RAGE and S100 proteins transcription levels in melanoma tumors

Estelle Leclerc¹, Stefan W. Vetter²

¹Department of Pharmaceutical Sciences, NDSU, Dept. 2665, Fargo ND, 58108-6950, USA, ²Department of Chemistry and Biochemistry, Florida Atlantic University, Boca Raton, USA. E-mail: Estelle.Leclerc@ndsu.edu

It has been suggested that the Receptor for Advanced Glycation Endproducts (RAGE) may play an important role in melanoma. Animal studies with anti-RAGE antibodies have shown that RAGE blockade leads to reduced tumor growth and metastasis formation. RAGE is a multiligand receptor and among its ligands are S100 proteins, which can be highly expressed in melanoma. Indeed, S100B is clinically used as a biomarker for melanoma diagnosis and prognosis.

We have surveyed 40 melanoma tumor samples for transcription of RAGE and four S100 proteins and compared them to normal skin tissue. We found tremendous differences between tumors. On average RAGE and S100A6 expression was moderately increased in melanoma. S100B was highly over-expressed whereas S100A2 was greatly under-expressed in melanoma tissue. Because tumor tissue is intrinsically heterogeneous we next analyzed three well characterized melanoma cell lines. A primary tumor cell line showed generally higher transcription levels for RAGE and S100 proteins compared to two metastatic cell lines. In all cell lines S100B was by far the dominant S100 protein exceeding S100A2 transcription levels by three orders of magnitude. Detailed profiling of S100 transcription in melanoma tumors, together with clinical data, may facilitate improved molecular diagnostic and treatment in the future.