complètement par ses caractères cytologiques au *C. glareolus* européen.

Voici maintenant quelques rectifications de données antérieures et quelques compléments: Chez *Arvicola scherman* Shaw et *Microtus nivalis* Martins, l'identification des hétérochromosomes par Renaud[1] (1938) et Matthey[2] (1938, 1947) était erronée. L'*X* et l'*Y* sont métacentriques et la pré-réduction est constante. Chez *M. orcadensis* Millais, où Matthey[3] (1951) hésitait entre 44 et 46, le nombre diploïde exact est de 46; l'*X* est métacentrique, l'*Y* punctiforme: *M. arvalis*, *M. incertus*, *M. orcadensis* ont exactement la même formule chromosomique et, comme les systématiciens l'admettent, sont des espèces très voisines.

Les Cricetinae néarctiques, *Neotoma floridana* Ord. et *Peromyscus leucopus* Rafin., ont respectivement 52 et 48 chromosomes; les numérations de Cross[4] (1931) sont donc exactes. L'*X* est long, acrocentrique, l'*Y* punctiforme. Cytologiquement, les hamsters du Nouveau-Monde sont donc très éloignés de ceux de l'Ancien-Monde et il semble logique de les placer dans une sous-famille spéciale (Sigmodontinae). Enfin, chez l'*Heteromyidae Dipodomys merriami* Mearns, il y a non pas 86 chromosomes (Cross[1], 1931) mais 70 seulement.

R. Matthey

Laboratoire de Zoologie de l'Université de Lausanne, le 29 juillet 1952.

Summary

Following the new squash-technic of Makino and Nishimura, it is now possible to work more quickly and with more accuracy on the chromosomes of mammals. The author has established the cytological conditions in seven species of Muridae and elucidated some doubtful points belonging 15 other species. *Microtus arvalis*, *M. orcadensis* and *M. incertus* have the same formule and must be considered as very akin. The chromosomic set of *Clethrionomys gapperi* (North-America) doesn't differ from that of *C. glareolus* (Europe). Three genera of Gerbillinae exhibit sex-chromosomes of the type found in palearctic Cricetinae.

By *Arvicola scherman* and *Microtus nivalis* a reinvestigation shows that *X* and *Y* are both metacentric. It seems preferable to put *Neotoma floridana* and *Peromyscus leucopus*, likely with the other genera of nearctic Cricetinae, in a special under-family, for they bear no cytological ressemblance with the true hamsters of the Old World. *Dipodomys merriami*, an Heteromyidae, has 70 and not 86 chromosomes (Cross, 1931).

There is in none species coexistence of pre- and post-reduction, although pictures of chiasmas may be sometimes observed. The conception of Koller and Darlington does not agree with the facts.

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[1] P. Renaud, R. suisse Zool. *45*, 349 (1938).

[2] R. Matthey, J. G. *36*, 73 (1938); Sci. Genet. *3*, 23 (1947).

[3] R. Matthey, R. suisse Zool. *58*, 201 (1951).

[4] J. Cross, J. Morph. *52*, 373 (1931).

Crossing-over between Alleles at the *w* Locus in *Drosophila melanogaster*

Work in this Department in the last few years has had as its main objective the investigation of the relationship between arrangement and function of genes[1]. As a result of this work, it was found among other things that crossing-over between alleles occurs in the mould *Aspergillus nidulans*[2].

The list of reported cases of crossing-over between alleles in other organisms is growing very rapidly, and a pressing question is how general a property of genes this happens to be. In some of the examples available in the literature, the loci investigated were studied thoroughly precisely because in the course of previous breeding experiments unexpected types had been obtained. This is true, e. g., for the *lz* locus in *Drosophila*, perhaps the most completely analysed example of this kind[3]. These *selected* loci cannot be included, of course, in a survey to infer how widespread crossing-over between alleles is. However, the following loci were adequately investigated apparently without previous knowledge of this kind. They constitute, therefore, an *unselected* sample: *S-ast*, *Sb–sbd* and *bx–bxd* (E. B. Lewis[4]), *sn* and *ras* (Ives and Noyes[5]), and *v* (Green[6]) in *Drosophila*; *bi* and *paba* (Roper[7]), and ad_1–ad_3 (Pontecorvo[8]) in *Aspergillus*; *i* (Giles[9]) in *Neurospora*; *G–S* in cotton (Stephens[10]); *R* (Stadler[11]) in maize; and *S* (D. Lewis[12]) in *Oenothera*. Crossing-over between alleles was detected in 10 out of these 13 loci, the negative ones being *ras*, *R* and *S*.

