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A potential immunological score might be developed on the basis of antibody profile analysis in melanomas

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Introduction: This study is focused on a major question of tumor immunology that is to reveal the potential role and capacity of immunocompetent cells found in solid tumors.

Objectives: We aimed to develop a new immunoglobulin profile analysis based on our findings on B cells (Tumor infiltrating B lymphocyte, TIL-B) infiltrating malignant melanomas.

Methods: Expressed heavy and light chain immunoglobulin variable region gene (VH-JH and $V\kappa$ -Jκ) usage was analysed at DNA level from various melanoma and breast cancer tissues. Cloned and sequenced heavy and light chain immunoglobulin variable region genes were sequenced and comparatively analysed at DNA and amino acid levels with Vector NTI Advance 11, Bioedit 7.0 Alignment editor, ClustalX2.0.11 multiple alignment and grouping TreeView 1.6.6 programs. Tissue samples of melanomas were processed for tissue microarrays (TMA Master for MIRAX Viewer 1.12, 3D Histech) and unique sialilated glycosphingolipides were

tested by immunohistochemistry.

Results: Comparative sequence data analysis revealed a pattern of immunoglobulin variable region genes with tumor associated antigen binding potentials. GD3 ganglioside expression was tested parallel to other tumorassociated antigens by immunohistochemistry on melanomas.

Conclusions: Our data indicate internationally as first that tumor associated sialilated glycosphingolipides are among the target molecules of these TIL-B immunoglobulines. The novel antibody profile analysis reveals important aspects of the patients' cancer related potential anti tumor humoral immune response.

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