Antibacterial Effect of Thirty New Heterocyclic Derivatives against Bacillus subtilis and salmonella enterica

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Abstract

Background and objective: Six families of thiazole, thiazolidine, imidazole, tetrahydropyrimidine, oxazolidine and thiazepine are new and important heterocyclic antibacterial compounds. Aim of this study is evalution the antibacterial effect of thirty new thiazole, thiazolidine, imidazole, tetrahydropyrimidine, oxazolidine and thiazepine derivatives against *Bacillus subtilis* and *salmonella enterica*.

Materials and methods: After derivatives were dissolved in DMSO, to evaluate the antibacterial effect, the disk diffusion method was applied to measure the growth inhibition zone diameter and broth microdilution was performed to determine the minimum inhibitory concentration (MIC) and then *minimum bactericidal concentration* (MBC) for all of derivatives compared with gentamicin and penicillin.

Results: Results showed of thirty derivatives tested, only imidazole derivative 3, thiazole derivative 23, thiazolidine derivative 25 had inhibitory effect on *B. subtilis* and wasn't showed inhibitory effect of all of derivatives on *s. enterica*. The maximum inhibitory effects on *B. subtilis* belonged to imidazole derivative 3 with inhibition zone diameter = 13.4, MIC = 256 and MBC = 512 μ g/ml. In antibiogram test the most susceptibility inhibitory effect on *B. subtilis* and *s. enterica* was recorded for penicillin and Gentamycin respectively.

Conclusion: In this study, the antibacterial effect of heterocyclic derivative was showed on *B. subtilis* and evalution effects of these derivatives in In Vivo, is The next step to identify more of these compounds.

Key words: antibacterial, heterocyclic derivatives, Bacillus subtilis, salmonella enterica.

Prevalence and Antimicrobial Susceptibilities of Bacteria Isolated from Sternal Wound Infections after the Coronary Artery Bypass Graft

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Abstract

Background and objective: Sternal ulcer infection is one of the complications of coronary artery bypass graft (CABG) surgery that although it has a low prevalence, but complications can be serious and risky for the patient. Infection occurs at 4 to 5 percent of people who are undergoing cardiac surgery. The aim of this study was to determine the prevalence rate and antibiotics susceptibility of sternal ulcer infection in patients with CABG surgery in Imam Ali Hospital Kermanshah, Iran, from March 2012 to February 2015.

Materials and method: This descriptive—analytic study was performed on 345 of CABG during 3-years period from March 2012 to February 2015 in Imam Ali Hospital Kermanshah, Iran. Sternal wound secretion samples of suspected patients were cultured and the bacterial identification tests were performed. Also, antibiogram test was done on the grown strains and antibacterial resistance patterns were determined. Statistical analysis was performed using the SPSS 16.

Results: Of 345 CABG surgeries, 17 patients had positive culture. The frequencies of the isolated strains include: *Staphylococcus aureus* with 4 cases (23.53%), *Staphylococcus epidermidis* with 4 cases (23.53%), *Escherichia coli* with 3 cases (17.64), *Klebsiella pneumoniae* with 3 cases (17.64), and *Pseudomonas aeruginosa* with 3 cases (17.64). The highest sensitivity rate was for Vancomycin, Penicillin, Gentamycin.

Conclusion: According to the result of the study and other similar studies, the most current bacteria that causing sternal wound infections are gram-negative bacteria. Therefore, to eliminate improper prescribing of medications, damage to the patient, and waste a lot of cost and time, Identifying susceptibility of these organisms is essential.

Keywords: Nosocomial infection, sternal infection, coronary artery bypass graft surgery

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The Similarity of the Nocleitide Sequence of 16S rRNA and rec A Genes between Strains of E. coli and P. mirabilis from Staghorn **Kidney**

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Abstract

Background and objective: Escherichia coli and Proteus mirabilis are the most isolated bacteria from kidney stones. 16S rRNA and recA genes show evolutionary relationship among bacteria. The aim of this study is to detect and isolate Escherichia coli and Proteus mirabilis from Staghorn kidney stones obtained from patients at LabafiNejad Hospital and investigation of genetic relationship between 16S rRNA and recA genes in these two bacteria.

Materials and methods: One hundred and fifty stone samples were obtained from patients referred to the surgical ward of LabafiNejad Hospital. They have examined for recognizing material of staghorn stones and exictene of bacteria. Cultured bacteria were identified by Phenotypic, biochemical and PCR tests, and antibiotic resistant of identified bacteria was performed. For investigation of genetic relationship between 16S rRNA and recA genes in identified strains of Escherichia coli and Proteus mirabilis were sequenced and phylogenetic tree was drawn for them by MEGA4 software.

Results: Results showed that out of 150 patients, 73.3% were male and 26.7% were female and 44% stones samples were culture positive. The most identified species consisted of Escherichia coli 22.8%, Proteus mirabilis 18.2%, Staphylococcus aureus 13.6%, Staphylococcus saprophyticus 12.2% and Staphylococcus epidermidis 12.2%. 16S rRNA gene sequences similarities in Escherichia coli and Proteus mirabilis strains were 96% and 97% respectively. Also the results of recA gene sequences analysis showed that all genes had 98% similarity. Among stones with positive bacterial cultures, the most composition of stone was Calcium oxalate 57.5%.

