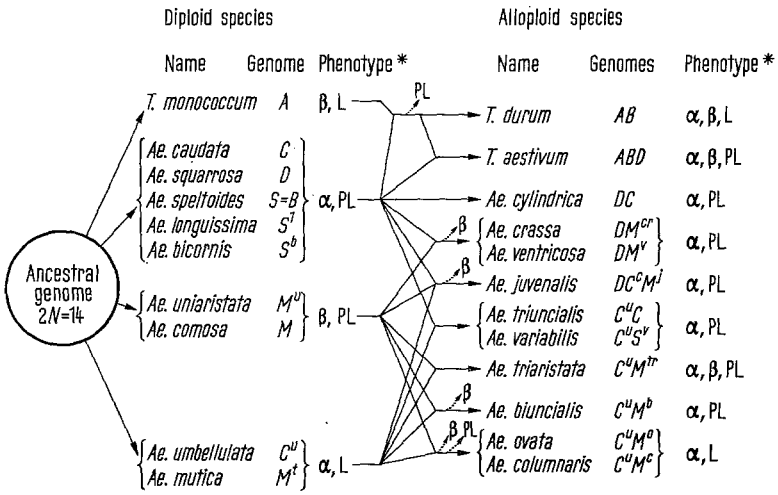
linoleate (PL) systems for β-sitosterol esters synthesis has been also recorded.

In diploid species, all 4 possible combinations of purothionin and sterol esters phenotypes are present. This points to heterogeneity within the α and β purothionins, but further characterization of purothionins from these species must wait until enough material is grown.

In alloploid species where the parental genomes have genetic information for electrophoretically different purothionins, the coexistence of the α and β forms is not always observed. A similar observation can be made with the β-sitosterol ester systems. It seems that duplicate genetic activity for similar systems represents an adaptive advantage but not necessarily a physiological one. Consequently redundant systems might be lost in the course of evolution following alloploid formation. It is to be noted that all observed losses affect the additional genomes and not the so-called pivotal genomes. This is consistent with the cytogenetical observation that pivotal genomes are completely homologous with known diploids, while the additional genomes are extensively modified and only partially homologous with diploid analyzers.



* Purothionin α or β; sterol esters PL *(palmitate-linoleate)* or L *(linoleate)*

Cytogenetical relationships in *Aegilops-Triticum* species and distribution of purothionins and β-sitosterol esters systems.

Resumen. En *Triticum durum* Desf. (genomios *AB*), el genomio *A* controla la sintesis de purotionina β y el genomio *B* la de purotionina α. Las especies diploides del grupo *Aegilops-Triticum* sintetizan α ó β, pero no las dos. En numerosos aloploides de este grupo se observa la pérdida de la actividad sintética para la purotionina correspondiente a uno de los genomios.

P. Carbonero and F. García-Olmedo

Instituto Nacional de Investigaciones Agronómicas, Madrid-3 (Spain), 2 June 1969

Complement with 38 Chromosomes in Two South American Populations of *Rattus rattus*

Since the appearance of technical improvements for chromosomal study, most papers dealing with the complement of the rat have been devoted to *Rattus norvegicus*[1-12]. On the other hand, only the recent report from Yosida[13] has analyzed the number and chromosomal morphology in *Rattus rattus*. From those papers it can be concluded that, although both varieties of rats exhibit chromosomal polymorphism, 42 seems to be the diploid chromosome number for *R. norvegicus* and *R. rattus*.

The present paper deals with 2 populations of *R. rattus*, having chromosome morphology and a diploid number different from those described in *R. norvegicus* and *R. rattus*.

Material and methods. A total of 16 animals (3 ♂ and 13 ♀) collected in Punta Lara, Province of Buenos Aires (Argentina) and the environs of São Leopoldo, State of Rio Grande do Sul (Brasil) were studied.

The animals were injected with 1 ml of a 0.04% colchicine solution and 3 h later were sacrificed. Chromosome spreads from bone marrow, spleen and testes were prepared as described elsewhere[10-12]. In each animal no fewer than 10 metaphases from each one of the tissues processed were analyzed.

