

ABSTRACT

Lung cancer is one of the major health problems in the world, is a common and severe disease, and its incidence is increasing. These features are added to the complexity of its treatment ---surgery, chemotherapy and radiotherapy---, which are aggressive, often costly and also require the collaboration of many different organized professionals. In this sense, the contribution of molecular biology with new concepts and challenges such as pharmacogenetics and pharmacogenomics has allowed not only the development of new drugs using predictive biomarkers, but also the analysis of the behavior of tumor cells, the study of gene mutations, polymorphisms, etc. and so on pathological analysis and individualized treatments through a better knowledge of prognostic factors and especially of the predictors of response.

In our work we sought to identify, by pharmacogenomic analysis, molecular markers in peripheral blood of patients with non---small cell lung cancer in locally---advanced stages not only to know and be able to predict the evolution and prognosis of the disease as the analysis of EGFR, VEGF and p16 inactivation, but to bring the best treatment option individually and achieve high success rates and minimum toxicity.