Discussion: In the present study, the phylogenetic results showed that the recA is better than 16S rRNA gene for investigation of genetic relationship between 16S rRNA and recA genes in identified strains Escherichia coli and Proteus mirabilis in kidney stone samples. With regard to the comparison of recA and 16S rRNA gene sequences, it is appeared that recA gene is slightly more accurate than 16S rRNA gene and it is better to use recA gene instead of 16S rRNA gene of course it needs more information.

Keywords: recA gene, 16S rRNA gene, kidney stone

Antibiotic resistance pattern of *Staphylococcus epidermidis* strains isolated from a referral hospital in Isfahan

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Abstract

Background and objectives: *Staphylococcus epidermidis* is a normal flora of human in different parts of the body which is known as an opportunistic pathogen in nosocomial infections. The aim of this study was to determine the antibiotic resistance patterns of *S. epidermidis* strains isolated from clinical samples in a referral hospital in Isfahan.

Materials and methods: In this study, total of 107 *S. epidermidis* strains isolated from different clinical samples in a referral hospital in Isfahan, during 2015. All isolates were identified at the species level using standard biochemical tests and PCR method by species specific primers. Antibiotic susceptibility of strains to 9 antibiotics was determined by disc diffusion method according to the guideline of Clinical and Laboratory Standards Institute (CLSI).

Results: The highest level of resistance was observed to erythromycin and also high resistance to clindamycin, cefoxitin, tetracycline and trimethoprim/sulfamethoxazole, was determined. All *S. epidermidis* strains sowed susceptibility to linezolid and quinupristin-dalfopristin.

Conclusion: Prevalence of resistance to broad spectrum of first and second lines antibiotics for treatment of *S. epidermidis* infections, indicating spread and distribution of these strains in this hospital in Isfahan. Lack of attention to antibiotic resistant *S. epidermidis* strains, which are members of human microbiota, could be an urgent for public health.

Keywords: S. epidermidis, antibiotic resistance, Isfahan, linezolid, quinupristin-dalfopristin

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Phytochemical, Antioxidant, and Antibacterial Properties of Medical Plant Salvia sharifii Rech. f. & Esfand

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Abstract

Background and objective: Salvia sharifii as medicinal plants has many therapeutic properties including; anti- microbial, anti- flatulence and anti- rheumatism. The goal of this study was to identify the active ingredients, antibacterial and antioxidant of aerial parts of Salvia sharifii collected from East of Iran.

Methods: The active component of the methanolic extract were separated and identified by gas chromatography (GC) and gas chromatography- mass spectrometry (GC-MS) methods. The essence of the aerial parts was extracted by Clevenger apparatus. The effect of essence against *Staphylococcus aureus* and *Escherichia coli* was tested by the micro dilution method. The total phenolic contents of the extracts were determined by Folin-Ciocalteu method and the antioxidant activity was evaluated using DPPH (2, 2 -diphenyl 1-1 picrylhydrazyl) assay.

Result: The result of this study revealed that Bornyl acetate (20.85%), β - Caryophyllene (15.79%) and Camphene (15.63%) were the most prevalent components of the methanolic extract. The minimum inhibitory concentration of the essential oils against Staphylococcus aureus and Escherichia coli were 3/75mg/ml and 7/5mg/ml respectively. Also, The amount of phenolic component of the methanolic extract was 9 µg/mg and the antioxidant activity of methanolic extract and essence were 32.1 and 58.2 µg/m respectively.

Conclusion: present Bornyl acetate in *Salvia sharifii*, the major compound in plant extract plays an important role in antimicrobial activity. Methanolic extract of *Salvia sharifii* has strong antioxidant activity.

Keyword: Staphylococcus aureus, Escherichia Coli, Salvia sharifii, Antioxidant activity, Micro dilution method

Frequency of Extended Spectrum Beta-lactamases Producing E. coli Strains Isolated from Urine of Inpatients in Yazd Hospitals and Detection of Resistance Pattern

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Abstract

Background and objective: Beta-lactamases are bacterial enzymes which cause hydrolysis of beta-lactam rings. Extended spectrum beta-lactamases cause bacterial resistance to penicillins, cephalosporins and aztreonam. *Escherichia coli* is a main cause of more than 80% of urinary tract infections. The aim of this descriptive-analytic study is to investigate the frequency of extended spectrum beta-lactamase in strains of *E. coli* separated from the urine specimens of inpatients in Yazd hospitals and to determine their sample of antibiotic resistance.

Materials and methods: A total of 300 *E. coli* strains were isolated from the inpatients in Yazd Shohadaye-Kargar and Shahid-Sadouqhi hospitals during January 2014 to November 2015; and were identified by biochemical tests. Antibiotic susceptibility tests were performed by disk diffusion according to CLSI. Confirmatory combination disk method was used for detection of ESBLs, and SPSS 16 software was applied to analyze the data.

