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Library Attendance Management System by Face Recognition using Deep Learning Algorithm

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Abstract

One the most challenging task is detecting faces in libraries because of complex background. So, in this application, library attendance management system is designed by face recognition using deep learning. Library visiting students or faculties attendance will be automatically managed by capturing face of the student/faculty member and deep learning helps in classification of face based on facial features.Its more user friendly and simple compared to state of art techniques for library attendance management. Convolutional neural network (CNN) is used as deep learning algorithm which classifies the obtained/ captured face with more than 95% accurately. The obtained attendance is saved in Ms-Excel with person name, time with date.CNN shows better performance compared with state of art machine learning techniques such as support vector machine, decision tree classifier,etc.

Keywords
Face Recognition; Deep learning; LMS;
Convolutional Neural Network (CNN).
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I. Introduction

Face recognition is recognising or confirming a person's identification from their face. It analyses patterns based on a person's facial features, compares the features, and saves the final features. A facial recognition system is a touchless method of managing students, faculty and visitors, unlike other biometric systems like fingerprints that collect identity through touch. The system notifies the appropriate identity in simple language if it notices anything unusual or an unknown face. An organisation can manage visitors and employees without physical contact using a facial recognition library attendance management system. It avoids the possibility of workplace theft or fatalities. In addition, these systems are capable of simultaneously detecting multiple faces. Face detection helps in the capture of terrorists, criminals and improves monitoring. Personal security is enhanced because hackers may steal or alter passwords or other sensitive information. Face recognition system have several advantages as, including social acceptance and simplicity. Just we need a device to capture photo, and it will work. Face recognition is simple and can even be done without the subject's in-depthknowledge. The CC-camera is present in almost all premises. Face detection is a necessary first step in identifying and locating human faces in images and videos.

The input layer has just one feature map, which feeds the CNN model with the normalised facial images. A face recognition-based attendance system for library means identifying students using a face biostatistics system based on high-definition tracking computer technologies and high-definition tracking. In addition, these systems are capable of simultaneously detecting numerous faces. The software photographed all allowed individuals, which then entered the data into a database. The system then maps the image into a face coordinate structure for storage.

A system that identifies the person's face is known as face recognition system. Due to its application in security systems, video surveillance, access control, and even social networks like Facebook and commercial spaces have become crucial tools for human-computer interaction. Face recognition has regained popularity after the rapid growth of artificial intelligence because of its non-intrusiveness and because, compared to other biometric techniques, it is the primary method of identifying a human being. Face recognition can be tested without the subject's

knowledge in an uncontrolled setting. When the history of facial recognition is examined, it becomes clear that numerous research articles have been published on the topic.

The system notifies the appropriate person if it notices anything unusual or an unknown face. This avoids the possibility of workplace theft or mishaps. In addition, these systems are capable of simultaneously detecting numerous faces. CNN is used in the face-recognition model. A CNN model is created in this study to increase the precision of facial data classification. The structure is comparable to the conventional machine learning model, but specific characteristics, such as input data, network width, and the whole layers used in CNN are different.

In facial recognition based on shallow learning, the traditional methods face a few challenges, such as the background of the photograph being complex, scene lighting, facial disguises, pose variation and changes in the background. To extract sample features from a few essential elements of images and depend on the artificial experience based on shallow learning. But the more complicated parts of the face from different background can be extracted based on deep learning knowledge. Deep learning is significantly advancing the resolution of problems that based on neural networks, the most significant part of the artificial intelligence sector. It is suitable for many sciences, business, and government areas since it has demonstrated promising results in exposing complicated structures in high-dimensional data.

It has destroyed chiefly records in various real-world contexts, including semantic segmentation, recognition on image, and natural language processing. With one or a few algorithms, it handles the issue of learning hierarchical representations. The deep learning approaches include the deep Belief network (DBN), stacked autoencoder, and convolutional neural network (CNN). In face and image recognition, CNN is mainly used as CNN has multiple layered structure with different uses. The goal of CNN, an artificial neural network that uses convolution, is to increase the number of features retrieved from the input data.

In different type of data recognition such as handwriting recognition, LeCun proposed CNN, which was first applied. In the field, for many scientists, the work of the LeCun network was the origin of the true inspiration and contemporary architectures; in ImageNet competition when Hinton, Sutskever and Krizhevsky published their work and achieved the rest results. It has shown that CNNs performances outperform recognition compared to handmade-based approaches and are recognised as one of the most prominent studies in computer vision. With the computational power of edge detection, semantic segmentation, scene recognition, and image recognition, CNN has achieved remarkable cutting-edge results in several areas, including Graphical Processing Units (GPUs).

This paper's significant contribution is the development of a robust face recognition algorithm that is highly accurate with complex background. We created a new CNN architecture in this article by introducing a Batch Normalization step after two separate layers. Three stages make up this paper's general structure of the face recognition process.

- Pre-processing is the 1st step which includes changing and resizing the colour space of the photographs.
- The extraction of facial features is the next step, which is followed by classification of the extracted feature set.
- The SoftMax Classifier in our system will carry out the system's final stage, in which categorization based on facial traits is pulled from CNN.

II. Literature Survey

We are all aware that a person may be recognised by their face, which is a distinctive and essential component of their physical makeup. Any face processing system must start with face detection, locating faces in an input image. This paper's goal is for face detection to present an algorithm used and reviewing methods. It detailed the algorithmic Haar cascade. In a natural time, environment for face detection robustly, we offer a methodology. Here, we utilise the open-source OpenCV platform's Haar cascade-style classifier to detect faces. This paper's main idea to reduce the crime rate is to test the use of deep learning neural networks for crime detection and effective criminal recognition in real-world situations.

For the police, tracking and manually doing this is very difficult. To trace the criminal person's identity, we used the proposed system. We can place CCTV in public places with technological advancements to capture the criminal's image. To detect the face automatically and recognise the face, this system will

be able. The criminal face recognition system can be used with the previously photographed faces and criminals' photos that are on hand in the police station. We sued some image processing tools and deep learning libraries to achieve this task. [1]

To explain and discuss how humans recognise familiar faces and the connection between recognition and other elements of face processing, the purpose of this study is to establish a theoretical model and a set of words. According to research, we can infer seven categories of information from faces. These are identity-specific semantics, facial speech codes, visually derived semantics, expression, name, structural, and pictorial. For face recognition units, facial speech analysis, and presentation analysis, a functional paradigm is put out in which structural encoding processes produce appropriate descriptions. A match between the previously recorded structural codes and structural encoding findings, included in face recognition units, characterising the appearance of recognised faces, is required to recognise identifiable faces.

