for feed. Salinity is one of the major abiotic environmental stresses, which affect on plant life and significantly reduces crop yield. It is known that under the action of salt stress a number of morphological and cytogenetic changes in cells cultured *in vitro* occurs. The aim of the work is to study the effects of salt stress on cytogenetic structure of cell populations of callus cultures of winter triticale using sodium chloride as a stressor.

The materials for studies were callus cultures derived from shoot apex explants of 3-day-old sterile seedlings of winter hexaploid triticale line 38/1296. Calli were planted on the modified Murashige Skoog medium containing sublethal concentration of sodium chloride 1.2 % established in our previous studies. Callus cultures grown on the medium free of NaCl as stress factor was a control. The cytogenetic analysis was carried out on calli culturing on 5th–7th day during I, III and VI passages. Passage duration was 21 days. Pressed temporary samples were prepared according to standard procedures. On average 100-150 metaphase and anaphase plates were analyzed in each variant of the experiment. Cytogenetic effect of NaCl on the triticale tissue culture was determined by the change in the ratio of cells of different ploidy levels, frequency of chromosome aberrations and mitotic abnormalities.

Resulted from the research in calli cultivated on the selective medium a significant increase in the number of aneuploid, diploid and tetraploid cells was detected. Also the appearance of haploid and pentaploid cells was observed. A significant difference between the control and experiment in portion of triploid cells was not detected, and polyploid cells almost were never found. The presence in the medium of sublethal concentrations of sodium chloride resulted in increased frequency of chromosomal aberrations, mainly as chromatid bridges and fragments. There were also isolated cells from multiple disorders, i.e. those which contained simultaneously both fragments and bridges. Disturbances of mitosis were mainly presented by multipolar mitoses and lagging chromosomes. In addition, at the sublethal concentration of NaCl the part of cells with micronuclei increased being a character of apoptosis, genomic instability and a significant indicator for genotoxic effect of sodium chloride on cells.

Thus, we have observed effect of salt stress on cytogenetic structure of cell populations of callus cultures of winter triticale during six passages in culture using sodium chloride as a selective agent. Cytogenetic analysis showed a high degree of heterogeneity and significant differences in cytological processes between callus cells that were grown on selective vs. control media. It was established that sublethal concentration of sodium chloride has clastogenic effect (chromosome aberrations) and causes turbagenic disturbances (lagging chromosomes, multipolar mitoses and binuclear cells) in callus cells of triticale. Analysis of genetic structure of cell populations cultured under sublethal concentration of the sodium chloride has demonstrated significant increase in aneuploidy and frequency of segregation to wheat and rye subgenomes as well as prevalence of cell populations with reduced number of chromosomes.

Модель внезапной экспансии – ограничение применения в сложных ситуациях

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При исследовании демографической истории для оценки времени увеличения численности вида на той или иной территории нередко используется модель внезапной экспансии (Rogers and Harpending, 1992). Степень чувствительности этой, достаточно простой, модели к нарушению изначальных допущений, в частности, к подразделенности популяции, остается неясной.

Модель внезапной экспансии тестировалась нами в ситуации, когда современная популяция образуется в результате смешения двух прежде изолированных популяций. Подобная ситуация является реалистичной и может возникнуть, например, во время

послеледникового расширения ареала, когда изолированные во время оледенения рефугиальные популяции испытывают рост численности и за счет увеличения скорости миграции/колонизации образуют смешанные популяции. Симуляции были проведены в программах fastsimcoal2 (ver 2.5.2.21) и Arlequin 3.1 с использованием параметров, соответствующих оценке демографической истории *Sorex araneus* L, 1758 (Mammalia, Lipotyphla).

Оценка времени экспансии (τ) демонстрирует бифазную зависимость от времени разделения популяций (*t*) и оказывается несколько завышенной при невысоких *t* и существенно заниженной в случае, если *t* достаточно велико. Несмотря на то, что в последнем случае распределение попарных нуклеотидных дистанций оказывается мультимодальным, тесты Таджимы и Фу указывают на рост численности, а raggedness index и SSD не позволяют отвергнуть модель внезапной экспансии. По нашему мнению, при оценке времени экспансии популяции модель внезапной экспансии должна использоваться с осторожностью в тех случаях, когда можно подозревать смешанное происхождение популяции.

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Sudden expansion model: limitations in complex situations

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To analyze the demographic history of populations researchers routinely employ the sudden expansion model (Rogers and Harpending, 1992). However, it remains unclear to what extent the model is robust to violation of the underlying assumptions, and, in particular to the presence of population subdivision.

We tested the performance of the sudden expansion model and the mismatch distribution analysis in a situation where the contemporary population originates as result of mixing between two ancestral populations that evolved in isolation for a certain time. Such scenario is realistic if we consider the post-LGM range expansion when glacial-refuge populations undergo demographic expansion and produce mixed populations due to increased migration/colonization rate. The simulations were performed in fastsimcoal2 (ver 2.5.2.21) / Arlequin 3.1 using model parameters that corresponded to estimated demographic history of *Sorex araneus* L, 1758 (Mammalia, Lipotyphla).

The results of the simulations indicate that the estimate of the expansion time (τ) shows a biphasic dependence on the time of divergence between the ancestral populations (*t*). The expansion time is slightly overestimated for younger *t* but is substantially underestimated for larger *t*. Although in the latter case the mismatch distribution is pronouncedly bimodal neither raggedness index nor the SSD test reject the sudden expansion model while the neutrality statistics (Fu's S and Tajima's D) are significantly negative. As a conclusion, we suggest that the results of the mismatch distribution analysis should be treated with caution if the population admixture is plausible.

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