

of this pure compound were determined. This method can be used as a template for isolation and purification of plant antioxidant compound.

Methods: The extraction of *Juniperus excelsa* leaves was done by using ethanol 80%, the fractionation of crude extract was done by using petroleum ether, chloroform, ethyl acetate and butanol. The n-butanol fraction which showed more antioxidant activity was subjected to purification by repeated silica gel, sephadex LH-20 and silica gel RP18. The antioxidant activity of pure compound was studied by using reducing power and DPPH radical scavenging. The concentration of pure compound required to scavenge 50% of DPPH free radicals (IC₅₀) was determined. Gallic acid and quercetin were used as standards.

Discussion and Conclusion: The IC₅₀ of gallic acid and quercetin were 21.2± 0.015 µg/ml. The IC₅₀ of the pure compound (176.355±4.9 µg/ml) was less than standards (P<0.05). In reducing power, the concentration of pure compound in absorbance 0.5 (145±13.77 µg/ml) was less than gallic acid (14.7± 0.93 µg/ml).

Keywords: *Juniperus excelsa*, Antioxidant activity, DPPH scavenging, reducing power, pure compound

P-500-The Spectrum of β-Thalassemia Mutations in Chaharmahal va Bakhtiari, Southwest Iran

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β-thalassemia is the most common single gene disorder in Iran. Mutations in β-globin gene may result in β-thalassemia major, which is one of the most common genetic disorders in Iran and some other countries. Knowing the β-globin mutation spectrum improves the efficiency of prenatal diagnosis in the affected fetuses of heterozygote couples. β-thalassemia patients were studied using polymerase chain reaction-amplification refractory mutation system (PCR-ARMS) to determine the spectrum of β-globin gene mutation in the people who involved with β-thalassemia major in this province. The most frequency mutation is Codons37/36 (%62), IVSII.1(G-A) (%18), IVS I.5(G-C) (%11), IVS I.10(G-A) (%10), %40 of patient homozygous and %60 of patient compound heterozygous. However, the frequencies of different mutations reported here are significantly different from those found in other part of the world and even other Iranian provinces. Reporting a number of these mutations in the neighboring region can be explained by gene flow phenomenon.

Keywords: Iran, β-Thalassemia, Mutation, PCR-ARMS

P-600-Fabrication of a bioscaffold from bovine tendon for possible applications in tissue engineering.

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Background: Tissue engineering is a new area of research that aims to repair damaged tissues and organs. Scaffolds are one of the most important parts of tissue engineering. Decellularized tissues and organs have been successfully used in a variety of tissue engineering/regenerative medicine applications. There are various methods for decellularization which are tissue-specific. The efficiency of cell removal from a tissue is dependent on the origin of the tissue and the specific physical, chemical, and enzymatic methods for decellularization used. The aim of this study was to fabricate a biological scaffold by decellularization of bovine tendon for possible applications in tissue engineering.

Methods and Results: After collection of the tendons from male bovine, a combination of physical, enzymatic and chemical methods were used. To do so, tendons were sliced and immersed in liquid nitrogen. Slices of tendon were then treated with trypsin/PBS (phosphate buffered saline) solution and were incubated in a shaker incubator. In the next step, the slices of tendon were treated with Triton X-100 for 24 h. Finally the decellularized tendon matrix (DTM) was sterilized with UV light and then washed with 70% ethanol and PBS.

Conclusions: Histological studies demonstrated that these procedures were suitable for decellularization of bovine tendon and also conservation of collagen type I, that is the most abundant fiber in the structure of connective tissues such as tendon, dermis, bone and gingiva. Designed scaffold with these properties may have useful applications in tissue engineering and regenerative medicine.

Keywords: tissue engineering, bioscaffold, decellularization method, tendon, collagen type I

P-0061-Based Molecular and Diagnostic Markers Type 2 Diabetes

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Abstract: Diabetes mellitus is one of the most common metabolic disease worldwide. Two main types of the disease are type 1 diabetes and type 2 diabetes. Type 2 diabetes occurs due to impaired insulin secretion and insulin action. Type 2 diabetes is a multi-factorial disease that genetics and environment play a role in its creation. Inheritance is polygenic. Genetic and non-genetic factors involved in type II diabetes. 1- genetic defects in beta cells (mutations in the HNF-1 alpha, HNF-4 alpha, HNF-1 beta, IPF-1 mutations in mitochondrial DNA), 2- defects in insulin action (insulin receptor defects, defects in insulin signal transduction pathway), 3-Chemical and pharmaceutical agents induce diabetes (vacor, glucocorticoids, diazoxide, thiazides) may cause changes in glucose homeostasis, 4-infectious agents 5- immune system- dependent diabetes 6-Genetic syndromes associated with diabetes. Recently, there is evidence that suggesting inflammatory cytokines secreted by adipose tissue, is involved in the development of type 2 diabetes. Among the inflammatory markers are TNF-α, IL-6 and c-reactive protein (CRP). TNF-α inhibits insulin delivery and it has an effect in