After accessing identity-specific semantic codes from person identification nodes, name codes are next retrieved. Additionally, it is suggested that the cognitive system decides for itself whether the first match is close enough to indicate actual recognition or only a likeness, with a number of factors supposedly influencing such determinations. Data from many different sources, such as laboratory testing, studies of frequent mistakes, and studies of individuals with various types of cerebral injury, are combined using this functional model. It also highlights the parallels and discrepancies between the processes in charge of object recognition, face and word.[2]

In computer vision and image analysis, face recognition presents a challenging problem. Information security is becoming increasingly important and complex. Currently, security cameras are prevalent in ATMs, banks, offices, universities, and other places with security systems. A biometric system called face recognition is used to recognize or authenticate a person from a digital image. In security face recognition system is used. A face recognition system should automatically recognize a face in a picture. This includes separating its traits before realizing them, which is challenging, regardless of illumination, ageing, lighting, expression, alterations, and stance. [3]

Face recognition has been one of the most successful uses of photo analysis and comprehension in recent years, particularly in the last few. This rise can be attributed to at least two factors: the broad spectrum of business and law enforcement applications and the maturation of usable technology after 30 years of research. Even if modern machine recognition systems have developed to a certain level of maturity, the restrictions placed on them by numerous practical applications limit their potential. For instance, it can still be challenging to identify faces in pictures of people taken outside in dynamic lighting or positions.

In other words, current systems still fall far short of what the human perception system is capable of. An up-to-date critical assessment of facial recognition studies using still images and videos is presented in this article. We wrote this survey study for two reasons: First, to offer a current evaluation of the relevant literature, and second, to provide some insights into the study of machine face recognition. To give a comprehensive survey, we categorize existing recognition approaches and provide in-depth descriptions of typical methods within each category. Additionally, pertinent subjects like psychophysical research, system evaluation, and lighting and position change problems are explored.[5]

The Scale Invariant Feature Transform (SIFT) method has proven effective for broad object detection and recognition. This research offers two novel face recognition methods based on the original SIFT algorithm: Partial-Descriptor-SIFT (PDSIFT) and Volume-SIFT (VSIFT). We contrast feature-based approaches, SIFT and PDSIFT, with holistic approaches, Fisher face (FLDA), the null space approach (NLDA), and Eigen feature Regularization and Extraction (ERE). Research on the AR and ORL databases demonstrates that PDSIFT performs noticeably better than the original SIFT technique. Moreover, PDSIFT powerfully beats NLDA and FLDA and can achieve performance levels comparable to ERE's most effective holistic technique. [7]

Face recognition is one of the most widely used visual analysis and comprehension techniques. This research presents a novel identity identification method based on the rank-level fusion of various face representations. In this research, we offer a face recognition method that combines Principal Component Analysis and Linear Discriminant Analysis, two well-known appearance-based methods. With the Borda count approach, fusion is

performed at the rank level. Our research shows that group face representations significantly outperform individual face representations regarding recognition accuracy. [9]

III. Proposed Method

Proposed method in this application is library attendance management system based on face recognition using deep learning algorithm.Deep learning algorithms helps in getting more precise results compared to state of art machine learning techniques.

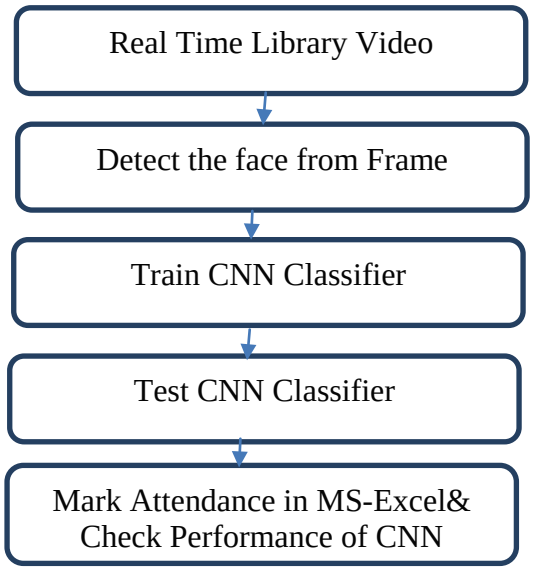


Fig.3.1 Block Diagram of Proposed Methodology

Above figure shows block diagram of proposed methodology, which shows total five steps. As mentioned in proposed block diagram, following steps are used for library attendance management,

a) Real Time Library Video
b) Detect the face from frame
c) Train CNN classifier
d) Test CNN classifier
e) Mark attendance in MS-Excel and check performance of CNN algorithm.

In first step, the input frame is considered as image and face detection algorithm is used as finding the face part from input frame. The detected face part from input frame is considered as facial features. Detected facial features from image are used for training the classifier. CNN algorithm will get train using saved images in database.

Same trained CNN is used for predicting the results for new test data. There are multiple layers are available in CNN. Obtained recognition results are even saved in MS-excel with Roll No., Name and time.
CNN Algorithm used is as shown below,

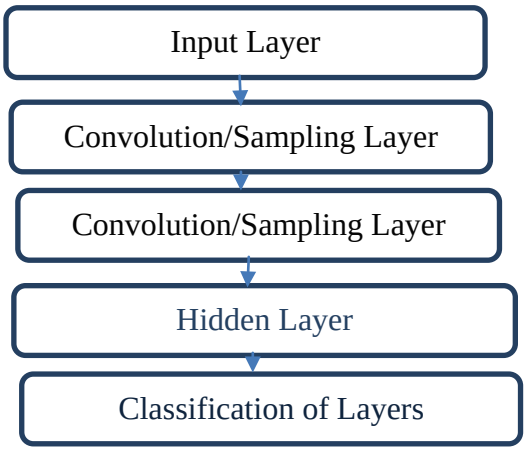


Fig.3.2 Structure of CNN model designed

As shown in above figure there are 5 layers used as 'input layer' which is first layer, while second and third layers are having same convolution / sampling layer.Fourth one is hidden layer and last layer is classification layer.

