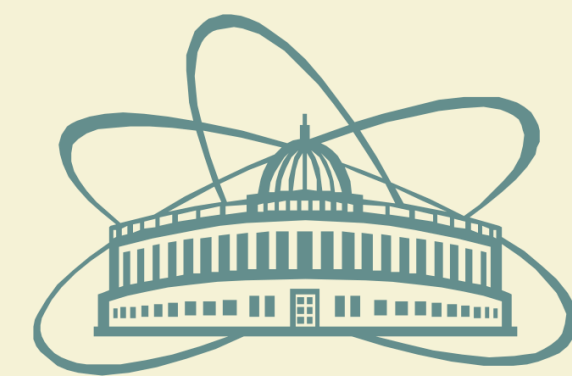


Radiation genomic research in the Laboratory of Nuclear Problems



AUTHORS N.E. Kharchenko, K.P. Afanasyeva, M.V. Alexandrova, I.D. Alexandrov

ORGANIZATION Joint Institute for Nuclear Research, Dubna, Moscow reg. Russia.

INTRODUCTION

In the modern world, living organisms are increasingly exposed to various sources of radiation. This is facilitated by the use of radiation in medicine, civil and military industries, as well as the presence of a radiation background in nature. The increased risk of genetic damage to living organisms makes radiobiological research more actual. And the simplest and most suitable object is the fruit fly (fig. 1).

