## GENETICS SOCIETY OF AUSTRALIA

### 12TH ANNUAL GENERAL MEETING

CANBERRA

20-21 JANUARY 1964

PROGRAMME

### ABSTRACTS

## SCANNED FROM THE ORIGINAL

## THE GENETICS SOCIETY OF AUSTRALIA TWELFTH ANNUAL MEETING, 1964.

#### PROGRAMME

Monday 20th January

9.00 am - 10.30 am

Registration for A.N.Z.A.A.S. at Academy of Science building.

11.00 am - 12.30 pm

F.H.W. Morley and J. Katznelson: "Genetic and morphological distinction between sub-species of <u>Trifolium subterraneum</u> L."

J. Sved: "The relationship between diploid and tetraploid recombination frequencies."

<u>D.W. Cooper</u>: "The inheritance of black pigmentation in a family of inbred Peppin Merinos."

<u>R.H. Hayman:</u> "Population studies on black sheep in the Australian Merino."

2.00 pm - 3.30 pm

<u>W.B. Mather</u>: "Temporal variation in <u>Drosophila</u> rubida inversion polymorphism."

S.H. James: "Cytogenetics of Isotoma petraea."

<u>O.R. Byrne</u>: "Polymorphism in the grasshopper, Austroicetes interioris."

J. Martin: "Non-random association of inversions in the midge <u>Chironomus intertinctus</u>."

4.00 pm - 5.30 pm

C. Folsome: "Unstable rII mutants of bacteriophage T4."

<u>B. Holloway</u>: "Host induced modification of <u>Pseudomonas</u> phage B3."

Miss B. Fargie and B. Holloway: "Chromosome mapping by transduction in <u>Pseudomonas</u> aeruginosa."

<u>N.H. Luig</u>: "Differential transmission of gametes in wheat in relation to Soviet genetics."

7.30 pm Business meeting

8.00 pm Dr. M. Demerec: "Evidence for evolutionary diver

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7.30 pm Business meeting

8.00 pm <u>Dr. M. Demerec</u>: "Evidence for evolutionary divergence between homologous regions of <u>Salmonella</u> typhimurium and <u>Escherichia</u> coli chromosomes."

9.00 pm Supper in the C.S.I.R.O. Biochemistry building.

#### Tuesday 21st January

9.00 am - 12.30 pm

Symposium: "The transfer of information in biological systems." (With section D of A.N.Z.A.A.S.- q.v.)

2.00 pm - 3.30 pm

J.W. James: "Selection response curves."

J.S.F. Barker: "Interspecific competition and population fitness."

<u>Miss C.M. Jacobson</u>: "An examination of X-ray induced apparent phenocopies of scutellar mutants in <u>Drosphila</u>."

Miss B. Kindred: "Selection for canalisation."

4.00 pm - 5.30 pm

<u>M. J. Whitten</u>: "Departure from asymmetry as a measure of genetic variability."

Miss M.K. Mader and P.A. Parsons: "Finger-print pattern variability."

P.A. Parsons: "Linkage in evolution."

8.00 pm - 9.30 pm

D.L. Hayman, Miss J.A. Marshall and P.G. Martin: "Morphological and autoradiographic studies of the chromosomes of some marsupials."

<u>M.J.D. White</u>: "Evolutionary loss of chiasmata in grasshoppers."

O.H. Frankel, Miss S. Lewis and Miss M. Roskams: "Evolution of morphogenetic control in a polyploid system."

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### THE GENETICS SOCIETY OF AUSTRALIA TWELFTH ANNUAL MEETING, 1964.

#### ABSTRACTS OF PAPERS

# F.H.W. Morley and J Katznelson: "Genetic and morphological distinction between sub-species of Trifolium subterraneum L."

Morphological criteria have been used to assign numerous lines to one of three sub-species. Crosses between sub-species give F1's with high pollen sterility and poor seed-set. Crosses within sub-species give a wide range of fertility levels, but fertility is relatively higher. The existence of partially inter-sterile groups within sub-species indicates a continuing state of sub-speciation.

Cytological examination of F1's disclosed chromosomal inversions, translocations, and failure of pairing. Within one sub-species meiotic irregularities were also found.

The distribution of the sub-species shows some adaptive specialisation, but the mechanisms are as yet uncertain.