Input layeris used at the starting which is compete input to the network. This input provides complete matrix format data to the network.while 2nd layer is used as convolution /sampling layer.Features of an image can be extracted using convolution layer while sampling layer is used for resizing the data. Hidden layer has multiple layers which means that activation function is not required separately. Classification layer consider entropy loss calculations which helps in comparison.

IV.Result Analysis

In results analysis there are two main steps as,

a) Training Faces in library
b) Testing new faces from library

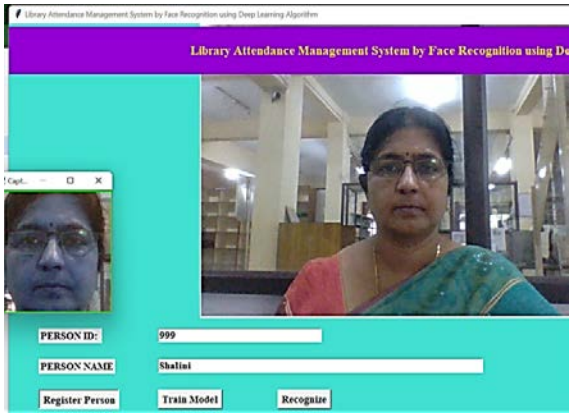


Fig.4.1 Detection of Face Part for Training CNN

Here, from the library we started detecting faces. If any face part found then we show the detected face part by Viola-Jones algorithm.

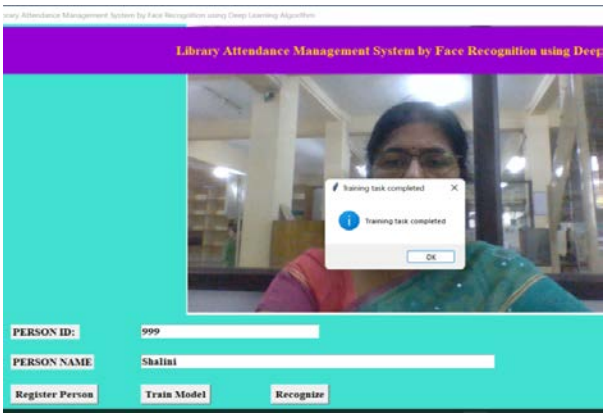


Fig.4.2 Training CNN Algorithm

Training face features to the CNN algorithm which is deep learning algorithm. Trained faces will be saved in database.

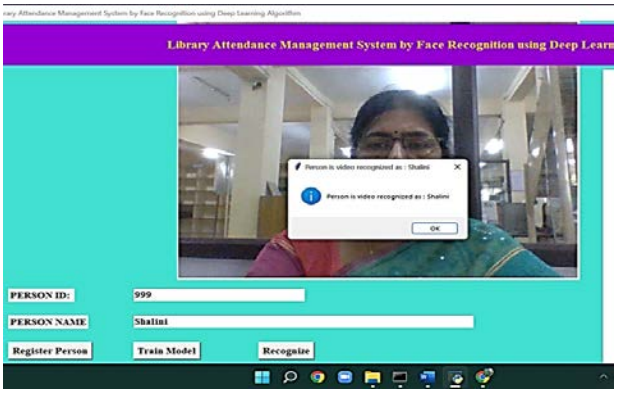


Fig. 4.3 Predicted Results as 'Shalini' using CNN

In prediction, trained model is used for predicting new face image. With the help of trained model, we can differentiate the faces and final predicted result is displayed on screen.

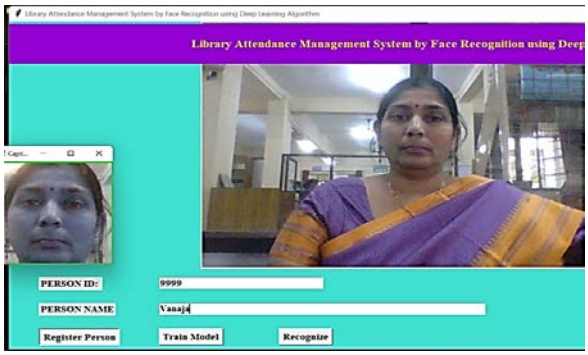


Fig.4.4 Detection of Face part for trainingCNN

Face is detected from screen for person-2. Detected face part can be further used for recognition using deep learning algorithm.

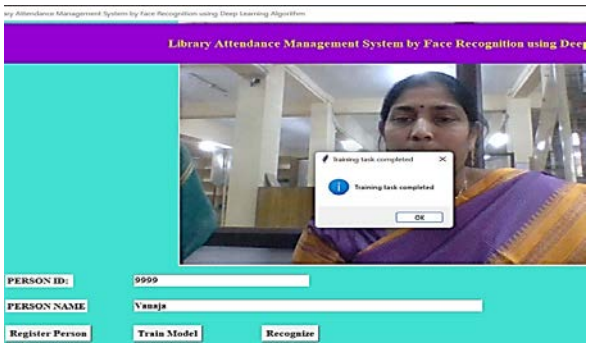


Fig.4.5 Training CNN Algorithm

With 2nd person face image, training task of CNN is completed. After training, trained images will be saved in one folder.

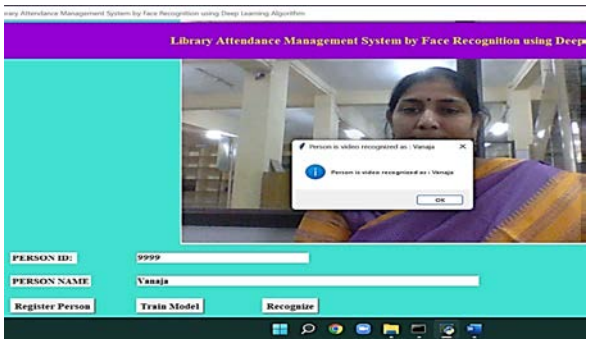
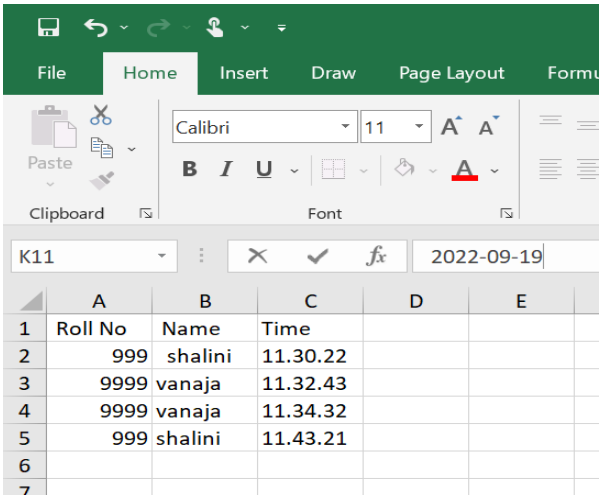


Fig.4.6Predicted results as 'Vanaja' using CNN

For second person prediction, CNN is used and obtained face recognition result as 'Vanaja' as shown on screen.



