**Supplemental Table 1.** Search Strategy and search terms documentation for each database

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| --- | --- | --- | --- |
| **PubMed\*** | **CINAHL** | **SCOPUS** | **EMBASE** |
| 1966-Sept 2018 | 1970-Sept 2018 | 1960-Sept 2018 | 1988-Sept 2018 |
| 1. "transcriptome analysis" OR "transcriptome profiling" OR "profiling" | 1. TX transcriptome analysis OR transcriptome profiling OR profiling | 1. transcriptome AND analysis OR transcriptome AND profiling OR profiling/ TW | 1. (('transcriptome'/exp OR transcriptome) OR 'transcriptome'/exp OR transcriptome) AND profiling OR profiling |
| 2. ("transcriptome analysis" OR "transcriptome profiling" OR "profiling") ("gene expression" [MeSH] | 2.TX transcriptome analysis OR "transcriptome profiling OR "profiling OR gene expression [MeSH] | 2 ‘gene expression’ | 2. ‘gene expression’/exp |
| 3. "microarray" OR "microarrays" OR "RNA sequencing" OR "RNA seq" or "RNAseq" | 3. TX "microarray" OR "microarrays" OR "RNA sequencing" OR "RNA seq" or "RNAseq" | 3. tx "microarray" OR "microarrays" OR "RNA sequencing" OR "RNA seq" OR "RNAseq".  | 3. 'microarray' OR 'microarrays' OR 'rna sequencing' OR 'rna seq' OR 'rnaseq' |
| 4. 1 OR 2 OR 3 | 4. 1 or 2 or 3 | 4. #1 OR #2 OR #3 | 4. #1 OR #2 OR #3 |
| 5. "food" [MeSH] OR "vegetable\*" OR "fruit\*" | 5. TX food [MeSH] OR vegetable\* OR fruit\* | 5. (food OR vegetable\* OR fruit\* ) | 5. food OR vegetable\* OR fruit\*/Exp |
| 6. "plant\*" OR "herb\*" OR "seeds" OR "extracts" OR “phyto\*” | 6. plant\* OR herb\* OR seeds OR extract\* OR phyto\* | 6. ( plant\* OR herb\* OR seeds OR extract\* OR phyto\* ) | 6. plant\* OR herb\* OR seeds OR extract\* OR phyto\* |
| 7. 5 OR 6 | 7. 5 or 6 | 7. #5 OR #6 | 7. #5 OR #6 |
| 8. “acute" OR "short-term" OR "short term" OR “single dose” | 8. “acute" OR "short-term" OR "short term" OR “single dose” | 8. TW “acute" OR "short-term" OR "short term" OR “single dose” | 8. 'acute' OR 'short-term' OR 'short term' OR 'single dose'/exp |
| 9. (“post-prandial” OR “post prandial” OR "postprandial") | 9. MESH post-prandial OR post prandial | 9. post-prandial OR post prandial | 9. ('post prandial' OR post) AND prandial:ab,ti |
| 10. 8 OR 9 | 10. 8 or 9 | 10. #8 OR #9 | 10. #8 OR #9 |
| 11. 4 AND 7  | 11. MH Clinical Trials/ | 11. MH Clinical Trials/ | 11. clinical AND 'trial'/exp |
| 12. 10 AND 11 | 12. 4 and 7 and 10  | 12. #4 AND #7 AND #10 AND #11 | 12. #4 AND #7 AND #10 AND #11 |
| 13. 4 AND 7 AND 10 | 13. 11 and 12 | 13. #12 AND clinical trial | 13. #12 AND ('clinical trial'/de  |
|  | [Filter human] | [filter human] | [filter human] |
| 521 articles  | 24 articles | 144 articles | 241 articles |
| Total before duplication removal 1148 |
| **Total after duplicate removal (218)= 947 + manual searches**  |

\*All terms were searched with and without filter [clinical trial]

