Scholarly Quarterly for Applied Biology
Year 7, Issue 2, Summer 2017
Qom Islamic Azad University
Faculty of Basic Sciences
Price: 3500T

License Owner: Qom Islamic Azad University

Managing Director: Manouchehr Fada'ian
Editor-in-chief: Ahmad Ali Pourbabaie
Acting Editor-in-chief: Farah Farahani
Internal Manager: Zahra Aqajani

Members of the Board:

Mohammad Kargar (Associate Professor, Department of Microbiology, Jahrom Islamic Azad University)
Ahmad Yazdani (Associate Professor, Department of Physics, Tarbiat Modarres University)
Safar Ali Talari (Associate Professor, Department of Parasitology, Kashan Medical Sciences University)
Alireza Babazadeh (Assistant Professor, Department of Physics, University of Qom)
Ahmad Ali Pourbabaie (Assistant Professor, Department of Microbiology, Qom Islamic Azad University)
Ramezan Ali Khavarinejad (Full Professor, Department of Bio-botany, University of Khawrazmi)
Mohammad Reza Zulfaqari (Associate Professor, Department of Microbiology, Qom Islamic Azad University)
Mohammad Soleymani (Assistant Professor, Department of Microbiology, Qom Islamic Azad University)
Manouchehr Fada'ian (Assistant Professor, Department of Organic Chemistry, Qom Islamic Azad University)
Naser Qa'emi (Associate Professor, Department of Biochemistry, University of Tehran)

Executive Manager: Yaser Sharifi | **Persian Editor: Zahra Mahmoudi**
English Editor: Ali Ebrahimi | **Pagination: Zeynab Mawlavi**

15 Khordad, Islamic Azad University, Qom | **Telephone and Telefax: 025-37780014**
Journal email: a-biology-j@qom-iau.ac.ir | **Journal Website: http://sjoapb.journal.qom-iau.ac.ir/**

Contents

Scholarly Quarterly for Applied Biology

Diagnosis of Bacterial Factors Causing Urinal Infection and Determination of their Antibiotic Sensitivity Model in Patients Having Diabetes Mellitus Type II in the City of Kermanshah

Farshad Yadollahi, Elaheh Tajbakhsh*, Hassan Momtaz

Department of Biology, Islamic Azad University, Shahr-e Kurd Branch, Shahr-e Kurd, Iran.

(Received: 8 April, 2017; Accepted: 26 May, 2017)

Abstract

Diabetes is among the most common and important diseases existing in the world and those suffering from this disease is exposed to great risk of being infection afflicted. Considering the great pandemic diabetes and threats from urinal infection, study of determinants of urinal infection and its proper treatment way are seriously thought as important. In this study, pathogen bacteria type was diagnosed with urine culture of 353 patients hiving diabetes mellitus type 2 and performance of biochemical tests on positive samples. After extracting DNA from separated bacteria, PCR test was done for crucial diagnosing of bacteria causing urinal infection; after this, suitable antibiotics was prescribed with the anti-biogram test on positive samples. Diabetic patients were reported to have 28.3% urine infection. Unmarked bacteriuria 22.1% and marked bacterriuria 6.22% were reported. The most common bacteria causing urine infection in these patients are: escherishia coli, klebsiella pneumonia, proteus, Staphylococcus saprophyticus, acinetobacter, citrobacter, enterobacter, pseudomonas auerogenisoa and providencia. Considering the fact that bacterial group causing urine infection in patients having diabetes mellitus type 2 is almost similar to non-diabetic patients suffering from urine infection in other studies; hence, primary antibiotic treatment for urinal infected patients in diabetic patients is identical for non-diabetic patients.

Keywords: Antibiotic resistance, Bacteriuria, Diabetes mellitus, PCR, Urinal infection.

* **Corresponding Author, Email:** ee_tajbakhsh@yahoo.com

Studying Biological Absorption Rate of Phenol and Aniline by palm kernel from Water Solutions

Uthman Sa'idikia[1], Farzaneh Badpa[2], Farzaneh Borhani[3*], Salimeh Mortazavi[4], Hedayatollah Mohammadzaie[5], Ashrafsadat Dehqani[6], Tahereh Dadgar[7], Maryam Rezaie[8], Fatemeh Darregiraie[9], Elham Dameni[10], Nasrin Ranjbar[11]

