Introducción

Tumor transformation is known to arise from the progressive accumulation of mutations in the genome. The subsequent progression of the disease is largely influenced by the specific alterations accumulated in the tumor genomes, as well as the evolution of tumor populations, their response to specific therapies and the emergence of resistant clones. The recent development of Next Generation Sequencing technologies has made possible to determine the genetic alterations present in a tumor genome, as well as their evolution during disease progression and after treatment. These technologies offer the opportunity to determine the complete sequence of a tumor genome by using whole-genome sequencing, or just the sequence of the more than 20,000 genes by using whole-exome sequencing. The recent application of either whole genome or whole-exome sequencing to the study of hematological tumors has revolutionized our understanding of the disease, with the identification of novel oncogenes and tumor suppressors involved in the development of these pathologies. Some of these alterations constitute novel prognostic factors with important implications in the clinical management of the patients. In addition, the characterization of driver genes, whose mutations are involved in the oncogenic transformation, represents novel diagnostic markers that might help in patient stratification, as well as provides novel pharmacological targets for the design of more specific therapies. The stratification of patients based on their tumor’s genome profile will also benefit the design of more accurate clinical trials aimed at targeting patients with tumors caused by the same genomic alterations. Together, novel sequencing technologies constitute an important advantage for the study and management of oncologic pathologies.