J. Sved: "The relationship between diploid and tetraploid recombination frequencies."

It is shown that the effect of multiple crossing-over may be to increase the tetraploid recombination frequency for a particular chromosome region above the corresponding diploid frequency, even though the mean frequency of crossing-over per strand may not be increased. Graphs are given showing the amount of such an increase which might be expected in practice. Corresponding to the diploid frequency of 50%, the upper limit of recombination in the tetraploid is shown to be 75%.

D.W. Cooper: "The inheritance of black pigmentation in a family of inbred Peppin Merinos."

The recurrence of pigmented sheep has been recorded in a family of inbred Peppin Merinos. A recessive gene <u>w</u> is postulated to account for the presence of the pigment. Pigmented animals are classified into three categories, head pattern, piebald and black spotted. The difference between the first as opposed to the second and third is tentatively supposed to be due to two allelic genes, <u>Pa</u> and <u>pa</u> respectively. A description of two types included in the classification'head pattern' will be given. Data on the inheritance of several blood groups in this family will also be briefly discussed.

<u>R.H. Hayman:</u> "Population studies on black sheep in the Australian Merino."

Two sources have been used to make an estimate of the frequency of the occurrence of black sheep in the Australian Merino, firstly the proportion of bales of black wool to all wool sold, and secondly information supplied by a number of studs on the frequency of occurrence of black animals in their flocks. If it is assumed that one gene is responsible for black pigmentation and that there is complete selection against pigmented animals, the presumed recessive homozygotes, it would seem that the frequency of this gene in all State populations (with the possible exception of Tasmania) is too high to be maintained by mutation alone. Possible explanations for the way in which these frequencies could have arisen will be considered.

#### <u>W.B. Mather</u>: "Temporal variation in <u>Drosophila</u> rubida inversion polymorphism."

It has been shown previously that the frequencies of the inversions found in the tropical Australian species <u>D. rubida</u> vary extensively over its known range. It has also been shown that at two stations only 20 miles apart, sampled at the same time, there is a significant frequency difference between the two stations, and between sexes within stations. In this paper a report on an investigation of inversion frequencies at various times of the year at two stations near Port Moresby will be given.

#### S.H. James: "Cytogenetics of Isotoma petraea."

<u>Isotoma petraea</u> occurs in fairly small isolated populations and is particularly characteristic of the granite outcrops east of Mt. Sterling in Western Australia. The pollination mechanism is flexible and is dependent upon environmental conditions - in mild weather cross-pollination is promoted while under hot conditions (which must be usual for the species) self-pollination is achieved. The chromosome number is 2n = 14, the chromosomes are more or less isobrachial, chiasmata are localised terminally, one per arm and fully terminalised at metaphase-1.

Cytologically the populations are of two types:- <u>TYPE I</u>: mainly structural homozygotes but including some small-ring interchange heterozygotes. <u>TYPE II</u>: totally composed of interchange heterozygotes, each population being uniform for a single meiotic configuration.

The constituent plants of TYPE II populations are complex heterozygotes and are maintained by a balanced lethal system operative through zygotic elimination. So far, rings of 6, 10, 12, 14, 6 + 6, and 6 + 8 have been observed in the complex heterozygote populations. Distributional and crossing studies indicate that the large-ring complex heterozygotes developed via the sequential fixation of interchanges in the heterozygous condition. It is suggested that the complex hybridity arose in the Lake Barlee area with the advent of a balanced lethal system, and that this system has migrated progressively across the area in a south-westerly direction converting primitively TYPE I populations to TYPE II, the constitution of the resultant population being the sum of that of the immigrants and the available interchange variability of the native population.

The above hypothesis is parallel to that proposed by C.D. Darlington. It is in contrast to that exploited by R.E. Cleland in his analysis of Oenothera phylogeny, namely that the large rings were achieved at one stroke as a result of crossing between segmentally differentiated but structurally homozygous races.

<u>O.R. Byrne:</u> "Polymorphism in the grasshopper <u>Austroicetes</u> <u>interioris</u>."

Populations of the above species are polymorphic for (a) pericentric inversions in three pairs of autosomes, (b) colour pattern, and (c) colour of hind tibia. A study has been made of this multiple polymorphism in a population at Port Augusta, South Australia. Data from three generations in the field have been obtained and will be presented.

J. Martin: "Non-random association of inversions in the midge

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J. Martin: "Non-random association of inversions in the midge Chironomus intertinctus."

