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Predictive biomarker discovery of treatment response in lung cancer: A metabolomic approach

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A lthough the broad range of chemotherapeutic agents approved in the late years, it is a challenge for oncologists to choose which drug or combination of drugs will represent the best option for each individual, since only a portion of patients will respond properly. In this regard a biomarker approach to predict patient response to treatment may be very helpful in the making decision process. Metabolomics, the unbiased identification and quantification of small molecule metabolites in biological samples, is particularly promising for biomarker development because altered metabolism is considered a hallmark of cancer. In this work, we have investigated the metabolome of 115 plasma samples from lung cancer patients by mean of liquid chromatography high resolution mass spectrometry. The obtained data matrix was analyzed according the clinical response to each therapy (Neoadjuvant and Inmunotherapy) in order to search for a predictive molecular signature in each group of patients.

Biography

Jose Perez Del Palacio is a Scientist with 18 years of industrial experience in a leading pharmaceutical research company (Merck Sharp & Dohme), working mainly in biochemistry and drug discovery. He has broad knowledge of bioanalysis technologies and metabolomics. He has additional experience and specialization in analytical methods development for HPLC, LC/MS/MS, GC and GC/MS systems. He is the author of several papers, scientific posters and presentations at international conferences and congresses.

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