	A	B	C	D	E
1	Roll No	Name	Time		
2	999	shalini	11.30.22		
3	9999	vanaja	11.32.43		
4	9999	vanaja	11.34.32		
5	999	shalini	11.43.21		
6					

Fig.4.7 Library Attendance is managed in MS-Excel

The obtained results are updatedin MS-Excel with the Roll No., Name and time at which the student has entered library.

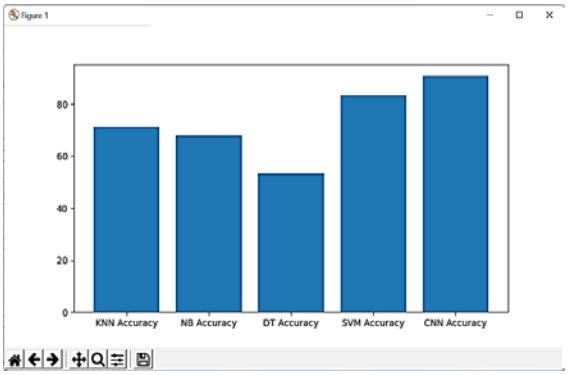


Fig.4.8 Accuracy classification of different algorithms

Accuracy of different classifiers are compared for face recognition and obtained results are shown in above bar graphs. With the help of above bar graph, we can say that proposed CNN algorithm gives better performance compared to state of art techniques such as KNN, NB, DT and SVM.

V. Conclusion

Face recognition in library is a challenging task which is handled in this application using deep learning. There are many traditional techniques have been used for attendance management in library. By studying fewer techniques and their limitations, in this application deep learning is used which gives very high accuracy than traditional algorithms such as SVM, KNN, Decision tree algorithms. In deep learning CNN algorithm is used for improving performance and for getting higher accuracy. With the help of accuracy comparison, we found that CNN has higher accuracy than state of art techniques.

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The Journal of Gene Medicine

Edited by: Gening Jiang

Impact factor (2021): 4.152

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GSK484, an inhibitor of peptidyl arginine deiminase 4, increases the radiosensitivity of colorectal cancer and inhibits neutrophil extracellular traps

Binbin Wang, Xiaojuan Su, Bo Zhang, Shiwen Pan

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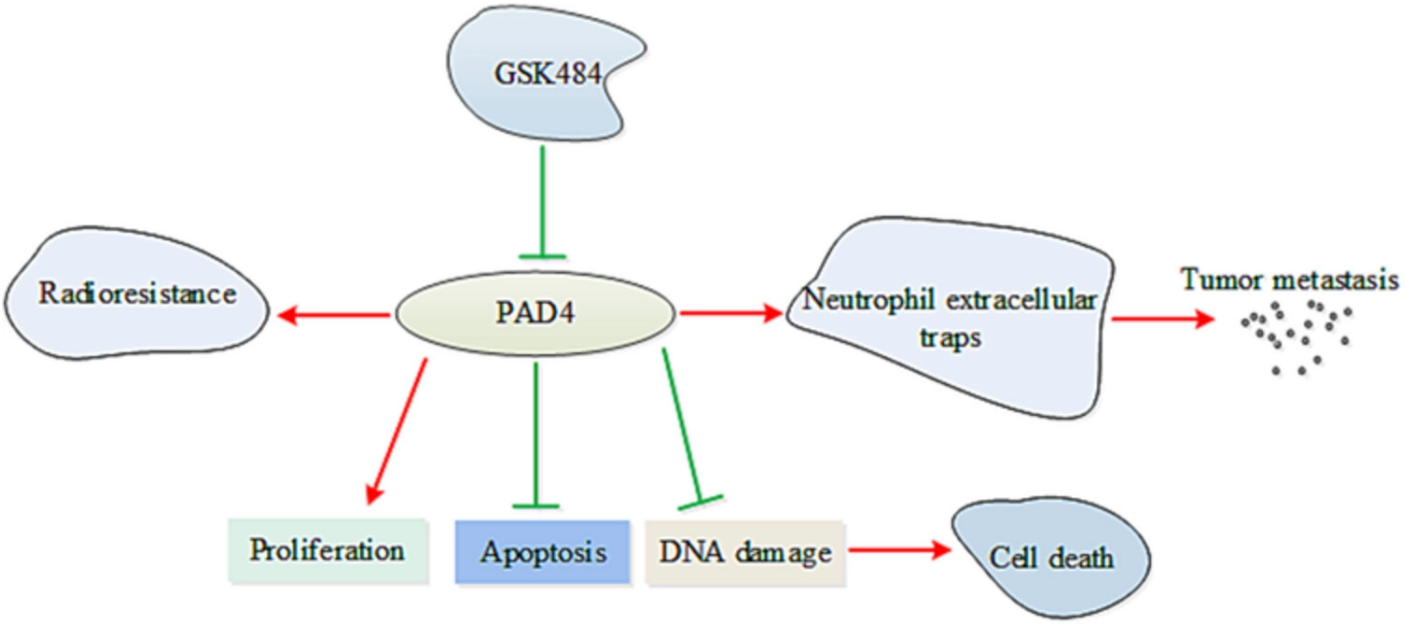

PAD4 inhibitor GSK484 inhibits colorectal cell proliferation, promotes the radiosensitivity of cells and induces cell death by promoting DNA double-strand breaks. Additionally, GSK484 inhibits the metastasis of colorectal cancer by promoting the formation of neutrophil extracellular traps.

