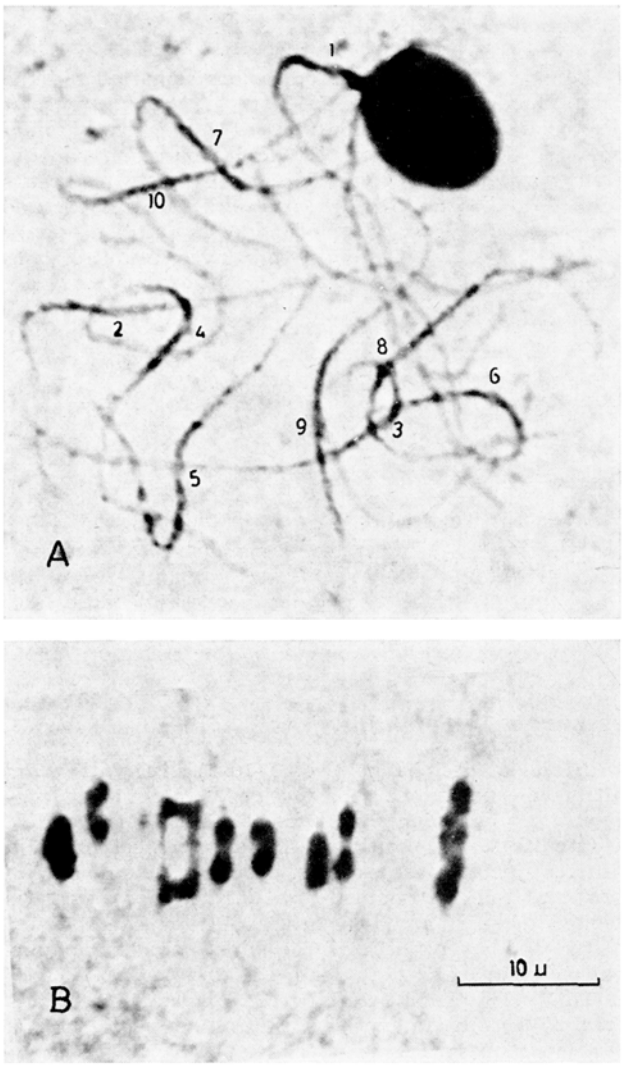
In the third plant (No. 1–16–3) heterozygous for 2 reciprocal translocations, the chromosomes involved, could not be numbered with accuracy because of the difficulty in obtaining completely analyzable cells at pachytene. The occurrence of 2 symmetrical 'cross-shaped' configurations in some of the cells 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.

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[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

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[3] A. GROP, D. GIERS and U. TETTENBORN, Experientia *25*, 778 (1969).

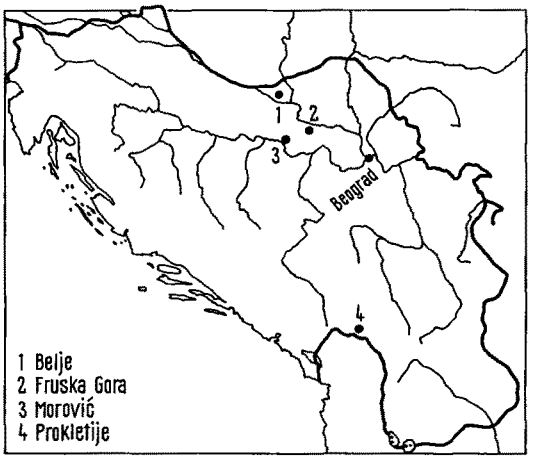

Fig. 1. Map of the locations where samples were taken.

$2n = 38$ and consists of 6 pairs of acrocentric and 12 pairs of meta- and submetacentric autosomes[4–8]. The authors previously mentioned suggested that during the process of domestication one centric fission occurred and was followed by a preferential selection of the 38-chromosome type.

