TESTS for these markers are usually performed by next generation sequencing (NGS) of tumor tissue or circulating tumor DNA (ctDNA) and have limitations such as sample accessibility/availability and under-sampling due to inter-/intra-tumor heterogeneity.

Previously we predicted GI using CTC phenotypic features without the use of NGS in metastatic castration-resistant prostate cancer (mCRPC) pts with high accuracy (~75%) (ASCO 2016). In addition, patients with phenotypically predicted GI (pGI) CTCs had significantly better PSA responses on Abiraterone + Veliparib (92%) vs. Abiraterone alone (23%) (ESMO 2016), and also responded better to platinum agents vs. taxane agents (ESMO 2017).

Here, we sought to develop and analytically validate an algorithm for predicting CTC pGI in TNBC.

Using this set of features and labels, a linear regression model was trained to predict the number of large scale transitions (LSTs) for each individual CTC genome within the training cohort and used as a ground truth or label for algorithm development.

Determination of the number of large scale transitions (LSTs) for each individual CTC genome within the training cohort and used as a ground truth or label for algorithm development.

The ability to identify PARPi/platinum sensitivity using an IF CTC staining method rapidly, at reduced cost and aid in the acceleration of drug development.

Further analytical validation in a larger cohort is ongoing.

Previous studies showed that pGI was an analytically validated biomarker with clinical utility to predict PARPi or platinum therapy response in mCRPC pts.

Here we show the same test concept can be applied to TNBC.

The ability to identify PARPi/platinum sensitivity using an IF CTC staining method for CTC phenotype without the use of NGS will help to stratify patients more rapidly, at reduced cost and aid in the acceleration of drug development.

CONCLUSIONS

• Genomic scars and HRD gene mutations are biomarkers for PARP inhibitor (PARPi) and platinum agent therapy response in breast cancer.

• Tests for these markers are usually performed by next generation sequencing (NGS) of tumor tissue or circulating tumor DNA (ctDNA) and have limitations such as sample accessibility/availability and under-sampling due to inter-/intra-tumor heterogeneity.

• Previously we predicted GI using CTC phenotypic features without the use of NGS in metastatic castration-resistant prostate cancer (mCRPC) pts with high accuracy (~75%) (ASCO 2016). In addition, patients with phenotypically predicted GI (pGI) CTCs had significantly better PSA responses on Abiraterone + Veliparib (92%) vs. Abiraterone alone (23%) (ESMO 2016), and also responded better to platinum agents vs. taxane agents (ESMO 2017).

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