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Qiuyuan Shao, Chunming Jiang, Qingyan Zhang, Jing Liu, Bo Jin, Min Zhao, Yangyang Xia

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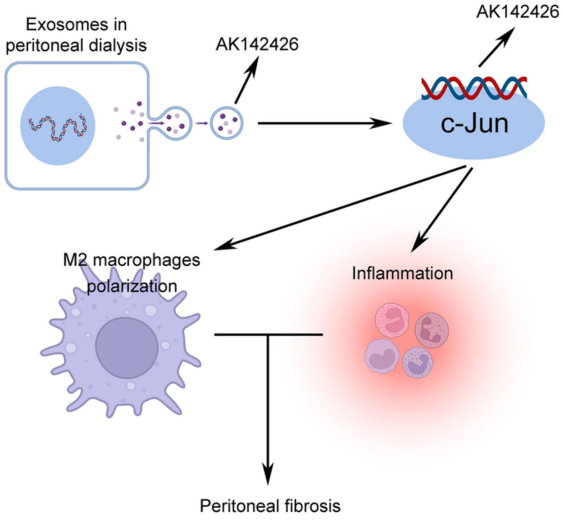

AK142426 in exosomes in peritoneal dialysis directly bound to c-Jun, and then induced M2 macrophage polarization and inflammation, thereby aggravating peritoneal fibrosis.

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A combined diagnostic model based on circulating tumor cell in patients with solitary pulmonary nodules

Dong Wang, Peng Li, Xiang Fei, Shuyu Che, Jinlong Li, Yunpeng Xuan, Jinglong Wang, Yudong Han, Weiqing Gu, Yongjie Wang

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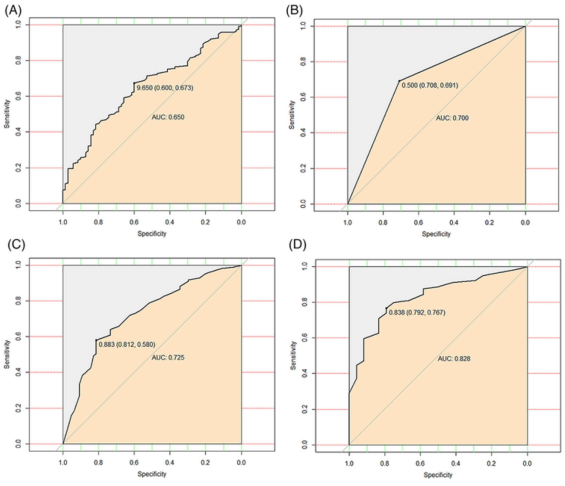

The AUCs of $FR^{+}CTC$ in diagnosing NSCLC were 0.650 (95% CI, 0.587–0.713) in the training set and 0.700 (95% CI, 0.603–0.796) in the validation set. When the $FR^{+}CTC$ was combined with age, sex, AGR and NSE, the AUCs were 0.725 (95% CI, 0.659–0.791) in the training set and 0.828 (95% CI, 0.754–0.902) in the validation set.

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Shazia Khan, Muhammad Umair, Safdar Abbas, Uroba Ali, Gohar Zaman, Muhammad Ansar, Rongrong Wang, Xue Zhang, Henry Houlden, Gaurav V. Harlalka, Asma Gul

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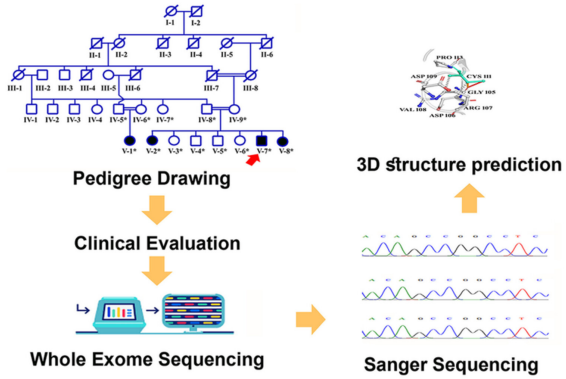

First, a clinical examination is carried out on the patient, including magnetic resonance imagining and a computed tomography scan. Standard procedures are used to perform whole exome sequencing and Sanger sequencing. To further understand the pathogenic nature of the mutation, 3D protein modeling is conducted.

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Prognostic analysis and validation of lncRNAs in bladder cancer on the basis of neutrophil extracellular traps

Lan Gu, Hao Guo, Long-Xiang Wu, Jun-Bin Yuan

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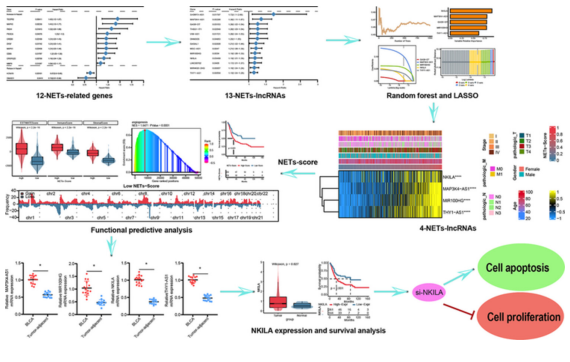

Four NET-lncRNAs in BLCA, MAP 3 K4-AS1, MIR100HG, NKILA and THY1-AS1, were identified via random forest (RF) and last absolute shrinkage and selection operator (LASSO) analyses. The NET-Score was obtained via the four NET-lncRNAs. Functional predictive and survival analysis was performed. Then, expression of four NET-lncRNAs was detected in tissues. Finally, *in vitro* experiments confirmed that si-NKILA promoted apoptosis and inhibited the proliferation of BLCA cells.

