Proceedings International
Platinum Open Access Journal (ISSN 2668-6384)

Proceedings, Abstract
Volume 4, Issue 1, 2022, 43
https://doi.org/10.33263/Proceedings41.043

The Journey from Melanocyte to Melanoma – Proteomic and Genomic Milestones †

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† Presented at 1st OncoHub Conference – Connecting Scientists for Next Generation Cancer Management (13-15 October 2021, virtual)

Received: 25.10.2021; Accepted: 5.02.2022; Published: 14.02.2022

Abstract: Within the largest organ with immune function, in the skin's complex structure, melanocyte is one of the cell types that is involved in the skin's main functions. In the process of melanocyte neoplastic transformation, several stages are favored by a pro-tumor inflammatory milieu. A tumorigenesis-friendly environment would increase the cell's genetic instability leading to tumorigenesis and, additionally ,metastasis. In the environment, immune cells and immune-related molecules seminally contribute to the inflammatory landscape. Melanomagenesis is not a straightforward process. To take place, various factors need to collide; environmental, genetic, and immune factors must include conjoint. Melanomas are heterogeneous as the transformed melanocyte has various genetic alterations, mutations specific to the site, to the degree of UV exposure, and/or specific for the genetic make-up of the host's organism. This variability suggests that melanoma has several causal pathways. Within our presentation, we will depict the transformation of a normal melanocyte through benign transformed melanocyte up to full-blown tumorigenesis. Skin melanomas have a high degree of cellular heterogeneity due to various genetic alterations, these mutations being specific to the site, to the degree of UV exposure, and/or specific for the genetic make-up of the host's organism. Various omics' technologies should evolve in novel toolkits for investigation, where probably temporal-omics approaches can identify cellular patterns related to disease progression. Integrating genetic profiling with all other types of proteomic/transcriptomic/metabolomic and correlating data with clinical and pathological parameters would lead to seminal improvements in diagnosis, prognosis, and therapy in skin melanoma.

Keywords: melanoma; proteomics; genomics.

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Funding

This research received no external funding.

Acknowledgments

This research has no acknowledgment.

Conflicts of Interest

The authors declare no conflict of interest.