | A.M.Clark - Mutagenic activity of heliotrine |
| 10.30 a.m. | Ellen M.Craig - Point mutation in relation to senescence |
| 11.00 a.m. | Tea |
| 11.30 a.m. | J. Langridge and B.Griffing - Inactivation by high temperature of gene functions in Arabidopsis |
| 12.00 noon | T. Nay - Hair cycles in inbred strains of mice |
| 12.30 p.m. | Berenice M.Kindred - Skin grafts between sib lines of inbred mice |
| 1.00 p.m. | Lunch |
| 2.00 p.m. | J.M.Rendel - High scutellar bristle number in Drosophila |
| 2.30 p.m. | B.L.Sheldon - Response to selection for bristle number |
| 3.00 p.m. | Anne Levy - Population studies with sex-linked genes in Drosophila |
| 3.30 p.m. | Tea |
| 4.00 p.m. | J.S.F.Barker - Selective mating in Drosophila |
| 4.30 p.m. | F.E.Binet and J.A.Morris - Flock structure for genetic improvement in poultry |

Evening Address:

8.00 p.m. L.H.Gray (Director of the Radiobiological Unit, Empire Cancer Campaign) - "Radiobiology and Radiotherapy".

Public Lecture Theatre, University.

Friday, 12th December:

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| 9.30 a.m. | B.W.Holloway and Barbara Fargie - Factors controlling fertility in Pseudomonas |
| 10.00 a.m. | J.A.Pateman - Aberrant recombination in Neurospora |
| 10.30 a.m. | G.W.Grigg - Conidial differentiation in Neurospora |
| 11.00 a.m. | Tea |

Friday, 12th December:

11.30 a.m. R.E.Wright - Extranuclear transmission in yeast heterokaryons

12.00 noon P.G.Martin - Differentiation of the nuclei of pollen grains

12.30 p.m. M.J.D.White and Lesley E.Andrew - Inversion polymorphism in the grasshopper Moraba scurra

1.00 p.m. Lunch

2.00 p.m. R.D.Brock and D.C.Wark - Radiation induced disease resistance

2.30 p.m. W.D.Jackson - Clinal variation in Eucalyptus

3.00 p.m. F.E.Binet and R.T.Leslie - Coefficients of inbreeding in the case of full-sib matings

3.30 p.m. Tea

4.00 p.m. A.S.Fraser -

"Is there need for an Australian Journal of Genetics and Biometry?"

General Business

Evening Address:

7.15 p.m. A.S.Fraser - "Evolution of Quantitative Genetic Systems".

Zoology Department Lecture Theatre.

## RADIATION BIOLOGY CONFERENCE

Members of the Genetics Society are reminded that the second Australasian Conference on Radiation Biology will take place in Melbourne from the 15th - 19th December. The sessions will be held at the Public Lecture Theatre, University.

## GENETICISTS' PICNIC

A picnic is being arranged for Sunday, 14th December, and all Members who are staying in Melbourne over that weekend are invited to attend.

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# GENETICS SOCIETY OF AUSTRALIA

## Amendment to Programme

**Thursday, 11th December**

9.30 a.m. BAKER, E. P. "Cytological Observations on Transference of Rust Resistance from *Agropyron elongatum* to Common Wheat".

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# CYTOLOGICAL OBSERVATIONS ON TRANSFERENCE OF RUST RESISTANCE FROM *Agropyron elongatum* TO COMMON WHEAT

Transference of the rust resistance from *Agropyron elongatum* to wheat has been of plant breeding interest following successful hybridization between the two genera. The initial successful step in this project was the production, in Canada, of a 56 chromosome derivative.

Backcrosses of Australian agronomic varieties (2n = 4 2) with this derivative produced resistant segregates in which it was shown that resistance depended on a single additional *Agropyron* chromosome. Resistant plants which segregated were found to contain 43 chromosomes. Their progeny consisted of 3 types of plants - susceptible (2n = 42); resistant which again segregated (2n - 43); and a low frequency of pure breeding resistant. The last category carried 44 chromosomes (22 bivalents).

The ratio of resistant to susceptible plants in a segregating line was 1: 1.6, suggesting a transmission rate of 40% for the *Agropyron* univalent through the female gametophyte.

