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Chitosan-PLGA Hybrid Nanocarriers Enhance Therapeutic Delivery of Doxorubicin for Hepatocellular Carcinoma



Article

Chitosan-PLGA Hybrid Nanocarriers Enhance Therapeutic Delivery of Doxorubicin for Hepatocellular Carcinoma

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Abstract

Hepatocellular carcinoma (HCC) is among the most prevalent and lethal malignancies worldwide, with limited therapeutic outcomes due to systemic toxicity and suboptimal efficacy of conventional chemotherapeutics such as doxorubicin (DOX). In this study, we formulated and standardized DOX-loaded chitosan/poly (lactic-co-glycolic acid) nanoparticles (DCLNs) via a nanoprecipitation method and evaluated their therapeutic potential in a diethylnitrosamine (DEN)-induced Wistar rat model of HCC. Physicochemical analyses confirmed nanoscale size, favorable zeta potential, and high encapsulation efficiency, while Fourier transform infrared spectroscopy (FTIR) verified polymer-drug interactions. Biochemical analysis revealed that DCLNs significantly normalized elevated liver function markers (Aspartate aminotransferase (AST), alanine aminotransferase (ALT), and alkaline phosphatase (ALP)), restored serum α -fetoprotein (AFP) to near-control levels, and reduced lipid peroxidation compared with free DOX and DEN controls. Anticancer profiling demonstrated marked recovery of superoxide dismutase (SOD), catalase (CAT), and glutathione peroxidase (GPx), indicating restoration of hepatic redox balance. Histopathological evaluation further corroborated these findings, showing recovery of hepatic lobular architecture and reduction in necrosis and inflammatory infiltrates in DCLN-treated Wistar Albino rats, while free DOX groups exhibited hepatocellular damage. Overall, the results demonstrate that encapsulating DOX in a chitosan/PLGA nanocarrier improves therapeutic efficacy, mitigates hepatotoxicity, and enhances antioxidant defense, establishing DCLNs as a favorable candidate for HCC.

Keywords: fungal chitosan; doxorubicin; liver cancer; biochemical and histopathological studies; *in vivo* hepatocellular carcinoma

1. Introduction

Cancer, a leading cause of global mortality with an ever-increasing incidence, remains one of the greatest challenges to human health, and despite decades of research, curative

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**A dual-organ genetic interplay between sensorineural hearing loss
and kidney disease: an update for clinicians**



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Genetic Diagnosis of Non-Syndromic Hearing Loss in South Indian Consanguineous Families Using Whole-Exome Sequencing



Genetic Diagnosis of Non-Syndromic Hearing Loss in South Indian Consanguineous Families Using Whole-Exome Sequencing

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Abstract

Background and Objective: Hereditary hearing loss is the most common auditory disability among various disabilities. Consanguineous populations have been found to have autosomal recessive disorders twice as often as in the general population. This study aimed to highlight the phenotypic and genetic complexity of non-syndromic hearing loss (NSHL) in South Indian consanguineous families. **Materials and Methods:** Whole-exome sequencing (WES) was performed on individuals with NSHL who were negative for common deafness-causing genes (GJB2, GJB3, SLC26A4, and MYO15A). The candidate variants identified were confirmed with BCFI regions identified using the Annotator tool. Sanger sequencing was performed for validation, followed by segregation analysis for the available family members. The effects of the candidate variants were analyzed using *in silico* structural approach and the ACMG guidelines. **Results:** WES identified variants, including a stop-gain, an indel, and a missense mutation, in the genes *SLC11A3*, *MYO15A*, and *MYO15A*. These variants were classified as likely pathogenic, one variant as a variant of uncertain significance (VUS), and one variant as likely benign. Homozygous variants in *SLC11A3* and *MYO15A* were identified within BCFI regions, including autosomal recessive inheritance. Additionally, two heterozygous variants in the *SLC11A3* and *MYO15A* genes were identified. This study indicates a high degree of genotypic and phenotypic heterogeneity of hearing loss among affected individuals. **Conclusion:** This integrated approach, which combines homozygosity mapping with WES, could be effective for diagnosing NSHL in affected individuals. Further genetic, genetic, and clinical studies on NSHL in consanguineous families is also warranted. Genetic testing in high-risk populations could be a valuable method for diagnosing genetic hearing loss in children.

Keywords: non-syndromic hearing loss; genetic heterogeneity; genetic testing; homozygosity mapping; APOC5A



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**Contribution of animals to biomedical advancements in the current era:
A narrative review**

Review Article

Thai Journal of Pharmaceutical Sciences



**Contribution of animals to biomedical
advancements in the current era: A
narrative review**

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ABSTRACT

Animal research has played a major role in the development of vaccinations and therapies for diseases such as cancer, pain, neurological, infectious, and chronic disease Regulatory System, Convention 2. For every principle drug available today, animal testing and research have contributed immensely. This narrative review aims to explore the contribution of animals to biomedical advancements in the current era, which involved a wealth of pre-estimated research using domesticated animals such as Sprague-Dawley Rats, and Mice. In current biomedical research, animals help develop new treatments for long-term diseases such as cancer, HIV, and Alzheimer's. Animals also aid in the development of antibodies and vaccines, act as disease models, help to test the therapeutic efficacy of drugs, and help in understanding complex biological systems. Among the specific developments are treatments for heart disease and diabetes, methods for organ transplantation, and knowledge of brain waves such as COVID-19. Several animal studies are listed in the current era of the current research process, from disease modeling to the identification of a cure, in both academic and industry. However, increasing animal welfare and ethical concerns have led to the emergence of alternative sources. With advances in computer science and simulation research, scientists are trying to replace animal models with large-scale in vitro and in silico models, and tissue-based models. While the majority of these technologies is in their early stages or recent status, a whole animal study, it appears that there is still a long way to go before animal studies are completely replaced by these technologies. Until then, the prudent and ethical utilization of animals, along with developing valid and reliable alternatives, appears to be an integral part of cutting-edge biomedical research.

Key words: Animal experiments, biomedical research, laboratory animals, medical advancements, toxicity research

INTRODUCTION

The involvement of animals in biomedical research continues to be crucial for understanding the origins, identification, and management of disease and disease

both humans and animals. In addition to providing knowledge, fundamental biological and medical research, the development of novel diagnostic and therapeutic approaches, the outcomes there would be how these research outcomes based on messenger ribonucleic acid (mRNA) of brain tissue

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