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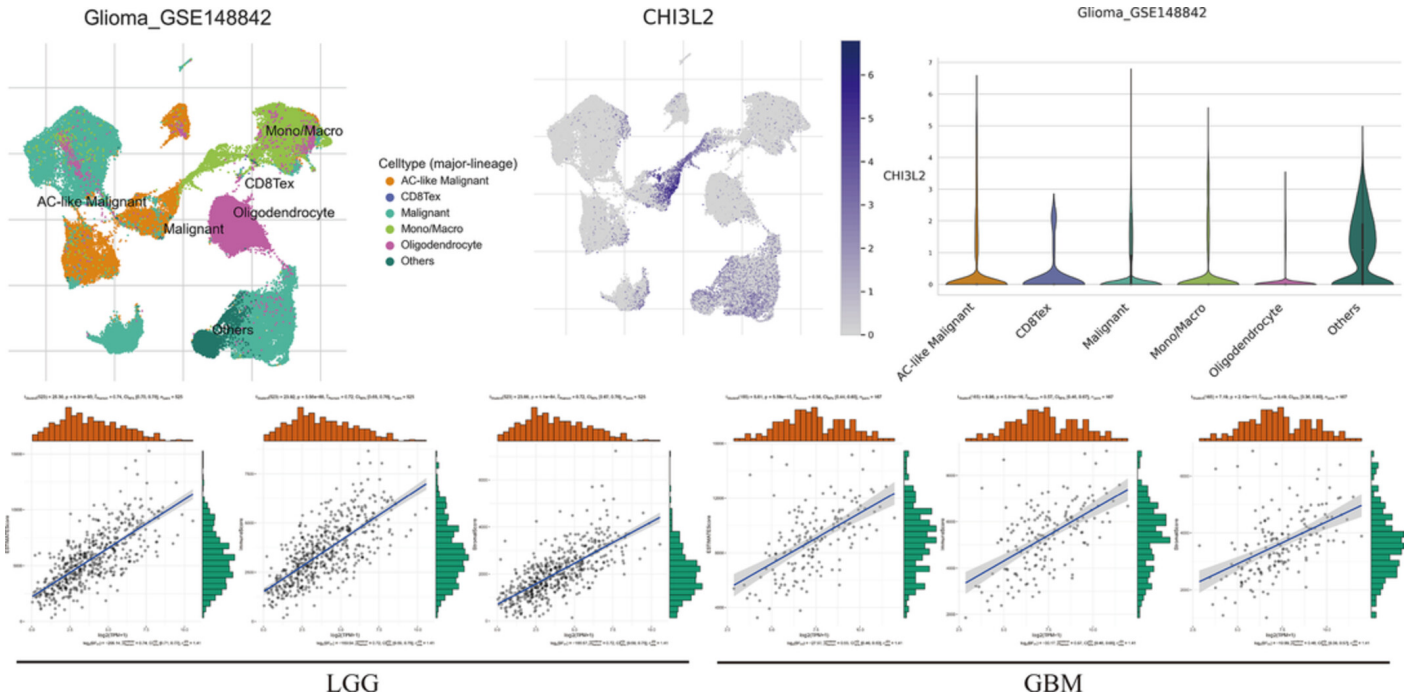
M2 macrophage marker CHI3L2 could serve as a potential prognostic and immunological biomarker in glioma by integrated single-cell and bulk RNA-Seq analysis

Wenbo Qian, Qi Wang, Chi Zhang, Junle Zhu, Qing Zhang, Chun Luo



We conducted this study for the first time by integrating bulk RNA-seq, proteomics and scRNA-seq proteomics to examine the roles of CHI3L2 in gliomas. The expression of CHI3L2 was markedly higher in glioma tissues compared with normal tissues by analysis of the data from the TCGA and CGGA datasets and as verified by GSE4290, GSE50161, qRT-PCR and IHC results, making our results more reliable. CHI3L2 was revealed to be significantly related to immunity, indicating its potential prognostic roles and immunological roles in glioma.

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CHI3L2 was revealed to be significantly related to immunity, indicating its potential prognostic roles and immunological roles in glioma.

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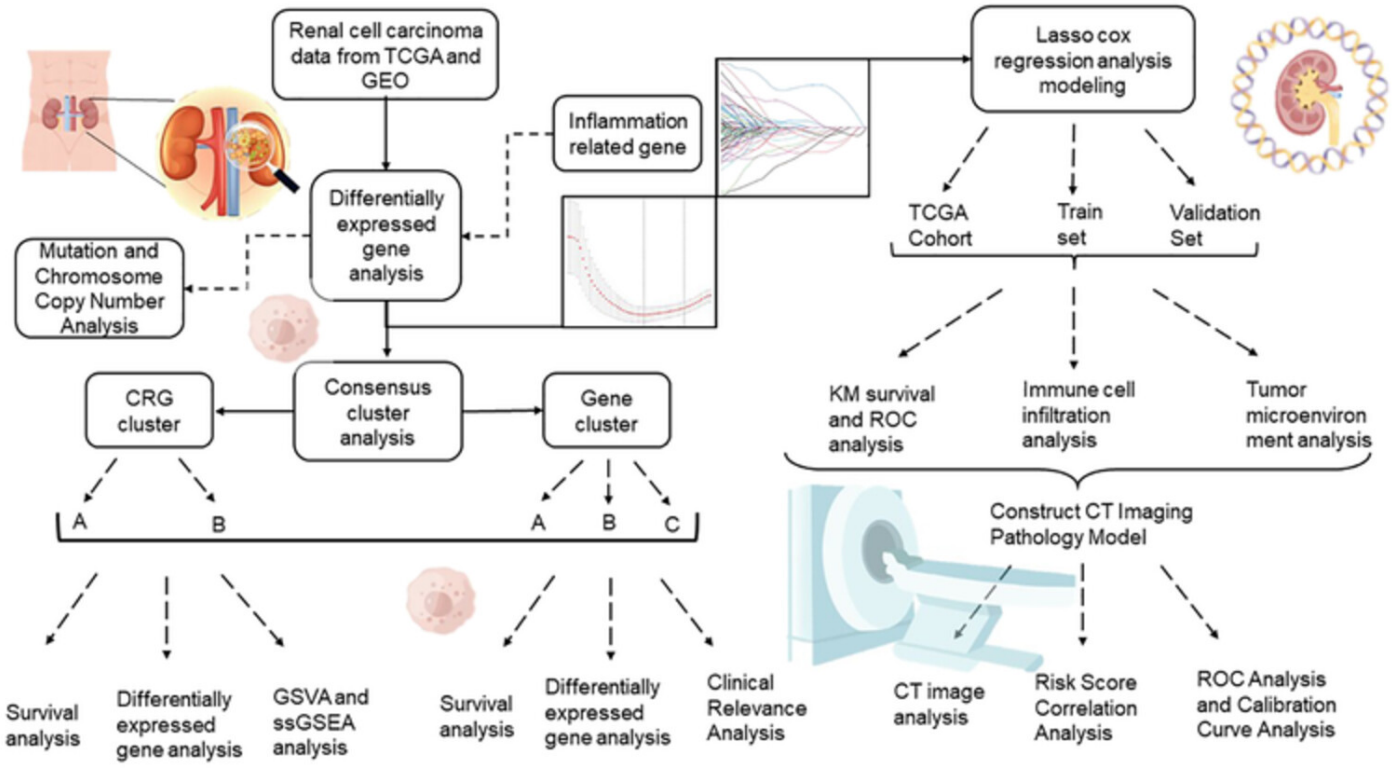
Transcriptome mapping of renal clear cell carcinoma revealed by machine learning algorithm based on enhanced computed tomography images



The key step of the study was to replace genetic testing with computed tomography images, obtain imaging features and construct imaging models with machine learning algorithms.

