Cancer Predisposition Genes in metastatic breast cancer –

Association with metastatic pattern, prognosis, patient and tumor characteristics

RESULTS

A total of 115 breast cancer patients were included in the prospective analysis evaluating the impact of germline mutations on metastatic pattern. Among them, 64 patients were classified as having multiple locoregional or distant metastases. The remaining patients were classified as having single metastases or as having metastases limited to the breast.

The influence of mutational type on metastatic pattern was assessed using Cox regression models, with one for each of the following predictor variables: Mutation in any of the analyzed genes, mutation in BRCA1/2, and PALB2. Kaplan-Meier Curves for the two variables are shown in Figures 1-2.

CONCLUSION

- The mutation in high and moderate risk breast cancer genes was frequent in metastatic breast cancer patients.
- The mutation frequency was substantially higher in the breast cancer gene compared to the other two genes. The results were consistent with recent results of studies of metastatic prostate cancer patients.
- Patients with brain and visceral metastases had the highest breast cancer gene mutation frequency.
- Results suggested that PALB2 mutation may be more frequent in patients with brain metastases.

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Table 1: Distribution of mutations across patient and tumor characteristics

Table 2: Distribution of mutations across risk factors for breast cancer

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