RAQUEL MARIA, RAMOS CALÇADA

Lukas Sommer Group

Stem Cell Biology, Institute of Anatomy
University of Zurich
Winterthurerstrasse 190, CH-8057 Zurich

raquelmaria.ramoscalcada@uzh.ch
www.anatomy.uzh.ch

KEYWORDS – Melanoma, human NCSCs, gene regulatory network.

MAIN FIELDS OF RESEARCH; ABSTRACT

Melanoma is the most deadly skin cancer, with a 5-year survival rate of approximately 15% to 20% for patients with metastatic disease. Its aggressiveness is mainly attributed to the metastatic potential of melanoma cells, which can still not be efficiently targeted despite the available therapies.

Melanoma arises from melanocytes, which in turn originate during embryonic development from neural crest stem cells (NCSCs). The neural crest is a transient and multipotent embryonic stem cell population in vertebrates that gives rise to most of the peripheral nervous system (neurons and glia), smooth muscle cells of the heart outflow track, craniofacial bone, cartilage and connective tissue, and skin melanocytes. Recent studies show that some transcription factors involved in mouse NCSC maintenance are also required for melanoma formation, such as Sox10.

An opening question in the field is whether the transcriptional network that regulates mouse NCSC self-renewal and multipotency is preserved in human NCSCs. Therefore, the first aim of my project is to define the gene regulatory network that underlies human NCSC multipotency. In a second phase of the project I will enquire whether some of the core transcription factors regulating human NCSCs are also required for melanoma initiation and/or progression.

SPECIAL TECHNIQUES AND EQUIPMENT

Human NCSC culture, RT-qPCR, FACS, fluorescence and confocal microscopy, siRNA-mediated knockdown approaches.