1&5. M.Sc. Student in Biochemistry, Iranshahr Medical Sciences University, Iranshahr, Iran
2. Department of Biology, Faculty of Basic Sciences, University of Isfahan, Isfahan, Iran
3&4. Lab Sciences Technician, Iranshahr Medical Sciences University, Iranshahr, Iran
6. M.Sc. Student in Hygiene Training and Health Promotion, Zahedan Medical Sciences, Zahedan, Iran
7. Islamic Azad University, Neishabour Branch, Neishabour, Iran
8. M.Sc., Zahedan Medical Sciences University, Zahedan, Iran
9. Dentistry MD, Zahedan Medical Sciences University, Zahedan, Iran
10. M.Sc. Student in Hygiene Training and Health Promotion, Zahedan Medical Sciences, Zahedan, Iran
11. M.Sc. of Biology, University of Urumiya, Urumiya, Iran

(Received: 2 March, 2016; Accepted: 15 May, 2017)

Abstract

Considering the increasing use of surface absorption process in eliminating bio-environment pollutants, selection of a suitable substance, technically and economically, as an absorbent has been one of the concerns of researchers of the field. This paper aims to explore the elimination rate of phenol and aniline by use of palm kernel modified from water solutions. In this applied-basic study, owing to the aims concerned at lab-scale and in a discontinued system, modified palm ash as an absorbent at 0.4, 0.6, 0.8 and one gram was used. Changes of effect of phenol and aniline density, PH, contact time and density of absorbent had been checked. All tests were applied based on water and sewage tests standard method and Excel software was used for analysis of data. Test results showed that modified palm kernel ash had a high output in eliminating phenol and aniline and surface absorption output of phenol and aniline had a direct relation with the increase of amount of absorbent; the best output of absorption with one gram absorbent amount and PH=6 with phenol density 150mg/litre, contact time 30m, PH=4 with Aniline density 50mg/litre in contact time of 45m were obtained.

Keywords: Aniline, Ash, Palm kernel, Phenol.

* **Corresponding Author, Email:** BorhaniFarzan@gmail.com

Scholarly Quarterly for Applied Biology

Determination of abundance of Allelic and Genotype of Gene DDX25 in Different Races of Iran

Sharareh Hosseinzadeh Kashani [1], Elham Siyasati Torbati [2*], Parviz Pakzad [3]

1. M.Sc.of Genetics, Islamic Azad University, North Branch, Tehran, Iran
2. Ph.D. of Genetics, Islamic Azad University, North Branch, Tehran, Iran
3. Ph.D. of Immunology, Islamic Azad University, North Branch, Tehran, Iran

(Received: 8 March, 2017; Accepted: 25 April, 2017)

Abstract

DDX25 gene is settled on chromosome 2411; it 14 exons and largely affects function of testicles and spermatogenesis. Abundance of allelic of DDX25 gene in every group might be different. This difference can result from pressures from geographical-environmental factors of different regions. This gene puts effects on gametogenesis trend and as less attention has been paid to the case and its scientific fields in Iran, this research deals with abundance of genotype of DDX25 gene in seven races of Fars, Kurds, Turks, Baluchis, Gilanis, Arabs and Afghans. In this plan, 180 people were investigated. DNA sampling was extracted by salting out and by use of PCR, the gene concerned was reproduced in the related SNP; next, PCR product is being sliced by use of RELP and Ase-I Andonuclease enzyme and produced parts were checked by means of electrophoresis. On calculating the abundance percentage of genotypes, 77.22% of the group had GG genotype, 6.11% had TT genotype and 16.66% had GT genotype. Abundance of allelic G equaled to 0.855 and for allelic T was 0.145. Based on calculations made by Kaido test and p value: 0.48 in the under-study group, there was no meaningful difference between races of Fars, Kurds, Turks, Baluchis, Gilanis, Arabs, Afghans and genotypes and the crowd was not in hardy Weinberg equation.

Keywords: Abundances of allelic, DDX25 Gene, Genotype, Iranian races.

* **Corresponding Author, Email:** emi_biotech2006@yahoo.com

Identification of Acute Adhesiveness, Necrosis and Hemolysis in Strains of UPEC and APEC Isolates from Clinical and Livestock Samples

Sepideh Shamsgoli [1], Gholamali Moradli [2*], Kiyomarz Amini [3]

1. MS Graduate, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Saveh Branch, Saveh, Iran

2. Assistant Professor, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Saveh Branch, Saveh, Iran

3. Assistant Professor, Department of Microbiology, Faculty of Basic Sciences, Islamic Azad University, Saveh Branch, Saveh, Iran

(Received: 6 April, 2016; Accepted: 26 May, 2017)

