Frequent genetic differences between matched primary and metastatic breast cancer provide an approach to identification of biomarkers for disease progression.

Breast cancer is a major cause of morbidity and mortality in women and its metastatic spread is the principal reason behind the fatal outcome. Metastasis-related research of breast cancer is however underdeveloped when compared with the abundant literature on primary tumors. We applied an unexplored approach comparing at high resolution the genomic profiles of primary tumors and synchronous axillary lymph node metastases from 13 patients with breast cancer. Overall, primary tumors displayed 20% higher number of aberrations than metastases. In all but two patients, we detected in total 157 statistically significant differences between primary lesions and matched metastases. We further observed differences that can be linked to metastatic disease and there was also an overlapping pattern of changes between different patients. Many of the differences described here have been previously linked to poor patient survival, suggesting that this is a viable approach toward finding biomarkers for disease progression and definition of new targets useful for development of anticancer drugs.
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extent, the role of primary tumors as a surrogate subject of study for the systemic disease.