

Investigation of the prevalence of Hepatitis B, C and HIV in major Thalassemia patients in Zahedan

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Abstract

Background and purpose: Major thalassemia patients due to the need for frequent and continuous blood transfusions ; they are exposed to blood-borne diseases, especially Hepatitis B, Hepatitis C and HIV. which is one of the most important health problems in the world and Iran today. The present study aims to determine the prevalence of Hepatitis B, Hepatitis C and HIV in patients with major thalassemia in Zahedan city.

Materials and methods: In this cross-sectional study, 816 patients with major thalassemia who had regular blood transfusions at Ali Asghar Hospital in Zahedan were investigated by census method. Demographic data And the results of Anti-HIV, HBs-Ag, HBs-Ab, Anti-HCV, Ferritin and CBC blood tests have been reviewed. Spss26 software was used for data analysis.

Results: The average number of referrals for transfusion was 25.71 ± 33.71 . 501 people (94.9%) had sufficient response to the hepatitis B vaccine and only 27 people (5.1%) had HBs-Ab levels less than or equal to 10 IU/ml. In this study, using chi-square analysis, a significant relationship between the age group of 30 to 60 years and hepatitis C has been observed ($P < 0.000$). However, no significant relationship between hepatitis B and HIV infection with gender and blood group variables has been observed.

Conclusion: HBsAg testing on donated blood and hepatitis B vaccination and the low prevalence of HIV among blood donors are directly related to the low prevalence of hepatitis B and HIV in major thalassemia patients. Considering that there is currently no vaccine against hepatitis C and HIV, careful screening of donated blood and the use of new laboratory methods and the use of high-sensitivity laboratory kits are necessary to reduce the transmission of HCV-Ag contamination for patients.

Keywords: Thalassemia, Hepatitis B, Hepatitis C, HIV

Prevalence of virulence genes in *A. baumannii* strains isolated from burn wound infection in Isfahan in 2022

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Abstract

Background and Aim: Antimicrobial resistance and biofilm formation are considered the main factors that increase the risk of life-threatening infections in burn patients. The purpose of this study was to investigate the antibiotic resistance and biofilm formation ability, as well as to determine the frequency of biofilm-related genes (*pgaA*, *abaI*, *csuE*, and *bap*) in *Acinetobacter baumannii* strains isolated from burn wound infection in Isfahan.

Material and Methods: A total of 50 *A. baumannii* isolates were collected from burn wounds samples of hospitalized patients in Imam Musa Kazim Burn Hospital of Isfahan, between February to July 2022. All isolates were preliminarily identified using morphological, physiological, and standard biochemical tests. Then, these isolates were confirmed as *A. baumannii* using specific primers for the *bla_{oxa-51}* gene. Antimicrobial susceptibility to 13 antibiotics was accomplished using the disk diffusion method and the biofilm formation ability of each strain was tested by the quantitative microtiter plate assay. Moreover, the frequency of four biofilm-related genes (*pgaA*, *bap*, *csuE*, and *abaI*) among *A. baumannii* strains was determined by specific primers.

Results: All strains were resistant to piperacillin-tazobactam, ceftazidime, cefotaxime, ceftriaxone, imipenem, and ciprofloxacin (100%), and were categorized as extensively drug-resistant (XDR). Overall, 26%, 60%, and 10% of strains were classified as strong, moderate, and weak biofilm producers, respectively. Among four examined biofilm-related genes, *bap* had the highest frequency (98%), followed by *csuE* (92%), *pgaA* (92%), and *abaI* (90%). Also, the presence of *pgaA* and *csuE* genes was significantly associated with the ability of biofilm formation.

Conclusion: The high prevalence of biofilm-forming XDR *A. baumannii* in the studied hospital in Isfahan indicated the importance of biofilm formation and virulence factors of *A. baumannii* strains in burned patients.

Key words: *A. baumannii*, Burn wound infection, antimicrobial resistance, biofilm formation

Molecular characterization of genes encoding virulence factors among community-acquired methicillin-resistant *Staphylococcus aureus* isolated from patients in Tehran during 2019-2022

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Abstract

Background: Community acquired methicillin resistant *Staphylococcus aureus* (CA-MRSA) infections have mostly been associated with skin and soft-tissue infections (ranging from impetigo to life-threatening necrotizing fasciitis). These strains bearing the staphylococcal cassette chromosome *mec* (SCC*mec*) types IV, V and VII element, Panton-Valentine leukocidin and SGA prophage type genes, and also are more frequently susceptible to a variety of non-beta-lactam antibiotics. In the current study we investigated the distribution of SCC*mec* types, prophage types and a variety of virulence factor genes among CA-MRSA strains isolated from patients in a referral hospital in Tehran during 2019-2022.

Materials and Methods: A total of 489 MRSA isolates were collected from a referral hospital laboratory in Tehran and identified using specific primers for *nucA*, *mecA* and *mecC* genes. The presence of different SCC*mec* types among confirmed MRSA was tested by a multiplex-PCR assay and CA-MRSA strains were typed using specific primers for different prophage types genes. Moreover, the frequency of staphylococcal enterotoxin (SE) genes (*sea-seq*), *pvl* and *tst* genes were also determined.

