

EGFR, HER2/neu, LAMC2 showed high expression whereas RHOC showed low expression with LN metastasis. The cutoff point of at least four proteins with cumulative score of 3 would reflect the best sensitivity and specificity. The 4-protein signature showed sensitivity of 90.1% and specificity of 64.1% and prognostic accuracy of 77.5% in correlation with LN metastasis in general for an overall 83 OSCC samples and in particular for each set of OSCC samples from each center demonstrates the robustness and accurateness of this 4-protein signature in predicting LN metastasis. Kaplan-Meier survival curves showed significant survival probability difference between two groups in 4-protein signature for overall 83 samples.

Conclusions: Four protein signature have been shown to have potential to be used as prognostic indicators of LN metastasis in OSCC. It can be an useful prognostic tool in the clinical setting to facilitate the prediction of LN metastasis. This study also concluded that the survival probability is inconclusive. However, it is found that the 4-protein signature has shown a trend for prediction of overall survival.

DOWN-EXPRESSION OF TETRASPANIN CD9 IS A SENSITIVE MARKER FOR IDENTIFYING PRE-MALIGNANT CHANGES IN THE ORAL EPITHELIUM. PROF. MARILENA VERED^A, DR. IDO GEORGY^B, MRS. SARA HAMER^A, PROF. AMOS BUCHNER^A, DR. AYELET ZLOTOGORSKI-HURVITZ^A.
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Objectives: Tetraspanins, cell surface proteins that mediate cell-cell and cell-extracellular matrix interactions, are capable to modify cell motility, thus being potential diagnostic markers in pre-malignant conditions. We examined the immunohistochemical expression of tetraspanins CD9, CD81 and CD63 in normal oral mucosa as well as in inflamed, dysplastic and neoplastic epithelial lesions.

Findings: Included were cases of normal oral mucosa (NOR, N=15), oral lichen planus (OLP, N=51), hyperkeratosis/mild dysplasia (HK, N=29), moderate-severe dysplasia (DYSP, N=22), oral squamous cell carcinoma (OSCC, N=31), and normal-looking mucosa nearby OSCC (N-OSCC, N=18). Staining, assessed as percent of stained cells multiplied by staining intensity (1=weak, 2=strong), was evaluated per epithelial thirds (basal, middle and upper) and then as total staining score (sum of all thirds). Statistical analysis was performed using One-way ANOVA. Receiver operating characteristic (ROC) curve was used for diagnostic sensitivity. Statistical significance was set at P<0.05. Expression of CD9 was highest in NOR compared to all other lesion types and higher in OLP, HK and DYSP than in N-OSCC and OSCC (p<0.001). A higher expression of CD81 in NOR, OLP and HK differentiated these lesions from DYSP, OSCC and N-OSCC (p<0.001). CD63 was usually inconclusive. CD9 was the only tetraspanin to significantly distinguish NOR from all other lesion types (area under ROC, 0.9; P < 0.001) with high sensitivity and specificity (80% for both, at a total staining score of 12.5).

Conclusions: CD9 could accurately discriminate between normal (high expression) and all other types of pathologies (lower expression) with high diagnostic sensitivity. In addition, expression of CD9 in neoplasia and the nearby histologically "normal-looking" epithelium was similar but significantly lower than in dysplasia and OLP. Therefore, the expression of CD9 could aid in defining the nature of equivocal histopathological changes in oral epithelial lesions.

HIGH THROUGHPUT SEQUENCING REVEALS CIRCADIAN RHYTHM GENE RORA IS COOPERATIVELY SUPPRESSED BY MULTIPLE MICRORNAS IN ORAL SQUAMOUS CELL CARCINOMA. PROF. JIALI ZHANG^A, DR. XUEQING ZHENG^B, DR. YANAN SUN^B, DR. YUEMEI PAN^B.
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Objectives: To explore the differentially expressed mRNAs and miRNAs in OSCC tissues, and identify the interaction network between miRNAs and transcription factors (TFs). Among them, the regulatory network of miRNAs - circadian gene ROR α on proliferation in OSCC was further elucidated.

Findings: RNA-seq and microRNA-seq analyses show that upregulation of microRNA in OSCC samples significantly contribute to the globally down-regulated transcription factors (TFs) in OSCC. Circadian rhythms genes including three members of retinoic acid receptor-related orphan receptor family (ROR α , ROR β and ROR γ) and CLOCK were among the down-regulated TFs. ROR α was predicted to be targeted by 25 co-upregulated miRNAs, of which, miR-503-5p, miR-450b-5p, miR-27a-3p, miR-181a-5p and miR-183-5p were further testified to directly target ROR α , resulting in a more stronger effect on ROR α suppression by mixing together. In addition, we showed that ROR α was significantly decreased in most OSCC samples (37 of 44, 84%), and significantly suppressed the proliferation of OSCC cells in vitro and in vivo. Attenuated ROR α decreased p53 protein expression and suppressed p53 phosphorylation activity.

Conclusions: The abnormal miRNAs-mediated TFs network could play important role in OSCC tumorigenesis. Among those TFs, circadian gene ROR α acted as a tumor suppressor in OSCC by inhibiting tumor proliferation and could be negatively regulated by miR-503-5p, miR-450b-5p, miR-27a-3p, miR-181a-5p and miR-183-5p cooperatively, which provides clues to understand the clinical link between circadian rhythms and cancer therapy.

COMPARATIVE STUDY OF KI67 AND MCM4-6 COMPLEX IN AMELOBLASTOMA AND UNICYSTIC AMELOBLASTOMA. MS. VANESA PEREIRA-PRADO^A, MS. DELMIRA APELLANIZ^A, PROF. ADALBERTO MOSQUEDA TAYLOR^B, DR. ROGLIO GONZALEZ-GONZALEZ^B, PROF. NELLY MOLINA FRECHERO^B, MS. GABRIELA VIGIL^A, MS. ESTEFANIA SICCO^A, PROF. RONELL BOLOGNA-MOLINA^A.
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Objectives: The aim of the present study was to determine the patterns of immunoeexpression of minichromosomal maintenance proteins (MCM) 4, 5, 6 and correlate them with the presence of Ki67, in order to evaluate their utility as possible