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A Comprehensive Analysis of Melanoma It's Causes, Symptoms, and Treatments

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Commentary

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DESCRIPTION

Malignant melanoma is a rapidly spreading metastatic tumour with a long history of rising incidence. Patients with advanced metastatic cancers, in particular, have a dismal prognosis. Melanoma has molecular characteristics not found in other cancers. Two factors are particularly important during the development of melanoma Melan oblasts, the neural crest-derived precursors of melanocytes, exhibit several mechanisms during embryogenesis that are usually associated with tumour cells, such as actively migrating, adapting to different cellular environments, and "invading" the epidermis. Melanoma cells, by forming stem-cell-like subpopulations, can differentiate into a variety of cell lineages, including neural, mesenchymal, and endothelial cells. These characteristics show that melanoma cells can reactivate neural crest differentiation and melan oblast migration pathways, indicating that malignant melanoma cells are highly plastic. During embryonic neural tube formation, the neural crest, a transient component of the ectoderm, is located between the neural tube and the epidermis.

Neural crest cells migrate during or shortly after neurulation, an embryological event marked by neural tube closure. They have been dubbed the fourth germinal layer due to their significance. Neural crest cells can differentiate into a variety of cell types, including autonomic nervous system neurons and glial cells, skeletal elements, and melanocytes. The ventral pathway and the dorsolateral pathway are the two main migration pathways of neural crest cells. Melan oblasts migrate primarily through the dorsolateral pathways between the somites and the ectoderm to their destination region, the epidermis, where they differentiate into melanocytes. In addition to its high differentiation plasticity, malignant melanoma is distinguished by having the highest mutation rate. However, in comparison to other cancers, only a few "drivers" of tumour development have been identified, and all of those frequently mutated driver genes appear to play only a secondary role in tumour metastasis.

MicroRNAs (miRNAs) are small non-coding RNAs that have the ability to regulate gene expression post-transcriptionally. In the nucleus, they are transcribed as long, double-stranded precursor molecules with a distinct stem-loop structure. An intracellular enzymatic cascade converts the precursor into two mature, single-stranded miRNAs that are complementary to each other and about 21 nucleotides long. The mature miRNA is annotated based on its location in the precursor molecule: the miRNA in the precursor arm with the 5 end is called 5p, and the miRNA in the 3 arm is called 3p.

To form the RNA-induced silencing complex, one mature miRNA molecule binds to one of the four human Argonaute proteins (RISC). The RISC identifies target messenger RNAs (mRNAs) *via* complementary base pairing, inhibits translation, and mediates target mRNA decay *via* hydrolytic cleavage or cellular degradation mechanisms. MiRNAs play a critical role in the regulation of all important cellular processes and are a major contributor to cancer formation and progression.

Many studies in melanoma show that miRNA expression is deregulated compared to normal human epidermal melanocytes, and that this deregulation is linked to important processes affecting tumour formation and progression. A comparative analysis of miRNA expression in Melan oblasts, differentiated melanocytes, and melanoma cells from primary tumours and metastases was used to identify miRNAs that drive melanoma development and progression.

This study discovered a strong and significant regulation of many miRNAs in melanoma cell lines compared to healthy cells, but a similar expression profile of miRNAs during the transition from Melan oblast to melanocyte development. Our findings support our hypothesis that these miRNAs are involved in tumorigenesis and make a significant difference when compared to comparable processes of proliferation or migration during embryonic development. Following this hypothesis, discovered many miRNAs that had not previously been described during the development of melanoma, but whose target gene analysis and comparison to known target genes from other cancers suggest a promising role as tumour driving candidates. This study lays the groundwork for more in-depth investigations into the novel miRNAs that may play a critical role in the development and progression of malignant melanoma.