

Distribution of molecular subtypes in endometrial cancer following the updated 2025 ESGO-ESTRO-ESP guidelines: A prospective cohort study.

03. Endometrial cancer

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Introduction/Background

Molecular classification has been proposed for endometrial cancer patients as a new triage tool for the administration of adjuvant therapy. Recently, the 2025 update of the ESGO-ESTRO-ESP guidelines have divided five distinct groups in the algorithm of molecular classification. This study aims to investigate the group prevalence of the 2025 updated molecular classification in endometrial cancer patients.

Methodology

We prospectively analyzed the records of patients with endometrial cancer that underwent testing in order to intergrade the new molecular classification from 2023 – 2025. Next-generation sequencing (NGS) was performed for polymerase epsilon (POLE) mutation and microsatellite instability (MSI) status, while immunohistochemistry was utilized to distinguish the various mutant-expression patterns of the p53 gene, the mismatch repair (MMR) status and the estrogen receptors (ER) status.

Results

224 patients met the inclusion criteria and were included in the study. The mean age of the patients was 61.1 years old, with a standard deviation (SD) of 10.6. The majority of the patients had endometrioid (n=90%) low grade (n=80%) disease. Concerning the 2025 updated molecular classification, a p53 mutation was present in 48 patients (21.9%) and a POLE mutation in 18 patients (8.2%). Furthermore, MMR deficiency (MMRd) or MSI-H results was detected in 48 patients (26.4%), while ER positivity was observed in 91 patients (85%). A complete molecular classification was available in 187 patients. There were 11 cases (4.9%) of multiple classifiers. Finally, 18 patients (9.6%) were categorized as POLEMut, 44 (23.5%) as MMRd, 78 (41.7%) as no specific molecular profile (NSMP) low-grade and ER-positive, 17 (9%) as NSMP high-grade or ER-negative and 30 (16%) as p53abn.

Conclusion

The new 2025 update of the ESGO-ESTRO-ESP guidelines better defines the groups, especially NSMP, in the algorithm of the molecular classification. However, large prospective trials are needed to validate the prognosis of each group.

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