ABSTRACT

Skin Cutaneous Melanoma (SKCM) is one of the combative cancers due to the higher estimation in diagnosis case and melanoma deaths between 2020 and 2040. The lack of early management has become the major factor hence the past few years' scientists have been studying the skin cutaneous melanoma using bioinformatics analysis to examine DEGs, generate the risk prediction model and proposing the protein interaction to target the protein. However, the diverse bioinformatics analysis approach and package seems to result in different output. Therefore, this study objective is to identify the aberrant gene in melanoma skin cancer between the primary tumor and metastatic using three packages in R (DESeq2, edgeR and limma) as well as predicting the prognosis model in white patients from gene and miRNA UCSC Xena dataset. The method begins by examining DEGs from genes and miRNAs, where the genes result in a total of 620, 674 and 38 DEGs gene and for miRNA 35, 94 and 22 DEGs were screened using DESeq2, edgeR and limma respectively. The results will be validated AUC > 0.8. The hsa-mir-203a, hsa-mir-205, hss-mir-203a(down-regulated), KRT75 and S100A7A were gene and miRNA that satisfied the AUC score and continue to be calculated for its correlation using spearman and miRTarBase. Finally, the RMST Kaplan-Meir curve was used to predict the SKCM patient model. There is no miRNA and gene pair from this study that satisfied the correlation analysis. Using the same five candidates of gene and miRNA the enrichment analysis was executed and resulted in KRT75 being involved in IL-17 signaling pathway. To conclude, the gene S100A7A might be a potential tool in diagnostic and prognostic of metastatic SKCM. The hsa-mir-205 and has-mir-203a result in distinguishing the primary and metastatic tumor.

Keywords: Metastatic SKCM*, UCSC Xena dataset, DEGs, ROC curve, Kaplan-Meir curve*