

ABSTRACT&REFERENCES

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**THE DEPENDENCE OF THE
SYNTHESIS OF MELANIN BY BLACK
YEAST *PSEUDONADSONIELLA BRUNNEA* ON THE
NUMBER OF COAL SOURCES IN THE CULTURE
MEDIUM**

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The aim of the study was to determine the effect of carbon source content in the culture medium on melanin synthesis by black yeast *Pseudonadsoniella brunnea* 470 FCKU.

Materials and Methods: Cultivation of *Pseudonadsoniella brunnea* strain was carried out on liquid nutrient medium, the main component of which was barley-malt extract. The concentration of the carbon source (carbohydrates) in the barley-malt extract solution was set at 2.0; 4.0; 6.0 and 8.0 % for the AST-2 areometer-sugar meter. 0.05 % L-tyrosine and 1 % peptone enzymatic were added to

these media. 0.05 % L-tyrosine and 1 % peptone enzymatic were added to these media. The acidity of the media at the level of 1–1.5 was carried out using sulfuric acid.

Result. Studies have shown that the amount of synthesized melanin by a strain of black yeast fungi *Pseudonadsoniella brunnea* 470 FCKU depends on the amount of carbon source in the culture medium. The amount of melanin synthesized by the *Pseudonadsoniella brunnea* strain increased by 5.8 and 5.1 times, with a decrease in the content of reducing sugars in the culture medium by 2 and 4 times, respectively.

Conclusions: Cultivation of *Pseudonadsoniella brunnea* 470 FCKU strain at low pH and carbon source content results in its protective function in the form of melanin release into the culture medium. The highest amount of melanin (394.03 mg/l) by strain *Pseudonadsoniella brunnea* was synthesized when carbon source was introduced into the culture medium at a concentration of 4.0 % by hydrometer, which corresponds to the content of 2.4–2.52 % reducing sugars (predominantly maltose)

Keywords: black yeast, melanin synthesis, optimal cultivation conditions

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DEVELOPMENT OF ANEXPRESS-METHOD FOR INFLUENCE AND GENOTYPING OF H1N1 AND H7N9 VIRUS AVIAN INFLUENZA A STRAINS BY PCR-RFLP ANALYSIS

p. 9–20

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Epizootic monitoring in recent years suggests that the highly pathogenic avian influenza A virus (H1N1) and (H7N9) actively circulate in the Eurasian countries. By 2016–2019 1.6 thousand outbreaks were recorded. For 2016–2019, 1.6 thousand cases of outbreaks were recorded. Of these, there are 872 cases in Europe. The monitoring of infected birds, both migratory and poultry, in places of cross-contact in Ukraine is relevant for preventing outbreaks of epizooties.

The aim of the study. To develop an express method for the identification and determination of bird flu virus A H1N1 and H7N9 strains, based on a polymerase chain reaction with analysis of restriction fragment length polymorphism (PCR-RFLP) of the virus RNA.

Results and discussion. The *in silico* analysis of the HA, NA, and NP gene amplicons allowed *in silico* to calculate the primers to the variable loci of the investigated genes, to calculate the reaction conditions, to determine restriction sites for the restriction enzyme to obtain theoretical PCR electrophoreograms. An express method for the detection and identification of influenza A H1N1 and H7N9 virus by three genes (HA, NA, and NP) of H1N1 and H7N9 RNA in polymerase chain reaction, combined with RFLP analysis, was developed. The method of rapid diagnostics is able to detect avian influenza virus A H1N1 and H7N9 and differentiate it from samples of other pathogens of viral infections of birds and animals. It was established, that the PCR-RFLP rapid diagnostic method is able to detect influenza A virus RNA of H1N1 and H7N9 strains with high sensitivity (100 % sensitivity).

Conclusions. The developed method of PCR-based rapid identification, combined with RFLP analysis, makes it possible to significantly simplify the method of identification due to specific amplification of an RNA region having a polymorphic restriction site. Testing of this locus is possible by pre-PCR and restriction of the amplified fragment. The method of express – diagnosis of PLR-RFLP has been established for detecting RNA virus influenza A of high pathogenic H1N1 and H7N9 strains with high indicators of sensitivity (100 % sensitivity)

Keywords: highly pathogenic avian influenza A virus H1N1, H7N9, express – diagnostic method for PCR-RFLP, conservative motifs, variable loci, polymorphism

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- DOI: 10.15587/2519-8025.2019.179207**
- INTRODUCTION AND ADAPTIVE CAPACITY OF PITTOSSPORUM TENUIFOLIUM GAERTN. IN CONDITIONS OF PROTECTED SOIL**
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The aim of the research – to study the complex of biological parameters and physiological specificity of plants of *P. tenuifolium* Gaertn variety as criteria of their adaptive possibilities under new conditions. Many researchers considered problems of adaptation under conditions of industrial interiors of separate varieties and groups of plants. Information, concerning the adaptive potential of varieties of Pittosporum genus is very limited. There are only brief reports about biological peculiarities of separate varieties of the genus under conditions of introduction (Tumak, Palamar 2007; Bojko, 2015, 2016, 2018; Larsen, 1979; Tranguillini, 1964).

As far as such studies for *P. Tenuifolium* variety are practically absent, problems of studying adaptive abilities of plants of this variety become especially urgent. In this connection plants of this variety were chosen as the **object** of the research. The phonological, comparative, morphological and anatomic research **methods** of were used in this work.

According to the results of phonological observations, plants of *Pittosporum tenuifolium* variety demonstrated adaptive changes, characterized by the period of forced rest and variation of terms and duration of this period, conditioned by keeping conditions.

