RETROSPECTIVE STUDY CORRELATING BETWEEN CLINICAL STAGING, PATHOLOGIC STAGING AND MOLECULAR SUBTYPES OF BREAST CANCER

Tarek Abd El-Halim El-Fayoumi, Mohamed Tarek El-Rakshy, Haytham Mahmoud Awad Fayed, Gehan Abd El Atti Khedr, Emad Nagui Fouad Estefanos
Surgical Oncology Unit, Department of General Surgery, Department of Clinical Oncology, Faculty of Medicine, Alexandria University, Alexandria, Egypt

Introduction

The biodiversity of breast cancer is reflected by the presence of different molecular subtypes. As medicine shifts to a more personalized approach, it is an important goal to correlate different molecular subtypes with clinical disease outcomes and targeted therapies as well as the diversity in systemic disease response, recurrence and survival rates. Breast cancer can be classified on a molecular basis into four different molecular subtypes depending on the expression of ER, PR, HER2 and Ki67. Molecular subtypes as new prognostic indicators have been received more and more attention. In these molecular subtypes, Luminal A subtype shows the best outcome, whereas HER2 overexpression and basal-like subtypes present the poorer outcome.

Aim of the work

The primary aim of this study was to correlate between different clinicopathological staging pattern and various molecular subtypes of breast cancer. Also, the Secondary aim was to determine the disease-free survival and overall survival of different molecular breast cancer subtypes.

Materials and methods

We retrospectively reviewed the medical records of breast cancer patients who were treated and followed-up at the clinical oncology department and surgical oncology unit, Alexandria main university hospital during the 2 years' period from June 2016 to June 2018. a total of 1071 breast cancer patients were presented during this period of time. Among 163 patients, only 118 have adequate clinical, pathological and treatment data suitable for analysis according to our inclusion and exclusion criteria and were included in our study. All information was obtained from medical records. Variables obtained from the registry included: patient profile and history; Age at diagnosis, family history, menopausal status, breastfeeding history, hormonal contraception intake, nature of complaints, date of diagnosis, recurrence and death.

Additionally, we collected clinical/pathological pattern of the tumor such as: Tumor size, site, lymph node involvement, number of lymph nodes involved, histological type, tumor grade, estrogen receptor, progesterone receptor, human epidermal growth factor receptor -2 (HER-2) receptor status and Ki 67 and luminal subtypes. Operative details including date of surgery, type of breast surgery (mastectomy or BCS), Axillary surgery (sentinel lymph node biopsy or axillary lymph node dissection), chemotherapy (type and number of cycles), targeted and hormonal therapy (type and duration of treatment).

Results

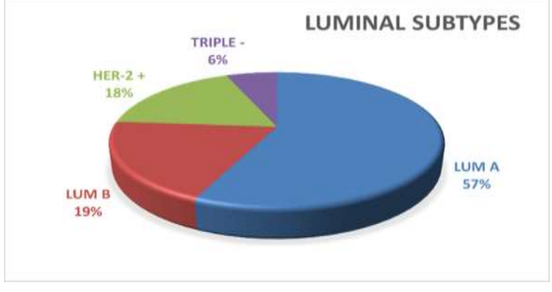

Figure: Distribution of four molecular subtypes of breast cancer (n = 118)

Table: Distribution of four molecular subtypes of breast cancer (n = 118)

DISEASE FREE SURVIVAL	Mean	% 1 year	% 2 year	% End of study	Log rank χ^2	Log rank p
Luminal subtype						
LUM A	32.57	86.1	69.9	59.0	5.098	0.165
LUM B	27.52	94.7	71.2	35.6		
HER +ve	24.26	100.0	49.7	0.0		
Triple -ve	19.41	57.1	38.1	38.1		
OVERALL SURVIVAL	Mean	% 1 year	% 2 year	% End of study	Log rank χ^2	Log rank p
Luminal subtype						
LUM A	33.44	92.9	78.7	0.0	11.478*	0.009*
LUM B	32.53	85.9	71.0	0.0		
HER +ve	22.49	85.7	37.1	0.0		
Triple -ve	24.00	85.7	35.7	35.7		

Conclusion

•The clinicopathological characteristics of the primary tumor are important for predicting the prognosis of different molecular subtypes among breast cancer patients.

•Factors affecting negatively on DFS were higher grade tumors, larger tumor size, equal or more than 3 positive axillary nodes and negative ER/PR status.

•Factors affecting negatively on OS were larger tumor size, more than 3 positive axillary nodes, higher grade tumors and HER2 positive status, TNBC.

Recommendations

•There is a need of further analysis in larger sample size and longer duration among breast cancer patients, for better understanding of the correlation between different molecular subtypes and their clinicopathological features as well as the impact of these correlations on the prognosis and overall survival.

•Our study has shown a lot of missing data increasing yearly during the period of our study leading to the reduction of our sample size. It is mandatory to rectify and have better reporting system for better analysis.

•All breast cancer patients need to be tested for ER, PR, HER2 and Ki67 in order to assess the need of systemic endocrine therapy as well as anti HER2 therapy.