Results: Totally, 463 strains (95%) were confirmed as MRSA, and 56 strains (12%) were positive for SCC*mec* types IV (a and c) and V which selected as CA-MRSA. Moreover, 4 different prophage types and 2 subtypes were identified among strains, in which all strains were positive for SGA, SGF, SGFa and SGFb prophage types. Also, 4 different prophage patterns were also detected among strains and pattern 1 consisted of all identified types was the most common pattern. On the other hand, except for *seb* and *seh* other 14 SE genes were detected among strains and 100% of strains were positive for *sea*, *sek* and *seq* genes. Furthermore, 5 different enterotoxin genes patterns were also determined, in which 18% of strains harbored 11 and 12 enterotoxin genes. Also, 29 and 100% of CA-MRSA strains were also carried *tst* and *pvl* genes, respectively.

Conclusion: The results of the present study indicated the prevalence of pathogenic CA-MRSA strains among patients in the studied hospital which provides a valuable scientific information on relationship between prophage types and virulence factors among these strains.

Key words: CA-MRSA, SCC*mec* type, SGA prophage type, staphylococcal enterotoxin, Panton-Valentine leucocidin, TSST-1

Prevalence of virulence genes in biofilm producing uropathogenic *Proteus mirabilis* strains isolated from patients with urinary tract infection in Isfahan during 2022

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Abstract

Background and Aim: *Proteus mirabilis* is the main pathogen causing complicated urinary tract infections (UTIs), especially catheter-associated UTIs (CAUTIs), which efficiently forms crystalline biofilm on different surfaces such as urethral indwelling catheters. The pathogenesis of *P. mirabilis* is related to its ability to produce a variety of virulence factors, such as biofilms, adhesion molecules, urease, hemolysin, swarming activity, proteases and siderophores. The aim of this study was to characterize the frequency of different virulence genes among biofilm producing uropathogenic *P. mirabilis* strains isolated from patients with UTI in a referral hospital in Isfahan during April-December 2022.

Material and Methods: In this study a total of 50 *P. mirabilis* isolates were collected from urine samples of 50 patients with UTI in a referral hospital in Isfahan and confirmed using polymerase chain reaction (PCR) by specific primers for *ureC* and *ureR* genes. All strains were tested for their ability to form biofilm using quantitative microtiter plate (MTP) assay, and the frequency of different virulence associated genes (*zapA*, *zapD*, *pta*, *hpmA*, *mrpA* and *hlyA*) among biofilm producing strains was determined by specific primers.

Results: All collected isolates were positive for *ureC* and *ureR* genes and confirmed as *P. mirabilis*. Also, all strains were able to form biofilm, in which 52, 44 and 4% of strains produced strong, moderate and weak biofilm, respectively. Moreover, *zapA* and *zapD* genes were detected in 100% of biofilm positive strains and the frequency of *hpmA*, *pta* and *mrpA* genes was limited to 96, 94 and 90% of strains. On the other hand, the *hlyA* gene was not detected in any studied *P. mirabilis* strains.

Conclusion: The high prevalence of biofilm producing *P. mirabilis* with a broad spectrum of virulence factors among patients with UTI in the studied hospital in Isfahan, indicating the clonal dissemination of biofilm producing pathogenic strains in Isfahan also the importance of *P. mirabilis* strains as a potential threat to patients' health.

Key words: *P. mirabilis*, complicated UTI, biofilm, virulence factors, urease, hemolysin

Psychological characteristics of Persons Living with HIV(PLWH)

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Abstract

Introduction: Although the annual incidence of HIV infection is decreasing globally, HIV prevalence is rising due to development of more effective treatment and higher survival [2]. Therefore, the health system is now facing emerging challenges of non-communicable diseases and mental health problems among PLWHA. The aim of this study is investigate the psychological and personality characteristics of PLWH for better planning for prevention and treatment.

Methods: This is a cross-sectional study on HIV⁺ patients from the referral center for HIV treatment and care in Rafsanjan in 2022. By consenting, 36 adult patients with HIV and 40 healthy controls participated in this study. An attempt was made to match the participants in terms of demographic variables. Psychometric evaluation was made with the MMPI (Minnesota Multiphasic Personality Inventory). Data were analyzed using SPSS-22 software and descriptive statistics and Yeoman-Whitney test.

Results: The results showed that there is a significant difference in the prevalence of depression disorders ($P=0.02$), mental weakness ($P=0.01$) and hypomania ($P=0.03$) between HIV positive people and control group people.

Conclusions: The result showed that nearly one among three individuals with positive HIV is suffering from mental disorder in Rafsanjan. This calls a need to integrate the mental health and psycho-social support into the HIV/AIDS care.

Keywords: MMPI; Psychological characteristics; HIV