**Saturday 19 May**

**Poster session II: Basic science**

**P128 Gene expression profile in laryngeal cancer by oligonucleotide microarrays analysis**

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Laryngeal cancer is one of the most frequent head and neck cancers, clearly determined by exogenous carcinogenic factors. More detailed recognition of molecular mechanisms in laryngeal carcinoma may allow to develop new treatment methods. At the same time, providing characteristics of genes and proteins expressed in laryngeal carcinomas shall allow to use them in diagnostics.

The aim of the study is the analysis of gene expression profile in laryngeal carcinoma.

The study comprised a group of 14 patients (12 males and 2 females) suffering from squamous cell laryngeal carcinoma, progression stages II to IV, diagnosed and treated surgically in the years 2003–2005 in the ENT of the Silesian Medical University (Katowice, Poland).

Total RNA was isolated both from squamous larynx cancer tissue and from fragments of macroscopically unchanged, healthy larynx tissue, collected from the same patient. RNA isolation was performed from some 40mg of frozen tissue, by means of RNeasy Midi and Mini Kit (Qiagen). For cDNA synthesis 5ug of RNA (GeneChip® Expression 3' Amplification One-Cycle cDNA Synthesis Kit, Affymetrix) has been used. Transcription in vitro followed (GeneChip® Expression 3' IVT Labeling Kit, Affymetrix), while the multiplied cRNA underwent fragmentation, applying high temperatures and magnesium ions. After 16-hour hybridisation on high density microarrays Human Genome U 133 Plus 2.0 (Affymetrix) read-out was performed, followed by data analysis.

After preliminary analysis using non-supervised methods, analysis was performed by means of non-parametric U Mann-Whitney test, with the assessment of percentage of false positive results (FDR) applying the method of Benjamini-Hochberg, as well as the Holm method. Using Mann-Whitney test, 1241 transcripts were singled out, differentiating between both groups at FDR = 5%. In the next stage that group was narrowed down to 398 genes, meeting the criteria assumed, analysing by means of parametric test. Two genes, angiopoietin like transcript (231773_at, ANGPTL1, angiopoietin-like 1) and undefined protein CGI-115 (219037_at) revealed a very substantial difference in expression, as well as complied with very rigorous criteria of error risk assessment for group of genes (FWER) applying Holm method.

Conclusions: Analysis of gene expression profile in laryngeal carcinoma allows to pick out new genes, which in future may become molecular markers of that carcinoma.

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Keywords: laryngeal cancer, gene expression profile, microarrays

**P129 The relationship between the expression of CD44 in SCC of the oral tongue and cervical lymph node metastasis**

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**Background:** Squamous cell carcinoma of the tongue are the most common oral cavity cancers in middle age. Presence of cervical lymph node metastasis at the time of diagnosis has a significant effect on treatment modalities and prognosis. CD44 is a transmembrane glycoprotein that is involved in cell adhesion to hyaluronan. It is suggested that CD44 expression plays a role in metastasis formation.

In this study, we tried to evaluate the expression rate of CD44 and cervical lymph node metastasis in squamous cell carcinoma of the oral tongue.

**Material and Method:** Between January 2005 and January 2006, we studied 39 patients diagnosed with SCC of the oral tongue in Omid hospital, Iran. The expression of CD44 was measured by immunohistochemistry in patients with and without cervical lymph node metastasis.

**Results:** The most common age group was 50–59 years. At the time of diagnosis, 20 (51.28%) of patients had cervical metastasis. CD44 expressions in 12 patients were homogenous and in 27 patients were non-homogenous. There was no statistically relationship between histopathologic grading and cervical metastasis (p = 0.429). In 19 (95%) of patients with cervical metastasis, expression of CD44 was significantly non-homogenous (p = 0.000).

**Conclusion:** It seems that CD44 as a marker can be used to predict cervical lymph node metastasis in the patients with SCC of oral tongue.

Keywords: tongue SCC, CD44, lymph node metastasis

**P130 Detection of serum cyfra 21–1 in patients with primary oral squamous cell carcinoma**

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Oral squamous cell carcinoma (OSCC) is the most common malignant tumor in oral and maxillofacial region with poor prognosis. Cyfra 21–1 is a useful tumor marker for squamous cell carcinoma, but the clinical value of Cyfra 21–1 in OSCC has not been confirmed. In order to investigate the diagnostic and prognostic value of serum Cyfra 21–1 in primary OSCC patients, preoperative serum Cyfra 21–1 concentration from 100 OSCC patients and 56 healthy persons was detected by enzyme-linked immunosorbent assay (ELISA), the cutoff value was calculated with a receiver operating characteristic (ROC) curve, the prognostic analysis was performed with Kaplan–Meier method and Cox regression models. Preoperative serum Cyfra 21–1 concentration in OSCC patients (1.18±1.20μg/L) was significantly higher (t = 6.585, P < 0.001) than that in healthy persons (0.40±0.16 μg/L); with the cutoff value of 0.65 μg/L, the diagnostic sensitivity and specificity was 0.570 and 0.964, respectively; it correlated significantly with tumor recurrence and survival rate, the higher serum Cyfra 21–1, the higher tumor recurrence rate and lower survival rate; serum Cyfra 21–1 was an independent prognostic factor for OSCC using univariate and multivariate Cox models. From these results, we suggest that preoperative serum Cyfra 21–1 concentration increases significantly in OSCC patients, with strong prognostic value as an independent factor.

Keywords: Cyfra 21–1, Oral squamous cell carcinoma, Prognosis, Serum

**P131 The effect of RNA interference of INOS gene expression on proliferation of squamous cell carcinoma of the tongue**

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**Objective:** The effect of nitric oxide (NO) and inducible nitric oxide synthase (NOS) on apoptosis and tumor cell proliferation was investigated.