

in many species has created great interest in diatoms as a source of biofuels. The aim of this study is to research a lipid producing diatom strain *Nitzschia communis* for flat-plate photobioreactor cultivation and determine the effect of different cell disruption methods on the lipid yield. *N. communis* (Marex number: 10S152) was collected for a European 7th Framework project titled; “Exploring Marine Resources for Bioactive Compounds: From Discovery to Sustainable Production and Industrial Applications (MAREX)” from Aegean Sea in Turkey and identified by molecular and morphological methods. The sequence data were submitted to NCBI database (GenBank Accession Number: JQ886460). *N. communis* cells were grown in 6 L flat-plate photobioreactor containing 5500 mL of F/2 medium under the light intensity of $95 \mu\text{mol photons m}^{-2} \text{s}^{-1}$ at $22 \pm 2^\circ\text{C}$ with the air flow rate of 8 L/min for 14 days. The growth rate and biomass productivity were determined at the end of the batch production process. Three different cell disruption methods (sonication, bead milling and homogenization treatments) were evaluated for the lipid extraction yield. The lipid concentration was determined gravimetrically.

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Maximizing biomass and bioactive molecule yields of *Padina pavonica* to determine seaweed-based products for industrial applications



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The objective of this study, which is supported by an EU Project (MAREX) was to investigate the growth and bioactive molecule yields of native brown seaweed species, *Padina pavonica*, which distributed along the coast of Turkey. Collected *Padina* individuals were placed in the growing vessels where a total of 12 treatment groups were applied in the laboratory. Growth rates of *Padina* were measured daily and presented as percentage. All data were analyzed using MEANS Procedure and represented as mean \pm sd. Biomass and extraction yields differences between the treatment groups were analyzed using Duncan's Multiple Comparison Test in SPSS statistic program and the values are ≤ 0.05 were accepted as significant. *P. pavonica* growth was found to be quite manageable for production. The highest biomass yield was recorded as $6.15 \pm 1.47\% \text{ day}^{-1}$ and the highest extract yield was found to be $16.88 \pm 2.80\%$ among the experimental treatment groups. From the result of the study, it was concluded that *P. pavonica* can be produced via biotechnological processes or optimized culture conditions in a sustainable program with the aim of developing *Padina*-based agents to the stage where they are available for various industrial applications.

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The combined effect of copper and salinity on the physiological and biochemical parameters of wheat (*Triticum aestivum* L.) cultivars



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Identification of tolerant to the combined effect of copper and salinity wheat varieties is very important, because heavy metal contamination and salinization due to irrigated agriculture is a big problem in Kazakhstan. Objective of the work was to study of separate and combined effect of copper and salinity (NaCl (0.25 mM) + CuSO₄ (50 mM)) on biomass, relative water content (RWC), proline content of 5 wheat varieties in hydroponics cultured conditions. For RWC and proline content were taken tolerant (Kazakhstanskaya rannaya), average tolerant (Kazakhstanskaya-3), sensitive (Shagala) wheat varieties. Wheat varieties on biomass accumulation by the shoots under combined effect of copper and salinity varieties arranged in the following order (% to control): Kazakhstanskaya rannaya (53%) > Kazakhstanskaya-3 (50%) > Meltur (33%) > Shagala (32%). RWC in the leaves of Kazakhstanskaya rannaya variety decreased by 8%, Kazakhstanskaya-3 – by 16%, Shagala – by 27%. On proline content amount of proline varieties arranged in the following order (% to control): Kazakhstanskaya rannaya (53%) > Kazakhstanskaya rannaya (707%) > Kazakhstanskaya-3 (516%) > Shagala (419%). RWC and proline content were greater in tolerant varieties than in sensitive.

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Physiological and biochemical features of *Cannabis ruderalis* in the Chui valley



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Currently, biochemical markers became widely used as method of the selection, taxonomy. Including genetics perspective plants of *Cannabis ruderalis* is also studied not well enough. The purpose of the research study of the genetic heterogeneity of different populations of cannabis using biochemical markers is the component composition of proteins, enzymes and DNA heterogeneity. Seeds of *C. ruderalis* were used as objects of study. Seeds were collected in the Chui valley. We selected 10 plants at each point of these plants and analyzed the structure of the harvest. Seed samples of the plants were analyzed with biochemical markers. Component composition of peroxidase, nonspecific esterase, amylase, acid phosphatase, soluble proteins, peptides and DNA of hemp seed varieties were studied under the study. The most heterogeneous composition was detected in the soluble proteins and polypeptides. Component composition of amylase was not so heterogeneous – only 4 ingredients were identified. But their location was sort-specific. Peroxidase spectrum consisted of 1–6 components. However, the difference between varieties by spectrum of this enzyme was greater than other markers enzymes were used. Thus, we show the differences between the varieties in composition of peroxidase, soluble proteins and peptides.

