tilis (L.) from Russia[4,5]. However, counts of 120 and 156 were later reported for the same species from Holland and Italy respectively[6,7]. Wide variation in chromosome number was also reported for *Entosphenus reissneri*, with counts of 94–96[8] and 165–174[9]. These discrepancies either represent true geographic variation in chromosome number or errors on part of the investigators. The possibility that these variations result from polyploidy was discussed by POTTER and ROTHWELL[3]. Aside from these two problems, the numbers of chromosomes in lampreys are beginning to show definite trends. The following species are allied by sharing high chromosome numbers: *Lampetra zanandreai*, $2n = 142$[7]; *L. planeri*, $2n = 146$[7]; *L. aepyptera*, $2n = 164$[2]; *P. marinus*, $2n = 168$[3]; and now *I. gagei*, $2n = 164$. Two species of lampreys from Australia, *Mordacia praecox* Potter[1] and *M. mordax* (Richardson)[10], have low diploid counts of 76.

Thus, Northern Hemisphere lampreys tend to have very high diploid chromosome numbers (142–168) and no, or very few, metacentric-submetacentric chromosomes; conversely, Southern Hemisphere lampreys have relatively low numbers (76) and many metacentric-submetacentric chromosomes. In addition, the chromosomes of the Southern Hemisphere lampreys[1,10] are roughly twice the size of the Northern Hemisphere species[2,3]. It was suggested that the high chromosome numbers of Northern Hemisphere lampreys were derived by polyploidization[2,3,11]. If this is the case, an ancestral Northern Hemisphere lamprey with a polyploid number of 140 to 170 acrocentric-telocentric chromosomes, may have invaded the Southern Hemisphere, subsequently undergoing karyotypic evolution involving centromeric fusion. This would have produced a karyotype of metacentric-submetacentric chromosomes, longer-sized chromosomes, and a low diploid number similar to that found in today's Southern Hemisphere lampreys.

The specimens used in this study were preserved and deposited in the University of Alabama Ichthyological Collection, catalogue Nos. 3370–3375.

Résumé. L'étude des chromosomes somatiques d'une lamproie de l'Amérique du Nord, *Ichthyomyzon gagei* Hubbs and Trautman montre que l'equipement chromosomique diploide est composé de 164 chromosomes, qui sont acrocentriques ou télocentriques et très petits (moins de 3,5 µm). Il n'y a pas de différences entre le karyotype de *I. gagei* et celui de *Lampetra aepyptera* (Abbott). Les rapports de *I. gagei* avec les autres lamproies et l'évolution du caryotype sont examinés.

W. M. HOWELL[12] and C. R. DUCKETT

Department of Biology, Samford University, Birmingham (Alabama 35209, USA), 7 August 1970.

[11] S. OHNO, V. WOLF and N. B. ATKIN, Hereditas *59*, 169 (1968).
[12] This research was supported by Samford University Research Fund, Grant No. 20, to HOWELL.

Some Observations on the Cytology of Induced Interchanges in *Sorghum*

The occurrence of plants with chromosomal interchanges in grain sorghums ($2n = 20$) have been reported among the progenies of haploids[1–3]. These studies were limited to observations on post-pachytene stages of meiosis. In the grain *Sorghum* variety I.S. 84, the pachytene stage of meiosis was found favourable for detailed study, which prompted the present study of induced interchanges. Dry seeds of this variety were irradiated with γ-rays at 10, 20, 30, 40 and 50 Kr at B.A.R.C., Bombay, and were sown directly in field plots. All the plants that survived and reached maturity were examined cytologically for chromosomal aberrations, employing standard acetocarmine technique.