Except for rare instances plants resistant to stem rust (*P. gr. tritici*) were also resistant to leaf rust (*P. triticina*). Occasional exceptions were resistant, however, to only one rust type. Cytologically such types were found to carry a telocentric univalent, indicating that resistance to the two species is carried on separate arms of the *Agropyron* chromosome.

Attempts are being made by X-radiation to translocate the resistances from the *Agropyron* chromosome into the wheat genome and to establish the normal 42 chromosome condition for agronomic reasons and for more direct use in further hybridization.

meeting 7

ANDREW.

GENETICS SOCIETY OF AUSTRALIA

ABSTRACTS OF PAPERS TO BE PRESENTED AT THE MELBOURNE MEETING,

11th - 12th DECEMBER, 1958

CHRISTIE, G.S., Pathology Department, University of Melbourne.

## General Biological Effects of Heliotrope Alkaloids

In Australia, natural outbreaks of chronic liver disease occur in sheep, horses and cattle. In Victoria, South Australia and the Riverina it has been shown that the outbreaks in sheep usually involve consumption of H. europeum by sheep. Extensive field and laboratory work by a group of C.S.I.R.O. biologists and chemists elucidated the natural history and clinical pathology of the disease, and demonstrated that the toxicity of the plant was due to its content of several related alkaloids. They were all esters of a basic alcohol possessing a pyrrolizidine ring and were thus members of an extensive group of such alkaloids occurring in several plant genera, especially Senecio, Erectites, Crotalaria and Heliotropium. Isolation of the heliotrope alkaloids permitted study of their hepatotoxic effect on laboratory animals in both acute and chronic forms.

Samples of one of the alkaloids, heliotrine, and of the C.S.I.R.O. strain of rat were made available for enzyme studies at the Department of Pathology. Histological control showed that in acute poisoning by 320 mg./kg. body wt., confluent necrosis of middle and inner zones occurred between the 16th and the 20th hour and was accompanied by unusually bizarre nuclear changes. Biochemically, there was a progressive fall of liver DNA. Loss of activity of mitochondrial DPN dependent respiratory enzymes, and disorganization of the TCA cycle occurred suddenly between the 14th and the 16th hours although enzyme systems not dependent on DPN, such as succinoxidase, choline oxidase and anaerobic glycolysis were little affected. It was concluded that the immediate cause of necrosis was a DPN deficiency state affecting the mitochondria. The nucleotide might be lost or inactivated or its synthesis in the nucleus impaired. The possibility that the action of the alkaloid might be primarily on the nucleus thus emerged, and further evidence was sought.

CLARK, A.M., Zoology Department, University of Melbourne.

## The Mutagenic activity of Heliotrine in Drosophila

Table 1

Production of sex-linked recessive lethals following injection into Canton S males of 0.08 microlitres of a 0.3% solution of heliotrine in saline. Three Basc females per male per brood. Brood intervals of 72 hours. Temperature: 25°C.

| | Brood | | | | |
|---|---|---|---|---|---|
| | 1 | 2 | 3 | 4 | 5 |
| Chromosomes tested | 558 | 563 | 233 | 116 | 102 |
| Lethals | 31 | 10 | 17 | 6 | 3 |
| Percent lethals | 5.6% | 1.8% | 7.3% | 5.2% | 2.9% |

Table 2

Production of sex-linked recessive lethals in mature spermatozoa. Single brood collected from males injected with 0.08 microlitres of heliotrine solution.

| | Concentration of heliotrine | | | | |
|---|---|---|---|---|---|
| | 0.1% | 0.3% | 0.5% | 1.0% | 1.3%. |
| Chromosomes tested | 917 | 558 | 647 | 205 | |
| Lethals | 29 | 31 | 55 | 33 | |
| Percent lethals | 3.2% | 5.6% | 8.5% | 16.1% | 30%. |
| (1¼ X rad~). | 1,200 r | 2,300 r | 3,000 r. | >6,000 r. | |

At concentrations higher than 1%, heliotrine treatment may yield up to 30% recessive lethals. However, only a single brood can then be obtained from the treated males. The alkaloid appears to prevent the maturation of immature germ cells. It is able to block spermiogenesis but does not appear to be directly spermicidal.

Structural rearrangements produced. Test Broods – ♂ not sterilized ∴ Heliotrine simply blocks maturation. complete block

CRAIG, Ellen M., 47 Prospect Hill Rd., Camberwell, Vic.

