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Polymorphism of genes of hemostasis system and methionine exchange in patients with female reproductive tumors.

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Background: Our purpose was to analyze the rates of polymorphic allelic variants of genes of hemostasis system and methionine exchange in patients with female reproductive tumors. **Methods:** The study included 51 patients with histologically verified gynecologic tumors (group 1), including 28 patients (group 1a) with malignant tumors (cervical cancer (CC) n = 8, ovarian cancer (OC) n = 8, endometrial cancer (EC) n = 8, other cancers n = 4) and 23 patients (group 1b) with benign tumors, and 47 women without tumors (group 2). 12 polymorphic loci were studied by RT-PCR in genomic DNA samples: F2 (G20210A, rs1799963), F5 (G1691A, rs6025), F7 (G10976A, rs6046), F13 (G226A, rs5985), FGB G(-455)A (rs1800790), ITGA2-α2 (C807T, rs1126643), ITGB3-b (T1565C, rs5918), PAI-1 4G(-675)5G, rs1799889), MTHFR (C677T, rs 1801133 and A1298C, rs1801131), MTR (A2756G, rs1805087), MTRR (A66G, rs1801394). Groups 1, 1a and 1b were compared with controls (p^1) and among themselves (p^2). **Results:** The ratio of genotype frequencies maintained in the Hardy-Weinberg equilibrium in all gene loci except F7 (G10976A) in group 1 (p = 0.03). An alternative allele in the F2 gene was found only in group 2 (1.1%). The frequency of an alternative allele in the F5 gene in group 1 was 2.9%, including 1a – 1.8%, 1b – 4.3%, group 2 – 2.1%; F7 – 16.7%, 14.3%, 19.6% and 17.0%; F13 – 23.5%, 23.2%, 23.9% and 34%; FGB – 26.5%, 25.0, 28.3% and 25.5%; ITGA2 – 53.9% (p^1= 0.03, OR = 1.89 (1.07-3.33), 48.2%, 60.9% (p^1= 0.01, OR = 5.21 (1.22-5.17) and 38.3%; ITGB3 – 13.7%, 10.7%, 17.4% and 16.0%; PAI-1 – 47.1% (p^1= 0.03, OR = 0.53 (0.30-0.93), 46.4%, 47.8% and 62.8%; MTHFR (T) – 28.4%, 30.4%, 26.1%, 34.0%; MTHFR (C) – 34.3%, 28.6%, 41.3% (p^1= 0.04, OR = 2.17 (1.02-4.61) and 24.5%; MTR – 18.6%, 19.6%, 17.4% and 27.7%; MTRR – 63.7%, 71.4%, 54.3% and 62.8%, respectively. TT genotype at the ITGA2-α2 (C807T) locus was more frequent in group 1 than in group 2 (23.5% vs 19.1%, p^1= 0.01, OR = 6.54 (2.61-16.40); CT genotype was more frequent in group 1a than in group 2 (67.9% vs 38.3%, p^1= 0.004, OR = 3.40 (1.27-9.13), and more frequent in EC than in group 2 (87.5% vs 38.3%, p^1= 0.03, OR = 11.28 (1.28-99.40). GG genotype at the MTRR (A66G) locus was more frequent in group 1a than in group 1b (53.6% vs 26.4%, p^2= 0.042). 5G5G genotype at the PAI-1 4G(-675)5G locus was more frequent in group 1 than in group 2 (31.4% vs 10.6%, p^1= 0.04, OR = 3.84 (1.28-11.53), and more frequent in OC than in group 2 (75% vs 11%, p^1= 0.0001, OR = 25.50 (3.96-160.20). AA genotype at the F7 (G10976A) locus was more frequent in CC patients than in group 2 (31.3% vs 17%, p^1= 0.03, OR = 15.33 (1.20-195.75). **Conclusions:** Carriage of the AA genotype at the F7 (G10976A) locus may increase the risk of developing CC, and the CT genotype at the ITGA2-α2 (C807T) locus may increase the risk of EC. On the contrary, the alternative 4G allele at the PAI-1 4G(-675)5G locus was less common in patients with malignant tumors, especially OC, than in the group without cancer. Research Sponsor: None.