editorial

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Inside Haematologica: new tools towards risk classification according to genetic lesions in acute lymphoblastic leukemia

Acute lymphoblastic leukemia (ALL) is a genetically and clinically heterogeneous disease, in which the underlying molecular genetic alterations may have independent prognostic value in the context of particular therapeutic protocols.[1] The availability of molecular methods to detect the most any prognostic relevant chromosomal alterations in childhood ALL has suggested that genetic features of leukemic cells are used to define risk classification of the individual patient.[2] Risk-classification may in turn lead to a risk-adapted treatment strategy.[3-8] In this issue of Haematologica, Martínez-Ramírez *et al*.[9] show that interphase fluorescence *in situ* hybridization analysis of AML1 and TEL gene abnormalities may be extremely useful for complementing cytogenetic studies, while Marín *et al*.[10] show that multiplex-PCR assay allows reliable and rapid detection of prognostically significant translocations in ALL.

References

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