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S100 protein in molecular subtypes of breast cancer

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Abstract

Background: Cancer research is mainly focused on the tumor cells themselves, the tumor microenvironment being largely neglected. Antigen presenting cells are a heterogeneous population that infiltrates the tumor and can be identified due to the expression of the S100 protein. The aim of this study was to analyze the S100 protein expression (intratumoral vs peritumoral region) in different molecular subtypes, as well as its interrelations with various parameters (such as hormonal receptors expression and HER2 status, patients' age, tumor's grade).

Material and methods: 66 cases of breast carcinomas were examined in terms of their molecular profile (the expression of ER, PR, HER2) and the expression of S100 in the intra- (S100it) and peritumoral areas (S100pt). The data were analyzed using the SPSS program, the values being considered statistically significant in the case of $p < 0.05$.

Results: Maximum numerical values of S100it and S100pt were achieved in case of HER2+ and triple-negative carcinomas, respectively. In the case of luminal A subtype, an inverse correlation was established between S100it and age ($p=0.019$). In the HER2+ subtype, S100it correlated with HER2+ protein expression ($p=0.005$). In the triple negative subtype, the tumor grade influenced S100it ($p=0.022$), and S100it correlated positively with S100pt ($p=0.041$).

Conclusions: The dynamics of S100 positive intratumoral cells is strongly influenced by the HER2 status and age.

Key words: breast carcinoma, S100, HER2, peritumoral stroma, molecular subtypes, dendritic cells.

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