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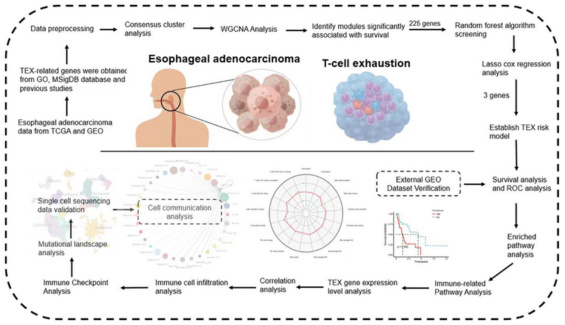
T-cell exhaustion: A potential target biomarker of the tumour microenvironment affecting oesophageal adenocarcinoma

Shiyu Peng, Xiaojiang Han, Wenbin Geng, Lifang Zhao

The Journal of Gene Medicine | Version of Record Online: 2 May 2023



The flow chart shows the process of data collection and processing for oesophageal adenocarcinoma. The prognosis model was obtained by unsupervised clustering, weighted correlation network analysis, LASSO–Cox regression and other algorithms.

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Su Jin Choi, John S. Yi, Jeong-A Lim, Thomas F. Tedder, Dwight D. Koeberl, William Jeck, Ankit K. Desai, Amy Rosenberg, Baodong Sun, Priya S. Kishnani

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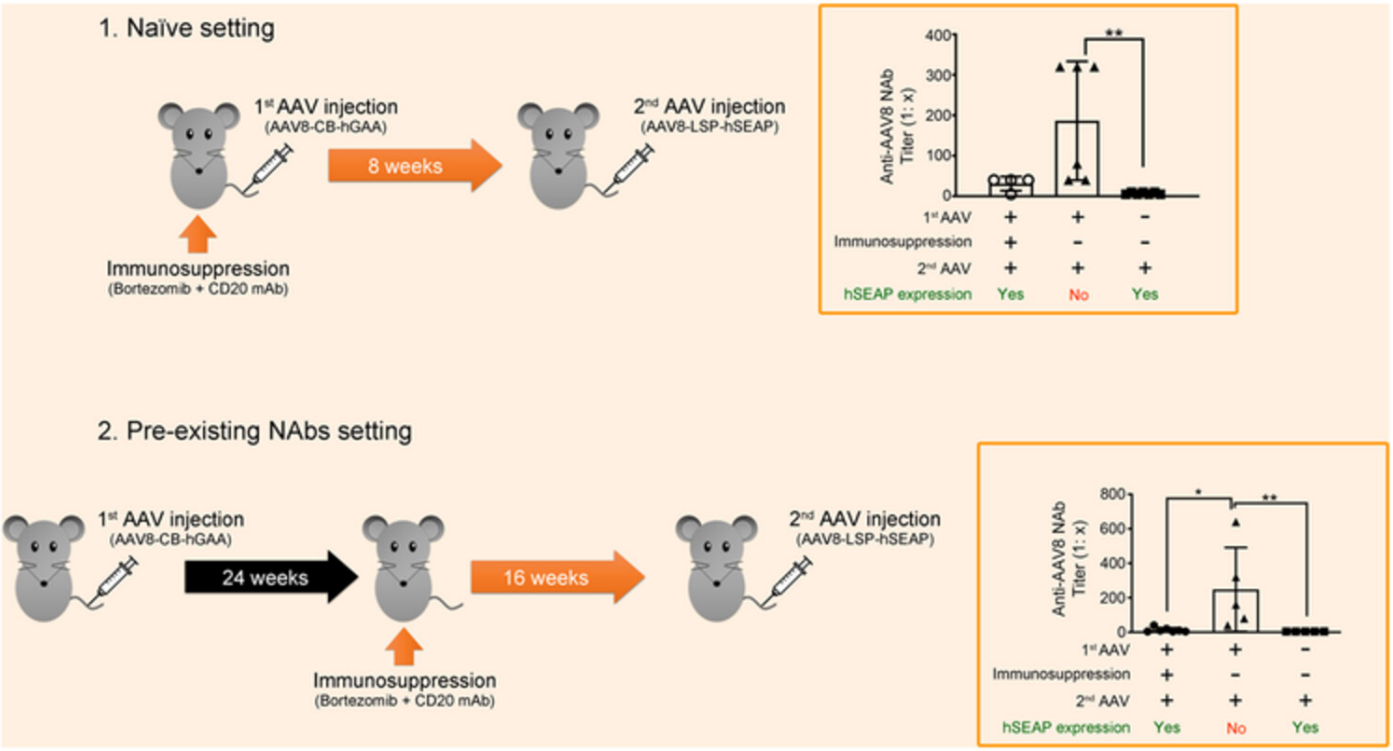

A combination immunosuppression treatment with bortezomib and a mouse-specific CD20 monoclonal antibody effectively suppressed anti-adeno-associated virus (AAV) neutralizing antibodies (NAbs) in naïve mice and in mice with pre-existing antibodies, allowing successful re-administration of the same AAV capsid vector.

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Monkeypox: Virology, laboratory diagnosis and therapeutic approach

Haleh Siami, Arghavan Asghari, Negin Parsamanesh

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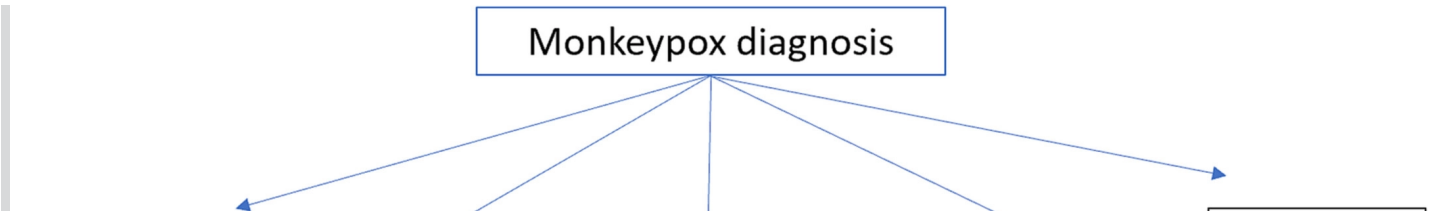

> Monkeypox infection outbreaks have been observed sporadically in Africa, usually as a result of interaction with wildlife reservoirs. Depending on the kind of exposure, patients with monkeypox may experience a febrile prodrome 5–13 days after exposure, which frequently includes lymphadenopathy, malaise, headaches, and muscle aches. A different diagnostic approach is available for monkeypox including, histopathological analysis, electron microscopy, immunoassays, polymerase chain reaction, genome sequencing, microarrays, loop-mediated isothermal amplification technology and CRISPR (i.e., "clustered regularly interspaced short palindromic repeats").