Point Mutation, Its Rate and Biochemical Effects Considered in Relation to Senescence

Theoretically, true point mutation is produced by chemical alteration in the structure of a single gene. It therefore should not require mitosis for its production. The number of point mutations should always be a function of time and the rate of point mutation largely independent of the number of mitoses. This becomes important when considering somatic mutation and its effects on normally non-mitotic essential parenchyma of the well-developed adult organism. As all types of mutation when dominant or homozygous are more often deleterious than otherwise, and as, in terms of biochemical genetics, each confers on its possessor a specific biosynthetic inability, it follows that point and occasionally other somatic mutations summate through the years in each parenchymal cell of a tissue to cause a slow deterioration in its independent synthetic ability. This may be compensated for at first by substances present in sap or circulation, either as diffusible products made in surplus by still unmutated or differently mutated other cells, or as essential substances absorbed. Finally, as somatic mutation continues, all

such compensatory mechanisms must break down, and senile deterioration becomes the inevitable outcome, accompanied by a lowering of resistance to disease and an end of the vigorous period of life. Nevertheless, all mutations cannot produce specific biosynthetic inabilities in their possessors. True advance in biochemical complexity could not have been made in evolution unless certain mutations confer added biosynthetic abilities, producing added independence of substances supplied in the environment (Horowitz, Proc. Nat. Acad. Sci. U.S. 31:153). Increased study of reverse mutation should evolve better reactivating methods whereby somatic cells might be induced to maintain their biosynthetic abilities and vigor in spite of increasing years, thus prolonging the useful part of life.

LANGRIDGE, J. and GRIFFING, B., Division of Plant Industry, C.S.I.R.O., Canberra.

The Inactivation by High Temperature of Gene Function in Arabidopsis

During a test of Bonner's hypothesis*, several races of Arabidopsis thaliana were found to have requirements for organic substances at temperatures above 28°C. In particular, two races from widely separated geographical regions required biotin for growth. The genetic implications of temperature sensitivity, and the probable adaptive and metabolic significance of the gene-temperature-biotin interaction are discussed.

* Bonner's (1957) hypothesis may be stated as follows:

(a) at certain temperature extremes plant growth is depressed by the inactivation of one or a few especially sensitive reactions, and
(b) such growth depression may be prevented by providing the plant with the normal products of the inhibited reactions.

NAY, T., C.S.I.R.O., Animal Genetics Section, University of Sydney.

Hair Cycles in Inbred Strains of Mice

Hair cycles in various inbred strains of mice have been observed. The strains differ both in timing and regularity of the second hair cycle, $C_3H$ mice having the most irregular and most delayed cycle.

KINDRED, Berenice M., C.S.I.R.O., Animal Genetics Section, University of Sydney.

## Skin Grafts between Sib Lines of Inbred Mice

Six inbred strains of mice have each been divided into five sib lines and these have been maintained as separate lines by sib matings. Skin grafts have been made between members of these lines to detect incompatibilities which may have arisen since the lines were separated. In A strain some grafts have been rejected and evidence is presented suggesting that the ability to reject grafts is inherited as a recessive character.

RENDEL, J.M., C.S.I.R.O., Animal Genetics Section, University of Sydney.

## Selection for Scutellar Bristle Number

Selection for high scutellar bristle number in sc flies results in an increase in average scutellar bristle number. This number is far more variable in sc than in + genotypes. As the number increased in sc flies of a selection line segregating for sc and +, no change in the number on + sibs was found until the average number on sc flies was about 3; a few + flies with 5 scutellar bristles then started to appear. As the sc flies increased in bristle number to 4 the variability began to be reduced and no sc flies with 5 bristles have yet been observed. As a few + flies with 5 bristles began to appear the variability of the + segregants began to increase and flies with 6 scutellar bristles soon followed. There is thus a region around 4 bristles in which genetic changes do not show at all readily. A change which will turn a + 5 bristle into a + 6 or a sc 1 into a sc 3 has little or no visible effect on a + 4 bristle of unselected type.

SHELDON, B.L., C.S.I.R.O., Animal Genetics Section, University of Sydney.