The comparative analysis of morphometric parameters of a sprout and leaf of plants, growing in interiors with different microclimatic conditions, revealed morphological changes, manifested in rates of annual growth, number of young leaves and their sizes, internode length. The anatomic construction of a leaf demonstrated the thickness increase of the adaxial epidermis by 32,5 %; thickness decrease of a leaf by 8 %. There was established the unessential increase of palisade coefficient, accompanied by redistribution between spongy and columnar mesophyll to the latter side. Adaptation at the physiological-biochemical level was manifested by changes of the quantitative content of pigments and their ratios under conditions of industrial interior.

Conclusions. The assessment of ecological-biological, morphological-anatomical and physiological peculiarities of plants of *Pittosporum tenuifolium* variety revealed adaptive changes, characterized by forced rest, variation of occurrence terms and duration of this period; morphological-anatomical changes in the sprout and leaf construction; change of the quantitative content of pigments and their ratios. The established changes favored the re-

sistance increase of *Pittosporum tenuifolium* plants under changed keeping conditions

Keywords: *Pittosporum tenuifolium*, adaptation, leaf, sprout, rest, anatomical structure, pigments, stability

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CYTOGENETIC EFFECTS IN CANCER PATIENTS LYMPHOCYTES DEPENDING ON THE RADIATION SOURCE AND THE LOCALITY OF RADIATION EXPOSURE IN EXPERIMENT EX VIVO

p. 25–31

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Aims: Estimation of the cytogenetic lesions yield and their distribution among cells in donor lymphocytes of cancer patients with different tumor localizations depending on the source of radiation and the locality of radiation exposure in a therapeutically significant dose in ex vivo experiment.

Methods: Cytogenetic analysis was performed in lymphocytes of 30 oncogynecological patients, lung cancer patients and head and neck cancer patients before the start of radiation treatment. Whole peripheral blood was irradiated at 2 Gy dose with a further simulation of partial body irradiation using gamma-irradiation ^{60}Co on the ROKUS-AM and megavolt irradiation on the linear accelerator Clinac 600C.

Results of research: An increase of radiation-specific chromosome damage frequency after gamma- and megavolt irradiation of cancer patients' lymphocytes at 2 Gy dose was shown. With the absence of dependence on the tumor localization the statistically significant excess of the chromosome exchanges level due to irradiation on linear accelerator in compare with gamma-irradiation was found. At 2 Gy dose point with a simulation of partial body irradiation a similar dependence on the applied source was observed. So, the increase of the chromosome type aberrations level was due to 2,5-fold increase of the dicentric and ring chromosomes number under the gamma-irradiation and 5-fold under megavolt irradiation. For local irradiation simulation for both sources the chromosome aberrations level significantly exceeded the values of the zero point, and the dicentrics distribution among cells was over-dispersed according to Poisson statistic.

Conclusion: Cytogenetic studies in ex vivo experiment showed that in donors' lymphocytes, regardless of the tumor location, megavolt irradiation demonstrated a more genotoxic effect in compare with gamma-irradiation. The data obtained indicated that the proposed test experiment of ex vivo irradiation with partial body radiation simulation can be successfully used to detect the fact of irradiation and to confirm, if present, its locality. The study results will contribute to the improvement of the radiobiological basis of cancer patients' radiation treatment and can be of use for the development of approaches to the individualization of therapeutic irradiation

Keywords: chromosome aberrations, cancer patients, lymphocytes, ex vivo experiment, partial-body simulation, gamma-irradiation, megavolt irradiation on linear accelerator

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- BIODIVERSITY OF THE STEPS OF THE LYSA HORA - AN ELEMENT OF THE REGIONAL ECOLOGICAL NETWORK OF THE ODESSA REGION**
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The article presents the results of studies of phytochemical diversity of the steppe tract Lysa Hora – an element of the regional ecological network of the Odessa region. The purpose of the study is to evaluate the ecological role of phytobiots of the Lysa Hora steppe tract, in particular in the spread of phytodiversity for the balanced development of the territory.

Methods. For the analysis of phytobiots classical methods researches were used. Identification of plant species was performed according to the relevant determinant (Definitior ..., 1987). The biomorphological structure of species of higher vascular plants is represented by the linear system of life forms of V.M. Golubev (1972) and K. Raunkier (1934). The ecological structure of plant groups was determined by NI Basilevich (1986), ecological-phytocenotic structure - according to A.D. Belgard (1950). The data collected during the field surveys were processed using the spreadsheet program Microsoft Excel and Statistica 7.0.

Research results. An assessment of the ecological role of the steppe tract of the Lysa Hora is given, according to the main ecological indicators: species richness, incidence and abundance of phytobiots. According to the results of our research, it has been established that 210 species of higher vascular plants belonging to 112 genera and 37 families occur in these territories. Most species of phytobiots belong to the Asteraceae – 17.1 %, Fabaceae and Lamiaceae – 11.4 %, Poaceae – 8 % to the leading families. The top ten genera of the spectrum also include the families Rosaceae, Scrophulariaceae, Rubiaceae, Brassicaceae, Boraginaceae, Plantaginaceae. In the spectrum of biomorphs, herbs are dominated by herbaceous plants – 50.1 %, perennials – 29.5 %. The location of the buds of renewal relative to the soil substrate is dominated by hemicryptophytes – 35.2 %, the proportion of terophytes is 29 %, phanerophytes – 5.2, geophytes – 4.2, chameophytes – 1.4 %. The habitat of rare and endangered species of higher vascular plants, which indicate the value of the Lysa Hora steppe tract in floristic terms, has also been established.

Conclusions. Steppe Tract Lysa Hora as an integral part of the regional eco-network, despite significant anthropogenic transformation, remains an important link in the spread of phyto-diversity and conservation of biota

Keywords: ecological network, steppe tract, anthropogenic transformation, ecological structure, Red Book of Ukraine

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