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WES-derived aneuploidy score (W-AS) identifies MMRd patients with reduced benefit from immunotherapy in endometrial cancer: Multi-omic analysis of the phase III AtTend/ENGOT-EN7 trial

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Background

The addition of Atezolizumab to standard chemotherapy significantly improves outcome in advanced/metastatic endometrial cancer with mismatch repair deficiency (MMRd). However, not all MMRd tumors benefited from the addition, and predictive biomarkers are not established.

Methods

Baseline surgical/biopsy specimens from 125 MMRd and 409 non-MMRd tumors from patients randomized in the AtTend trial were processed for multiomic analysis, including RNAseq (ongoing), Whole Exome Sequencing (WES by Twist Exome 2.0, analysed through Dragen v.4.2.4 and ASCETS) and multiplexed immunofluorescence with an 18-antibody panel. Univariable Cox proportional hazards models were used to explore the prognostic and predictive effect on progression free survival (PFS) and overall survival (OS).

Results

WES was finalized for 234 patients overall, including all available MMRd samples (110/125, 88.0%). Key findings from the analysis of individual mutations include: low incidence of POLE mutations (1/234); a dual MMRd/BRCA1/2-mutated profile (14/234); a high frequency of MSH3 mutations in MMRd patients (29/110). No individual mutation was associated with outcome, but MMRd tumors with combined alterations in APC and CTNNB1 (WNT pathway) (23/110, 20.9%) showed worse PFS (HR 1.91, 95% CI 1.10-3.33, p=0.0201). W-AS > 0.2 was found in 10/110 (9.1%) MMRd tumors and was associated with worse PFS (HR 2.81, 95%CI 1.33-5.97, p=0.0049) and OS (HR 2.51, 95%CI 1.12-5.65, p=0.0211). W-AS-high tumors did not benefit from atezolizumab in PFS (interaction p=0.0016. Low AS: HR 0.28, 95%CI 0.16-0.47, p<0.0001; High AS: HR 3.60, 95%CI 0.71-18.29, p=0.1006). Preliminary data suggested a lower immune cell infiltration in W-AS-high tumors, characterized by a reduced proportion of CD4+ helper T cells and an increased proportion of M2 macrophages.

Conclusions

If externally validated, W-AS may identify patients with MMRd tumors who derive limited benefit from adding immunotherapy to standard chemotherapy. Genetic assessment of W-AS, MSH3 and WNT genes should be considered in the prognostic workup of advanced/metastatic endometrial cancer.

Clinical trial identification

EudraCT 2018-001072-37; NCT03603184.

Legal entity responsible for the study

Istituto di Ricerche Farmacologiche Mario Negri, IRCCS.

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