

Methylation and gene expression differences between ASC/TMS1 and MyD88 genes in healthy and cancer laryngeal tissue



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Objective: There are no biomarkers for diagnosis, prognosis and treatment of patients with laryngeal carcinoma. Methylation changes of ASC/TMS1 and MyD88 genes, in healthy and cancer tissue, might be related with development and progression of cancer. The study explored is there a difference in gene's methylation in healthy and tumor tissue and does it correlate with protein expression.

Results: The overall methylation of MyD88 gene is significantly higher in healthy tissue and this finding correlates with protein expression (**Fig. 1 and Fig. 3**) and the overall methylation of ASC/TMS1 gene is unchanged but the protein expression of ASC/TMS1 is significantly higher in cancer. (**Fig.2 and Fig.4**)

Methods: The total of 36 patients were enrolled in the study. Methylation of bisulphite converted DNA was quantified by pyrosequencing in fresh frozen cancer and adjacent non-malignant tissues.

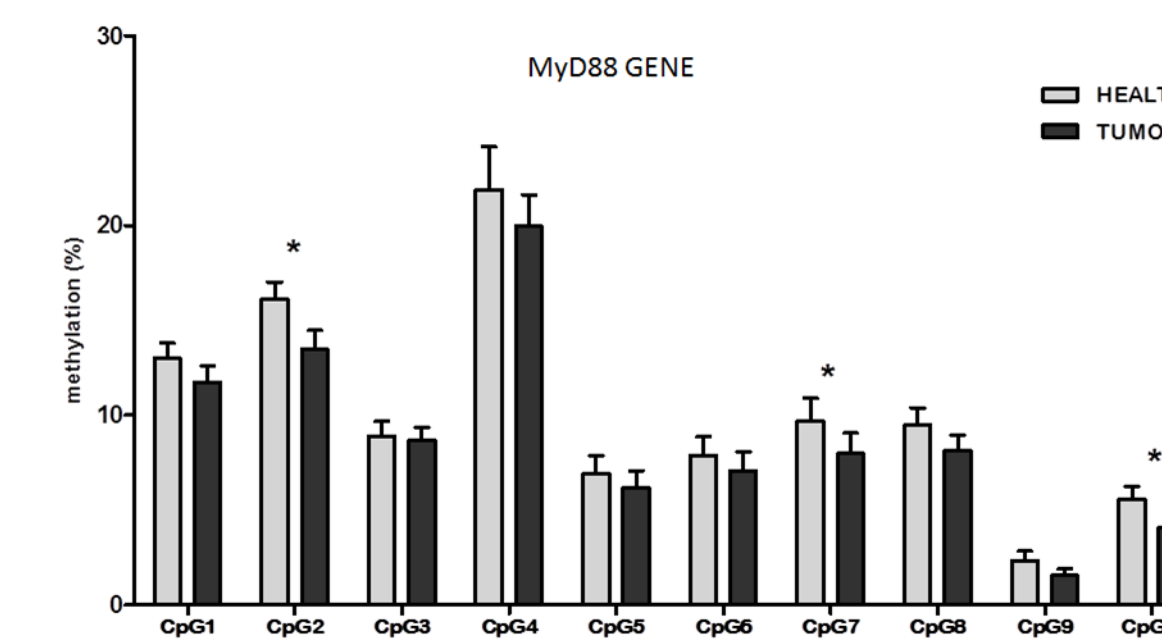


Figure 1: The graph (GraphPad Prism 5.0) showing overall methylation status (%) of CpG islands promotor region of **MyD88** gene in healthy and tumor tissue. * CpG islands (CpG2($p=0,0267$), CpG7($p=0,0174$), and CpG10 ($p=0,0407$) showing significant contribution in overall difference in the methylation status. Paired t-test; $p \leq 0,05$. Results are shown as mean $\pm$ SEM

