

Antibacterial Activity of Seaweeds against Urinary Tract Infection with Special Reference to the Virulence Genes

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Background: Seeking natural and safe sources for the treatment of multidrug resistance bacteria (MDR) has become a global need. This study showed the ability of some common Egyptian seaweeds as promising treatment bases for human urinary tract infection (UTI) diseases and as new antibacterial agents to replace synthetic antibacterial drugs. **Aim:** To evaluate the effect of seasonal variation on the antibacterial activity of some seaweeds against the bacterial isolates causing urinary tract infection (UTI) diseases and investigated its virulence genes factors in order to genetically compare the virulence activities of the affected UTI strains after seaweed extracts treatment. **Material and Methods:** Pathogenic UTI bacterial isolates were collected from urinary tract infected patients at Tanta University hospitals, Department of Urology. After morphological and biochemical investigations, the bacterial isolates were classified into 3 groups of Gram-negative species of *Escherichia* sp., *Klebsiella* sp. and *Proteus* sp., which were the main cause of the UTI infection and were identified using Vitek system 2 technique. Different seaweeds (macroalgae) belonging to different divisions viz. *Enteromorpha intestinalis* and *Ulva lactuca* (Chlorophyta), *Petalonia fascia* and *Sargassum vulgare* (Phaeophyta), *Gelidium spinosum* and *Jania rubens* (Rhodophyta) were collected seasonally during 2015-2016 from Abu-Qir Bay, Alexandria, Egypt. In order to extract the antimicrobial material, diverse polar solvents (85%) of acetone, chloroform, diethyl ether, ethanol, hexane, methanol, and water were used. PCR was used to investigate the virulence genes responsible for multidrug resistance of the UTI bacterial strains. **Results:** The highest antibacterial activity was recorded for the screened green algal species in spring season followed by winter, summer and finally autumn seasons. The red algal species reached its maximum antibacterial activity in summer season followed by autumn, winter, and spring seasons. The brown algal species were detected only in spring season and showed the lowest antibacterial activity. Collectively, the strongest antibacterial activity was recorded for the ethanolic extract (85 %) of *Ulva lactuca* green seaweed in spring season. The UV absorption of these 5 fractions showed the same absorption peaks at 245, 401 and 666 nm, respectively by using UV spectrophotometer (UV 2101/pc). Therefore, these 5 fractions were pooled together to obtain the active compound of *Ulva lactuca* ethanolic extract. The phytochemical screening of this active compound indicated the presence of phenolic, flavonoid, saponins, alkaloids and glycosides secondary metabolites. FTIR analysis indicated the presence of u OH group, u CH aliphatic (CH, CH₂ and CH₃), u C=O, u C=C, u C-O, u aromatic phenyl ring (CH, CH₂ and CH₃). All the strains contained ureC genes in a rate of 96.66%. The PCR amplicons of hpmA gene was detected in the three bacterial strains. **Conclusion:** Seaweed derived compounds proved their ability as new natural and safe source for antibacterial agents, which could reduce the virulence genes activity and prevent the resistance and pathogenicity of these kind of pathogenic bacteria

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