Recently we analyzed chromosomes of the several (9) specimens of Wild Pig belonging to 4 populations from different parts of Yugoslavia (Belje; Morović; Fruška Gora; Prokletije; Figure 1). The animals studied were shot in the wild and metaphase plates were obtained from primary cultures of heart, testis, lung, and kidney tissues, and from a leukocyte culture as well. All analyzed specimens had chromosome complements with diploid number $2n = 38$, characterized by the presence of 6 pairs of acrocentric and 12 pairs of meta- and submetacentric autosomes (Figures 2 and 3), in every detail identical to the chromosome complement of the Domestic Pig. They were also identical with the chromosome

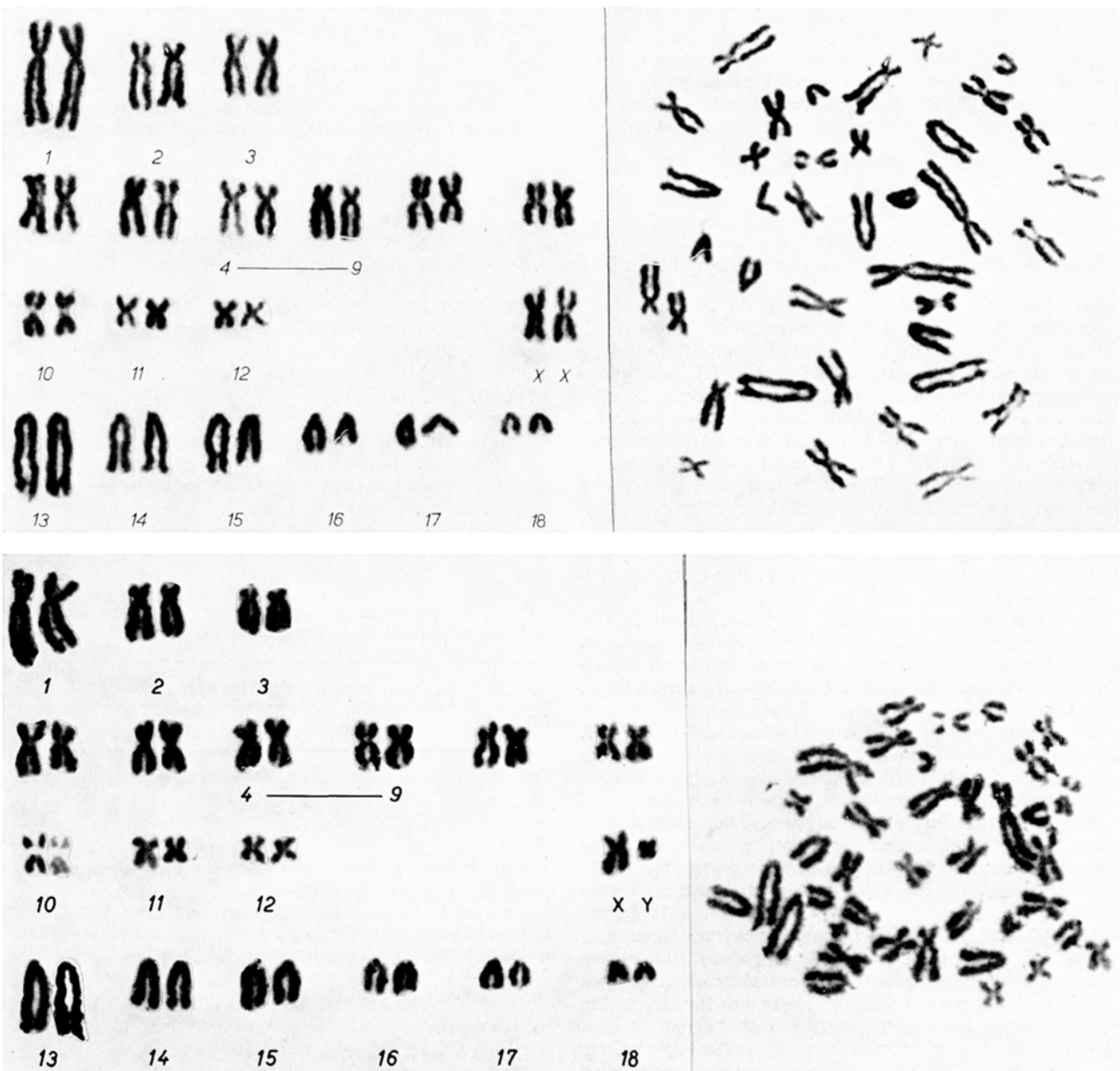

Fig. 2 and 3. Metaphase plate and karyogram of a female and a male wild pig (*Sus scrofa* L.).

complement of the Wild Pig from Japan (*Sus vittatus leucomystax*), according to the findings of MURAMOTO et al.[9].

