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Abstracts

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Papillary thyroid carcinoma arising in struma ovarii: diagnostic pitfalls and clinicopathological insights from a rare case

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Background & Objectives: Struma ovarii is a rare monodermal ovarian teratoma predominantly composed of thyroid tissue, accounting for approximately 3–5% of ovarian teratomas. Malignant transformation is uncommon, occurring in about 5–10% of cases, most frequently as papillary thyroid carcinoma (PTC). The applicability of thyroid carcinoma diagnostic criteria to ovarian counterparts remains controversial, and standardized management strategies are lacking.

Methods: A 71-year-old woman presented with abnormal uterine bleeding. Imaging revealed a multiloculated cystic adnexal mass with a solid component. Tumour markers and thyroid function tests were within normal limits. The patient underwent total hysterectomy with bilateral salpingo-oophorectomy with intraoperative frozen section evaluation.

Results: Gross examination demonstrated an 8.5 cm cystic ovarian lesion containing a 3.5 cm multinodular solid component with yellow, gelatinous appearance. Frozen section suggested a benign cystic lesion. However, extensive histopathological sampling revealed that the tumour was entirely composed of thyroid tissue, consistent with struma ovarii. Within this background, focal areas exhibited classical features of PTC, including papillary architecture and characteristic nuclear changes.

Conclusion: Malignant struma ovarii is a rare entity with nonspecific clinical, radiological, and intraoperative findings, often leading to diagnostic challenges. Preoperative diagnosis is difficult, as imaging and laboratory parameters are typically non-specific and thyroid function is usually normal. Histopathological evaluation remains the gold standard, requiring careful sampling due to the focal nature of malignancy. Although most cases present at early stage and have favourable prognosis, long-term follow-up is recommended due to the potential for late recurrence or metastasis. This case highlights the critical importance of thorough gross and microscopic examination in identifying malignant transformation within struma ovarii and underscores ongoing challenges in establishing uniform diagnostic and therapeutic guidelines.

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HPV positive cervical squamous cell carcinoma: association of tumour grade with presence of different HPV genotypes and their load

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Background & Objectives: Cervical cancer ranks as the eighth most common cancer worldwide and the ninth leading cause of cancer-related death according to GLOBOCAN 2022. Alarmingly, in Latvia it is the second most common malignancy in females under 45 years of age and the third leading cause of cancer-related death among women (data from the Latvian Centre of Disease and Prevention Control). Majority of cervical cancers are associated with high-risk human papilloma virus (hrHPV) infection. In this study we investigated the associations between cancer grades and genotypes and viral loads of infecting hrHPVs.

Methods: Study cohort consisted of formalin-fixed paraffin embedded cervical tissues (FFPE-blocks) of women (n=77), median age 60 years, observed in P. Stradins Clinical Universiy hospital. Tumour grades determined by pathologist. DNA extracted from sectioned FFPE-blocks (Qiagen) was subjected to PCR detecting 14 hrHPV genotypes (semiquantitative Anyplex or quantitative Allplex HPV14, Seegene, South Korea).

Results: All 77 were cases of cervical squamous cell carcinomas (CSCC). All CSCCs were positive for at least one hrHPV, mainly HPV16 (73/77, 94.8%) followed by HPV33 (23/77, 29.8%). Other genotypes were significantly less prevalent ($p<0.05$). Of 77 CSCCs, 53,2% carried two and 15,6%, three hrHPVs, most commonly HPV16+HPV33+ (27.3%) and HPV16+HPV18+ (6.5%). Tumour grades correlated positively with presence of several hrHPVs,

specifically HPV16 together with hrHPV of other α-species, specifically α7+α9 combination. Significant correlation between tumour grades was also observed with the overall viral load and loads of HPV16 and HPV39, while for HPV66 and HPV31 loads the correlation was negative (p<0,001 for all).

Conclusion: To conclude, we have demonstrated that presence of multiple hrHPV genotypes, specifically of different α-series with high viral loads is a marker of CSCC of higher morphological grade.

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Unknown mutations in POLE gene: are they true unsignificant?

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Background & Objectives: Screening for pathogenic mutations in the *POLE* gene is essential in endometrial cancer, as these mutations are associated with a high number of DNA alterations, leading to an increased tumour mutational burden (TMB) and improved patient outcomes. Several panels based on next-generation sequencing (NGS) or quantitative PCR (qPCR) technologies have been developed for *POLE* mutation screening, proving highly effective in identifying known pathogenic variants in clinical practice. In contrast, Sanger sequencing enables the detection of all types of genetic variations.

Methods: The aim of our study was to investigate *POLE* gene mutations in a series of 104 patients with endometrial cancer. We performed mutation screening using both Sanger sequencing and the Idylla™ POLE-POLD1 mutation assay on FFPE tumour tissues.

Results: Our results identified five known pathogenic mutations located in exons 9, 11, 13, and 14 (P286R, F367S, V411L, and A456P, respectively), as well as twelve variants of unknown significance. In silico prediction analysis suggested that only one variant, M359V (exon 11), is likely benign, whereas the remaining non-classified variants were predicted to be deleterious or protein-truncating.

Conclusion: Deleterious variants affecting conserved regions of the protein or causing truncation within the exonuclease domain of *POLE* may impair polymerase proofreading function. This impairment can increase tumour mutational burden and potentially contribute to poor response to conventional platinum-based chemotherapy.

Therefore, integrating in silico prediction results for variants of unknown significance may be valuable, particularly in cases where patients show limited response to chemotherapy and where TMB assessment is not available.

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Small sample, big diagnosis: two cases of carcinosarcoma of the cervix and endometrium on curettage samples

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Background & Objectives: Carcinosarcoma (malignant mixed Mullerian tumour) is a rare, aggressive biphasic neoplasm composed of malignant epithelial and mesenchymal components. Endometrial carcinosarcoma accounts for less than 5% of uterine malignancies, while primary cervical carcinosarcoma is exceedingly rare. Diagnosis on curettage is challenging due to limited sampling and tumour heterogeneity. We aimed to highlight the key histopathological features and diagnostic pitfalls of carcinosarcoma through two cases diagnosed on curettage.

Methods: Two patients diagnosed with gynaecologic carcinosarcoma on curettage were retrospectively evaluated. Clinical, histopathological, and immunohistochemical findings were reviewed.

Results: The first case was a 77-year-old postmenopausal woman with vaginal bleeding. MRI revealed a cervical mass, and endocervical curettage was performed. Microscopically, the cervical tumour showed a carcinomatous component (90%) consisting predominantly of high-grade serous carcinoma with focal clear cell carcinoma and neuroendocrine differentiation, while the sarcomatous component (10%) showed pleomorphic spindle and epithelioid cells in a myxoid stroma. p53 showed a mutant pattern with complete loss, and Ki-67 was 70–80%. Notably, unlike previously reported cases in the literature, the tumour cells also exhibited TTF-1 positivity. Radiological and clinical work-up demonstrated no thyroid or pulmonary lesion.

The second case was a 56-year-old woman with abnormal uterine bleeding with no endometrial thickening on