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Correspondence

Prognosis of patients with multifocal breast cancer

Dear Editor,

In their report, Kim et al [1] provide further evidence that different foci of multifocal breast cancer occasionally arise from different progenitor cells. They conclude that the current College of American Pathologists' guideline that suggests using "only the largest tumor for tumor staging and determination of treatment methods" is "insufficient."

I agree with the authors' conclusion for 2 reasons. First, for most invasive breast cancers (hormone receptor positive/HER2 negative and lymph node negative), the National Comprehensive Cancer Network already endorses molecular profiling (quantitative messenger RNA assessment) to predict prognosis with adjuvant hormonal therapy or chemotherapy or both, rather than the size of the largest tumor [2]. Their endorsement is based on multiple reports of these assays being of greater value than metrics such as tumor size and grade. Also, the American Joint Commission on Cancer similarly has now included pathologic prognostic staging with quantitative messenger RNA (mRNA) profiling as part of staging for this same group of invasive breast cancers [2].

However, the National Comprehensive Cancer Network has not addressed how this change applies to multifocal or synchronous invasive breast cancers. Based on the results reported by Kim et al and the other studies, they cite in their report that, because different tumors in a patient with multifocal or synchronous invasive cancers can demonstrate molecular differences, these same different tumors would be expected to harbor different quantitative mRNA profiles as well, as has been shown by Karsten et al [3]. If recurrence risks from each of multiple tumors are considered independent events, then it follows that for a single tumor, a lower risk of recurrence and therefore lower absolute systemic adjuvant therapy benefit would be expected when compared with the higher recurrence risk expected from one or the other or both from each of 2 tumors. For example, if a patient has 2 tumors, each with a 20% recurrence risk based on quantitative mRNA profiling (and therefore an 80% likelihood of no recurrence from each), then the risk of recurrence from one or the other or both would be $1.00 - (0.8 \times 0.8) = 0.36$. In other words, the risk of recurrence from one or the other or both would be estimated to be 36%.

The incorporation of quantitative mRNA profiling into standard guidelines enhances our ability to predict prognosis and benefit from adjuvant systemic therapies. In part because of the occasional somatic molecular differences noted by Kim et al in different tumors of patients with multifocal disease, quantitative mRNA profiles of each tumor in a patient with multifocal or synchronous invasive breast cancers should help impart more precise prognostic and benefit estimates for patients with multifocal or synchronous tumors.

Steven Sorscher, MD
Oncology Division, Wake Forest School of Medicine, Winston-Salem, NC 27157, USA
E:mail address: ssorsche@wakehealth.edu

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References

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Prognosis of patients with multifocal breast cancer—reply

Dear Editor:

We thank Dr Sorscher for his interest in our article on clonality analysis of multifocal breast cancers. Disappointingly, multiple breast cancer has not been included in the eighth American Joint Committee on Cancer staging system as an independent risk factor. The current TNM staging system adopts the size of the largest invasive tumor for T