

ABSTRACT

Colorectal cancer ranks amongst the most common types of cancer within the Western world and despite continuous improvements of treatment strategies frequently ends in death of the patients. For a long time, it was believed that mainly mutations within well-characterized protein-coding genes contributed to the development and progression of colorectal cancer. However, increasing evidence shows that genetic alterations apart from this coding genome also play a significant role in tumorigenesis. Since this discovery, molecules called non-coding RNAs (ncRNAs) have been gaining more and more traction amongst cancer researchers. These ncRNAs do not influence cells like protein-coding RNAs (“messenger RNAs”; mRNAs) through the expression of functional proteins, but rather they ensure the cells’ physiological integrity through the regulation of other genes. If their function is lost or if the strictly regulated intracellular level of these ncRNAs is disturbed, cells might lose the ability of growth control, the fine balance between controlled cell death and survival, and in turn develop into cancer cells. Therefore, it is of great importance to unravel the extensive effects of ncRNAs and their role in colorectal cancer development. To this end, we will use various state-of-the-art molecular biology methods and genetic tests in different colorectal cancer models, which should help to shed light on the influence of ncRNAs in colorectal cancer. Taken together, the discoveries made by this project will contribute to (1) better understanding basic mechanisms in colorectal cancer initiation, (2) better predicting the course and outlook of the disease in individual patients and, (3) facilitating the discovery of novel therapeutic approaches in colorectal cancer treatment.