Bioinformatic study reveals the difference in the expression level of ADAMDEC-1 in TCGA cancer panel

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Background: Cancer is the leading cause of death and a significant obstacle to raising life expectancy in every country in the world. According to the World Health Organization (WHO) estimates, cancer is considered as the first or second leading cause of death in 112 of 183 countries. Currently, metastasis is known as one of the main reasons for tumor progression. Mounting evidence indicates that tumor progression is frequently linked to the secretion of metalloproteinases that enable tissue invasion and intravasation by cancer cells via extracellular matrix (ECM) degradation. A Disintegrin and Metalloproteinase (ADAM) is a family of peptidase proteins that have diverse roles in tissue homeostasis and immunity. The biological function of ADAM-like DECysin-1 (ADAMDEC-1) still is unknown in diverse cancers. Hence, we evaluated the role of ADAMDEC-1 as a unique member of the ADAM family in The Cancer Genome Atlas (TCGA) cancers.

Methods: We performed a comprehensive bioinformatics analysis of expression of the ADAMDEC-1 across TCGA cancers (with tumor and normal samples) in various cancers. Besides, we conducted the correlation analysis to find genes related to ADAMDEC-1 expression.

Results: Our results demonstrated that the expression level of ADAMDEC1 is different (decreased or increased) in various tumor tissue compared with normal tissue depending on the cancer type. Moreover, TCGA analysis revealed 34 gene candidates that exhibited a positive correlation with ADAMDEC-1 across TCGA cancers.

Conclusion: Our study displayed that ADAMDEC1 can be considered as an influential biomarker in various cancer progression with diagnostic and prognostic advantages.

Keywords: Cancer, Tumor biomarkers, The Cancer Genome Atlas (TCGA), A disintegrin and metalloprotease like decysin (ADAMDEC1)