Background

Biomarkers to predict treatment outcomes for individual patients (pts) on standard of care Tx is an unmet medical need in the management of mCRPC. Using pre-treatment blood draws, we previously reported a phenotypic CTC heterogeneity algorithm that predicts progression-free survival times on ARSi vs. Taxanes. We have also defined distinct genomic subtypes to which different driver genetics and genetic instability are linked. We sought to correlate CTC phenotypic drug sensitivity by determining OnTx CTC phenotypic and genotypic profiles to assess the effect of specific drug classes.

Methods: CTC Morphology and Heterogeneity Analysis

CTC Counts OnTx are Independent of Baseline Counts

CTC Heterogeneity Decreases Following Treatment in Patients Receiving 1st and 2nd Line, But Not 3rd Line Therapy

OnTx CTC Counts Associated with Worse Survival Than Baseline Counts for Patients Receiving ARSi and Taxanes

Therapy Specific CTC Morphology Changes Are Observed Between Patients Treated with ARSi, Taxanes and Platinum

Presence of Specific OnTx CTC Cell Types Associated with Therapy Resistance and Poor OS

Presence of Specific OnTx CTC Cell Types Are Prognostic of Therapy Resistance and Poor OS

Conclusions

- Post treatment changes in specific CTC subtypes vary by drug class.
- CTC count and CTC subtypes are present in OnTx blood samples. Presence of OnTx CTCs are generally associated with worse overall survival compared with CTCs in baseline draws.
- CTC heterogeneity and discrete CTC subtypes impact patient survival by Tx class.
- Models to improve prediction of therapeutic benefit can be developed utilizing CTC phenotypic profiling.