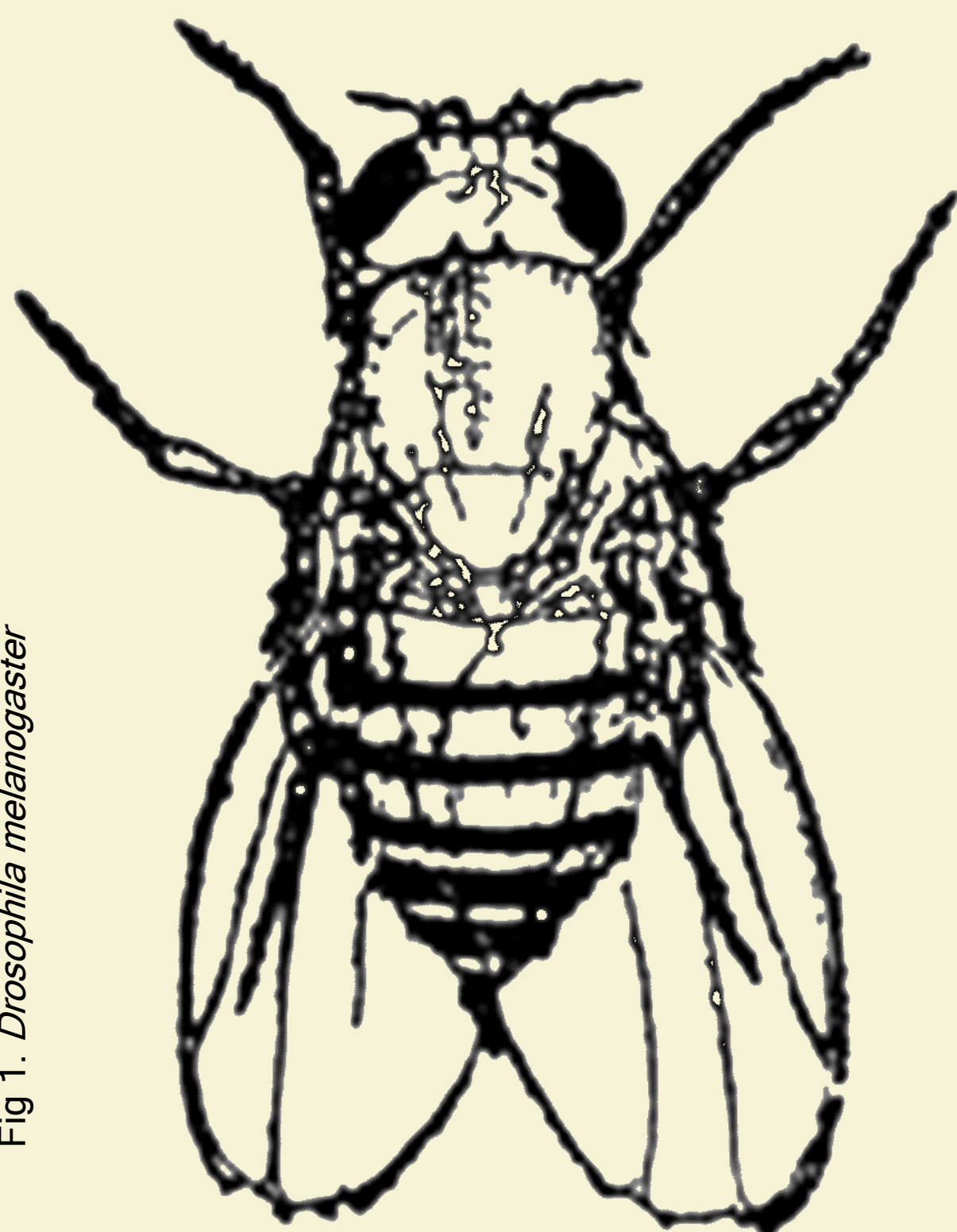


Fig 1. *Drosophila melanogaster*

METHODOLOGY

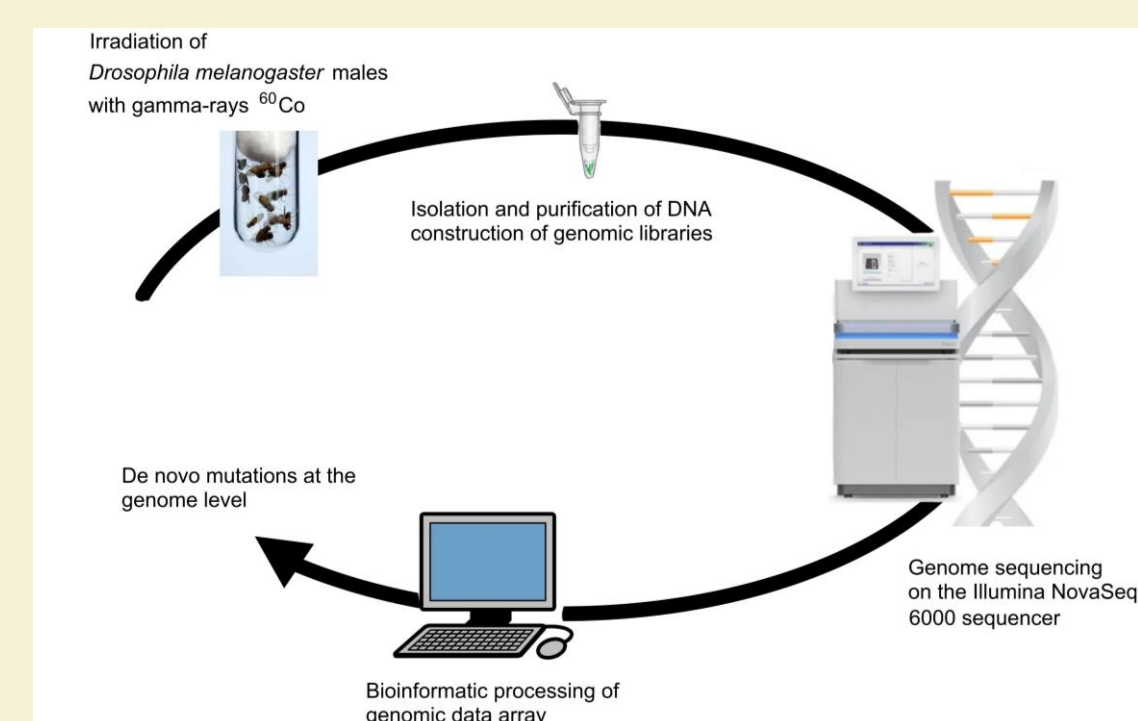


Fig. 2. Stages of experiment

To study the genomic changes under conditions of a homogeneous genetic genotype, the isogenic line of *Drosophila melanogaster* constructed by our group was used. Irradiation of males was carried out on a ROKUS-M machine. The source: ^{60}Co γ -rays, the dose: 40 Gy. DNA was isolated from individual F_1 flies of the offspring of control and irradiated males according to the protocol we developed. DNA library preparation and sequencing were performed on the basis of Ldt Evrogen. Bioinformatics analysis was performed in collaboration with the Clinical Bioinformatics Laboratory. See Fig. 2.

RESULTS At this stage of the bioinformatics analysis of the data, five types of changes have been identified: small deletions (size from 29 to 543 p.n.), extended deletions (size 3618 and 71462 p.n.), inversions, duplication and translocation. At the same time, only small deletions (130 and 100 bp, respectively) were detected in control samples 1 and 2. The frequency of occurrence of this type of change is 0.66 per 1 gene. In the induced samples, small deletions were also observed, but their frequency is 2.33 per genome, which is 3.5 times higher than in the controls. Small deletions in induced samples predominate. However, 4 remaining types of changes are also observed (large deletions, inversions, translocations and duplications). The absence of such changes in the control makes it possible to assume their true radiation nature. In total, in one radiation-induced mutant, up to 8 lesions of one type or another localized in one or different chromosomes were observed. The number and type of changes for each sample, see fig. 3. Their localization and distribution over the genome, see fig. 4.