Results: Out of 300 *E. coli* isolates, 111(37%) were identified as ESBL producer and 81(73%) were belonged to women and. Among ESBL producer isolates, the highest rate of resistance was related to Cefotaxime (100%), Ceftazidime (100%), Co-trimoxazole (89.2%), Nalidixic acid (81.1%), Ceftriaxon (62.2%), Ciprofloxacin (60.3%), Ofloxacin (60.3%), Norfloxacin (59.4%) and Gentamicin (42.3%) respectively.

Conclusion: The results showed that the frequency of ESBLs was 37% among *E.coli* isolates and regarding to the multidrug-resistant and ESBLs producing strains, it is suggested that if necessary, ESBLs phenotypic confirmatory test should be performed with susceptibility tests in the laboratories.

Key words: ESBLs, Disk Diffusion, Escherichia coli, Combination Disk.

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Prophage Typing and SCCmec Typing of Methicillin Resistant Staphylococcus aureus Strains Isolated from Patients in Isfahan

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Abstract

Background and objective: Staphylococcus aureus is an important agent of nosocomial infections which has high potential to acquire resistance to different antibiotics. The aim of this study was to type and determine the antibiotic resistance patterns of methicillin resistant S. aureus strains isolated from patients in a hospital in Isfahan, Iran.

Materials and methods: In this study a total of 117 S. aureus strains were collected during 6 months in 2015 form outpatients and hospitalized patients in a hospital in Isfahan. All isolates were identified at the species level using standard biochemical tests and also specific primers. Antibiotic susceptibility of S. aureus strains to 11 antibiotics was determined by the guidelines of CLSI, also presence of mecA gene among MRSA strains was tested. SCCmec typing and prophage typing of isolates was carried out using multiplex-PCR assay by specific primers.

Results: All isolates were confirmed as *S. aureus* strains using phenotypic and genotypic methods. The highest antibiotic resistance was observed to erythromycin and followed by tetracycline and the lowest resistance was to vancomycin, linezolid and quinupristin-dalfopristin. Forty one percent of strains showed resistance to oxacillin and cefoxitin and also were positive for mecA gene, were confirmed as MRSA strains. Among MRSA strains, the highest rate of resistance was to erythromycin, ciprofloxacin, tetracycline, clindamycin, gentamicin and SXT, respectively. All MRSA strains harbored SCCmecc type III and classified as hospital acquired MRSA. Four different prophage types and 1 prophage pattern were found among isolates.

Conclusion: The prevalence of MRSA strains in this study was higher than other reports, and all isolates were classified as HA-MRSA strains. Vancomycin, linezolid and quinupristin-dalfopristin were the most effective antibiotics for treatment of infections caused by MRSA, in present study. High prevalence of antibiotic resistant clonal groups of MRSA strains which have potential to produce broad spectrum of virulence factors is a risk to public health.

Key words: S. aureus, antibiotic resistance, methicillin, prophage typing, SCCmec typing

The Antibacterial Activity of Coriander (Coriandrum sativum) on Pathogenic Microorganisms "in vitro"

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Abstract

Background and objective: Antibiotic resistance is a serious threat to human health, especially vulnerable groups such as children, the elderly and individuals with poor immune systems. So finding natural, cheap and effective antimicrobial compounds is necessary. The aim of this study was to investigate the antimicrobial effect of coriander (Coriandrum sativum) on a number of infective bacteria including *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa*. **Materials and methods**: This experimental study was carried out from February 2014 until May 2015 in the industrial microbiology laboratory, Ferdowsi University of Mashhad. We used maceration method, aqueous and ethanolic solvents for the extraction of coriander (Coriandrum sativum). Plate count agar and disc diffusion method were used to determine the sensitivity of strains. The minimum inhibitory concentration (MIC) and minimum bactericidal concentration (MBC) were measured using microplate.

Results: The results showed good antibacterial effects on pathogenic strains. The most considerable effect of ethanolic coriander extract was observed on *Staphylococcus aureus* at a concentration of 80 mg/ml. The minimum inhibition zone in this concentration belonged to *Pseudomonas aeruginosa*. MIC of ethanolic extract of the *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* were 25.6, 12.5and 25mg/ml, respectively and MBC of them were 25.6, 25 and 50mg/ml, respectively. Ethanolic coriander extract has a higher antimicrobial effect than aqueous extract, so MIC and MBC of aqueous coriand erextracts on *Staphylococcus aureus*, *Escherichia coli* and *Pseudomonas aeruginosa* were, 12.5, 25 and 50 mg/ml and MBC regarding them were 25,50 and 100 mg/ml, respectively.

Conclusion: Our results showed that coriander herbs has significant antimicrobial effects on pathogenic bacteria, suggesting that the highest antimicrobial effect was observed on *Staphylococcus aureus*as a gram-positive organism and the lowest antimicrobial effect was on *Pseudomonas aeruginosa* as a gram-negative one.

Keywords: Coriander, Extract, Pseudomonas aeruginosa, Staphylococcus aureus, Escherichia coli

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