

## Cancer stem cell miRNAs in early diagnosis and prognosis of colorectal cancer patients

Cristiano Farace<sup>1</sup>, Andrea Pisano<sup>1</sup>, Fabrizio Scognamillo<sup>2</sup>, Andrea Montella<sup>1</sup> and Roberto Madeddu<sup>1</sup>

<sup>1</sup>Dept. of Biomedical Sciences, University of Sassari, Sassari, Italia

<sup>2</sup>Dept. of Surgical, Microsurgical and Medical Specialities, University of Sassari, Sassari, Italia

Colorectal cancer is a leading tumor whose worldwide patients' mortality is still increasing in the last years, calling for more early and robust diagnostic and therapeutic procedures. To this end, a number of molecules have been investigated as diagnostic biomarker and therapeutic targets in biological matrix of patients, but a real translation into the clinical practice is still missing. Cancer stem cells (CSC) denote a small subpopulation of the cancer cell with the unique ability to initiate and propagate the tumor mass. Moreover, CSC have been shown to play a crucial role in epithelial-to-mesenchymal transition, a phenotype switch at the bottom of the metastatic process. Hence, CSC and their regulatory molecules represent optimal cellular and molecular targets in cancer eradication strategies. On the other hand, microRNA (miRNA) represent a class of small RNA with gene expression function and high potential as biomarker. In presence of a specific miRNA, the related mRNA is committed degradation, resulting in the specific downregulation of its expression. Since miRNAs are 19-23bp long, these short molecules display high stability and integrity in body tissues and fluids. Hence, miRNA represent optimal tissue- and blood-based candidate biomarker in diagnosis, prognosis and therapeutic intervention and prediction.

Here, we unraveled the role of colorectal CSC-related miRNA in colorectal cancer patients' clinic. Firstly, we assessed through qRT-PCR a set of 9 miRNA in CSC models derived from 3 different established cell lines (HCT-116, HT-29 and T84). Then, the same miRNA were investigated in tumor and healthy tissues, and blood of 13 colorectal cancer patients, and statistical analysis tasks applied to highlight miRNA contribute in colorectal cancer clinic. The results analysis have shown that 1) CSC display different miRNA pattern in relation to the molecular background of the established cells; 2) some CSC-related miRNA are overexpressed in cancer tissues and blood, corroborating our hypothesis; 3) a pattern of miRNA was correlated with cancer staging, sex, AST, alkaline phosphatase, LDL, triglycerides; 4) some miRNA were positively correlated with metastases (miR16). Hence, we found a pattern of CSC-related candidate miRNA which play important role in colorectal patients' clinic, even at level of cancer staging and metastases, paving the way to new miRNA-based biomarkers useful in colorectal cancer early diagnosis and prognosis.