

LETTER TO THE EDITOR

Prognostic value of the S-phase fraction of breast cancer

Sir – The publication in the November issue of the *British Journal of Cancer* of an article entitled ‘Lack of prognostic significance of DNA ploidy and S-phase fraction in breast cancer’, raises a number of questions, which the accompanying editorial by W. Miller, while attempting to justify the decision to publish the aforementioned article, does not answer. Most of the points I wish to discuss in my letter concern the general field of prognostic factors and their application to breast cancer treatment.

The authors critically reassess the results on DNA-ploidy and SPF in the literature. Some of the criticisms, in particular concerning the use of multivariate analysis are justified. But there are some discrepancies in the comparison of their own results with those of previous studies. Thus, although the Stanton paper clearly presents negative results – it suffices to read its title – at the end of the discussion, they agree that most authors have provided evidence showing that SPF is a significant prognostic factor. Taking the comparison a little further, they state that their own data are in general agreement with the literature, since they at least observed a trend. A statistical explanation (type II error) is even proposed. In fact their conclusion is the same as that of a recent review on the subject (O’Reilly & Richards, 1992), i.e. that SPF is a significant prognostic factor, worth pursuing, but that DNA-ploidy is not. This is certainly not the impression that the reader would get from the title and the abstract.

How can we now improve our understanding of the value of DNA flow cytometry in defining breast cancer prognosis? Technical aspects can certainly be proposed. It is striking that the data on ³H-thymidine labelling of surgical biopsies of breast cancer seem to be more homogeneous (Meyer, 1986; Hery *et al.*, 1987; Tubiana *et al.*, 1989; Silvestrini *et al.*, 1989). The mitotic index has also been successfully used for over 35 years, as part of histopathological grading (Bloom & Richardson, 1957). Therefore, the proliferative activity of breast cancers appears to be an important biological determinant of outcome, but, from a methodological point of view, the best way to measure it still remains an unresolved question.

In a study, soon to be published, six experienced ‘cytometrists’ were asked to classify some 400 DNA histograms of breast cancers. The interesting conclusion of this work was that the prognostic significance of DNA ploidy was maximal for the histograms that were agreed on, whereas for those for which opinions diverged, the outcome was similar to that of the aneuploid group (Joensu *et al.*, 1992). The major role of subjective elements in the interpretation of DNA histograms may be an important limitation of DNA flow cytometry, and attempts to standardise this interpretation should be instituted prior to its routine use in clinical practice.

In the excellent ‘evaluation guidelines’ for prognostic fac-

tors, the technical aspects were adequately dealt with (McGuire, 1991), but the ever expanding field of prognostic factors raises the general problem of their multiple intercorrelations, potentially generating confusion for their practical application. One of the aspects that is seldom tackled concerns the search for an explanation of their association with clinical outcome. Along these lines, it is indicative that the results of the largest cytogenetic study published to date suggest the existence of a possible unique pathway of genetic evolution of breast cancers, involving unbalanced chromosome translocations, endoreduplication and further chromosome losses (Dutrillaux *et al.*, 1991). This was achieved by analysing the proportion of rearranged chromosomes against the modal number of chromosome counts. Most importantly, it was consequently shown that the loss of both oestrogen and progesterone receptors was more frequent as the karyotypes became more complex (Magdelenat *et al.*, 1992). A similar pattern has been confirmed for S-phase fraction (Remvikos *et al.*, 1992) or histopathological grade (Zafrani & Dutrillaux, unpublished results). Although at present the data are insufficient to discuss the chronology of the events, it can be hypothesised that a set of biological parameters (including S-phase fraction) correlate with the state of genetic evolution, a finding that could explain their potential prognostic value.

Finally, it must be stressed that S-phase fractions of breast cancer present the additional value of interaction with treatment. We have previously suggested the existence of a relationship between S-phase fraction and response to neoadjuvant chemotherapy (Remvikos *et al.*, 1989). This has been confirmed by different groups (Spyratos *et al.*, 1992; O’Reilly *et al.*, 1992). One can speculate that different therapeutic strategies could be developed, not only based on prognosis, but also designed to achieve improved efficacy against tumours with different proliferative characteristics, much in the same way as it has been proposed that accelerated fractionation radiotherapy should be used for fast growing tumours (Peters *et al.*, 1988).

In the light of these comments, the decision to publish or not to publish the negative results of the study by Stanton *et al.* appears to be a secondary point. Although it is claimed that it counterbalances some other overoptimistic studies, its contribution to our knowledge on breast cancer proliferation and its prognostic value is quite limited.

Yours etc,

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