

YKL-40 AND miR-214 EXPRESSION IN SYSTEMIC SCLEROSIS

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Aim: was to examine protein and mRNA levels of YKL-40 and its regulation in Systemic sclerosis (SSc).

Methods: Forty female patients with SSc and fourteen healthy subjects are enrolled in our study. Patients are further subdivided into such with diffuse cutaneous (dcSSc) or limited cutaneous SSc (lcSSc). Serum levels of YKL-40 are examined by ELISA. Bioinformatic tools are used to predict miRNA targeting the 3'UTR of YKL-40 mRNA. Expression levels of YKL-40 mRNA and miR-214 in white blood cells (WBC) are measured by RT-PCR. miR-214 levels in plasma are also assessed.

Results: The *in silico* analysis revealed several miRNAs targeting *YKL-40* mRNA, from which miR-214 was selected. YKL-40 serum levels were significantly higher in patients. Expression levels of *YKL-40* mRNA and miR-214 in WBC were unchanged in all SSc patients and in the subgroups compared to healthy subjects. miR-214 expression in plasma of SSc patients was significantly down-regulated compared to controls. Similar profile is observed in patient subgroups when matched with controls. ROC and area under the curve analysis showed that both serum protein levels of YKL-40 and miR-214 expression levels have discriminatory capacity to distinguish patients with SSc, dcSSc and lcSSc from healthy subjects.

Conclusion: YKL-40 and miR-214 are differently expressed in SSc. Down-regulation of miR-214 expression in plasma could be associated with increased serum protein levels of YKL-40. Both, YKL-40 serum concentrations and miR-214 plasma fold change values might serve as possible diagnostic biomarkers in SSc.

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