214P: Landscape of homologous recombination repair gene mutations in different molecular subtypes of breast cancer

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Background

Breast cancer (BC) is one of the most prevalent malignancies throughout the world. Important therapeutic progress has been achieved over the past decade, and the identification of genomic alterations in the homologous recombination repair (HRR) pathway sensitizes tumors to therapeutics such as PARP inhibitors and platinum-based chemotherapy. Here we evaluated the characteristics of HRR related gene mutations in patients with different molecular subtypes of BC.

Results

Table 1 Molecular subtypes of breast cancer & mutant HRR genes

	HR+	TNBC	HER2+
All patients	75	29	17
HRR mutation	33	10	15
Top 5 mutant genes (Gene, No. of mutations)	*BRCA2,13*	*BRCA1,3*	*CDK12,9*
	CDK12,6	*NBN,2*	*BRIP1,4*
	BRCA1,5	*BRCA2,1*	*BRCA1,3*
	NBN,5	*ATRX,1*	*BRCA2,2*
	ATM,4	*PALB2,1*	*ATRX,1*

Methods

A total of 121 patients with BC were enrolled into the study. All samples were collected and detected by DNA based NGS with a 1021 gene panel which containing 36 HRR genes (CHEK1/2, BRCA1/2, BRIP1, CDK12, ATM/ATR, FANCA/C/D2/E/F/G/L/M, MRE11A, NBN, RAD50/51/52, RAD51B/C/D et al).

Results

Among the 65 HR+ BC patients receiving adjuvant therapy, 9 (9/65, 13.9%) patients received platinum-based adjuvant therapy. The medium follow-up time was 34 m (range 18-68 m). For the 3 patients who had relapsed, the 2 patients with HRR gene mutations had longer DFS (48 m and 68 m, respectively) than the other one without HRR gene mutations had shorter DFS (18 m).

Conclusions

In terms of HRR gene mutations, HR+, TNBC and HER2+ BC have different mutation landscape. Mutations in HRR genes may serve as a biomarker for platinum-based adjuvant therapy for HR+ BC patients, which warrants further studies.