**Supplemental Table 2.** Summary of genes identified from transcriptome profiling after acute dietary plant intake.

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| --- | --- | --- | --- | --- |
| **First Author****[year]** | **Study****population** | **Highest gene expressions reported§** | **Proposed mechanism of action**  | **Conclusions** |
| Upregulated genes[number] | Downregulated genes[number] |
| D'Amore [2016] | healthy adultsMean age 29  | *ACADM, ACAT1**RXRβ; RXRs, HSPA1A, PRDX3*[6] | *SCD5, IRAK3, NF-κB, IL-8* *CXCR4, CCNK, HIF1A, CRY2**AGO2*[9] | Activation of PPARα/PGC1α promote gene transcriptionIn fatty acid oxidation &mitochondrial function | EVOO with high phenols:1.improves insulin sensitivity2. modulates multiple inflammatory pathways in healthy adults 3. changes transcriptome in cancer & proliferation4. affects miRNome: -insulin resistance: miR-107-inflammation: miR-181b-5p, miR-23b-3p- cancer: miR-19a-3p, miR-519b-3p  |
| Camargo [2010] | MetS adults40-70 years | *CCR2, CA1, CPVL, FN1,* *RAPIGAP, GYPB, SELENBP1*[19] | *PTGS2, IL-1B, IL-6, OSM, CCL3, CXCL1, CXCL2, CXCL3, CXCR4, NAMPT, DUSP1, DUSP2, EGR1, EGR2, EGR3, EREG, FOSB, G0S2, JUN, JUNB, NFKBIA, NFKBIZ, NR4A1, NR4A2, PER1, SOCS3, SOD2, TAGAP, TNFAIP3, ZFP36, AREG, CA2, CD69, CD83, CDKN2A, RASGEF1B*[79] | Exert anti-inflammatory effect on pathways of:- NF-κB/AP-1 -MAPK -cytokine-cytokine receptor interaction-arachidonic acid metabolism | 1. Suppresses expression of proinflammatory genes2. Induces changes in transcriptome for:-Cell death-cell migration-cell division-cell proliferation -transcription |
| Konstantinidou [2009a] | healthy adults22-28 years | *OGT, TXNL2, ADHFE1, SLC11A2, DUSP8, RORA, IL-10, SOS1, COL4A4, STAT4, DCLRE1C, POLK, ATF7, MAP3K15, NALP1, XAF1, PRKAG2, OSBPL7, ACAD11, AAK1, PLA2G6, INPP5F, ABCA7, ABCB1, SPTLC2, AKAP13, IKAROS**CDC14, USP48, USP52, ADAM17, USP6*[259] | *NQO1, NDUFA5, NCB5OR, CD69, IL-8, CCL17, CXCR4, IFN-γ, CLC, LEF1, FPR1, DDIT4, XRCC4, CDKN2B, LMNA, PDCD10, SCARB2, CYCS, TNFRSF21, ITG3BP, JDP2, IL-1β, SULT1B1, PLA2G7, SC5DL, ID11, SCP2, CHPT1, ACOX3, THBD, AKT3*[246] | *-ABCA7* & *ABCA1* mediate HDL cholesterol formation-USP48 and AKAP13 play a role in NF-κB activation involved in cancer/proliferative pathways | 1. Short-term protective effects of olive oil extract is mediated via gene expression changes2. Highest gene upregulation is reported for metabolism, DNA repair, anti-inflammatory response, oxidative stress and tissue remodeling3. Highest gene downregulation is reported for cancer, inflammation, and DNA damage |

