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Identification of ZMYND19 as a novel biomarker of colorectal cancer: RNA-sequencing and machine learning analysis

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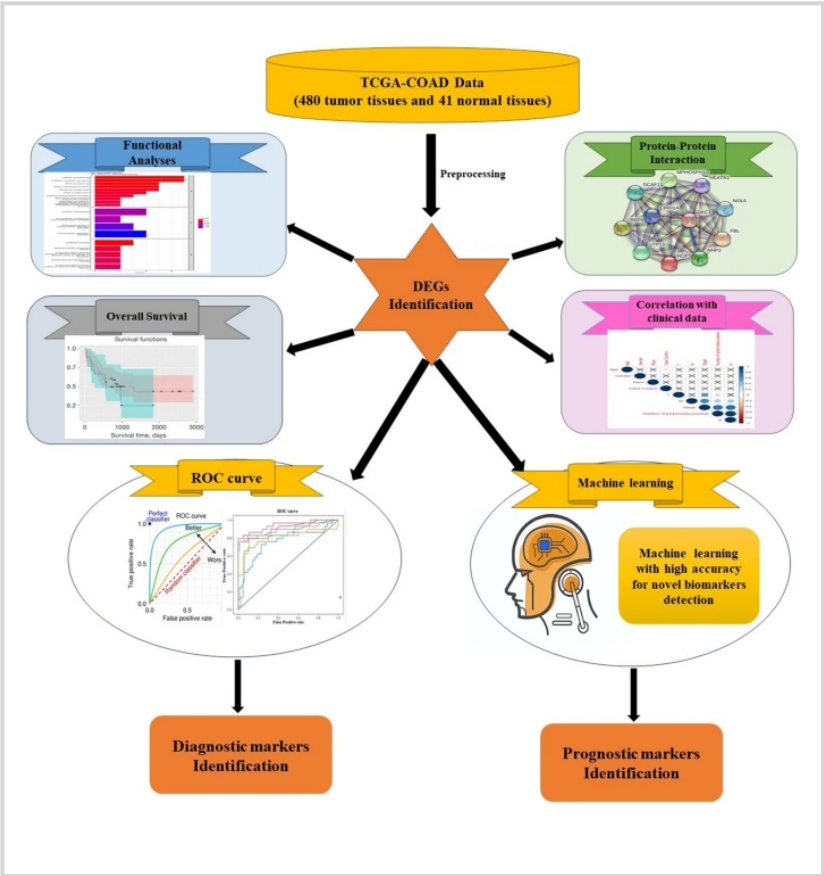
Abstract

Colorectal cancer (CRC) is the third most common cause of cancer-related deaths. The five-year relative survival rate for CRC is estimated to be approximately 90% for patients diagnosed with early stages and 14% for those diagnosed at an advanced stages of disease, respectively. Hence, the development of accurate prognostic markers is required. Bioinformatics enables the identification of dysregulated pathways and novel biomarkers. RNA expression profiling was performed in CRC patients from the TCGA database using a Machine

Learning approach to identify differential expression genes (DEGs). Survival curves were assessed using Kaplan–Meier analysis to identify prognostic biomarkers. Furthermore, the molecular pathways, protein–protein interaction, the co-expression of DEGs, and the correlation between DEGs and clinical data have been evaluated. The diagnostic markers were then determined based on machine learning analysis. The results indicated that key upregulated genes are associated with the RNA processing and heterocycle metabolic process, including C10orf2, NOP2, DKC1, BYSL, RRP12, PUS7, MTHFD1L, and PPAT. Furthermore, the survival analysis identified NOP58, OSBPL3, DNAJC2, and ZMYND19 as prognostic markers. The combineROC curve analysis indicated that the combination of C10orf2 -PPAT- ZMYND19 can be considered as diagnostic markers with sensitivity, specificity, and AUC values of 0.98, 1.00, and 0.99, respectively. Eventually, ZMYND19 gene was validated in CRC patients. In conclusion, novel biomarkers of CRC have been identified that may be a promising strategy for early diagnosis, potential treatment, and better prognosis.

Graphical abstract



Abbreviations

CRC: Colorectal cancer

DEGs: Differential expression genes

COAD: Colon adenocarcinomas

READ: Rectum adenocarcinomas

TCGA: The Cancer Genome Atlas

SVM: Support vector machine

KNN: K-nearest neighbors algorithm

DTs: Decision Tree

RF algorithm: Random Forest

ML: Machine learning

ROC curve: Receiver operating characteristic curve

AUC: Area under the *Curve*

GDAC: Global Data Assembly Centres

GEO: Gene expression omnibus

FFPE: Formalin-fixed *Paraffin*-embedded

IOSCA: Infantile-onset spinocerebellar ataxia

PEO: Progressive external ophthalmoplegia

snoRNPs: Small nucleolar RNPs

HCC: Hepatocellular carcinoma

OS: Overall survival

ccRCC: Clear cell renal cell carcinoma

PC: Prostate cancer

CDKs: Cyclin-dependent kinases

OC: Ovarian cancer

DL: Deep learning

ESCC: Esophageal squamous cell carcinoma

NSCLC: Non-small cell lung cancer

HNSCC: Head and neck squamous cell carcinoma

LASSO: Least absolute shrinkage and selection operator

DEMs: Differentially expressed miRNA

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Contributions

GK-T, EN, RM, AA, and MD have gathered study data and written the manuscript. MK, SMH, MM, MG-M, GAF, MAK, MN, and AA have provided critical revision of the final manuscript. EN and AA have contributed to the study design and approved the final version of the manuscript. All the authors read and approved the final version of the manuscript.

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Ethics declarations

Conflict of interest

The authors have no conflict of interest to disclose.

Additional information

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