We thought that an ideal *unselected* locus for a search for crossing-over between alleles was *w* in Drosophila: at this classical locus a large number of alleles are known, with distinguishable and pleiotropic effects, suitable closely linked markers can be placed on both sides and the cytological situation does not suggest any peculiarity. As described below we have succeeded in obtaining cross-overs between alleles among the first 5,000 gametes from two heterozygous combinations (w/w^{bl} and w/w^{co}) out of eight tested (w/w^{sat}; w/w^{bf_2}; w^e/w^a; w^e/w^{sat}; w^e/w^{bl}; w^e/w^h, and the two already mentioned) with eight different alleles in all.

The experimental procedure was the following. Indicating with w^x and w^y any two mutant alleles, females of constitution

$$\frac{sc\ w^x\ ec\ cv}{+\ w^y\ +\ +},$$

or of constitution

$$\frac{y\ w^x\ ec}{+\ w^y\ +}$$

were crossed to males $sc\ w^x\ ec\ cv$, or $y\ w^x\ ec$, respectively, and the progeny examined for eye colours different from

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[1] G. Pontecorvo, Biochem. Soc. Sym. *4*, 40 (1950); Advances in Enzymology *13*, 121 (1952); Sympos. Soc. Exp. Biol. *6*, 218 (1952); Advances in Genetics *5* (in the press); Sympos. Soc. Exp. Biol. *7* (in the press). – J. A. Roper, Nature *166*, 956 (1950); Exper. *8*, 14 (1952); Advances in Genetics *5* (in the press).

[2] G. Pontecorvo, Advances in Genetics *5* (in the press). – J. A. Roper, Nature *166*, 956 (1950); Advances in Genetics *5* (in the press).

[3] C. P. Oliver and M. M. Green, Genetics *29*, 331 (1944). – M. M. Green and K. C. Green, Proc. Nat. Acad. Sci. *35*, 586 (1949).

[4] E. B. Lewis, Cold Spring Harb. Sympos. Quant. Biol. *16*, 159 (1952).

[5] P. T. Ives and D. T. Noyes, Anat. Rec. *3*, 257 (1951).

[6] M. M. Green (personal communication).

[7] J. A. Roper, Nature *166*, 956 (1950); Exper. *8*, 14 (1952); Advances in Genetics *5* (in the press).

[8] G. Pontecorvo, Advances in Genetics *5* (in the press).

[9] N. H. Giles, Cold Spring Harb. Sympos. Quant. Biol. *16*, 283 (1952).

[10] S. G. Stephens, Cold Spring Harb. Sympos. Quant. Biol. *16*, 131 (1952).

[11] L. J. Stadler, Cold Spring Harb. Sympos. Quant. Biol. *16*, 49 (1952).

[12] D. Lewis, Heredity *3*, 339 (1949).

those of w^x, w^y or w^x/w^y. In the experimental crosses carried out so far the classification was discontinued after examining about 5000 flies unless at least one new type had arisen among them. In two of the crosses indicated below new types did actually arise and, in order to make sure that they were not accidental, a further large number of progeny was classified. We propose, of course, to re-examine at a later date further progeny from the combinations which gave negative results in the first sample of 5000.

Results of backcrosses of females heterozygous for two white alleles

Genotype of backcrossed females	No. of progeny examined	No. and genotype of unusual types
$\frac{sc\quad w\quad ec\quad cv}{+\quad w^{sat}\quad +\quad +}$	5,000	0
$\frac{sc\quad w\quad ec\quad cv}{+\quad w^{bl}\quad +\quad +}$	38,225	3 *sc* males 2 $\frac{sc\ +\ +\ +}{sc\ w\ ec\ cv}$ females
$\frac{sc\quad w\quad ec\quad cv}{+\quad w^{bf_2}\quad +\quad +}$	5,000	0
$\frac{sc\quad w\quad ec\quad cv}{+\quad w^{co}\quad +\quad +}$	21,067	2 *sc* males 3 $\frac{sc\ +\ +\ +}{sc\ w\ ec\ cv}$ females
$\frac{y\quad w^e\quad ec}{+\quad w^a\quad +}$	5,000	0
$\frac{y\quad w^e\quad ec}{+\quad w^{sat}\quad +}$	5,000	0
$\frac{y\quad w^e\quad ec}{+\quad w^{bl}\quad +}$	4,881	0
$\frac{y\quad w^e\quad ec}{+\quad w^h\quad +}$	4,847	0
	89,020	10

