Microarray-Based Differential Gene Expression Profiling of the Metabolic Syndrome in Arabs with Psoriasis in Bahrain

Background Psoriasis doubles the risk of the metabolic syndrome and its associated comorbidities. Our objective was to investigate the gene expression of the metabolic syndrome in patients with psoriasis and to measure the protein level of the differentially expressed genes.

Methods Eighteen patients with psoriasis off treatment were recruited and assigned into two groups based on the presence or absence of the metabolic syndrome. Patients were assessed for psoriasis and metabolic syndrome clinically and biochemically. Gene regulation was explored by microarray, where two selected upregulated genes were further assessed using polymerase chain reaction and their translated protein was measured using enzyme linked immunosorbent assay.

Results Analysis showed REL was 11 folds upregulated in microarray ($p<0.005$), two folds upregulated in polymerase chain reaction ($p<0.05$) and expressed at level of 7.140 ng/mL ($p<0.05$) in enzyme linked immunosorbent assay in cases compared to controls (0). On the other hands, WSB1 was nine folds upregulated in microarray ($p<0.005$), two folds upregulated in polymerase chain reaction ($p<0.05$) and unexpectedly unexpressed in enzyme linked immunosorbent assay in cases compared to controls ($p<0.05$).

Conclusions The strongly differentially expressed REL and WSB1 can be used as a prognostic tool or a therapeutic target in clinical practice.