

# Zróżnicowanie polipów nosa w badaniach techniką mikromacierzy oligonukleoty do wy ch \*

Diversity of nasal polyps in microarray technology research

**Beata Rostkowska-Nadolska, Małgorzata Kapral, Katarzyna Gruna-Pelczar, Marcin Frączek, Wojciech Gawron, Urszula Mazurek**

## Summary

Nasal polyps, according to many authors, generate as a result of chronic inflammation process with activation of cytokines, immunological reaction mediators that regulate proliferation, differentiation and cell apoptosis. Clarifying molecular mechanisms present in those disturbances may have diagnostic and prognostic value in evaluation of recurrence, dynamics and differentiation of nasal polyps as well as in their therapy. **Aim.** The aim of the work was an analysis of nasal polyps on the basis of molecular, histopathological and clinical picture as well as comparing differentiated genes transcription in nasal polyps and proper nasal mucosa. **Material and method.** Oligonucleotide array with HGU 133A - Affymetrix were used to analyze the expression of 22 283 genes in nasal polyp tissues from 17 patients. The control group consisted of 8 tissue samples from patients after nasal septoplasty surgery. **Results.** All the samples could be classified to nasal polyps group or proper mucosa group, it reflected significant differences in genes profile expression in both groups. The evaluation of 22 283 genes transcriptions showed that in most cases nasal polyps tissue reflect classification connected with dominant inflammation cells infiltration. The data obtained let distinguish subgroups connected with clinical condition of the patients. The subgroup with massive nasal and sinus polyposis, eosinophilia and differentiated lower respiratory airways hyperactivity and the subgroup without eosinophilia infiltration may be distinguished. The data obtained suggest that molecular mechanisms may influence on the promotion and kind of inflammation process as well as the clinical course of nasal polyps.