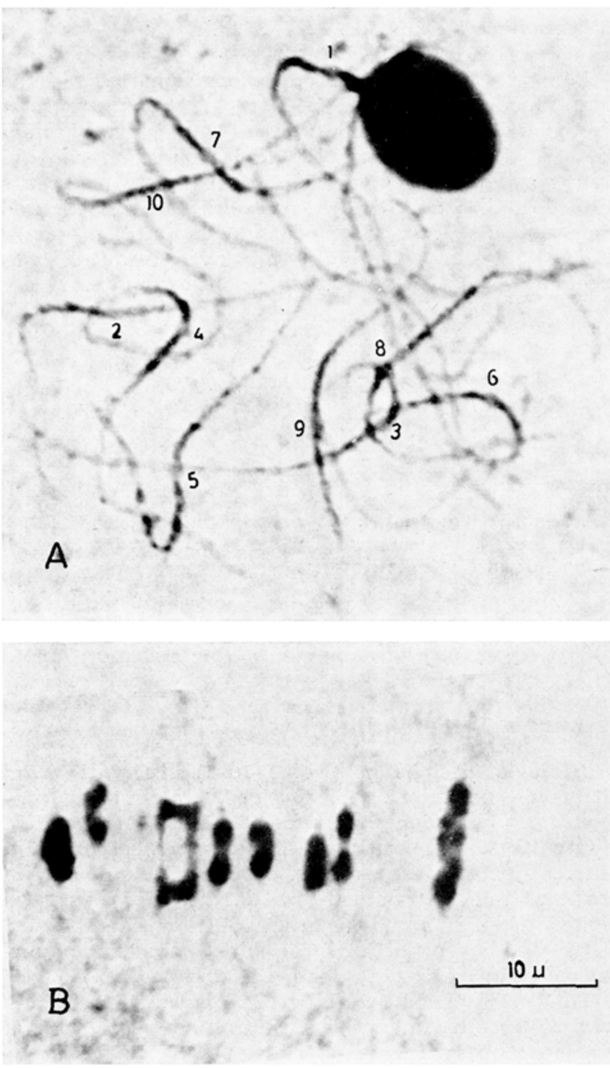
Figure A depicts the pachytene stage in the untreated material. The 10 differentiated pachytene bivalents can be traced, end to end, and basically they conform to the pattern observed originally in *S. subglabrescens*[4] and in other grain sorghums[5]. The ten chromosome types were given reference numbers 1–10 in the order of decreasing length. Most of the chromosome types can be recognized on the basis of total length, arm ratio, degree of heterochromatinization and the presence of conspicuous chromomeres on specific loci. The longest chromosome is the nucleolar chromosome (No. 1). Chromosome 2 has submedian centromere. Chromosome 6 has a subterminal and 7 a submedian centromere. All the remaining chromosomes (3, 4, 5, 8, 9 and 10) have approximately median centromeres.

Cytological screening of about 500 treated plants led to the isolation of 2 plants, each with a single reciprocal translocation and another heterozygous for 2 translocations. In each of these plants no fewer than 10 pachytene and 100 metaphase I cells were studied. In the plant with single interchange (No. 1–10–5) observations on analyzable pachytene cells revealed 'cross-shaped' configurations involving chromosomes 6 and 7. Appreciable variability in the position of the cross was observed in different pairing associations. However, the points of breakage were determined to lie in the heterochromatic regions of short and long arms of the chromosomes 6 and 7. Consequently, 1 of the 4 paired arms of the interchange complex at pachytene was observed to be very much shorter, thereby limiting the frequency of chiasma formation in it. As expected, the formation of chain of 4 at metaphase I was observed in 63% of the cells examined. A ring of 4 was realized in 8% of the cells at this stage and the rest forming only bivalents.

In the second plant (No. 1–11–3) the nucleolar chromosome was observed to form a pairing association with chromosome 10 of the complement. Judging from pachytene configurations it can be ascertained, that the translocation break points lie approximately in the middle of the long arm euchromatic regions of both the chromosomes. Analysis at metaphase I revealed, 39% of the cells with a ring of 4 and 21% with a chain of 4 chromosomes. The remaining 40% formed only bivalents.

