Novel biomarkers and risk score for the prognosis of early stage colorectal cancer patients and for providing personalized medicine

CSIC has developed a risk score method based on six novel biomarkers for determining the prognosis of patients at early stage of colorectal cancer (CRC), and for selecting those patients that would require combination chemotherapy and thereafter for deciding the best adjuvant chemotherapy.
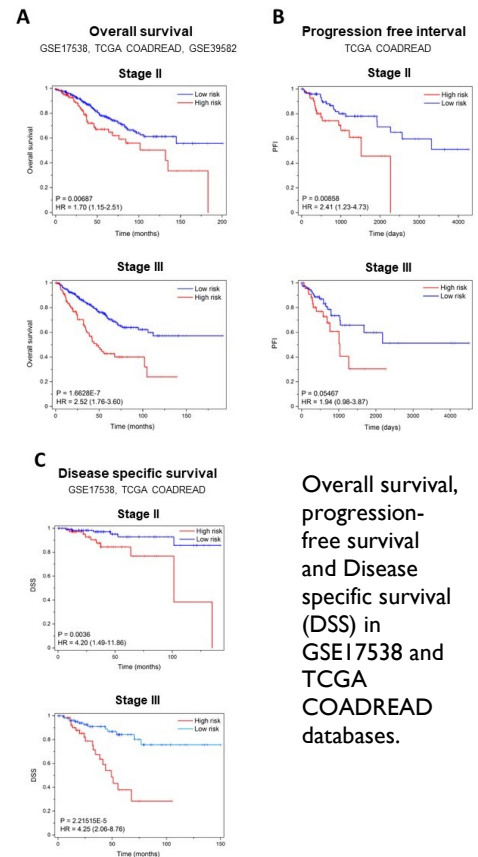
Industrial partners from the pharmaceutical industry are being sought to collaborate through a patent licence agreement

An offer for Patent Licensing

This technology enables Point-of-Care (PoC) Testing and Personalized Medicine (PM) for CRC.

CRC is considered a heterogeneous disease with different outcomes according to the molecular subtypes. This heterogeneity is reflected in differential epigenetic and genetic events as microsatellite and chromosomal instability (MSI, CIN), CpG island methylator phenotype (CIMP), P53, KRAS and BRAF mutations (among others) that lead to different pathogenesis and drug sensitivity. This heterogeneity has been addressed by implementing global gene expression classifiers. Still, given the CRC heterogeneity and the various clinical outcomes, novel and simpler predictive algorithms are necessary to facilitate clinical decision-making and individually-designed management approaches. Current pathological staging presents some predictive limitations, as a significant number of CRC patients relapse after surgical resection and are likely to develop metastasis within 5 years. Particularly necessary is the stratification of stage II and stage III patients to prevent recurrence and poor outcome and to identify those patients who would benefit more of aggressive therapies.

This technology gives solutions to all these needs.

Overall survival, progression-free survival and Disease specific survival (DSS) in GSE17538 and TCGA COADREAD databases.

Main innovations and advantages

- It has been identified genes whose expression levels provide a reliable method for the identification of patients with CRC with good or bad prognosis or for selecting patients suffering CRC to receive adjuvant combination chemotherapy. Taking a sample from the patient the expression level of at least one gene selected from a group of genes is enough for the prognosis of CRC using standard quantitative PCR techniques for determining gene expression.

- It has been developed an algorithm for calculating a risk score for CRC patients based on the expression levels of these genes, confirming its predictive value in different datasets.

- The prognosis, the selection of the adjuvant, the selection of the patient suffering CRC to receive adjuvant combination chemotherapy can be done using a computer program to simplify, facilitate and systematize the process (to create a point of care).

- This technology enables PoC Testing and PM for CRC.

Patent Status

European patent application filed

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