	Control			Irradiated								
	C1	C2	C3	1	2	3	4	5	6	7	8	9
Small deletions	1	1		7	2		1	1	3	5		2
Extended deletions							2					
Inversions				1								
Translocations					1		1		1	1		
Duplications						1	2		1			

Fig. 3. The number and type of changes for each sample

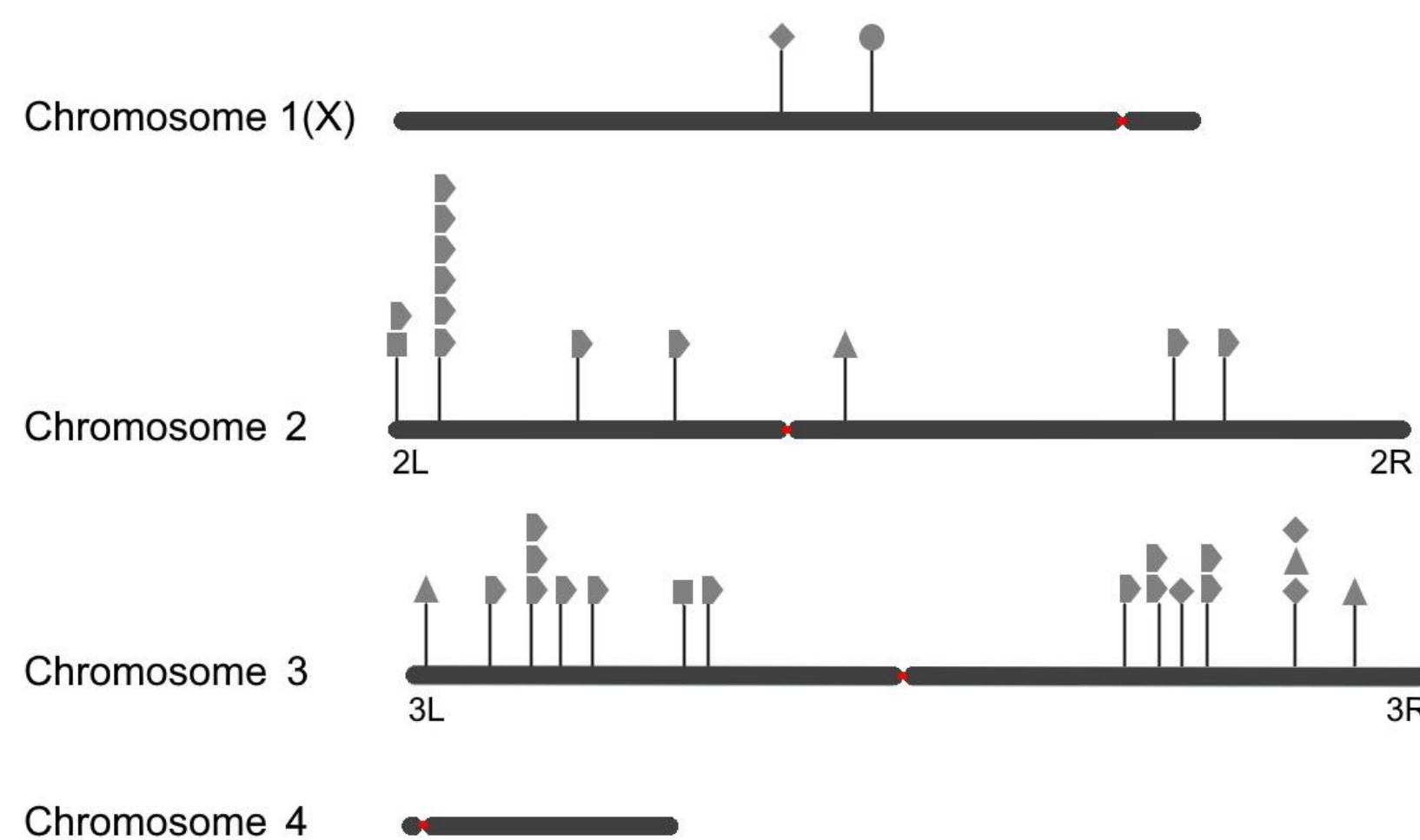


Fig. 4. Localization and distribution of the changes over the genome

CONCLUSION

The methods chosen in the experiment, correctly selected protocols and high-quality execution made it possible to successfully conduct a pilot experiment.

To a first approximation, we can say that

1. Radiation increases the occurrence of small deletions by 3.5 times.
2. Such types of changes as large deletions, inversions, duplications and translocations are characteristic of radiation mutagenesis.

PROSPECTS FOR FURTHER RESEARCH

1. Continued bioinformatics analysis of minor DNA changes (base substitutions, indels).
2. An increase in the sample of the control and gamma-induced groups to obtain not only a qualitative picture, but also quantitative dependences.
3. Conducting experiments with neutrons and carbon ions to reveal the role of various types of radiation in mutagenesis at the genome level.