This paper follows one presented to the Society at Brisbane in 1961, in which was discussed the non random association of a third chromosome inversion with the sex-determining region. The present paper concerns two second chromosome inversions which show little evidence of heterosis when considered singly, but show a strong non random association in south Victorian populC. Folsome: "Unstable rII mutants of bacteriophage T4"

Mutants which revert to  $r^+$  with extraordinarily high frequencies (0.000,01 to 0.5) have been studied. Revertant phages obtained from unstable rII mutants (U rII) specifically backmutate to the original U rII type regarding genetic site and reversion index. Neither base pair alterations nor genetic recombination is sufficient as a mechanism to explain the genetic behaviour of U rII mutants. A model based upon the formation of interstrand DNA loops will be presented.

B. Holloway: "Host induced modification of Pseudomonas phage B3"

Growth of a bacteriophage on a particular bacterial host can sometimes cause genetic alterations of the bacteriophage. These are usually manifested by changes in the ability of the phage to multiply in one or another host. This phenomenon raises two questions: (i) What is the nature of the change in the bacteriophage genetic structure? (ii) What part does the host genome play in this effect? Experiments with phage B3 in <u>Ps. aeruginosa</u> have indicated a different structure of the phage DNA for host-modified B3, as demonstrated by the frequency of naturally occurring single strand breaks. By sexual recombination and transduction studies of the host bacteria, a region of the host chromosome has been found which controls host-induced modification in an as yet unknown fashion.

#### Miss B. Fargie and B. Holloway: "Chromosome mapping by transduction in Pseudomonas aeruginosa."

Joint transduction of genetic markers by phage F116 has been used to elucidate the genetic map of <u>Pseudomonas</u> <u>aeruginosa</u>. The results show that in this bacterium genes concerned with sequential steps in the various biosynthetic pathways are not clustered together on the chromosome, but are distributed over its whole length. On the other hand, several clusters are found of genes concerned with unrelated biochemical steps. The pathways under examination include tryptophan, methionine, threonine, arginine, isoleucine and valine, lysine and histidine.

<u>N.H. Luig</u>: "Differential transmission of gametes in wheat in relation to Soviet genetics."

Results obtained by the author when studying single factor differences in wheat (resistance to stem rust and to leaf rust) are compared with those reported by Soviet workers. The former data are highly heterogeneous when statistically analysed, and this includes F2, F3, and F4 single factor segregation ratios. Studying segregation for the same factor pairs but using different parents gave similar differences, and this was true for linked and independently inherited factor pairs. The paper also deals with morphological, physiological and cytological abnormalities in hybrids as well as in homozygous lines and varieties.

J.W. James: "Selection response curves."

The estimation of the rate of decay of response to selection for a quantitative character is illustrated on data from four selection experiments, and the relation of the "rate of decay" to different models of the selective process is considered. The possibility of predicting ultimate limits to selective advance from response in early generations is also examined.

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J.S.F. Barker: "Interspecific competition and population fitness"

Claringbold and Barker have described a model for the estimation of population fitness, which is based on the outcome of competition between a standard tester population of one species and a population of another species whose fitness is to be estimated. This model is similar to others developed to describe interspecific competition, and is similarly unrealistic in ignoring (a) deterministic oscillations in population size, and (b) stochastic fluctuations.

In some experiments, heterogeneity, a reversal of the change in species frequency, and indeterminacy in outcome have been observed. Possible explanations of these in terms of genetic change in the populations, genetic heterogeneity in the founding population, effects of varying population density, and stochastic fluctuations will be considered, as well as the relevance of these experiments to studies of interspecific competition and the estimation of relative fitness of populations.

# Miss C.M. Jacobson: "An examination of X-ray induced apparent phenocopies of scutellar mutants in Drosophila."

Phenocopies of some mutant lines of <u>Drosophila</u>, which have either increased or decreased numbers of scutellar bristles, can be produced by X-irradiation. Both the dosage and the age at which it is given affect the result. However, the actual interruption to normal development produced by X-ray treatment can be shown histologically to differ from that produced by mutation in these cases. To date, the results of this investigation are consistent with those obtained in similar studies on mouse vibrissa number, which were discussed at the last meeting.

Miss B. Kindred: "Selection for canalisation."

A character which is well canalised will be resistant to environmental as well as genetic variation. An attempt is being made to select for good and poor canalisation of (a) scutellar bristles in <u>Drosophila</u> by selecting on response to different temperatures during development, and (b) secondary vibrissae in mice by selecting on symmetry.

