Secondary myeloid neoplasias: an emerging group of diseases

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Secondary myeloid neoplasias are a heterogeneous group of diseases characterized by the proliferation of myeloid cells; they were recently recognized by the World Health Organization (WHO) as an entity. The wide use of chemotherapy and better diagnosis of hematological malignancies has caused a growth in the number of secondary malignancies. Most of them are myeloid: a) myelodysplastic syndromes (MDS), a heterogeneous group of clonal hematopoietic stem cell disorders characterized by ineffective hematopoiesis and dysplastic changes in bone marrow and peripheral blood with the risk of transformation to acute myeloid leukemia (AML) or b) sometimes the previous disease directly evolves to an overt AML. Usually the prognosis of patients with a secondary myeloid neoplasia is poor, especially when the previous disease is a MDS. However, patients may achieve a complete response. In this situation, progenitor stem cell transplantation is the best therapy.

Cytogenetic analysis still plays a pivotal role in the diagnosis of hematological diseases. Cytogenetics and mutational analysis are the main prognostic tools in both AML and MDS. For this reason, cytogenetic studies are critical in the correct management of these diseases. There are several cytogenetic abnormalities associated with better prognosis, such as translocations involving core binding factors in AML patients, and losses in 20q, 5q or chromosome Y in MDS. In contrast, many others abnormalities are associated with dismal prognoses, such as the presence of a complex karyotype, abnormalities of either chromosome 3 or chromosome 7 and, in case of AML, the loss of the long arm of chromosome 5.

All of these abnormalities are included in the new staging system for MDS (IPSS-2). Recently new data regarding the presence of abnormalities in chromosome 7 in primary MDS showed that the presence of a partial deletion of the long arm of this chromosome (7q-) is associated with a better prognosis than monosomy 7.[1] This abnormality is a common event in secondary MDS and AML and the potential value of this observation in secondary MDS should be addressed. In this issue of the *Revista Brasileira de Hematologia e Hemoterapia* a new observation highlighted the importance of performing cytogenetic studies in secondary MDS.[2]

Over recent years, the wide use of microarrays and, more recently, the possibility of sequencing the human genome have provided new insights into knowledge of the molecular mechanisms involved in MDS and AML. Analysis of the gene expression profile by means of microarray technology demonstrated the presence of new pathways involved in the pathogenesis of these disorders, although studies focusing on secondary myeloid diseases are lacking.[3] Since the sequencing of the entire genome of the first hematological malignancy, a patient with AML,[4] several papers have shown the interest of the detection of new genes involved in these diseases.[5] Some of these papers have also described the involvement of new functions involved in myeloid diseases such as the spliceosome mechanism that could play an essential role in the genesis of both MDS and AML.[6] Therefore, near future investigations should provide more information of the genes involved in secondary myeloid diseases. The challenges will be to understand these genes which are thought to be drivers in the genesis of secondary myeloid neoplasias and, more importantly, to identify new therapeutic targets.

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