Abstract

The word lymphoma defines a group of cancers affecting the lymphocytes. There are about 40 different types of lymphoma described by the World Health Organization (2008), affecting Natural Killer cells, and T- and B- lymphocytes. Therefore, because of the wide variety of lymphomas, and the multiple mechanisms of the disease, the diagnosis is very difficult in some cases. Furthermore, unlike other human cancers, the success of the treatment for the different types of lymphoma depends on the accurate identification of the disease, rather than its early detection. Thus, regular diagnosis involves determination of immunoglobulin or T-cell receptor rearrangements, and lineage assignment. However, the specificity of these methods is not enough to detect specific gene mutations associated with different types of lymphoma. Fluorescent in Situ Hybridization (FISH) is a method practiced to consistently demonstrate gene fusion and chromosomal alterations in sample cells from fresh fine needle aspirates and biopsies kept in paraffin. In fact, this method normally uses two kinds of probes to detect chromosomal translocations. Dual-fusion and break-apart probes are different in the information they provide, sensitivity and ease of interpretation. However, they are successfully used for the identification of a number of lymphomas. Despite FISH’s accuracy for detecting gene translocation and other chromosomal alterations, the use of a tree color, dual fusion probe has also been introduced for the detection of cryptic chromosomal rearrangements. For example, IGH-MYC cryptic re-arrangements, detected using this method, have been found to be present in rare cases of NHL, with clinical and prognostic significance. In conclusion, molecular methods for the diagnosis of lymphoma like FISH, used in different versions can help the accurate identification of the different subtypes of this disease, which influences the treatment that patients receive, improving their prognostic.

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References