Abstract

Uropathogenic Escherichia Coli and Avian pathogenic Escherichia coli involve a wide range of acute factors in man and livestock. These factors play a role in creating colonization, attack and subsequently reduced response of the host immune system that include cnf, hly, afa and pap genes. This study aims to keep track of genes of adhesiveness, necrosis and hemolysis of UPEC, APEC pathogens of Escherichia coli isolates from man and livestock. Totally 36 isolates of Escherichia coli of clinical samples from the patients having urine infection received at the Kerman hospitals and 36 isolates of Escherichia coli of livestock from faculty of veterinary of Kerman province. Isolates were diagnosed based on biochemical tests and standard bacteriology. Examination of genes showed that in livestock samples a number 10 isolates (27.7%) contain acute genes and 22 isolates (61.1%) in human samples proved positive for the presence of genes. No traces of cnf and cfa genes were found in human and livestock. More abundance is reported for pap gene with (33.33%) in livestock samples and (13.8%) in human samples. PCR method is a way to quickly diagnose acute factors in Escherichia coli isolated from Human and livestock samplings way of spread and source of contamination of which can help study epidemiology and quick battle against disease.

Keywords: Acute genes, Multiplex-PCR, Uropathogenic Escherichia Coli (UPEC).

* **Corresponding Author, Email:** Moradli.mic@gmail.com

Scholarly Quarterly for Applied Biology

Identification of Bacteria Producing Biosurfactant Isolated from oil-tainted soils of Borujerd Town

Mohsen Mirzaie[1*], Reza Yari[2], Morteza Chelowie[3]

1. Assistant Professor, Department of Lab Sciences, Islamic Azad University, Borujerd Branch, Borujerd, Iran
2. Assistant Professor, Department of Biology, Islamic Azad University, Borujerd Branch, Borujerd, Iran
3. M.Sc., Department of Biology, Faculty of Sciences, Islamic Azad University, Borujerd, Iran

(Received: 7 March, 2017; Accepted: 30 April, 2017)

Abstract

Biosurfactant is a valuable substance that is widely used in industries like petroleum, medicine, pharmacology, hygienic cosmetics, nutrition and agriculture. This paper aims to identify local bacteria generating biosurfactant existing in the soil tainted with oil disposals. Sampling was taken from oil-tainted soils around Borujerd town. After dilution and culturing, various bacteria were isolated. Bacteria generating biosurfactant were isolated by use of biosurfactant production tests like blood hemolysis test in blood agar medium, emulsifying activity, droplet disintegration, crude oil spread and oil hydrocarbons decomposition. The strongest bacterial species producing biosurfactant is being selected and cultured in bushnell haas broth with gas oil in shaker incubator. After production and delivering biosurfactant from colony concerned for identifying type and species of bacteria, biochemical tests along with 16sr PCR, sRNA and succession determination were made. With the various tests, it was known that bacteria produces lots of biosurfactant. In software study, it was proved, after succession, bacteria has genetic similarity of 97% with type and species of Bacillus subtilis. Considering the abundance of this bacteria in soil and its high ability in producing biosurfactant and expanded oil substances pollution in the country, this bacteria can be used in removing bio-environmental contaminations.

Keywords: Bacillus subtilis, Biosurfactant, Environmental contamination, Oil.

* **Corresponding Author, Email:** mirzaei.iaub@gmail.com

Identification, Culture and Reproduction of Stem Cells of human Spermatogonia

Zaynab Piravar[1], Shokoh Chegini[2*]

1. Ph.D, Department of Biology, Islamic Azad University, Tehran Central Branch, Ayatollah Rafsanjani Building, Tehran, Iran

2. MS Graduate, Department of Biology, Islamic Azad University, Tehran Central Branch, Ayatollah Rafsanjani Building, Tehran, Iran

(Received: 31 October, 2016; Accepted: 25 December, 2016)

Abstract

Spermatogonial Stem Cells or SSCs are a group of stem cells which produce sperm for maintaining reproduction during all lifecycle of men. In non-primate mammals, these stem cells are called A-single (As), A-paired (Apr) and A-aligloed (Aal) respectively that are prefabricates of spermatogonial cells. In man, due to limited studies on SSC cells, there are a few findings at hand. There are two different types of spermatogonia A: Adark and Adark. Apale as spare spermatogonia and Apale as renewing spermatogonia or renewing stem cell. Regulating SSCs including survival and various divisions depends on micro-environment of these cells in toxic epidermal tubes of testicular tissue. The signals arising from somatic cells existing in the micro-environment lead SSCs towards renewing stem cell or distinction of spermatozoa. Although various expressive markers or indicators can help isolation and enrichment of SCCs, specific marker for these cells has not yet been known. Testicular cells along with feeder cells have prepared possible growth and spread of these SSCs for a long time; hormones, different growth factors and their role in the process of reproducing spermatogonia stem cells have been studied.

Keywords: Culture system, Micro-environment, Spermatogonia stem cells, SSC-specific markers.

* **Corresponding Author, Email:** shokouhchegini@yahoo.com