

during ossiculoplasty. A new strategy of IM of hearing threshold (HT) evaluation was developed by a team of engineers and surgeons on the basis of previously performed researches.

Subjects and Methods: Patients (n = 25) underwent two-stage canal wall-up tympanoplasty due to chronic otitis media with cholesteatoma. During the second look surgery performed 12 months later ossiculoplasty was monitored intraoperatively by LDV and round window electrocochleography (RW-ECoChG). Both measures were performed via an enlarged posterior tympanotomy. LDV and RW-ECoChG intraoperative tests recorded simultaneously for the same stimulation set. Intraoperative HT was defined automatically in auditory steady state response (ASSR) option as well as prosthesis vibration by LDV. Using both intraoperative techniques various configurations of prosthesis placement were tested. On the basis of the preoperative tonal audiometry and post-ossiculoplasty RW-ECoChG & LDV thresholds a mini-software calculated an optimal ABGC. Prosthesis moveability tested simultaneously by LDV was showed and correlated with RW-ECoChG thresholds.

Results: Postop ABG closure ranged between 15 to 45 dB. HT improvement evaluated intraoperatively correlated with postop ABGC ($r > 0.5$; $p < 0.05$). Various prosthesis configurations and placements resulted in measurable changes in the RW-ECoChG thresholds. LDV appeared sensitive mostly to prosthesis position changes manifesting by movability improvement at 0.5- and 1.0kHz.

Conclusions: RW-ECoChG measured in ASSR option was found to be an objective and sensitive technique for IM of HT improvement significantly corresponding with postop ABG-C. LDV showed their usefulness to control prosthesis position changes by confirming better acoustic energy transfer through the reconstructed ossicular chain.

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Basic and translational research in cholesteatoma and ear surgery (N633)

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Preliminary Analysis of Genetic Alterations in Cholesteatoma

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Learning Objectives:

The Clinic is operating annually over 100 cholesteatomas (655 operations in the years 2010 -2015). Because of a

common bacterial infection a bacteriologic analysis indicates for *Pseudomonas aeruginosa*, *Proteus mirabilis* and *Staphylococcus aureus* as the most commonly detected in middle ear infection.

Having in mind a literature suggestion of a partial analogy between oncogenesis and cholesteatoma formation and own experience in identification of oncogenes and tumor suppressor genes modulating progression of laryngeal cancer we have undertaken a molecular analysis targeting for an identification of genetic background of cholesteatoma. Array-CGH scanning of a genome indicated for frequent gains and losses of gene copy number in the genome. The results will be further analyzed to identify amplified regions potentially indicating location of oncogenes and homozygous deletions covering loci of tumor suppressor genes involved in cholesteatoma.

Independently a molecular cytogenetic technique was applied to analyze 8q24 chromosome region to estimate an amplification and potential rearrangement(s) of c-Myc oncogene. Fluorescent in situ Hybridization (FISH) with the use of specific DNA probes (regular fluorescent, break a part) is being applied.

The results will be presented during the meeting.

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Inflammatory pathways in middle ear cholesteatoma

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Learning Objectives:

Introduction: Middle ear cholesteatoma (MEC), accompanied by chronic inflammatory response is characterized by invasive growth and osteolytic activity.

Aim: Present the cellular and inflammatory pathways in the pathogenesis of cholesteatoma and adjacent tissues.

Material and methods: Congenital, acquired MEC (study groups) and retroauricular skin specimens (control group, CS) were investigated for markers of inflammation using various immunohistochemistry, Western Blot, cell culture and flow cytometry techniques. Studied markers included proliferation and apoptosis of keratinocytes (PCNA, Ki67, p53, p21, APO2.7), angiogenesis and inflammation (TGF- α), proteasomal degradation pathway (low-molecular mass polypeptide-7 subunit of the immunoproteasome (LMP7), and selected molecular signalling (the DNA-binding high-mobility box 1 (HMGB1) in the protein advanced glycation endproducts (RAGE) axis.

Results: The significantly more intense expression of LMP7 and p21-positive cells was seen in MEC. The LMP7(+) cells