Abstract

Cutaneous melanoma is a very aggressive cancer with increasing incidence. It originates from transformed pigmented skin cells (melanocytes). The main risk factor for melanoma development is exposure to UV light and repeated sunburns. In approximately 10% of cases, melanoma occurs on a hereditary basis. Patients with cutaneous melanoma diagnosed in early stages have very good prognosis, with surgical resection of the primary tumour being mostly sufficient for treatment. In contrast, the advanced melanoma stages with metastases are often progressive and refractory to conventional therapies. Cutaneous melanoma is referred to as an immunogenic tumour that is frequently infiltrated by cells of the immune system. Tumours with immune cell infiltration show better prognosis. Spontaneous regression may occur. Over the last few years, progress has been made in the treatment of melanoma using checkpoints molecules (anti-CTLA-4 and anti-PD-1) to activate patients own immune system to recognize tumour lesions. In the tumour microenvironment, cytokines play an important role, enabling communication between cells and regulation of cell proliferation and migration and thus the tumour development. Cytokines (IL-2, IFNα) can be used in adjuvant therapy of melanoma.

This work analysed levels of expressed cytokines in a porcine model of hereditary cutaneous melanoma – MeLiM pig. In this unique model, cytokine expression was monitored at the mRNA and protein levels during initial stages of melanoma regression. Increased expression of IL-6 in the tumour tissue, compared to adjacent healthy skin, was detected. Subsequently, significant changes in cytokine levels were discussed with findings from other studies. Analysis of immunological changes during melanoma spontaneous regression on MeLiM model might help us to understand the tumour biology and has a potential to bring new knowledge applicable in human medicine.

Key words: cutaneous melanoma, cytokines, IL-4, IL-6, IL-8, MeLiM, pig model, spontaneous regression