## Response to Selection for Bristle Number in Drosophila

A brief review will be given of the response to selection in four bristle selection lines of Drosophila melanogaster derived from the same Oregon wild type stock. In particular it will be shown that the response in one low line, at least from generation 13 on, has been accompanied by selection for the heterozygote of a gene which is an autosomal recessive, the homozygous recessives being fully viable but completely sterile as females, partly sterile as males. The gene was presumably present but not expressed in the base population. The homozygous recessives are reduced to only a couple of bristles on the abdominal segments, but the heterozygotes are not different from those homozygous for the normal allele. The

increase in frequency of the gene in this line is therefore probably due to the heterozygotes being more fertile than the homozygous normals.

LEVY, Anne., Genetics Department, University of Adelaide.

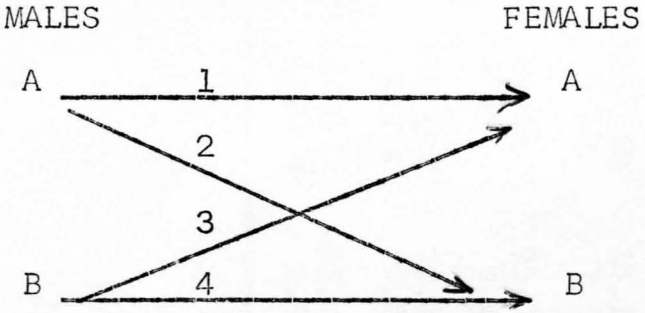
Population Studies with Sex-linked Genes in Drosophila melanogaster

Using a modified form of the population cage described by Thomson (1957), inbred lines of Drosophila melanogaster with pairs of allelic sex-linked eye-colour genes have been maintained as populations for 34 weeks to date. Samples from each cage are examined fortnightly, and gene frequency changes observed. Results of competition between apricot and white, and blood and white, will be presented, and several cases of probable equilibrium discussed in relation to Bennett's (1957) conditions for selectively balanced polymorphism at a sex-linked locus.

BARKER, J.S.F., Department of Animal Husbandry, University of Sydney.

Methods of Analysis of Selective Mating in D. melanogaster

When selective mating between two groups is being studied, there are four possible mating types.




Four methods have been used to measure the degree of selective mating:-

(1) Pair matings: Each of the matings studied separately.
(2) Male Choice : Males of one type placed with females of both.
(3) Female Choice: Females of one type placed with males of both.
(4) Multiple Choice: Both types of males and both types of females.

These methods have been used to study selective mating between wild type and the sex-linked mutant yellow (y). Here there are 2 male and 3 female genotypes to be considered. Results are given in the table. The differences between the methods will be discussed in

Numbers and percentages of fertilized females obtained using four methods of analysis of selective matings between yellow and wild-type D. melanogaster

| Method | Male Genotype | Female Genotype | | | | | |
|---|---|---|---|---|---|---|---|
| | | $+/+$ | | $+/y$ | | $y/y$ | |
| | | No. fertilised / No. tested | % | No. fertilised / No. tested | % | No. fertilised / No. tested | % |
| Pair Matings | + | 81/114 | 71.1 | 126/148 | 85.1 | 85/108 | 78.7 |
| | y | 2/145 | 1.4 | 8/102 | 7.8 | 54/108 | 50.0 |
| Male Choice | + | 39/46 | 84.8 | 44/46 | 95.7 | 41/46 | 89.1 |
| | y | 4/49 | 8.2 | 3/49 | 6.1 | 40/49 | 81.6 |
| Female Choice | + | 87/146 | 59.6 | 152/194 | 78.4 | 44/104 | 42.3 |
| | y | 5/146 | 3.4 | 1/194 | 0.5 | 40/104 | 38.5 |
| Multiple Choice | + | 63/70 | 90.0 | 64/70 | 91.4 | 51/70 | 72.9 |
| | y | 1/70 | 1.4 | 2/70 | 2.9 | 18/70 | 25.7 |

terms of differences between the males in vigour and the distastefulness of y males to wild-type females.

Results from such studies (usually only male and female choice) have been used by various authors to predict the effect of selective mating on gene frequency. Male and female mating ratios (Merrell 1950) have been developed for this purpose. It will be shown (1) that these do not give an adequate prediction, and (2) that any prediction should be based on multiple choice data.

