compared in two groups: less than 16-Ala and at least 16-Ala. The stages of pT1a and pT1a (m) were found in 20 alleles in the less than 16-Ala group, whereas in 16 alleles of the at least 16-Ala group, pT1b-pT2(m) was the most common ($p = 0.039$). Lymph node metastases were found more frequently in the less than 16-Ala group than in the at least 16-Ala group but this difference was not statistically significant (10 vs. 3 respectively; $p = 0.680$).

Conclusions: The analysis of the length of the polyAla tract may be a useful diagnostic tool in predicting the course of PTC in patients with a positive family history.

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Thyroid

PSAT384

Familial Non-Medullary Thyroid Cancer — Does The Number Of Alanine Residues In The FOXE1 Gene Play A Role?

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Familial non-medullary thyroid cancer (FNMTC) constitutes about 3–9% of all thyroid cancers. One of the genes believed to predispose to non-syndromic FNMTC is FOXE1. It contains a polyalanine tract (polyAla) with a variable number (11–22) of alanine residues. This length polymorphism could lead to changes in the FOXE1-encoded protein (FOXE1 transcription factor) structure and predispose to papillary thyroid cancer (PTC).

The aim of the study was to investigate the relationship between the length of the polyAla tract and the stage of PTC at diagnosis (according to AJCC 8th edition) in patients with FNMTC.

The study included 27 patients (from twenty families) with familial PTC (at least two family members were diagnosed with the disease). The length of the polyAla tract of the FOXE1 gene was analyzed. The following numbers of polyAla variants were detected: 11-Ala – 2, 12-Ala – 1, 14-Ala – 23, 16-Ala – 28 alleles. The staging at diagnosis was