Daily Drinking Orange Juice may Fine-Tune Genes Tied to Cardiovascular Wellness

A group of researchers investigated how chronic orange juice (OJ) intake affects the transcriptomes of peripheral blood mononuclear cells (PBMCs) in healthy adults, and whether responses vary by body mass index (BMI) status. This was a single-arm pre–post intervention without a control beverage; findings show transcriptomic associations and do not establish causality. Fold-change ranges for individual genes were reported in supplementary data but were not emphasized in the main text.

Nutrigenomic Potential of Citrus Flavanones

What if a breakfast staple could quietly tune the genes that steer blood pressure, lipids, and inflammation? Citrus fruits, especially OJ, supply flavanones such as hesperidin and naringenin that may influence vascular tone, lipid handling, and immune signaling. Yet, most people ask whether a daily glass truly alters biology in ways that matter, and whether body weight affects the response.

Mapping gene activity in circulating immune cells can link a kitchen habit to outcomes families care about, although the mechanistic paper did not newly assess clinical endpoints; prior publications from the same cohort reported reductions in blood pressure and body-fat percentage with 500 mL/day OJ over 60 days.

Multi-Omics and Computational Analyses

Pathway enrichment was performed using GeneTrail with the Kyoto Encyclopedia of Genes and Genomes (KEGG), WikiPathways, and BioCarta; protein-protein interaction networks were analyzed using the Search Tool for the Retrieval of Interacting Genes/Proteins (STRING).

Predicted transcription factors were identified with Enrichr. MicroRNA (miRNA) targets were derived via Mienturnet/miRTarBase; long non-coding RNA (lncRNA) targets via LncRRIsearch; small nucleolar RNA (snoRNA) changes were also cataloged. Disease associations employed the Comparative Toxicogenomics Database.

Transcriptomic Remodeling after Orange Juice Intake

Chronic OJ intake remodeled the PBMC transcriptome: 3,790 oligonucleotides changed, including 1,705 protein-coding genes (mostly downregulated), 66 miRNAs, 19 lncRNAs, and 67 snoRNAs. Principal components, partial least squares–discriminant analysis (PLS-DA), and clustering analyses successfully separated T60 from T0, indicating a consistent intervention signal.

Enriched pathways mapped to blood pressure control (aldosterone synthesis/secretion, renin secretion, angiotensin-converting enzyme inhibitor-related signaling), lipid metabolism (thermogenesis, adipogenesis, mitochondrial fatty-acid β-oxidation), inflammation (toll-like receptor, tumor necrosis factor, interleukin-17 (IL17)), cell adhesion (focal adhesion, actin cytoskeleton), and major signaling axes (mitogen-activated protein kinase (MAPK), vascular endothelial growth factor receptor 2 (VEGFR2), phosphoinositide 3-kinase-Akt (PI3K-Akt), epidermal growth factor (EGF) receptor, cyclic adenosine monophosphate (cAMP), insulin, and advanced glycation end product–receptor for advanced glycation end products). Additional enrichment included AHR signaling and endoplasmic reticulum (ER) protein processing.

Protein-protein interaction hubs included serine/threonine kinase AKT1, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), catenin beta-1 (CTNNB1), heat-shock protein 90 alpha (HSP90AA1), and eukaryotic elongation factor 2 (EEF2).

BMI-Specific Transcriptomic Differences

Overweight participants exhibited a unique modulation of lipid metabolism and adipogenesis pathways, characterized by distinct regulation of glycogen synthase kinase 3 beta (GSK3B), G protein-coupled receptor kinase 6 (GRK6), and miRNAs, including miR-548i and miR-1292-3p. Normal-weight participants exhibited unique modulation of inflammatory pathways, characterized by changes in signal transducer and activator of transcription 3 (STAT3), solute carrier family 16 member 6 (SLC16A6), B-cell lymphoma 2 (BCL2), MAPK1, and miR-1185-2-5p. Thus, two people drinking the same OJ may experience different molecular benefits depending on BMI.

Conclusion

Daily OJ, a familiar food, reprogrammed immune-cell gene networks tied to blood pressure, lipids, and inflammation, with layered changes across protein-coding genes, miRNA, lncRNA, and snoRNA. Predicted interactions between flavanone metabolites and transcription factors, including NFKB1, AHR, and PPARA, provide mechanistic plausibility.

Importantly, BMI-stratified effects revealed that lipid pathways dominated in overweight adults, while inflammation pathways shifted in normal-weight adults. However, the results are limited by the small sample size (n=20), the absence of a control beverage, the use of a microarray platform, and the exploratory nature of in-silico docking, which remains hypothesis-generating.

Future studies should integrate fold-change magnitude data with targeted functional assays to validate these transcriptomic signatures. For individuals and clinicians, this supports tailoring “simple” dietary advice to body weight, to turn an everyday drink into a more precise cardiometabolic lever.

Personalized nutrition requires both molecular evidence and practical application; these findings offer early molecular insights that can inform such individualized dietary guidance. Further research is needed to confirm and translate these transcriptomic effects into clinical outcomes.

Source:

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