BINET, F.E. and MORRIS, J.A., C.S.I.R.O., Poultry Research Centre, Werribee.

Optimal Structure of Flocks for Genetic Improvement of Poultry, with Respect to Sex-limited, Measurable Characters.

Lush, in his early papers (1947) established formulae for the weights to be given to the performance of an individual and to the mean performance of its sibs; the weighted sum is then used as a Selection Index: the weights are such as to maximise the correlation of the Index with Breeding Value of the individual. More recently (1957) Osborne obtained new formulae from which an Index (based on the weighted sums of (i) individual performance, (ii) mean of performance of full sibs, and (iii) mean performance of half sibs) can be calculated: this Index assures (for a given flock-structure) greater accuracy than any other Index (ignoring performance of prior and subsequent generations) does. When using Osborne's Index, selection accuracy (given fixed genetic parameters) depends on Flock-Structure, i.e., on the number of progeny per dam, the number of dams (per sire) leaving progeny. Genetic progress, however, depends not only on selection - accuracy, but also on selection-intensity and realized genetic variation: as these latter two also depend on Flock-Structure, the expression for genetic progress must be written down explicitely, as a function of the numerical components of Flock-Structure. The paper to be read contains a formula for that function from which formula (for fixed flock-sites and fixed genetic parameters) the number of sires and dams maximizing genetic progress, have been computed on an Electronic Computer.

HOLLOWAY, B.W. and FARGIE, Barbara, Bacteriology Department, University of Melbourne.

## Factors Controlling Fertility in Pseudomonas Aeruginosa

The mechanism of sexual reproduction in both Escherichia coli K12 and Pseudomonas aeruginosa involves an unusual type of mating factor. It can apparently be both cytoplasmic and nuclear in location, and depending on its location shows different properties i.e. it is an episome. The behaviour of this fertility factor in P. aeruginosa, the FP factor, has been studied and its behaviour compared with the F factor in E. coli. The two are very similar but show some interesting differences. The segregation pattern of two factors is different. Furthermore in P. aeruginosa not all FP+ strains can donate FP to FP- strains. The segregation of the ability to donate FP will be discussed, and a comparison of the FP factors from two different strains of P. aeruginosa will be made. A search for High Frequency Recombination (Hfr) mutants in P. aeruginosa has been made but none have yet been found, although some evidence suggests that they may exist but be unstable. Attempts to 'cure' FP carrying strains of the fertility factor have been made but as yet have not been successful.

PATEMAN, J.A., Botany Department, University of Melbourne.

## Aberrant Recombination at the am Locus in Neurospora crassa

A number of independently induced mutant alleles are known at the "amination deficient" locus in N. crassa. Strains carrying one of these mutant alleles do not produce demonstrable glutamic dehydrogenase and grow on minimal medium only after a lag period. Previous work with four different am mutants has shown that certain combinations of these am alleles in pairs in heterocaryons were complementary. In addition, apparently true wild-type ascospores were found in low frequency in the progeny of most crosses between strains which carried non-complementary am alleles.

The frequencies of wild-type production by various crosses between non-complementary am alleles were not easily explained in terms of recombination due to crossing over of the classical type. Consequently it was decided to repeat one of these crosses, with marker genes on each side of the am locus. A total of 47 wild-types were obtained in a sample of $2.76 \times 10^6$ ascospores from marked am x am crosses. These results will be discussed in detail. At the present time the data do not seem explicable in terms either of crossing over or of "gene conversion".

GRIGG, G.W., C.S.I.R.O., Animal Genetics Section, University of Sydney.

## The Control of Conidial Differentiation in Neurospora crassa

The ability of a culture to produce a macroconidum or a microconidium is determined (irreversibly) at a particular period during development.

The determinative periods for macroconidiation and microconidation are not always coincident. In some strains prevention of conidial formation for a period encompassing the earlier of the two determinative periods followed by a removal of the restriction allowing conidiation to proceed causes a complete switch in the conidial character so that strains which are normally macroconidiate may be induced to produce only microconidia. The phenotypic changes are not due to permanent genetic changes in the cultures.

This phenomenon was observed only if normal growth proceeded when conidial differentiation was prevented.

