The Terminology of "Carcinoma Cell Leukemia"—Is an Alternative Needed?

To the Editor:

I refer to the article of Nasr et al.1 entitled "Carcinoma Cell Leukemia" published in a recent issue of Blood. I would like to express my reservation about the use of the phrase "carcinoma cell leukemia" to describe circulating carcinoma cells. Although it could be argued that the historical meaning of the word leukemia (Gr. leukos white + haima blood = white blood)2 may be applicable to conditions characterized by circulating cancer cells in peripheral blood, use of such terminology, in my opinion, may be a source for future confusion. In clinical practice, it is customary to use the terms leukemia and carcinoma to describe hematological malignancies and nonhematological malignancies, respectively. This distinction has clear advantages in that it differentiates the eminently treatable neoplasms of hematopoietic tissue from those of nonhematopoietic cells with very different biological behavior and prognosis. The distinction is particularly useful when counseling patients with leukemias who are terrified by the words carcinoma and cancer. The hybrid term "carcinoma cell leukemia" may blur this distinction, potentially leading to confusion. The term "carcinocytaemia"3 may be a preferable term because it is more accurately descriptive. My viewpoint may sound pedantic but I feel it is imperative that incorrect use of terminology should be discouraged to avoid creating confusion in the future.

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REFERENCES


Cutaneous T-Cell Lymphomas and Bacterial Superantigens

To the Editor:

Epidermotropic cutaneous T-cell lymphomas (CTCL), ie, mycosis fungoides (MF) and Sezary syndrome (SS), result from the malignant, clonal lymphoproliferation of cells exhibiting at their surface the CD3+CD4+ phenotype of mature helper/inducer T cells.1 The expression by most Sezary cells of the T-cell receptor (TCR) αβ heterodimer and the presence at their surface of the CD45RO marker of memory T cells raised the hypothesis that an antigen-specific stimulation of Sezary cells could be involved in the pathogenesis of CTCL.2 In this field, Jakow et al.3 recently reported the results from a study addressing the immunopathogenic role of staphylococcal superantigens in CTCL. As it is widely known by clinicians that infection of the skin may exacerbate exfoliation and erythema in patients with MF/SS, the purpose of this study is of interest. However, the methodology used in this work and some of the authors’ conclusions appeal specific comments and criticisms. First, the investigators claimed that they showed evidence for an oligoclonal expansion of Vβ2+ T cells in the skin samples from MF/SS patients showing a cutaneous infection with Staphylococcus aureus strains producing toxic shock syndrome toxin-1 (TSST-1), a toxin with superantigenic properties which selectively stimulate TCR/Vβ2-bearing CD4 lymphocytes. Considering that the Vβ family-specific reverse transcriptase-polymerase chain reaction (RT-PCR) is only a semi-quantitative method, it appears that the relative expression of Vβ2 in the skin from infected patients does not differ significantly from the one observed in the noninfected subgroup, or neither with the levels evidenced in the normal skin from controls. Indeed, it would have been warranted to correlate the results from the RT-PCR analysis with those obtained by using immunostaining techniques with anti-Vβ2 monoclonal antibodies, which would allow a more quantitative evaluation together with a statistical analysis of the Vβ2 representation in both the skin and the blood compartments.4

Furthermore, we5 and other investigators6 have shown that differently from a classical antigen-specific immune response, superantigen dependent T-cell expansions exhibit a high diversity of the TCRβ V-D-J junctional segments in terms of amino acid length and protein sequence. Because the RT-PCR amplification of the Vβ/C-J junctional segments does not allow to assess the diversity of this hypervariable, so-called complementary determining region 3 (CDR3), but only indicate the repertoire of Vβ segments used by the T-cell infiltrate, we believe that the data from Jackow et al failed to show that the representation of the Vβ2 subset was driven by a superantigenic stimulation.

Another important question is whether a superantigen is able to induce the activation of malignant cells in patients with CTCL. Functional in vitro studies have been hampered by the difficulty to expand Sezary cells by using classical mitogenic stimulations, contrasting with the proliferation of Vβ2-expressing T cells from patients with SS induced by TSST-1.5 However, because there was no determination of the Vβ segment used by the malignant clone in Jakow’s study, the Vβ2 subset might include both normal and tumoral cells. Indeed, the use of clonotypic tools such as CDR3 length analysis and CDR3 sequencing is warranted to evaluate the contribution of tumoral cells to the proliferative response toward a bacterial superantigen.

Finally, the lack of a biased usage of Vβ segments by Sezary cells emphasizes that a common superantigenic, chronic stimulation is not involved in the initiation of MF/SS.6 Even though these data do not rule out the possibility that bacterial superantigens might be involved in the exacerbation of the Sezary cell expansion and/or the cutaneous inflammation observed in patients with CTCL, further investigations are warranted to address these hypotheses.

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