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Production of L-Asparaginase by Yemeni Filamentous Fungi

Yemen with its diverse climatic regions represents a rich resource for bioactive compounds obtained from microorganisms. This study was designed to screen fungal isolates obtained from the Microbiology branch, Biological Sciences Department, Faculty of Science, Sana'a University for their ability to produce L-asparaginase enzyme. In preliminary screening for L-asparaginase, among 77 fungal isolates about 29 fungal isolates representing 37.66% were high producers of L-asparaginase. These fungal isolates belonged to the genera Aspergillus, Eupenicillium, Fusarium, Penicillium, and Stachyobotrys. These 29 fungal isolates were screened for their ability to produce L-asparaginase using the agar well diffusion method. 12 fungal isolates out of 29 showed the ability to produce extracellular L-asparaginase. These isolates belonged to 8 species which were: A. sulphurs, A. ustus, F. sacchari, P. chrysogenum, P. citrinum, P. corylophilum, P. melinii, and P. subturcoseum. Only 5 isolates were obtained for the determination of enzymatic activity, among them P. chrysogenum showed the highest activity (279.8696U ml-1) followed by A. ustus (170.9435U ml-1). This finding is the first report on the L-asparaginase production from filamentous fungi in Yemen.

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Utilization of Molecular Simulation Applications for Stability Testing of Anthocyanin Compounds in Black Elderberry

Recently, many studies on the molecular activity of compounds have been carried out using simulations through computer programs or in silico simulations. Anthocyanins are one of the compounds that are often used as food coloring agents and can function as antioxidants to prevent blockage of blood vessels, as an anti-cancer that can prevent the development of cancer cells and tumors and have anti-inflammatory effects. The purpose of the research is to determine the stability of anthocyanins using molecular simulations and determine the best mixing sequence of ingredients to produce the most stable anthocyanin mixture.
Based on the results of the simulations carried out, it can be proven that the final 3 sets (the modeled compound belonging to namely AP and AZ followed by a number based on the simulation order) selected are AP17, AP18, and AZ17. The AP17 set had the lowest potential energy at the end of molecular dynamics simulations, but molecular visualization showed structural instability indicated by the formation of gaps in the molecular conformation. The AP18 set had the second lowest potential energy at the end of molecular dynamics simulations and molecular visualization showed molecular conformation that tended to be stable during molecular simulations with no change in structure. The AZ17 set had the highest potential energy of the final 3 sets selected and molecular visualization showed a gap in the conformation at the beginning of the simulation, but over time the gap became denser, indicating that the molecule became more stable over time.
Based on the research results, the AP18 set was chosen because it has relatively low potential energy and it can be proven that the structure visualization of this set tends to be more stable over time during molecular dynamics simulations.

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Detection of extended-spectrum betalactamase and carbapenemase-producing Enterobacteriaceae in Tunisia

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The emergence of dramatic urinary tract infections (UTIs) caused by the members of the Enterobacteriales is an important public health problem in the community as well as in Tunisian hospitals. This study aims to investigate the prevalence of extended-spectrum ?-lactamase (ESBL) and carbapenemase-producing uropathogenic isolates of Escherichia coli (E. coli) and Klebsiella pneumoniae (K. pneumoniae).
Based on decreased susceptibility to ?-lactams antibiotics and analyzed for the presence of ESBL and carbapenemase genes by Real Time- polymerase chain reaction (RT-PCR), 56 uropathogenic isolates of E. coli (n = 36) and K. pneumoniae (n = 20) were confirmed positive for ESBLs. The CTX-M-type ?-lactamases were mostly detected in E. coli isolates (21 strains, 58.33% [95% CI 38.09% - 72.06%]) followed by blaSHV-like (18 strains, 50% [95% CI 32.92% - 67.07%]), blaTEM-like and blaCMY-2-like simultaneously (15 strains, 41.67% [95% CI 25.51% - 59.24%]). Furthermore, the RT-PCR system on the K. pneumoniae strains demonstrated that blaSHV-12-like was the most predominant (16 strains, 80% [95% CI 56.33% - 94.26%]) followed by blaTEM-like (14 strains, 70% [95% CI 45.72% - 88.10%]), blaCTX-M belonging to groups 9 and 1 (11 strains, 55% [95% CI 31.52% - 76.94%]) and finally blaCMY-2-like (10 strains, 50% [95% CI 27.19% - 72.80%]). In addition, E. coli and K. pneumoniae strains harbored a carbapenemase gene blaOXA-48-like with 22.2% [95% CI 10.11% - 39.15%]; 20% [95% CI 12.83% - 43.66%], respectively.
Our results confirm the need to monitor the resistance to extended-spectrum ?-lactams and to carbapenems among enterobacteria in Tunisia.