

EPIGENETIC CHROMATIN MODIFICATIONS IN *BRASSICA* GENOMES

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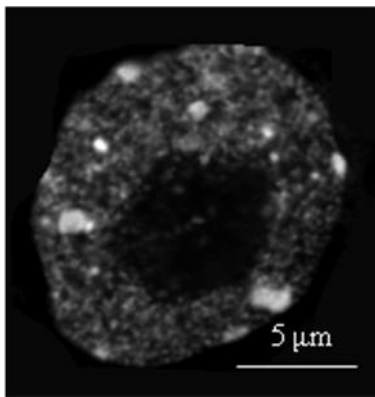


Fig. 1. Chromocenters in *B.rapa* interphase nucleus

1. Introduction

Posttranslational histone modifications have significant influence on spatial chromatin structure, thus play a crucial role in chromatin condensation and the expression of genetic information. Histone modifications are highly conserved among eukaryotes, although nuclear distribution of these modifications vary between different species [1]. Histone methylation and acetylation are the main epigenetic modifications, which influence chromatin condensation [2]. Hence, confocal microscopy was applied to determine chromatin structure in interphase nuclei of *Brassica* species, which differ in genome size, ploidy level and nuclear phenotype.

2. Methods

Immunostaining method with specific antibodies were applied for three *Brassica* species, two diploids and one allotetraploid. Fluorescence of DAPI and Alexa 488 was registered using an Olympus FV1000 (Olympus, Poland) confocal system equipped with an Olympus IX81 inverted microscope. Axial series of 2D fluorescence images of optical sections through nuclei (z-stacks) were collected using two separate photomultipliers (R6357, Hamamatsu, Japan).

3. Results

Analysis of spatial distribution of several forms of methylated and acetylated histone H3 and H4 revealed, that some of these modifications are specific only for euchromatin or heterochromatin (chromocenters), while others are specific for both types of chromatin within one species. Additionally, differences between species were found. The Z-stacks analysis allowed us to establish precise localization of every examined modification.

4. References

- [1] J. Fuchs, D. Demidov, A. Houben and I. Schubert, Chromosomal histone modification patterns – from conservation to diversity, *Trends in Plant Science*, **11**: 199-208 (2006).
- [2] Z. Jasencakova, A. Meister, J. Walter and I. Schubert, Histone H4 acetylation of euchromatin and heterochromatin is cell cycle dependent and correlated with replication rather than with transcription, *Plant Cell* **12**: 2087-2100 (2000).