Especially differences were identified among varieties of amylase composition.

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Microclonal propagation of the rare species of the rubber plant tau-saghyz (*Scorzonera tau-saghyz* Lipsch. et Bosse)



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Rubber plant Tau-saghyz (*Scorzonera tau-saghyz* Lipsch. et Bosse) belongs to the family Asteraceae, a rare, endemic species with a reduced amount. This is a perennial plant 25–40 cm high, with the powerful branching caudexes and deep rod root. The content of rubber in roots is about 20–40% of the dry weight of roots it depend on an age and a cultivar. It was established that the physiological statement of explants and compound of a medium influence on an efficiency in vitro cultivation. A rapid multiplication rate could be obtained from leaf explants by combining the phytohormones in MS medium. Addition of GA to MS medium containing BA and NAA resulted in an increase in mean numbers as well as mean length of the shoot. It implies that cytokinin in combination with GA and auxin plays vital role in organogenesis and further regeneration from leaf explants of *S. tau-saghyz*. This is the first report in *S.-saghyz* with protocol for direct organogenesis and regeneration from leaf explants. Our protocol has great potential for rapid multiplication, propagation and conservation of rare species *S. tau-saghyz* Lipsch. et Bosse and also for creation a collection of Tau-saghyz, representing scientific and commercial interest.

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Transgenic expression of rotavirus capsid protein (VP7) in alfalfa for edible vaccine



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Rotavirus is the cause of severe diarrheal disease in infants and young children worldwide. WHO has estimated that the number of deaths from rotavirus is over half a million in children under 5 years old every year. The plant system is the ideal strategies for the production and oral delivery of vaccines. The VP7 gene (0.98 kb) encoding surface antigen of human rotavirus was employed to develop edible vaccine using transgenic plant. Gateway vector pB7WG2D harboring bar gene as a selectable marker was used for the construction of plant transformation vector. Alfalfa was

transformed with agrobacterium-mediated method. A hundred of transgenic plants were obtained and confirmed by genomic PCR, of which six transgenic lines expressing VP7 protein in high level were selected by ELISA, which were reconfirmed by Southern Blot analysis. The VP7 protein in transgenic plants was also identified by Western Blot analysis. To test immunogenicity, alfalfa extracts were orally administered to mice once daily for 3 weeks, and mice fed with the transgenic alfalfa line elicited IgG and IgA antibody responses. In future, we will assess the neutralizing activity of the antibodies raised from the mice immunized with the transgenic plants.

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Research concerning the quality of some food industry rye batches



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There are numerous ways in which rye can now be used in food industry. Considering the continuous ascending trend in the number of food commodities manufactured using rye, we aimed the improvement of rye based recipes for increasing the nutritional value in the biotechnology of bakery products. We used 10 batches of rye received for processing into breadstuffs, in a special facility. The available standards for the assessment of chemical, physical and sensory parameters of rye seeds and flour were used. The study was focused on sensory analysis, hectoliter mass, humidity and foreign material assessment. The taste, appearance, color and smell of rye seeds were found to be normal, adequate for healthy rye. The rye seeds mass was proven to have mineral (stones) and organic impurities (flaw seeds, straws, leaves). All rye flour investigated was found to have normal appearance, smell, taste and color, all features being appropriate for the plant species. Results concerning aflatoxin, ochratoxin, deoxinivalenol and zearalenone content indicated no exceeding of the residue limits. The sensorial analysis results allow the ranking of the analyzed rye samples into breadstuffs rye, according to the accepted standards. The analyzed rye seeds and flour are appropriate for being processed into breadstuffs.

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Heat stress affects XET activity in durum wheat roots: Biotechnological implications



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Biotechnological alterations of expression, intracellular traffic, localization and activity of plant cell-wall modifying enzymes is a key target to improve crop physiological characteristics. In this