Expression of CXCR4, JUNB and PD-L1 in circulating tumor cells isolated from patients with prostate cancer

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Background & objectives

Previous studies have indicated that the chemokine receptor CXCR4 and the transcription factor JUNB contribute to migration, invasion, and metastasis. Programmed cell death protein 1 (PD-1) and the corresponding ligand (PD-L1) provide cancer cells protection against the immune system. Recent publications of our group have shown that CXCR4, JUNB, and PD-L1 which belong to the same signal transduction pathway, were overexpressed in CTCs isolated from breast and lung cancer patients. Moreover, the expression was related to patients' clinical outcome.

The aim of this study was to investigate the expression of CXCR4, JUNB, and PD-L1 in prostate cancer patients' CTCs, examine their clinical relevance and unravel possible correlations between them.

Methods

Thirty-six patients with prostate cancer were enrolled in this study. CTCs were isolated using Ficoll density gradient. Two different triple immunofluorescence staining experiments were performed, the first using antibodies against CK (positive epithelial marker for CTCs), PD-L1, and CD45 (hematopoietic marker), and the second for CK, CXCR4, and JUNB. Results were conducted using VyCAP microscopy.

Results

Fourteen out of 36 prostate cancer patients (39%), were positive for CTCs. The most frequent phenotype was the (CK+/PD-L1+/CD45-): 71% (10/14 patients) and the less frequent was (CK+/PD-L1-/CD45-): 29% (4/14). Furthermore, at the second staining, the most common phenotype was (CK+/JUNB+/CXCR4+): 71% (10/14 patients) and 60% average percentage of total CTCs. The less frequent phenotype was the (CK+/CXCR4-/JUNB+): 14% (2/14 patients) and 8% average percentage in total CTCs.

Conclusion

Our results revealed that CXCR4, JUNB, and PD-L1, consistent with our previous publications in breast and lung cancer, were overexpressed in CTCs from prostate cancer patients, indicating their role in tumor progression and metastasis**.** Further analysis will illustrate the potential association of these molecules with patients' clinical outcomes.