

# Gene network analysis of melanoma cancer development

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Cancer is defined as a disorder characterized by uncontrolled cell growth and it is considered one of the leading causes of death worldwide. Cutaneous melanoma cancer, which affects melanocytes, has the highest growth rates in cancer in the last decade. Its appearance is somehow related to changes in specific genes and their own networks in the organism. Through a data mining approach, this study sought to identify genes that may potentially be involved with melanoma skin cancer development. Gene candidates were collected after extensive search at Pubmed database. As a control, genes related to the maintenance of a healthy skin were collected at GeneCards database. Then, the interactions between genes in each group were mapped, and a score related to this interaction was defined by the STRING database. A topological analysis of the interaction networks was performed with the Cytoscape software, which showed that both networks, melanoma and healthy skin, exhibit a power law behavior. Based on the score generated by STRING, the genes were clustered using K-means. Genes with the highest scores were identified as leaders. For the melanoma group, suggested genes leaders were: TP53, AKT1, JUN and STAT3 MYC. For healthy skin group, suggested genes leaders were UBC, TP53, JUN, AKT1, CREBBP, EP300 and SRC. At present, we are investigating the results in order to identify genes that could be closely related to gene leaders, according to the current methodology, without being previously described as related to melanoma development.

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