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Identification of Molecular Markers Involved in the Invasion and Metastasis of Cutaneous Melanoma †

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Abstract: Cutaneous melanoma is one of the most aggressive types of cancer and often proves fatal in metastatic stages. The use of high-throughput technologies has revealed its heterogeneous nature and high mutational burden, which has hindered the establishment of specific markers that drive melanoma progression and the subsequent development of targeted treatment. The research is ongoing, and it aims to discover reliable biomarkers for the diagnosis and development of novel, efficient treatment. In this context, our study aimed to investigate the molecular mechanisms that aid the transition of melanoma from the primary stage to the metastatic stages to reveal the genes and microRNAs that facilitate metastatic colonization. Primary melanoma cell cultures were evaluated compared with melanoma cell lines derived from lymph nodes and brain metastases. Briefly, ARN was isolated reverse-transcribed to cDNA, and the expression of 252 genes and 84 miRNAs was analyzed using qPCR array. The results highlighted the involvement of several genes and miRNAs in melanoma invasion and metastasis. Regarding gene expression, aberrant regulation of several markers involved in ECM remodeling, migration, and angiogenesis was detected (e.g., *MMP2, RHOU, VEGFA, etc.*) between primary and metastatic samples. For miRNAs, the most significant dysregulation was registered for miR-100, miR-125b, miR-129, and some members of the let-7 family. Interestingly, these markers were oppositely expressed between different metastatic samples, suggesting that melanoma metastasis might be predominantly situs-specific, aligning the results with the parallel progression model theory.

Keywords: melanoma; metastasis; gene expression; microRNAs; qPCR array.

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Conflicts of Interest

The authors declare no conflict of interest.