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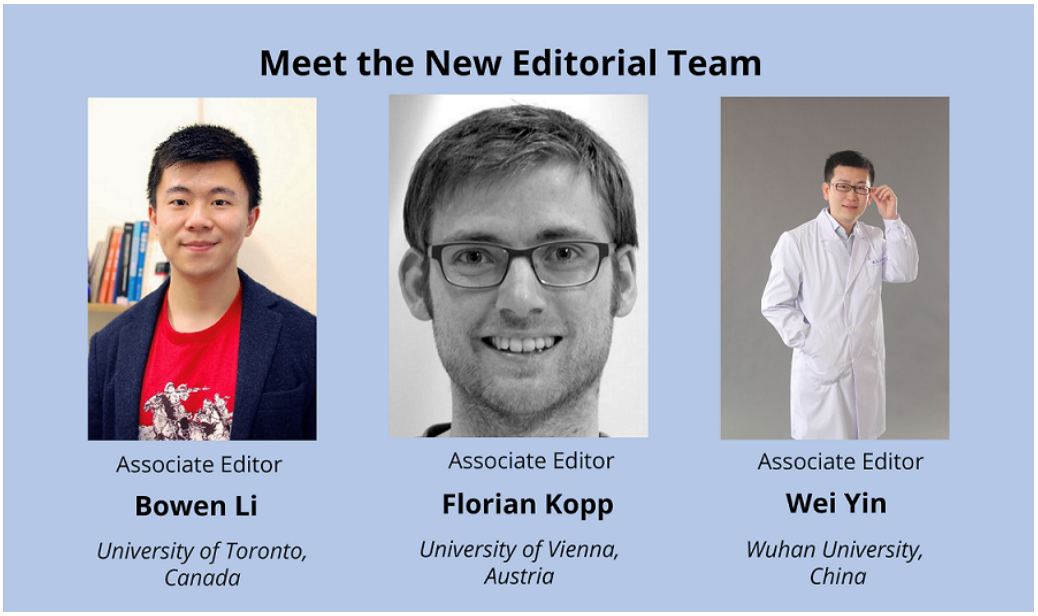

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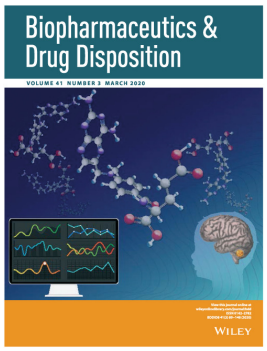

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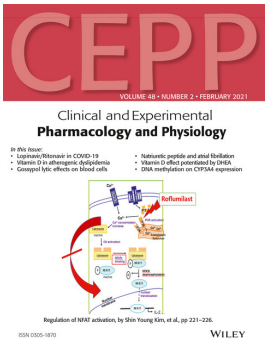

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J Gene Med. 2021 Aug;23(8):e3346. doi: 10.1002/jgm.3346. Epub 2021 May 22.

PCSK9 genetic (rs11591147) and epigenetic (DNA methylation) modifications associated with PCSK9 expression and serum proteins in CAD patients

Nivas Shyamala [1], Kishore Kumar Gundapaneni [1], Rajesh Kumar Galimudi [1 2], Mohini Aiyengar Tupurani [1], Chiranjeevi Padala [1 3], Kaushik Puranam [1], Keerthi Kupsal [1], Ramanjaneyulu Kummari [1], Srilatha Reddy Gantala [1], Krishna Reddy Nallamala [4], Sanjib K Sahu [4], Surekha Rani Hanumanth [1]

Affiliations

PMID: 33885177 DOI: 10.1002/jgm.3346

Abstract

Introduction: Proprotein convertase subtilisin/kexin type 9 (PCSK9) genetic polymorphisms play a significant role in cholesterol homeostasis. Therefore, we aimed to investigate the association of PCSK9 genetic variations NM_174936.3:c.137G>T (R46L, rs11591147) and NM_174936.3:c.1120G>T (D374Y, rs137852912), as well as promoter DNA methylation status, with mRNA expression and circulating serum protein levels in coronary artery disease (CAD) patients.

Methods: The present study includes 300 CAD cases and 300 controls from South India. Biochemical assays were performed using commercially available kits. PCSK9 rs11591147 and rs137852912 polymorphisms were analyzed by the polymerase chain reaction (PCR)-restriction fragment length polymorphism method, whereas promoter DNA methylation status and gene expression were determined using methylation specific PCR and quantitative PCR respectively.

Results: The genotypic distribution of PCSK9 rs11591147 revealed that individuals with the TT-genotype and T-allele have a reduced risk for CAD. Furthermore, patients with the PCSK9 rs11591147 TT genotype have a significantly lower total cholesterol and low-density lipoprotein-cholesterol levels and also higher high-density lipoprotein-cholesterol levels than individuals with the GG genotype. Logistic regression analysis has shown that the GG and GT ($p = 1.51 \times 10^{-8}$, $p = 1.47 \times 10^{-9}$) genotypes predicted the risk for CAD with an odds ratio of 5.8 and 7.3 respectively. In addition, individuals with the TT genotype were hypermethylated at promoter DNA of PCSK9, resulting in lower mRNA expression and circulating serum proteins than in individuals with the GG genotype. In silico analyses revealed that rs11591147 T-allele has protein destabilizing capacity.

Conclusions: In conclusion, the present study indicates that the PCSK9 gene expression and circulating serum protein levels are not only associated with rs11591147 genotype, but also with promoter DNA methylation. Furthermore, the findings with respect to both single nucleotide polymorphism and promoter DNA methylation may open avenues for novel treatment possibilities targeting PCSK9 for CAD management.

Keywords: LDL-C; genotypes; methylation-specific PCR; promoter DNA methylation; proprotein convertase subtilisin/kexin type 9; qPCR.

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