<u>M.J. Whitten</u>: "Departure from asymmetry as a measure of genetic variability."

Eye development in <u>Drosophila melanogaster</u> can be altered by the presence (on chromosome II) of a major gene, together with minor modifiers some of which are linked to the major gene. Penetrance of the mutant is dependent on the complement of modifiers present, as well as various environmental factors, such as parental age. Since each eye is independently affected the four possible phenotypic classes can be tested against a model of fluctuating asymmetry. Using this model one can measure the genetic and environmental contributions to phenotypic variance. The method has been used to determine additive genetic variability and hence to assay the efficiency of selection on penetrance of the major gene.

## Miss M.K. Mader and P.A. Parsons: "Finger-print pattern variability."

Based on a survey of finger ridge-counts of unrelated persons of British origin, it has been shown that total ridgecount for the right hand, the left hand, and for the sum of both hands is greater in males than females. However, ridgecount variability is greater in females than males. Similar results occur for triradius counts.

The greater female variability could be a manifestation of the Lyon hypothesis, whereby in females either one of the two X chromosomes is inactivated in different cells of the same individual if it is assumed that polymorphic can linked and (b) stochastic fluctuations.

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The greater female variability could be a manifestation of the Lyon hypothesis, whereby in females either one of the two X chromosomes is inactivated in different cells of the same individual, if it is assumed that polymorphic sex-linked polygenes occur for finger-print patterns.

Comments will be made on finger-print patterns as a useful character for research in physical anthropology and human genetics.

P.A. Parsons: "Linkage in evolution."

Interactions between genes or blocks of genes on the same chromosome and the degree of linkage between them are controlled by natural selection. All variations between extremely tight linkage as in "gene complexes" controlling polymorphisms, and looser linkage as in linked inversion polymorphic systems occur.

Models will be examined for equilibria for two linked loci. It will be shown for certain models that linked interacting systems controlling polymorphisms can be envisaged as covering the whole chromosome, even apart from various mechanisms whereby crossing-over is restricted, such as inversions, localisation of chiasmata and the restriction of recombination to one sex, though interactions over long distances will be relatively rare since natural selection will on the whole favour closer linkage between the interacting loci. The intensity of natural selection will, however, depend on the reproductive potential of the species.

It is but one step to interactions between genes on different chromosomes controlling polymorphisms, where in general interactions might occur so as to minimise the "genetic load."

<u>D.L. Hayman, Miss J.A. Marshall and P.G. Martin</u>: "Morphological and autoradiographic studies of the chromosomes of some marsupials."

Morphological variation of the X chromosome associated with sex chromosome balance and with some other factors is to be described. The synthesis of DNA in all chromosomes has been followed by using tritiated thymidine and autoradiography. This has allowed certain deductions to be made relevant to the morphology of the chromosomes.

M.J.D. White: "Evolutionary loss of chiasmata in grasshoppers."

All grasshoppers previously studied have chiasmata in males (and presumably in females also). These chiasmata are clearly visible at diplotene-diakinesis-first metaphase because of opening-out of the "reductional split" after the end of pachytene.

In members of the African subfamily Thericleinae, there are no recognizable diplotene or diakinesis stages and hence the transition from pachytene to premetaphase I is direct. In the majority of the species chiasmata are revealed about half way through first metaphase, when the reductional split opens out between them. In some species chiasmata are only revealed momentarily, in first anaphase.

In three species of Thericleinae chiasmata seem to be genuinely absent at all stages in the males, although present in the females (the genetic system being apparently as in <u>Droso-</u><u>phila</u>).

It is suggested that in all Thericleinae the "mechanical" function of the chiasmata (holding the chromosomes together in bivalents) is more or less vestigial, in the males. These forms are hence cytogenetically pre-adapted for the final loss of chiasmata which has occurred in the males of three species. O.H. Frankel, Miss S. Lewis and Miss M. Roskams: "Evolution of morphogenetic control in a polyploid system."

In common wheat (<u>Triticum vulgare</u>) normal flower morphogenesis is an invariant character. It is controlled by a factor associated with Q, which in turn controls the "vulgare syndrome". In speltoid mutants, where Q is deleted or inactivated, we have obtained, as previously reported, a range of genetically stable genotypes in which flower morphogenesis is impaired. In certain compactoids this extends in the supernormal direction, with extra flowers in the empty glumes.

