Biological activities of some Acacia spp. (Fabaceae) against new clinical isolates identified by ribosomal RNA gene-based phylogenetic analysis.

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Abstract:

Abstract Nowadays, most of the pathogenic bacteria become resistant to antibiotics. Therefore, the pharmaceutical properties of the natural plant extracts have become of interest to researchers as alternative antimicrobial agents. In this study, antibacterial activities of extract gained from Acacia etbaica, Acacia laeta, Acacia origena and Acacia pycnantha have been evaluated against isolated pathogenic bacteria (Strains MFM-01, MFM-10 and AH-09) using agar well diffusion methods. The bacterial strains were isolated from infected individuals, and their exact identification was detected on the basis of 16S rRNA gene amplification and sequence determination. Alignment results and the comparison of 16 S rRNA A gene sequences of the isolates to 16 S rRNA gene sequences available in Gen Bank data base as well as the phylogenetic analysis confirmed the accurate position of the isolates as Klebsiella oxytoca strain MFM-01, Staphylococcus aureus strain MFM-10 and Klebsiella pneumoniae strain AH-09. Except for cold water, all tested solvents (Chloroform, petroleum ether, methanol, diethyl ether, and acetone) showed variation in their activity against studied bacteria. GC-MS analysis of ethanol extracts showed that four investigated Acacia species have different phyto components. Eight important pharmaceutical components were found in the legume of Acacia etbaica, seven in the legume of Acacia laeta, fifteen in the legume of Acacia origena and nine in the leaves of Acacia pycnantha. A dendrogram was constructed based on chemical composition, revealed that Acacia laeta is more closely related to Acacia etbaica forming on eclade, whereas Acacia origena less similar to other species. Our results demonstrated that, investigated plants and chemical compounds present could be used as promising antibacterial agents

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