

## MicroRNAs identify high-risk colon cancer patients

Choosing the optimal anticancer treatment for each patient requires proper disease staging. Staging is usually assessed according to the TNM system: tumour size (T), number of nearby lymph nodes affected (N), and metastasis, or spread to other organs (M). In general, this is a very useful system to know how advanced the disease is, which helps oncologists decide how aggressive the treatment must be. However, this system has some limitations and it might not be precise for all patients. In the last few years, molecular biology has shed light on cancer mechanisms and has allowed the development of new drugs. Molecular markers might also be useful in the clinical setting for predicting how aggressive a tumour will be, which would improve the accuracy of the TNM system.

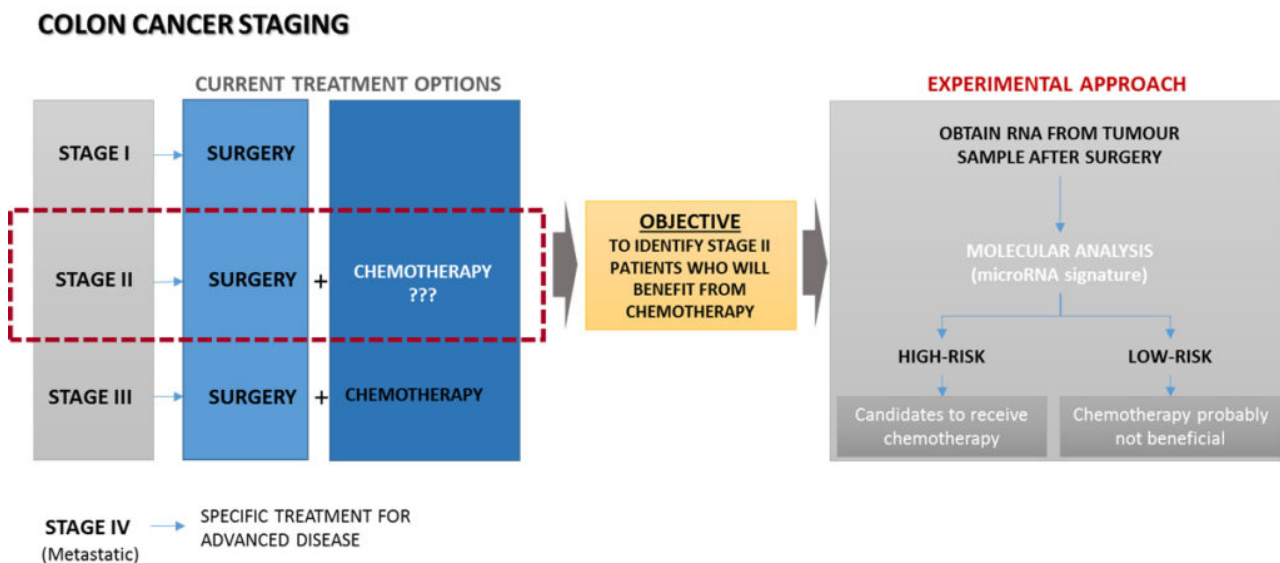


Fig. 1.

Colon cancer is a perfect example of a disease where molecular markers are needed to improve disease staging and treatment decisions. At present, patients diagnosed with stage I colon cancer will receive surgical treatment only – with a very good prognosis. Patients with stage III colon cancer will receive surgery first, after which chemotherapy will be added. However, it is not clear whether chemotherapy should be added to patients with stage II colon cancer. If these stage II patients could be precisely classified into high- and low-risk groups based on molecular information, it would mean important clinical progress in clinical decision-making: the prognosis of high-risk patients would likely be improved with chemotherapy after surgery, while unnecessary treatments and their adverse effects could be avoided in low-risk patients who can potentially be cured with surgery alone.

In our study, we investigated a group of molecules called microRNAs, which were discovered in 1993 and which regulate gene expression. We evaluated a six-microRNA signature previously described as a potential prognostic marker in colon cancer by a Chinese group (Zhang et al. *Lancet Oncology* 2013). We analyzed the expression of these six microRNAs in tumor tissue and examined the effect of the microRNA signature in 71 European patients diagnosed with stage II colon cancer. We observed some differences in the microRNA expression pattern between our study and the Chinese one, which could be explained by ethnic differences or differences in the technical methods used to determine microRNA expression. Although the prognostic impact of the six-microRNA signature was partially validated in our patients, we were able to modify the microRNA signature and improve results. Using only three of the six microRNAs (miR-103a-3p, miR-143-5p, and miR-215), we were able to classify patients as high- or low-risk. Patients identified as high-risk stage II may benefit from being treated with chemotherapy after surgery, like patients with stage III disease, while patients diagnosed as low-risk stage II will probably not benefit from adding postsurgical treatment and can thus avoid potential toxicities and side effects.

In the last few years, many molecular signatures have been developed to help us diagnose and treat patients better. However, research groups around the world work with different techniques, reagents or samples, and sometimes these differences make it difficult to reproduce experiments and gene expression assessment in different laboratories. Our results highlight the need to standardize methods and to validate results in different groups of patients so that these markers can be used in real-life medicine and patients can benefit from these scientific advances.

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## **Publication**

[Identifying High-Risk Stage II Colon Cancer Patients: A Three-MicroRNA-Based Score as a Prognostic Biomarker.](#)

Caritg O, Navarro A, Moreno I, Martínez-Rodenas F, Cordeiro A, Muñoz C, Ruiz-Martinez M, Santasusagna S, Castellano JJ, Monzó M  
*Clin Colorectal Cancer. 2016 Dec*