NEW TECHNIQUES TO IMPROVE THE DETECTION OF MINIMAL RESIDUAL DISEASE IN PEDIATRIC PATIENTS WITH ACUTE LYMPHOBLASTIC LEUKEMIA AND BCR-ABL1 REARRANGEMENT IN SPAIN

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Leukemias are caused by determined genetic abnormalities. The Philadelphia chromosome (Ph+) is formed by the fusion of two genes, BCR and ABL1, resulting in an abnormal gene that alters the normal cellular processes. The chimeric BCR-ABL1 gene can be found in different types of leukemia, either chronic or acute, at all ages, although is more frequent in adults. Some years ago, a specific treatment against this genetic abnormality was discovered, and the outcome of patients improved dramatically. However, Ph+ acute leukemia is still considered as a high-risk subtype of leukemia and some patients need very aggressive treatments with chemotherapy and hematopoietic stem cell transplantation. We need to follow precisely the levels of residual disease that may remain after the administration of the treatment, in order to identify those high-risk patients who would benefit from those intensive therapies. There are different methods to follow the minimal residual disease, but these techniques are complex and sometimes the results among them are not concordant.

Our project aims to implement a new technique based on next generation sequencing that will allow an easy and fast identification of the BCR-ABL1 gene at the DNA level, to design a sensitive and personalized follow-up of the minimal residual disease for each patient with Ph+ acute leukemia.