Results and discussion. The 16 specimens of *R. rattus* studied had a diploid number of 38 chromosomes. The analysis of the complement showed the existence of 9 pairs of metacentric, 3 pairs of subterminal, and 7 pairs of acrocentric chromosomes. Although *X*-chromosomes were difficult to identify with accuracy, it could be determined that they were second or third in size among the acrocentric elements. The *Y*-chromosome was the smallest acrocentric chromosome of the set (Figure 1).

[1] S. Makino and T. C. Hsu, Cytologia *19*, 23 (1954).
[2] J. H. Tjio and A. Levan, Hereditas *42*, 218 (1956).
[3] P. H. Fitzgerald, Expl. Cell Res. *25*, 191 (1961).
[4] P. C. Nowell, S. Ferry and D. H. Hungerford, J. natn. Cancer Inst. *30*, 687 (1963).
[5] M. Vrba, Folia biol. *10*, 75 (1964).
[6] G. Dowd, K. Dunn and W. C. Moloney, Blood *23*, 564 (1964).
[7] W. O. Rieke and M. R. Schwartz, Anat. Rec. *150*, 383 (1964).
[8] T. H. Yosida and K. Amano, Chromosoma *16*, 658 (1965).
[9] N. Takagi and S. Makino, Chromosoma *18*, 359 (1966).
[10] N. O. Bianchi and O. Molina, Naturwissenschaften *53*, 590 (1966).
[11] N. O. Bianchi and O. Molina, J. Hered. *57*, 231 (1966).
[12] N. O. Bianchi, Cytologia *31*, 276 (1966).
[13] T. H. Yosida, A. Nakamura and T. Fukiyama, Chromosoma *16*, 70 (1965).

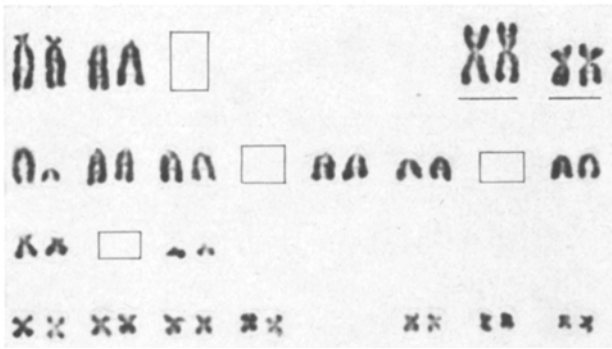


Fig. 1. Karyotype of male *R. rattus* with 38 chromosomes. The first pair in the second row are the *XY* chromosomes. Squares point out the absence of pairs 3, 6, 9 and 12 of *R. norvegicus*; underlined pairs are the new chromosomes not observed in *R. norvegicus* (compare with karyotype in Figure 2).

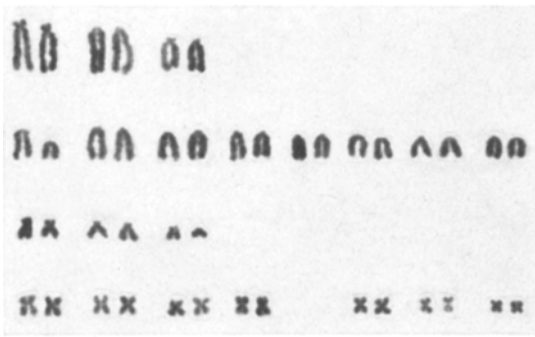


Fig. 2. Karyotype of male *R. norvegicus* with 42 chromosomes. The first pair in the second row are the *XY* chromosomes (chromosomes are arranged according with NOWELL et al.[4]).

Since no *R. rattus* with 42 chromosomes was found, we decided to compare the karyotype of our sample with the karyotype of a sample of *R. norvegicus* collected in a neighbouring area. Consequently, chromosome spreads from 5 wild *R. norvegicus* (2 ♂ and 3 ♀) trapped in La Plata city (Province of Buenos Aires) were prepared and studied. Diploid number in these animals was 42. Karyotypes were constructed according to the system proposed by NOWELL et al.[4] (Figure 2).

