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In reply: In reply to the Letter to the Editor by Drs Rakha, Ellis and Reis-Filho, regarding our article,¹ we would like to clarify the following:

Triple-negative (ER/PR/HER2-negative) breast cancer constitutes more than one entity with heterogeneous and poorly understood growth and invasive mechanisms. Despite concordance between histopathology, immunohistochemistry and cDNA analysis, a pragmatic approach should be considered for identification of these tumors for treatment.² We agree that negativity for ER/PR/HER2 is not an obligated criteria to classify breast tumors as basal-like carcinomas, but for the purpose of our study, we only selected the triple-negative tumors for analyzing several biological markers. The use of both terms indistinctly throughout the text might have led to some confusion.

From a histopathological point of view, it is true that basal-like breast carcinomas are heterogeneous groups of high-grade invasive ductal neoplasms (NOS), which also include most of the myoepithelial, medullary, adenoid cystic, metaplastic and spindle cell carcinomas.³ Apparently, they are not specific markers to classify these tumors. Recently, it has been stated that the immunohistochemical pattern that best defines basal-like breast carcinomas is the triple negativity in association with the positivity for EGFR and/or basal cytokeratins (CKs) (ie, CK5/6, CK14 and CK17).⁴ Few investigators have analyzed all three CKs together, as we did. Nevertheless, in our cases, we did not find any statistical correlation between expression of several CKs (data not included in our paper). Furthermore, how basal CK expression contributes to the adverse prognosis of these tumors is currently unknown. Among our triple-negative cases

with myoepithelial differentiation, we also observed a heterogeneous pattern of CK expression. Moreover, positive S100 expression was observed more frequently than SMA expression, and interestingly, in other studies, SMA expression was detected more frequently than p63.³ It means that the characterization of these neoplasms is still blurry.

The level of EGFR expression has been revealed as an independent predictor of tumor response to radiation therapy.⁵ The contribution of our immunohistochemical study in this field is that, in fact, in triple-negative breast carcinomas, several growth-factor receptors (ie, EGFR, IGF1R, PDGFR α , and so on) are involved, and therefore, they could explain the aggressive clinical behavior in some cases.

Other markers, such as p53 overexpression, have been considered a common marker of basal-like breast carcinoma,⁶ but it has also been detected in 11.3% of ER-positive breast carcinomas.⁷ Therefore, current evidence is still insufficient to support the routine analysis of p53 in clinical practice.⁸

Dendrograms of expression profiling/hierarchical clustering analysis are not available for most institutions. Of note, comparative studies with different gene sets for breast cancer diagnosis achieved 77–81% agreement for outcome classification,⁹ as with immunohistochemistry and conventional histopathology.

In summary, the data reviewed above indicate that characterization and/or classification of these neoplasms is still undergoing investigation. Therefore, more research should be conducted in this field to define the underlying mechanisms, which in turn will provide better understanding of breast neoplasms for more accurate patient treatment.

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