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Comparative metabolite profiling of a metastatic and primary melanoma cell line using untargeted metabolomics: a case study

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Abstract: Melanoma accounts for more than 60% of deaths associated with skin cancer, making its early detection through dermatological screening essential for improved treatment outcomes. Early detection and successful treatment of melanoma can dramatically increase the 5-year survival rate from 14 to 98%. To support such efforts, comprehensive identification of metabolite patterns capable of describing cancer progression will help support the foundational knowledge necessary to build early detection platforms for intervention prior to metastasis. Using an UPLC-MS, as part of a cell-based, untargeted metabolomics approach, we profiled the metabolomes of WM-226-4 and WM-115 cells. Derived from the metastatic and the primary sites of the same individual, these two cell lines represent a paired melanoma cancer cell line. Progenesis and MetaboAnalyst, platforms dedicated to metabolomics data analysis, were used to establish a panel of differentially expressed metabolites across these two stages of melanoma. In addition, *mummichog* was used to identify the affected pathways. A total of 12 differentially expressed metabolites including amino acids, carnitine, acylcarnitine, and a limited set of lipids were identified. The significantly differing metabolites are components of a diverse set of metabolic pathways (e.g., glycerophospholipid metabolism, carnitine shuttle, tryptophan metabolism), that have biological implications for the survival and dissemination of metastatic melanoma cells.

Keywords: untargeted metabolomics; melanoma; metastasis; carnitine shuttle; glycerophospholipid metabolism; UPLC-MS