It will be noted that out of 89,020 flies examined the ten which have a wild-type allele are all cross-overs between *sc* and *ec*. If the wild-type allele had arisen independently of crossing-over, we would have expected only one in twenty to be cross-overs, the map distance between *sc* and *ec* being 5·5. Furthermore, in each cross not all the cross-overs should be of one type. Even without this, the probability of our results being due to accidental coincidence of back-mutation and crossing-over is exceedingly small. We can conclude that crossing-over is not independent, and is probably the cause, of the origin of the wild-type allele in the two crosses given above. It is to be noted, furthermore, that not one case of origin of the wild-type allele without crossing-over has been obtained in the 89,020 flies examined: clearly the rate of back-mutation is not unduly high.

These preliminary results only show that crossing-over between certain alleles at the *w* locus occurs and is correlated with the origin of a new allele. We are now continuing an extensive search with other combinations, particularly of alleles with intermediate effects from which it is hoped to be able to distinguish phenotypically both reciprocal types of recombinant. Should it be possible to exclude unequal crossing-over, this new addition to the list of *unselected* loci where crossing-over between alleles has been observed, would further support the idea that this is a very widespread property of genes[1].

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Department of Genetics, University of Glasgow, July 14, 1952.

Zusammenfassung

An einem besonders günstigen Beispiel (*w*-Locus von *Drosophila melanogaster*) soll zur Klärung der Frage beigetragen werden, wieweit Crossing-over zwischen Allelen ein allgemein genetisches Phänomen darstellt. Es wurden vorläufig 8 heterozygote Kombinationen von 8 Allelen geprüft, wobei die Chromosomen mit *sc*, *ec*, *cv* oder *y*, *ec* markiert waren. Bisher wurden Ausnahmetiere (Entstehung neuer Allele) bei w, w^{bl} und w, w^{co} gefunden, und zwar 10 von 59292 Fliegen. Da alle 10 Fliegen gleichzeitig Crossovers zwischen *sc* und *ec* sind, entstehen die Ausnahmetypen offenbar durch Crossing-over und nicht durch Rückmutation. Weitere Versuche sind jedoch nötig, um sicherzustellen, dass es sich nicht um ungleiches Crossing-over handelt.

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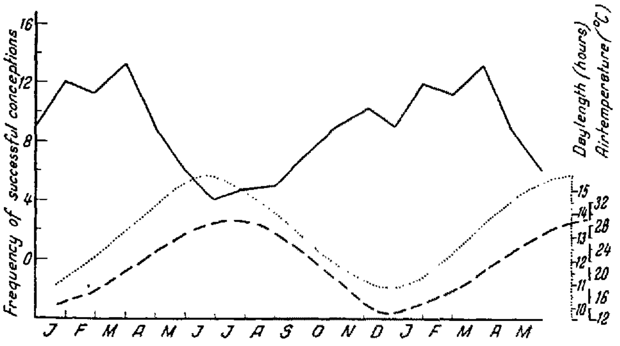
[1] G. PONTECORVO, Sympos. Soc. Exp. Biol. 7 (in the press).

Frequency of Successful Conception under Free Mating Conditions in the Egyptian Buffaloes

Seasonal changes in the conception percentage has been recorded in many species; i.e. in monkeys (CORNER[1]), in mares (HAMMOND[2]) and in ewes (YEATES[3]). In cattle, environmental temperature affects reproduction (ANDERSON[4]), while daylight is also an important factor in this respect (MERCIER and SALISBURY[5]).



Frequency of successful conceptions in the buffalo in relation to air temperature and daylength (30°N).

——— Frequency of succesful conceptions.

· · · · Daylength (hours).

- - - - - Air temperature (°C).

The number af animals used in the present investigation was 772 female buffaloes ranging in age from 2 to 10 years. These observations were recorded at a breeding farm in the North of Delta. The animals were fed green fodder during winter months and concentrates during

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[1] G. W. CORNER, Amer. Scientist. *39*, 50 (1951).

[2] J. HAMMOND, Nature London *153*, 702 (1944).

[3] N. T. M. YEATES, Nature London *160*, 429 (1947).

[4] J. ANDERSON, Ist. int. Congr. Physiol, Path. Reprod. Milano (1948).

[5] E. MERCIER and G. W. SALISBURY, J. Dairy Sci. *10*, 747 (1947).