

Cancer immunology of Cutaneous Melanoma: A Systems Biology Approach.

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Abstract

Cutaneous melanoma is a melanocyte skin cancer and it is one of the most aggressive tumors in humans. It causes a great number of deaths worldwide, and in Brazil approximately 1,300 melanoma patients die each year. The Cancer Genome Atlas (TCGA) database contains genomics, epigenomics and transcriptomics data from 471 samples of skin cutaneous melanoma (SKCM). A few studies have applied systems biology approaches to investigate melanoma progression. However, they failed to integrate several layers of “omics” data in order to elucidate the mechanisms by which melanoma cells become resistant to the immune system. We propose here to perform an integrative omics analysis with the SKCM data available in TCGA. For this, we will utilize established models coupled with hub detection algorithms. The identification of hub genes can help us to unravel the role of immune system in SKCM progression.

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