Predictive metabolomics signature of relapse in metastasic colorectal cancer

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Colorectal liver metastasis (CRLM) is the main cause of colorectal cancer (CRC) deaths. Understanding the molecular profile of each CRC can help to predict its prognosis and response diversity among patients. The goal of this work was to identify a precise metabolomics signature of disease relapse in CRLM patients after metastasectomy. A pilot metabolomics study was conducted at the University Hospital of Jaén using plasma samples from 39 patients with CRLM before and after metastasectomy. Paired samples were analysed using reverse phase (RP) and hydrophilic interaction liquid chromatography (HILIC) coupled to high-resolution mass spectrometry (HRMS). The molecular profiling of recurrence 2 years post metastasectomy was carried out by univariate and multivariate statistical strategies. An optimized untargeted metabolomics approach detected a predictive signature in plasma based on: lysoPE(16:0), lysoPE(18:2), lysoPE(18:0), lysoPE(22:6), lysoPC(P-16:0), unknown lysoPC, galacturonic acid, taurodeoxycholic and taurochenodeoxycholic acids, taurine, hypoxanthine and bilirubin. These potential biomarkers enabled a precise classification of recurrent patients with CRLM after the resection of the hepatic metastasis with an area under the ROC curve (AUC) of 0.791 (95% CI 0.533-0.981). In summary, metabolomics analyses led to the identification of twelve circulating metabolites easily detectable in plasma that can predict the recurrence in CRLM patients undergoing surgery.