Predicting the clinical course of Hodgkin lymphoma

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We read with great interest the editorial by DeVita (A breakthrough in Hodgkin's disease. *Nat. Rev. Clin. Oncol.* **7**, 179; 2010)[1] concerning a paper recently published in the *New England Journal of Medicine*. In that paper, Steidl *et al.*[2] demonstrated that the percentage of CD68 positive macrophages infiltrating the diagnostic biopsy specimen was an independent predictor of disease-specific survival in classic Hodgkin lymphoma, outperforming the International Prognostic Score.[3] Steidl and colleagues included gene-expression profiling in their assessments, which was concordant with macrophage infiltration using immunohistochemistry. The concordance between gene-expression profiling and immunohistochemistry should be considered as an important achievement, because it makes a very simple assay have great prognostic value. We agree that this research represents a breakthrough in Hodgkin disease and these data will be very useful to design the best treatment of patients with classic Hodgkin lymphoma that deserve special care, especially to avoid overtreatment and late toxic effects. However, Steidl and colleagues did not include any comment about ^{18}FDG PET, which nowadays seems to have a very important role in the evaluation of chemosensitivity and response to treatment in Hodgkin lymphoma.[4–6] We speculate that the macrophage infiltration could be a consequence of the inflammatory microenvironment which is detected by PET and that persists at early assessment in patients who will eventually fail to respond to treatment. A correlation between the findings of macrophage infiltration and PET data would be extremely interesting and useful to better understand the biology and the relevance of each new prognostic factor that predicts the clinical course of Hodgkin lymphoma.

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doi:10.1038/nrclinonc.2010.36-c1

Competing interests
The authors declare no competing interests.

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