[1] J. E. ENDRIZZI and D. T. MORGAN JR., J. Hered. *46*, 201 (1955).
[2] K. F. SCHERTZ, Crop Sci. *3*, 445 (1963).
[3] V. R. REDDI, Cytologia *35*, in press (1970).
[4] J. VENKATESWARLU and V. R. REDDI, J. Ind. Bot. Soc. *35*, 344 (1956).
[5] M. L. MAGOON and M. S. RAMANNA, Caryologia *14*, 391 (1961).

In the third plant (No. 1–16–3) heterozygous for 2 reciprocal translocations, the chromosomes involved, could not be numbered with accuracy because of the difficulty in obtaining completely analyzable cells at pachytene. The occurrence of 2 symmetrical 'cross-shaped' configurations in some of the cells examined, suggests, that 2 different pairs of non-homologous chromosomes with median centromeres have undergone interchanges in this plant. At metaphase I, 1 or 2 rings of 4 were observed in 76% of the cells (Figure B). The formation of 1 or 2 chains of 4 occurred in 15% of the cells while the remaining 9% formed only bivalents. The orientation of rings and chains of 4 was adjacent or alternate. Occasionally, 1 of the rings on the metaphase plate showed a diamond shaped configuration which may lead to irregular segregation of chromosomes (Figure B). Only 16% of the cells showed alternate orientation and 75% mostly adjacent orientation of rings and chains of 4. On an average 20% of pollen grains were observed to be well filled and normal which is only slightly greater than the frequency of cells showing alternate orientation.



A) Pachytene stage in I.S. 84 untreated plant. B) Metaphase I in plant No. 1-16-3, showing 2 rings of 4 chromosomes and 6 bivalents.

On the other hand, the 2 plants with single translocation formed a higher proportion of viable pollen grains. To a large extent, this appears to be due to increased number of cells forming bivalents only. The present findings seem to agree with those of ENDRIZZI and MORGAN[1] and differ considerably from the results reported in other translocation heterozygotes of *Sorghum*[6].

The recovery of a plant in the treated material with 2 interchanges, reported here, will be of particular interest and indicates the possibility of developing multiple translocation stocks for their use in current cytogenetic studies of *Sorghum*[7].

Zusammenfassung. Es wurden die induzierten Chromosomenbrüche durch Röntgenbestrahlung von Sorghumsamen und die Translokationen in der Meiose der Pollenkörner untersucht.

V. R. REDDI, E. V. V. BHASKARA RAO and D. PURNACHANDRA RAO

Department of Botany, Andhra University, Waltair (India), 27 July 1970.

[6] C. C. HUANG, J. G. ROSS and H. D. HAENSEL, Can. J. Genet. Cytol. *5*, 227 (1963).

[7] We are thankful to Prof. J. VENKATESWARLU for facilities and encouragement and to Council of Scientific and Industrial Research (New Delhi) for financial assistance to two of us (E.V.V.B.R. and D.P.R.).

Chromosome Complement of the European Wild Pig (*Sus scrofa* L.)

Chromosomes of the European Wild Pig have been studied by several authors. In 1966 MCFEE et al.[1] reported for the Wild Pigs in Tennessee (which were imported in 1912 from Germany) a diploid number of $2n = 36$ and a chromosome complement containing 4 pairs of acrocentric and 13 pairs of meta- and submetacentric autosomes. However, they also found that 27% of the animals studied had 37 chromosomes, which they postulated to have resulted from the entry of domestic breeding into the wild herd. Their findings were confirmed by RARY et al.[2] who studied animals from the same area in Tennessee, and by GROP et al.[3] whose specimens came from 4 different localities in Germany.

Such chromosome complement differs from the complement of the Domestic Pig which has a diploid number

[1] A. F. MCFEE, M. W. BANNER and J. M. RARY, Cytogenetics *5*, 75 (1966).
[2] J. M. RARY, V. G. HENRY, G. H. MATSCHKE and R. L. MURPHREE, J. Hered. *59*, 201 (1968).
[3] A. GROP, D. GIERS and U. TETTENBORN, Experientia *25*, 778 (1969).