The comparison of the 2 complements showed that the karyotype of 38 chromosomes differed from that of 42 in the following features: (a) absence of the subterminal pairs 3 and 12; (b) absence of 2 pairs of acrocentric chromosomes of the group 4–10; (c) existence of 2 pairs of large metacentric chromosomes (Figures 1 and 2).

The diploid number of 42 chromosomes is probably the most general for rats. Therefore, it is possible to assume that the complement of 38 chromosomes has arisen from that of 42 by means of a process of chromosomal rearrangement, the following being the most probable mechanism: (a) deletion of the short arms of pairs 3 and 12, or alternatively, pericentric inversion transforming the subterminal 3 and 12 chromosomes into acrocentric elements; (b) centric fusion between the rearranged pairs 3 and 12 and 2 pairs of acrocentric chromosomes.

The external appearance of our specimens does not seem to differ from that habitually described in *R. rattus*. However, the lack of animals with 42 chromosomes prevented us from determining whether or not the 2 types of *R. rattus* have the same phenotype.

Finally, the existence of a similar chromosome complement in 2 *R. rattus* populations separated by more than 1200 km poses a very interesting question: Is the *R. rattus* with 38 chromosomes widespread all over the South American continent? Further rat samplings involving different regions of South America will be necessary to answer the question.

Resumen. Se estudiaron los cromosomas de 16 ejemplares de *Rattus rattus* provenientes de la Provincia de Buenos Aires (Argentina) y del Estado de Rio Grande do Sul (Brasil). En todos los animales el complemento estuvo formado por 38 cromosomas. Considerando que en las ratas el complemento de 42 cromosomas es probablemente el mas generalizado, se sugiere que el complemento de 38 cromosomas ha derivado del de 42 mediante un proceso de reordenamiento cromosómico con fusión céntrica.

N. O. BIANCHI[14], J. PAULETE-VANRELL[15] and L. A. DE VIDAL RIOJA[14]

Comisión de Investigaciones Científicas de la Provincia de Buenos Aires, La Plata (Argentina) and Universidad de São Leopoldo, Facultad de Filosofía, Ciências e Letras, São Leopoldo (R. G. do Sul, Brasil), 3 March 1969

[14] Comisión de Investigaciones Científicas de la Provincia de Buenos Aires, La Plata (Argentina).

[15] Universidad de São Leopoldo, Facultad de Filosofía, Ciências e Letras, São Leopoldo (R. G. do Sul, Brasil).

Properties of Mycobacteriophage C2[1]

Mycobacteriophage C2 was isolated by MANKIEWICZ[2] in 1965 from sputum of a patient with alveolar cell carcinoma. This communication describes studies on the morphology, nucleic acid characterization of C2 and phage-*Mycobacterium smegmatis* relationship.

Experimental. Phage C2 and its host, *M. smegmatis*, strain ATCC 607, were supplied by Dr. E. MANKIEWICZ. Electron microscopy: phage was propagated on ATCC 607 grown in YOUMANS and KARLSON[3] medium, purified by differential centrifugation and suspended in 1% ammonium acetate. A drop of phage suspension or phage-infected bacterial culture was placed on a Formvar-carbon-coated grid, and negatively stained with 2% neutral potassium phosphotungstate (PTA). Specimens were examined with a Phillips EM 200 electron microscope. Nucleic acid studies: phage C2 was propagated, harvested and purified by the method of SELLERS and RUNNALS[4] modified by the use of RVA agar medium[5] instead of Leventhal's agar. Acridine orange staining of phage nucleic acid was done by the procedure of MAYOR and HILL[6]. Phage DNA was extracted with phenol at room temperature, purified[7] and its infectivity tested against *M. smegmatis*, BCG, *C. hoffmani*, *E. coli* and mouse L cells. DNA concentration was measured by spectrophotometry (Beckman DB-G) and diphenylamine reaction[8] and its buoyant density in CsCl was kindly