

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  $\leq 0.05$  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) + CuSO<sub>4</sub> (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%) > Meltun (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.