INTRODUCTION

Despite accumulating evidences suggesting that immune cells are generic constituents of tumors (1), the role that the immune system plays in tumorigenesis is still a matter of debate.

Characterization of the immune phenotype of tumors during progression could aid in developing patient-tailored therapy strategies.

Here, we sought to identify differences in the expression pattern of immune-related genes comparing paired samples of primary breast tumors and metastasis from patients participant in the GEICAM/2009-03 (ConverHER) study.

OBJECTIVES

To characterize the immune phenotype during breast cancer progression in terms of:

- PD-L1 expression and
- Immune gene expression analysis.

DIFFERENTIAL GENE EXPRESSION

- We analyzed in 44 matched, 1 primary and 1 metastatic non-matched tissues from 46 patients participating in the ConverHER study, PD-L1 expression by immunohistochemistry (IHC) by using a specific antibody for tumor and immune cells detection (2) (Figure 1).

- Significant features (p-value < 0.05) were assessed for functional enrichment of KEGG pathways and GO terms.

RESULTS

- Prevalence of PD-L1 in immune infiltrating cells (IC) was lowest in ER+HER2- specimens (Figure 2). PD1L1 expression in tumor cells (TC) was observed in 1/90 samples.

- No significant changes in PD-L1 IC were observed between matched pairs (Figures 3 and 4).

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- No changes in pre-specified immune signatures were observed (Figure 5).

- Metastases had decreased Notch pathway, innate inflammation and TGFβ-activated fibroblasts signatures (Figure 6).

CONCLUSIONS

- PD-L1 expression and immune gene signatures did not significantly change between primary and metastatic BC.

- However, metastasis had decreased TGFβ-activated fibroblasts, innate inflammation and Notch pathway signatures.

- The results in the current study need to be further corroborated in an independent dataset.

REFERENCES


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