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From Science^{to} Knowledge



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PREPARATION OF AMINO ACID-FUNCTIONALIZED CARBON QUANTUM DOTS USING CLEMENTINE PEEL – POTENTIAL APPLICATION IN BIOMEDICAL ANALYSIS AND AS FLUORESCENT PROBE FOR Fe³⁺ DETECTION

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Luminiscent carbon quantum dots (CQDs) are widely known as zero-dimensional nanomaterials which have attracted extensive attention, especially in green chemistry and biomedicine. Due to their excellent biocompatibility and low toxicity, water solubility, stability in high ionic media and great optical properties, CQDs have been widely used as functional optical materials in fluorescence sensing. In this study, preparation and modification of CQDs using clementine peel as carbon precursor and amino acids with different chemical complexity (glycine and arginine - nitrogen dopants) has been presented. It has been demonstrated that increasing nitrogen content in CQDs samples has increased the quantum yield percentage of prepared CQDs. Some differences in sample properties were observed regarding structural and chemical diversity, biological and antioxidant activity. The antiproliferative effect of CQD@Gly against pancreatic cancer cell lines (CFPAC-1) was demonstrated. Based on the DPPH assay results, the CQD@Arg demonstrated the highest antiradical activity $81.39 \pm 0.39\%$, and EC_{50} was determined to be $EC_{50} = 53.78 \pm 0.97 \mu\text{g/mL}$ ($R^2 = 0.9357$). Furthermore, due to the highest determined quantum yield, CQD@Arg sample was further used for the ion sensing and cellular imaging of cancer cells. The CQD@Arg was applied as a fluorescent nanoprobe for Fe³⁺ detection, with a good linear correlation in the concentration range from $7.0 \mu\text{mol dm}^{-3}$ to $50.0 \mu\text{mol dm}^{-3}$ with $R^2 = 0.9931$ and limit of detection (LOD) of $4.57 \pm 0.27 \mu\text{mol dm}^{-3}$. In order to investigate the applicability of prepared CQDs in cell imaging, MCF-7 cells were incubated with CQD@Arg and imaged by confocal microscopy. This study implies the potential application of the prepared CQDs in bioimaging and ion sensing, and also as a fluorescent probe with diverse biological and pharmacological activities in general. This work has been supported by Croatian Science Foundation under the project "Application of innovative techniques of the extraction of bioactive compounds from by-products of plant origin" (UIP-2017-05-9909). We would like to thank also to Sugato Hajra and professor Hoe-Joon Kim for the XRD and EDS measurements (supported by Basic Science Research Program through the National Research Foundation of Korea (NRF) and funded by the Ministry of Science and ICT of Korea (2021R1C1C1011588)). The authors thank Daniel Berkesi (University of Szeged, Hungary) for the HR-TEM measurements.

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BIVALVES DISCLOSE NOVEL PATTERN OF SATELLITE DNA ORGANIZATION, HIGHLY DISPERSED AND CLOSELY CONNECTED TO HELITRON MOBILE ELEMENTS

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Several features have already qualified commercially and ecologically important bivalve species from the family Ostreidae as valuable non-standard model organisms, confirmed by an exponentially increasing number of genome sequencing projects and genome research on this group of organisms. The ubiquitous and in the same time still the least understood DNA components of every eukaryotic genome are repetitive DNA sequences. They cause significant technical problems in DNA sequencing and assembly and frequently are omitted or underrepresented in genome assemblies, consequently being called the "dark matter of the genome". Repetitive DNA sequences are divided into two major groups, satellite DNAs (satDNAs) composed of sequences repeated in tandem, and transposable elements (TEs) interspersed throughout the genome. In this work we have revealed a completely new principle of satDNA organization in respect to the generally accepted paradigm that satDNAs typically form long arrays of monomers, composing heterochromatic chromosomal compartments. We have identified complete inventory of satDNAs, the satellitome, of the invasive Pacific oyster *Crassostrea gigas*, consisting of 52 satDNAs. While heterochromatin in this species is extremely scarce, satellitome analysis disclosed novel and unusual, highly scattered arrangement of relatively short satDNA arrays across the whole genome. The inspection of the organizational forms of the most abundant satDNAs displayed their association with constitutive parts of Helitron TEs. In addition, Helitron-related satDNAs exhibit an advantage in the number of chromosomes occupied, indicating that these TEs are a significant factor in their genome-wide propagation, as well as in forming of genome architecture of *C. gigas*.