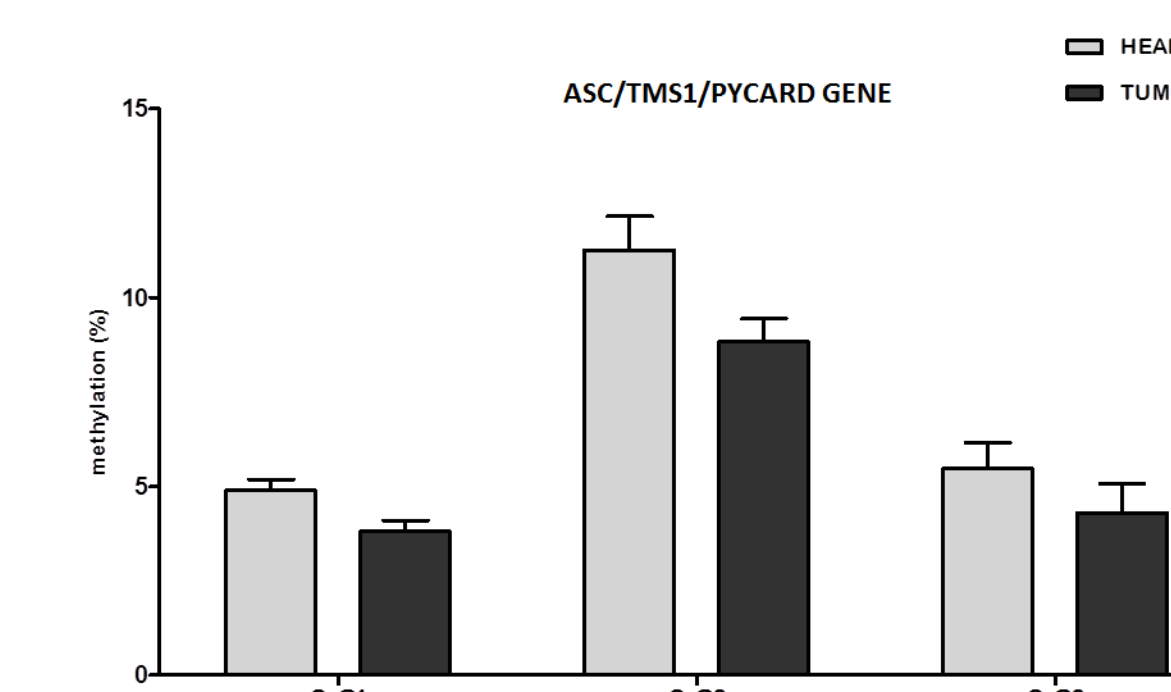


Figure 2. The graph (GraphPad Prism 5.0) showing overall methylation status of CpG islands promotor region of **ASC/TMS1/PYCARD** gene in healthy and tumor tissue. There is no statistically significant difference between healthy and tumor tissue of the larynx $p=0,1562$ ($p > 0,05$). Paired t-test; $p \leq 0,05$. Results are shown as mean $\pm$ SEM