A temperature dependent gene acon$^{t}$ is described which reduced the length of the aerial hyphae of strains carrying it. Its time of expression is relatively independent of the physiological age of the culture. The gene was not expressed if the conidial character was determined before this time is reached. The mutant character of the gene was not modified by any growth substance in conidiating complete medium.

A number of apparently unconnected characters such as colour, growth rate, number of conidia produced, size and shape of conidia, mean number of nuclei per conidium and length of aerial hyphae are affected by the peach-microconidial gene m (pe$^{m}$).

WRIGHT, R.E., Department of Bacteriology, University of Melbourne.

## Extranuclear Transmission in Yeast Heterokaryons

The use of yeast heterokaryons in establishing cytoplasmic transmission has been examined and the extranuclear nature of factors associated with respiration in yeast has been confirmed.

The method involves the examination of bud clones from isolated heterokaryons for changes in respiratory phenotype not associated with recombination of nuclear markers.

Matings involved two auxotrophic stocks, one of which was unable to use oxygen ($R^{-}$) while the other had normal respiration ($R^{+}$).

Auxotrophic progeny were obtained from 91 of 530 mating pairs. The nuclear markers of these auxotrophs were the same as those of the respective parental stocks. Since ascus analysis had indicated that nuclear fusion was followed by frequent recombination of these markers it was concluded that the nuclei of the auxotrophic progeny originated by assortment of parental-type nuclei from heterokaryons rather than by segregation from heterozygotes.

In $Arg^{-}R^{-}$ X $Thz^{-}R^{+}$ crosses 5 of 17 mating pairs which produced $Arg^{-}$ progeny gave some $R^{+}$ types and 6 of 23 giving $Thz^{-}$ progeny gave some $R^{-}$ types.

The frequency of these changes was related to the suppressiveness of the $R^{-}$ parent.

Similar changes in respiration were not found among the auxotrophic progeny in control experiments involving $R^{-}$ x $R^{-}$ and $R^{+}$ x $R^{+}$ crosses.

Thus it was concluded that the observed changes in respiration resulted from extranuclear transmission factors concerned with normal respiration and its suppression.

MARTIN, P.G., Zoology Department, University of Adelaide.

## Differentiation of the Nuclei of Pollen Grains

La Cour (1949) showed that at the first mitosis in the pollen grain, the vegetative nucleus arrived in a region rich in RNP, the generative nucleus in a region with little RNP. He suggested that this unequal distribution of cytoplasm was the cause of differentiation. Investigations were carried out on P.G.I. in maize and agave to determine whether there was also an unequal distribution of nuclear contents. After fixation in10% neutral formalin, removal of nucleic acids and staining with fast green at pH 8.0, the amounts of fast green in nucleoli were measured microphotometrically. It was found that the amounts in the vegetative and generative nuclei soon after mitosis were very different but that their sum equalled the amount in pre-mitotic nuclei. It is suggested that, at P.G.I. in these two species, some nucleolar components (possibly basic proteins are distributed unequally and without loss and that this may be important in differentiation.

WHITE, M.J.D. and ANDREW, Lesley E., Zoology Department,
University of Melbourne.

Effects of Inversion Polymorphism on Viability and Biometrical Characters in the Grasshopper Moraba scurra

Investigations on the frequencies of cytological heterozygotes and homozygotes carried out in 1958 confirm previous conclusions that the cytological polymorphisms of the CD and EF chromosome pairs are associated with heterotic effects on viability. A powerful genetic interaction exists between these two heterotic systems as far as viability is concerned, so that the two polymorphisms are not combined at random in the adult populations. Preliminary studies on some biometrical characters suggest that in one population at any rate (Wombat, N.S.W.) the Standard sequences of both the CD and EF chromosomes increase the size of the insect, while the Blundell and Tidbinbilla sequences diminish size. The analysis of variance is complicated, however, by the fact that there is significant heterogeneity among the variances of the different genotypes, the double heterozygotes (St/Bl, St/Tid) having the highest variance. Although it would be rash to conclude too much from a single sample, we are inclined to interpret this result as indicating that each inversion sequence (Standard CD, Blundell CD, Standard EF, Tidbinbilla EF) has a characteristic effect on size and that the greater variance of the double heterozygotes is due to the fact that they can carry any combination of four sequences, each of which has its own range of effect on size, due to genic heterogeneity of each cytological sequence.