In the absence of Q, i.e. in speltoids, two further genetic systems are revealed. Firstly, there is a second (dominant) gene, tentatively called A, in the presence of which all flowers from the <u>second</u> onward, are normal. A is thus an analogue of Q shifted one step up on the spikelet axis. Secondly, there is a complex polygenic system which is capable of producing all intergrades of flower morphogenesis, from completely normal to the virtual absence of flowers. We have recently succeeded in establishing genetically stable lines along the entire fertility/sterility gradient. Normal fertility, it has now been found, can be attained by selection within this system, even in the <u>absence</u> of A.

Flower morphogenesis in vulgare and in the speltoids differs not only genetically, but also physiologically. In vulgare the flower formation is uniformly normal in all experimental environments applied, including drastic heat and radiation shocks; in the speltoid series, frequencies of flower formation are strongly affected by suitable combinations of daylength and temperature applied during the critical period of flower formation.

Thus, in vulgare, flower morphogenesis is buffered genetically against mutation and recombination among a multitude of polygenes, and physiologically against environmental shocks.

It can be readily understood that there can be no more than one canalization factor even in a hexaploid; and it is not surprising that the typical polymeric series have been found in genes conditioning relatively superficial functions. Canalization systems are opportunistic; their transformation in polyploids may shed light on the evolutionary changes in gene function itself.

It had previously been thought that at the diploid level the polygenic system may have been in control of flower morphogenesis, and that canalization by Q evolved at the tetraploid or hexaploid levels, possibly as a result of selection under cultivation, so that the polygenic system could now be regarded as a relic system. Recent experiments have rendered this hypothesis highly improbable. Firstly, we now know that the gene A is located on chromosome 5D, the homeologue in the D genome of 5A, on which Q is located. It does seem plausible that A acted as the canalization factor in the (diploid) D genome, with a shift of action - and hence with ostensible inactivation - in the polyploid state. There is no trace of a corresponding gene in the B genome at the hexaploid level, which we assume is due to the much greater age of the tetraploid association of the A and B genomes.

Further, we now know that the hexaploid <u>T. spelta</u> possesses a canalization factor for flower morphogenesis, though it lacks the gene complex Q of <u>T. vulgare</u>. This is in line with ideas recently expressed by Murumatsu and by Swaminathan on the nature and origin of Q. It also encourages the speculation that In common wheat (<u>Triticum vulgare</u>) normal flower morphogenesis is an invariant character. It is controlled by a factor associated with Q, which in turn controls the "vulgare syndrome". In speltoid mutants, where Q is deleted or inactivated, we have obtained, as previously reported, a range of genetically stable genotypes in which flower morphogenesis is impaired. In certain compactoids this extends in the supernormal direction, with extra flowers in the empty glumes.

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Thus, in vulgare, flower morphogenesis is buffered genetically against mutation and recombination among a multitude of polygenes, and physiologically against environmental shocks.

It can be readily understood that there can be no more than one canalization factor even in a hexaploid; and it is not surprising that the typical polymeric series have been found in genes conditioning relatively superficial functions. Canalization systems are opportunistic; their transformation in polyploids may shed light on the evolutionary changes in gene function itself.

It had previously been thought that at the diploid level the polygenic system may have been in control of flower morphogenesis, and that canalization by Q evolved at the tetraploid or hexaploid levels, possibly as a result of selection under cultivation, so that the polygenic system could now be regarded as a relic system. Recent experiments have rendered this hypothesis highly improbable. Firstly, we now know that the gene A is located on chromosome 5D, the homeologue in the D genome of 5A, on which Q is located. It does seem plausible that A acted as the canalization factor in the (diploid) D genome, with a shift of action - and hence with ostensible inactivation - in the polyploid state. There is no trace of a corresponding gene in the B genome at the hexaploid level, which we assume is due to the much greater age of the tetraploid association of the A and B genomes.

Further, we now know that the hexaploid <u>T. spelta</u> possesses a canalization factor for flower morphogenesis, though it lacks the gene complex Q of <u>T. vulgare</u>. This is in line with ideas recently expressed by Murumatsu and by Swaminathan on the nature and origin of Q. It also encourages the speculation that the flower morphogenetic component of the Q complex may have been an ancient and perhaps the crucial component of what has become the complex supergene Q, which has assumed such a controlling part in the evolution of <u>T. vulgare</u>.