Poster ID: P856
Topic: Stammzelltransplantation

Bewertung der Proteinexpression und Zählung zirkulierender Tumorzellen bei verschiedenen Krebsarten

Assessment of Protein Expression and Enumeration of Circulating Tumor Cells in Various Cancer Types

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Introduction: Cancer is a leading cause of death worldwide and its monitoring is characterized by high invasiveness and low accuracy. Circulating tumor cells (CTCs) can provide information concerning cancer evolution through stages and resistance to therapy, by utilizing CTCs enumeration and their immunophenotype. The aim of the present study was to evaluate the use of CTCs number and immunophenotype as a monitoring tool for cancer.

Methods: Blood samples were collected for 4 types of cancer, namely breast (1207 patients), melanoma (111 patients), pancreatic (172 patients) and prostate (378 patients). Flow Cytometry was used for CTCs enumeration and immunophenotyping. Protein expression of 6 biomarkers, such as EpCAM, PanCK, MUC1, CD63, cMET and PSMA was monitored for four cancer stages (I-IV), whereas, using linear regression, the averages of CTCs numbers in the 4 stages were modelled for each cancer.

Results: Over-expression of MUC1 was found only in breast cancer. Similarly, CD63 was over-expressed only in melanoma, PSMA only in prostate cancer, whereas higher expression values of cMET in pancreatic cancer. In addition, higher expression values of EpCAM and PanCK were found in Stage I, while a partial loss in their expression was observed in latter stages (II-IV). Finally, for all 4 types, CTCs were found to increase linearly with cancer stage with a mean coefficient of determination equal to 0.996.

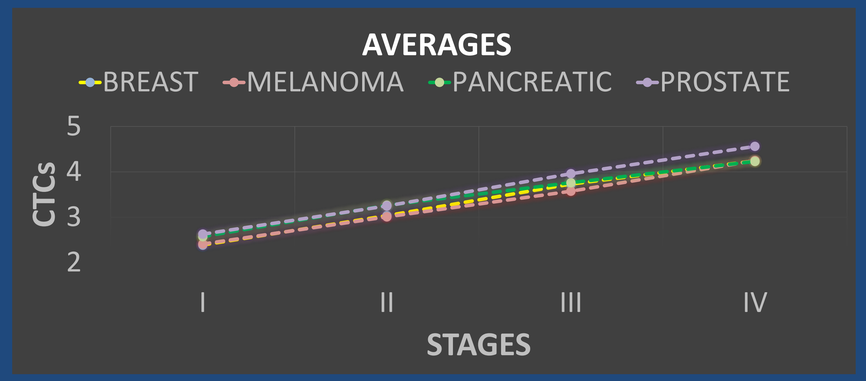

Figure 1: Linear Correlation of CTCs Number with Stages

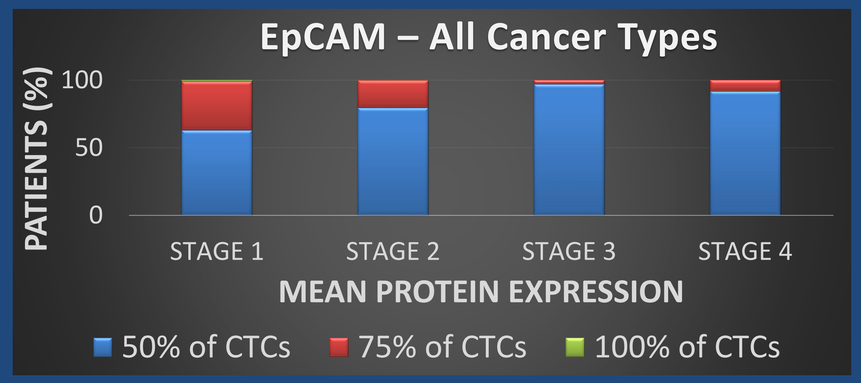

Figure 2: Mean Protein Expression of EpCAM with Stages

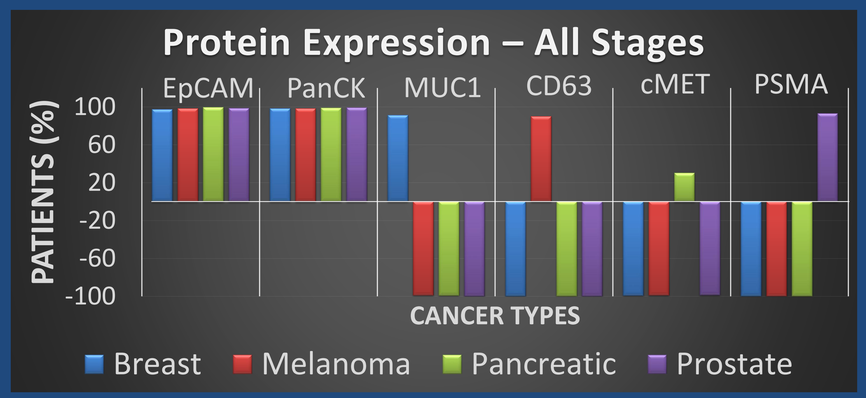

Figure 3: Protein Expression with Cancer Types

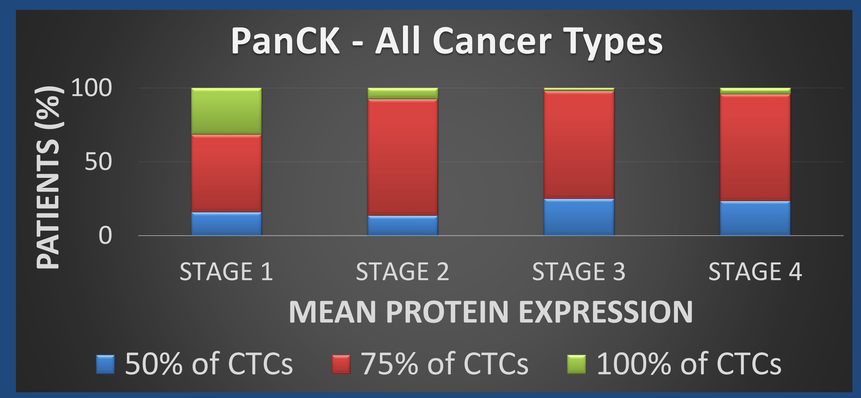

Figure 4: Mean Protein Expression of PanCK with Stages

Conclusions: MUC1, CD63 and PSMA were found expressed in breast, melanoma and prostate cancer respectively. Higher expression values of cMET in pancreatic cancer indicates resistance and metastasis. In addition, higher expression values of EpCAM and PanCK were found in Stage I, while a partial loss in their expression was observed in latter stages (II-IV). This decrease can be observed in tumor budding at the invasive margin of cancers (EpCAM) and due to cellular de-differentiation (PanCK). Finally, CTCs counts increase linearly with cancer stages, indicating that CTCs are correlated with tumor stage, while higher likelihood of metastasis and cancer aggressiveness are related to increased CTCs. Summarizing, CTCs enumeration and immunophenotyping could be helpful for better monitoring of cancer. However, further investigation is needed to understand the detailed expression CTCs patterns and their significance in cancer.

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