BROCK, R.D. and WARK, D.C., C.S.I.R.O., Division of Plant Industry,
Canberra.

Radiation Induced Disease Resistance

Mutants resistant to blue mould of tobacco (N. tabacum) and to root-knot nematode of tomatoes (L. esculentum) have been induced by X and U.V. irradiation.

Blue mould resistance in tobacco has been located in R-2 progeny following U.V. treatment of pollen grains. This resistance is inherited as a single recessive gene with low penetrance (5-20%). Resistance in a naturally occurring mutant of N. tabacum is inherited as a single dominant gene. It seems likely that these genes differ from those conferring resistance in N. debneyi.

A number of tomato mutants resistant to root-knot nematode (M. javanica) were isolated in the R-1 after X-ray and U.V. irradiation of pollen. In every case resistance was inherited as a single dominant gene and other genes were mutated in the same cell at the

time of treatment. The mutants exhibit a similar resistance pattern to the gene Mi from L. peruvianum which also confers resistance to M. javanica.

JACKSON, W.D., Botany Department, University of Tasmania.

## Clinal Variation in Eucalyptus

Population studies of the Tasmanian eucalypt species vernicosa, subcrenulata, and johnstonii, show that these are not distinct and separable forms, but represent points in one continuous morphological gradient which is clinal with respect to intensity of alpine environment, varying with altitude, aspect, soil fertility, and geographic position.

The characters showing clinal variation include stature, and size and shape of leaves and fruits, characters on which the taxonomic separation into species was originally made. Because of the completely transitional character of the clinal variation, it is proposed to combine the forms into a single superspecies, E. vernicosa, and name cline forms as reference points in the range, adding two additional names to obtain a uniformly graded series.

The superspecies demonstrates the interplay of several environmental factors each affecting clinal variation, and the assemblage of correlated variability along each particular gradient. It provides a suitable case to test the inversely apposed concepts of allopatric introgression of Anderson, and the evolution of a cline in the Huxleyan sense by the sole agency of strong natural selection causing gene substitution.

An analysis of the variation in ten clinal characters shows that the expression is largely genetically fixed at all levels. Progeny tests of open pollinated parents show that the segregation is maintained at a fairly uniform level throughout. The variation in most characters does not show any disproportionate increase in the steep part of the cline. However, in certain characters where there is significant heterogeneity in the variance, it can be shown that this heterogeneity is not due to regions of high genetic variance. Homogeneity is not restored by the removal of a few anomalous populations, but is completely restored by transformation which remove dependence between the variance and the mean. If the 10 characters are combined into a single index of morphological difference the variance of this index in individuals is almost constant over the complete clinal range, indicating that there are no regions with a disproportionate increase in genetical recombination.

Taken as evidence against the formation of the cline by intro-

gression are the correlated variability and lack of marked segregation in progenies, the uniform level of variance in individual characters, and the uniform level of recombination in these characters. All evidence seems to favour the concept of cline formation by natural selection successively increasing the Darwinian fitness, the basis of selection changing as each locus is fitted. This process can proceed without the necessity of isolation, except in so far that separation in space and time is sufficient for differences in selective advantage to exceed gene migration.

BINET, F.E. and LESLIE, R.T., C.S.I.R.O., Poultry Research Centre, Werribee, and Statistic Department, University of Melbourne.

Coefficients of Inbreeding, in the Case of Full-sib Matings

By using the method of Generating Functions, it is shown that in case of full-sib-matings in each generation, the Coefficient of Inbreeding in the n-th generation (assuming that in the "zero -th" generation, where the inbreeding began, this coefficient was zero) is

$$1 - 0.948e^{-0.212n}\left[1 + (-1)^n\, 0.0557e^{-0.962n}\right]$$

FRASER, A.S., C.S.I.R.O., Animal Genetics Section, University of Sydney

Evolution of Quantitative Genetic Systems

The analysis of a quantitative genetic system has, until recently, been based on the assumption that the various components are fixed, and although they determine the effects of selection, are not themsleves predominantly affected by selection. These views have become harder and harder to maintain, and recent experiments in many fields have shown their validity to be tenuous.

The concepts of "developmental canalisation" and "genetical homeostasis" have when applied experimentally shown that a re-organisation of our concepts of quantitative variation is necessary, and that new tools of analysis, both experimental and theoretical are required.