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GENETIC PARTICULARITIES OF POPULATIONS OF DIANTHUS ARENARIUS IN BALTIIC REGION AND BELARUS

Genetic diversity of populations reflects their adaptation to environmental conditions and its knowledge helps to choose appropriate protection measures for rare and endangered species. Dianthus arenarius is endangered perennial plant species, included in Annex II of the European Council Habitats Directive 92/43/EEC as well as in the Latvian endangered plant list. In Latvia, Lithuania and Belarus D. arenarius create a complex of several perennial subspecies. In this research genetic particularities of D. arenarius populations were studied in two aspects: genetic diversity within and between different localities and diversification of localities on plants chromosome level, including endopolyploidy. In total, 505 D. arenarius mature leaf samples were collected in 2015 and 2016 in middle of June from 12 localities in Baltic region and Belarus: 8 sampling sites from Latvia, 3 from Lithuania, and 1 from Belarus. Leafs were dried in silica gel and kept till analysis. For investigation of genetic diversity retrotransposon based markers iPBS were applied. 51 primers previously effective on different eukaryote species were tested and 3 of them which represent higher level of polymorphism were used for further population’s characterisation. Differences in genetic variation between localities within and between countries were shown. Determination of DNA content (C-value) level of individual cells in leaves of mature plants was performed by the BD FACSJazz® cell sorter (BD Biosciences, USA) with flow cytometer function. Samples for flow cytometry were prepared with the DNA staining kit (Sysmex Partec, PI Absolute, GmbH, Germany), cells nuclei were stained with 10 μL propidium iodide. Cell counting events were triggered by forward-scattered signal. The excitation of the cell fluorescence was made by 488 nm Coherent Sapphire Solid State (blue) laser. Flow cytometry analysis of DNA content in D. arenarius leaves from different localities revealed presence of several relative fluorescence peaks from 2C up to 18C. Differences between localities regarding endopolyploidy were found.

TRANSGENERATIONAL EFFECTS OF THE PLANT INSIDE AND OUTSIDE CHERNOBYL ZONE

The research was directed to provide fundamental aspects of understanding adjust of the metabolic pathways in living cells under chronic irradiation in contaminated by radioactive isotopes Chernobyl zone and inheritance its influence aftermath at outside on clean site. More than 30 years were passed after Chernobyl catastrophe on sequence there surrounding lands remain heavily contaminated by long-living radioactive isotopes for many years to come. A number of studies addressed numerous questions about changes in metabolic processes running by irradiated plants. For instance these include: genome hypermethylation, up regulation of antioxidant system, signal transduction system, adjusted of reparation enzymes, etc. Nevertheless, there is still no common understanding of how different metabolic pathways are playing together as a coordinated ensemble on the whole plant system level. Thus complex studies of Chernobyl grown plants using post genomic methodologies such as genomics, transcriptomics and proteomics might provide detailed insight into the biochemistry of living plant cells under influence chronic ionizing radiation.

This research identified some genetic changes during eight generation grown plant soybean and flax and a set of differentially synthesis proteins of the plants as results of adaptation toward increased level of