Since at least one of our samples came from the area in which a chance for a cross with domestic breed never existed (Prokletije – the area inhabited by Moslems who for religious reasons never raised pigs), the differences between chromosome complements of Balkan Wild Pig populations and those from Germany suggest a case of intraspecific chromosomal polimorphysm with at least 2 chromosomal types ($2n = 36$ and $2n = 38$). There is little doubt that Domestic Pig originated from the 38-chromosomes type which inhabits southern and eastern parts of Europe and probably most of Asia. Further studies are necessary to find out the exact areas of the 36- and 38-chromosomes types and to shed more light on the nature of the Robertsonian changes which caused this variation[10].

Résumé. Le complément chromosomique des sangliers des régions de l'Est et du Sud de la Yougoslavie est caractérisé par un nombre diploïde $2n = 38$ et il est composé de 6 paires d'autosomes acrocentriques et de 12 paires d'autosomes méta- et submétacentriques, ce qui signifie qu'il est identique au complément du porc domestique et qu'il diffère du complément chromosomique des sangliers d'Allemagne. Il est évident qu'il s'agit là d'un cas de polymorphisme chromosomique intraspécifique avec au moins deux types de nombre diploïde ($2n = 36$ et $2n = 38$) résultant des variations de Robertson. Il est très probable que le porc domestique tire son origine d'un type à 38 chromosomes.

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[10] We thank to the managers of 'Jelen' and 'Morović' Game Preserves through whose kind cooperation the studied animals were provided.

Autoradiographic Evidence for a Thymidine Precursor Pool in the Root of *Allium cepa*

In order to determine the possible presence of a thymidine precursor pool in the onion root (*Allium cepa*), the regional pattern of DNA synthesis was followed by means of a tritiated-thymidine (^{3}H-TdR) continuous labeling procedure coupled with autoradiography.

Methods. A commercial onion bulb (*Allium cepa* L., $2n = 16$) was grown in a vial of tap water at room temperature until the growing roots reached a length of approximately 2 cm. The bulb was then transferred to a solution of ^{3}H-TdR with a concentration of 5 μC/ml (specific activity 6.25 C/m*M*), and representative root were removed and fixed in Carnoy's fixative following a 24 h continuous label in ^{3}H-TdR and after 1, 8, and 20 h chase periods in unlabeled tap water.

The roots were embedded and sectioned longitudinally at a thickness of 8 μm and stained by the Feulgen method[1]. All the autoradiograms were prepared by the stripping-film method[2], incubated at 4 °C in the dark for 10 days, and developed together.

The percentage of labeled nuclei was determined in the meristem and in the elongation region. Nuclear grain counts were determined in autoradiographs for each chase interval in the respective regions with the aid of a quadrille-reticle having 400 squares. Grain counts were corrected for background by counting, in each autoradiograph nearest each of the regions under study, the number of grains in a known area of film with no underlying root tissue.

Results. The percentage of nuclei showing incorporation of ^{3}H-TdR in the meristem and elongation region is shown in Table I. Note that for every chase period, greater percentages of nuclei are labeled in the elongation region as compared to the meristematic region. It is of particular interest that in the meristematic region there is a pronounced elevation in the percentage labeled nuclei preceding a progressive decline. It can be seen from Table II, that for each chase interval the average nuclear grain count of the elongation region is significantly higher than that of the meristematic region. Furthermore, with increasing chase periods the nuclei of both regions show a progressive increase in grain counts.

Discussion. One might predict a continual decrease in the percentage labeled nuclei in the meristematic region due to division and displacement of nuclei by the growing meristem. The initial rise in percent labeled meristematic nuclei (Table I) is interpreted as evidence for the presence

Table I. The percent of nuclei labeled after exposure to ^{3}H-TdR for 24 h and subsequent exposures to unlabeled medium

Amount of time in unlabeled medium (h)	Nuclei labeled (%)	
	Meristem	Elongation
0	75[a]	87
1	90	99
8	82	86
20	69	85

A minimum of 6 roots were utilized for each interval.
The 0 h sections correspond to roots exposed to ^{3}H-TdR for 24 h and sacrificed immediately after. The 1, 8, and 20 h sections correspond to roots subsequently exposed to unlabeled medium for 1, 8, and 20 h. [a]

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