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Expression profiling of inflammation-related genes in type-II diabetic individuals

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Type-II diabetes has been emerged as a growing health issue that has affected more than 170 million individuals worldwide. According to WHO, number of affected individuals by type-2 diabetes is expected to rise in Pakistan from 4.3 million in 1995 to 14.5 million in 2025, making Pakistan at number four among the top ten countries of the world affected by diabetes. It is well known that diabetes is associated with inflammation and altered immune response; however, the specific cellular and molecular mechanisms involved are not fully resolved. To investigate the mechanism that contributes to the pathology of disease, we performed gene expression profiling of white blood cells in subjects with and without type 2 diabetes mellitus, taking obesity factor into account as well. We categorized subjects according to their HBA1C and BMI level into three groups; subjects with HBA1C level >8.0 were included in group I, 8-10 in group II and >10 in group III. Thirty genes involved in inflammation related pathways including pro- and anti-inflammatory cytokines like *CCR1, CCR2, CCR3, CCR4, CCR5, CCL15, CXCL10, CXCL11, CXCL12, TNFα, IL-4, IL-6, IL-10, IL-17A, AKT2* and *TNFR1*, etc., were profiled for gene expression using Real-Time PCR. Among genes tested, *AKT2, CASP1, CASP5, CCR1, CCR2, IL-17A* and *PPARG* genes were found to be upregulated, while *CCR4, CXCL12, PPARGC1A* and *TNFα* were down-regulated in diabetic individuals in HBA1C-dependent manner. However, obese individuals showed a different pattern of expression than lean individuals. The identification of peripheral inflammatory cytokines associated with type-II diabetes as biomarkers has a potential for better diagnosis, optimized patient care and novel drug research.

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Increased luteolin and myricetin biosynthesis in the suspension culture of *Scrophularia striata* Boiss. by chitosan

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Manipulation of cell culture media by elicitors is one of most important strategies of biotechnology to induce secondary metabolism for the production of valuable metabolites. Natural elicitors such as chitosan are exogenous biotic compounds extracted from arthropods exoskeleton and fungal cell walls often act as specific elicitors in a number of plant cell cultures for efficient induction of valuable medicinally secondary metabolites. In this investigation, inducing effect of chitosan on physiological, biochemical and molecular parameters were investigated in cell suspension cultures of *Scrophularia striata* Boiss. Cells were treated with 10 mg/L chitosan and harvested for 3, 5 and 7 days after elicitation. Luteolin (Lut) and Myricetin (Myr) quantified by high-performance liquid chromatography (HPLC). Cell samples were used to elucidate the expression level of *phenylalanine ammonia-lyase* (PAL) and *p-coumarate 3-hydroxylase* (C3H) genes by semi-quantitative RT-PCR. Following treatments of chitosan, the results showed that the cell growth and viability of cells was decreased as compared to control. In addition, chitosan increased Lut and Myr contents. Cells elicited with chitosan for 5 days yielded the highest amount of Lut (12.69-fold) and Myr (11.15-fold) compared to the control cells. The expression of PAL and C3H genes by chitosan was increased, reaching a peak at 5 days after treatment (2.2-fold and 2-fold higher than control cells, respectively). Chitosan up-regulates the production of Lut and Myr, by effecting on gene expression of flavonoids biosynthesis pathway.

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