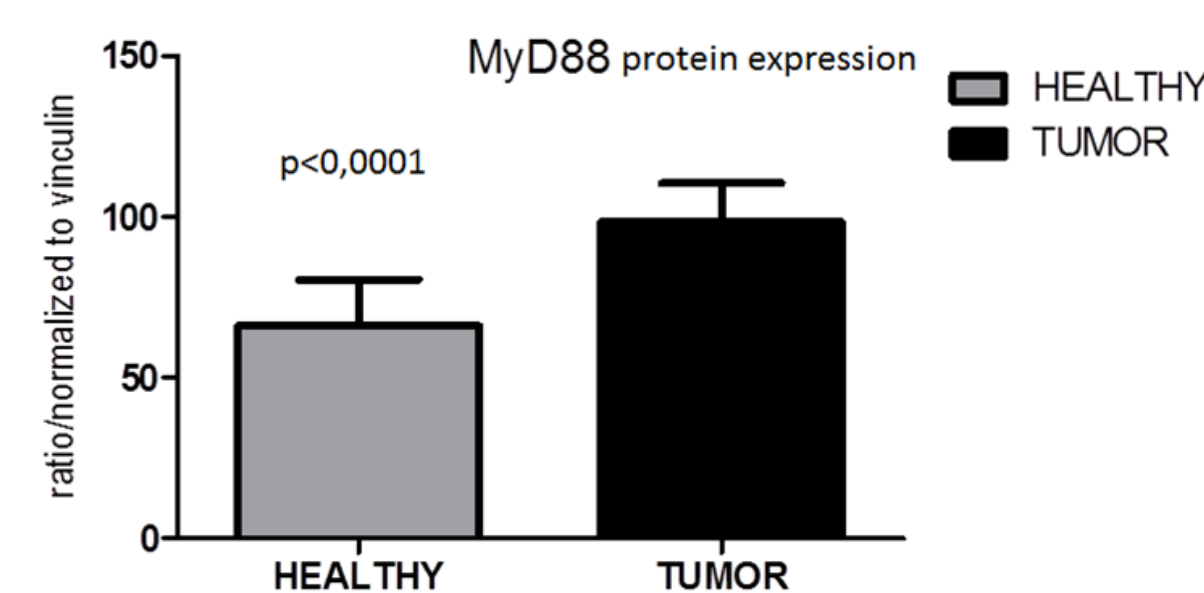


Figure 3. The graph (GraphPad Prism 5.0) of densitometric quantification of protein MYD88 bends. The graph shows statistically significant difference ($p < 0,0001$) in **MyD88** protein expression between healthy and tumor tissue. Paired t-test; $p \leq 0,05$. The values are shown as mean value $\pm$ SEM

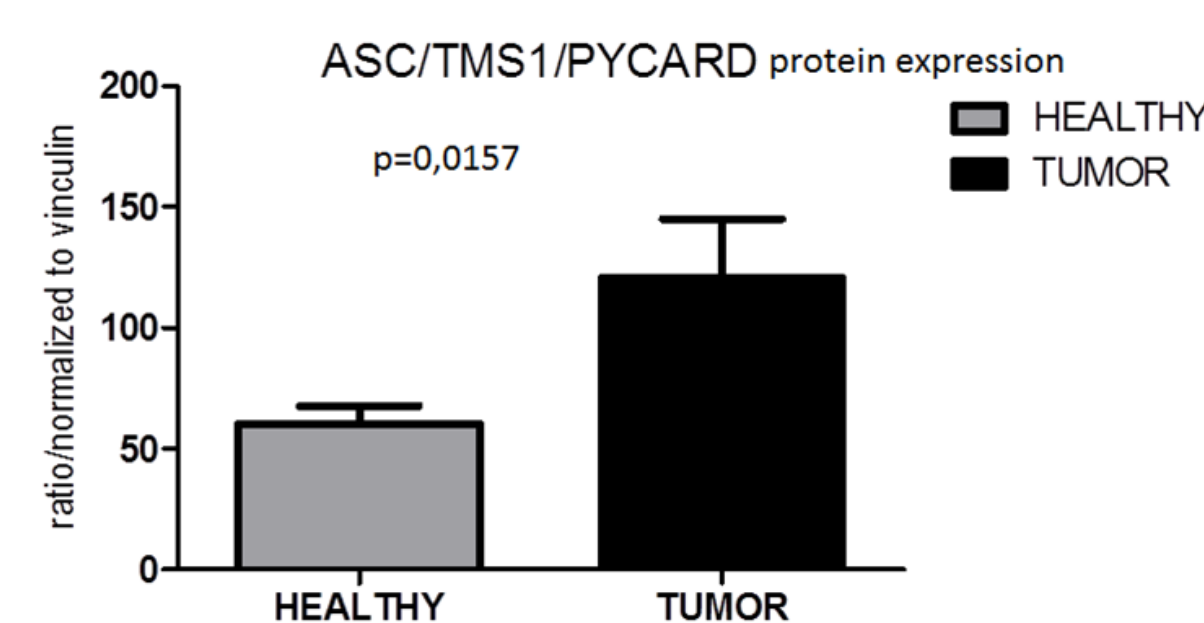


Figure 4. The graph (GraphPad Prism 5.0) of densitometric quantification of protein ASC/TMS1/PYCARD bends. The graph shows statistically significant difference ($p=0,0157$) in **ASC/TMS1/PYCARD** protein expression between healthy and tumor tissue. Paired t-test; $p \leq 0,05$. The values are shown as mean value $\pm$ SEM

Conclusion: The methylation status of the ASC/TMS1 and MyD88 genes are promising prognostic biomarker candidates and may lead to earlier detection of laryngeal cancer.