

**Ayyildiz, D., and Arga, K.Y. (2017). Hypothesis: Are There Molecular Signatures of Yoga Practice in Peripheral Blood Mononuclear Cells? OMICS 21, 426-428.**

**Abstract:**

As a follow-up to the observations made by Qu et al. (2013), we performed an advanced analyses of the gene expression profiles in that study from a systems biology perspective, and employing our multistage integrated analysis methodology (Calimlioglu et al., 2015) to study transcriptomic, proteomic, regulatory, and metabolic signatures of yoga practices in PBMCs.

Statistically significant differences ( $p < 0.05$ ) in the expression levels of 217 genes (among samples belonging to subjects before and after attending the yoga program) lend support for the effect of yoga practices on regulation of gene expression. Proteins encoded by these differentially expressed genes primarily displayed binding and catalytic activities. Enrichment analyses of the differentially expressed genes resulted in significant ( $p < 0.05$ ) associations with several disease pathways, including type 2 diabetes (39 genes), multiple sclerosis (9 genes), colorectal cancer (9 genes), prostate cancer (5 genes), thyroid cancer (3 genes), and lymphoma (3 genes), as well as the ubiquitin-mediated proteolysis pathway (7 genes), which has been implicated in a number of pathological conditions such as neurodegenerative disorders and cancers wherein protein misfolding may play a role. Three genes (BCL2, CASP9, and PXN) that play a role in apoptotic signaling in response to DNA damage were found to be downregulated upon yoga practice.

Although we caution the readers that yoga practice and study of its molecular correlates may be influenced by direct and indirect environmental and endogenous factors that can remain unaccounted for, we suggest that the potential molecular signatures of yoga practice in PBMCs presented here and by Qu et al. (2013) offer new insights into multistage integrated analysis of gene expression profiles as we report here.