**Supplemental Table 2.** continued…

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| --- | --- | --- | --- | --- |
| **First Author****[year]** | **Study****population** | **Highest gene expressions reported** | **Proposed mechanism of action**  | **Conclusions** |
| Upregulated genes[number] | Downregulated genes[number] |
| Barrera‑Reyes[2018] | Healthy adultsMean age 28 | *ADRB2, IL8RA, IL8RB,* Protein Tyrosine PhosphataseReceptor Type C (*PTPRC), TPT1, ORM1**PTPRC,TIGIT, TPT1*[37 genes] | *FPR1, IL-8*, Sestrin 3 (*SESN3*), *CD36*, Hemoglobin SubunitAlpha 1/2 (*HBA1*/*HBA2)* | decreased ROS production Ca2+ modulation  inflammatory response modulation | Cocoa decreases production of ROS.Cocoa exerts anti-inflammatory effects  |
| Smolders [2018] | Healthy adultsMean age 60 | U0126streptozocinPD98059SP600125(all upstream transcription regulators) | INS, Insulin, Ins1\*\*\*CREB1, GATA4, calcitriol, AGT, lysophosphatidic acidPDGF BB, decitabineHNF4A, dexamethasoneFADD,Cg,MAP2K1/2ATP, SOX11,aldosteroneEGF, butyric acid,Ca2+Pkc(s), GnRH analog | Downregulation of Glucose metabolism & carotenoid metabolismUpregulation of beta cell development amyloids & kinesins | Theobromine inhibits activation of glycogen/glucose breakdown gene expressionsTheobromine does not change lipid & cholesterol metabolism related gene expressions |
| Beltran [2015] | Healthy male adults23-35 years | *CXCL8, CCL3, CCL2, IL-6, TNF-α, CX3CR1, IL-10, ID3, ZNF593, UTF1, MXI1, TBPL1, SRSF2, DDX5, ENY2, NFE2, CRYM, WDR77, E4F1, JUNB, CBX4, FAM1, MED17, TAF7, MED13, MED16, TOB2, RXRB, MED14, HR, THRAP3, MED12, MED24, BAZ1B, MED1, MED30, TAF11, TLR2, CD36, TNFAIP3, IRF8, IFNG, CMPK2, NR1D1, IRAK1, PAF1, IL18, GFI1, RARA* | *EGR3* | antioxidant activity of polyphenols due to:- heme-oxygenase (HO)-biliverdin reductase AxisRegulate energy homeostasis via: AMPK/MTOR pathway | Hibiscus polyphenols regulate:-mitochondrial function, -energy homeostasis -cardiovascular system (blood pressure)-metabolic function- cortisol levels -post-translational modification,-cell cycle, -RNA trafficking and cellular function -glucocorticoid receptor signaling pathway |

**Supplemental Table 2.** continued…

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| --- | --- | --- | --- | --- |
| **First Author****[year]** | **Study****population** | **Highest gene expressions reported** | **Proposed mechanism of action**  | **Conclusions** |
| Upregulated genes[number] | Downregulated genes[number] |
| Charron [2015] | Healthy adults40-80 years | *AHR, ARNT, HIF1A, JUN, NFAM1\*, OSM\*, REL*[7] | None reported | *AHR* expression:-mediates β-catenin degradation to protect from cancer-modulates immuneFunction (T-cells)HIF1Adimerizes with ARNT to form HIF-1increases: -glucose metabolism- angiogenesis*JUN* expression may inhibit tumorigenesis | Garlic intake activats 7 genes involved in: -xenobiotic metabolism- inflammation-immunity-apoptosis-tumorigenesis. |
| De Smet[2015] | Healthy adults21-55 years | None reported | immune response genes [20]\*\**A2M, ADAM9, AIP, ANXA1**ARHGDIB, BCL6, CD family genes* | - Plant sterol may decrease cellular oxycholesterol of intestinal T-cells thereby diminishing their expansion. | -No change in gene expressions involved in plant stanol -Genes involved in T-cell pathways are downregulated in proximal parts of small intestine-Plant sterols may have a key role in modulation of immune response |
| Esser[2015] | Healthy & obese adult males50-70 years Obese only | SFA intake: *ABCA1, ABCG1*MUFA intake: PPAR-ɑ target genes*, TNF-α, IL1-β, CD14, CD180, TLR5, TLR6, TLR7 AND MAP2K4*MUFA intake:GPI-anchored protein synthesis genes | SFA intake: *SREBP2, LDLR, desaturase enzyme genes*, *FADS1 & 2, SCD*MUFA intake:G-protein-coupled receptors | -SFA reduced gene expression for cholesterol biosynthesis, and increased gene expressions involved in cholesterol efflux.SREBP2 mechanism unknown-MUFA upregulates β-oxidation & activates transcriptional response of inflammatory genes over time | BMI significantly affects immune-related gene expression profiles after sunflower oil extract interventionMUFA increases PPAR-ɑ & inflammatory pathway gene expressions |

**Supplemental Table 2.** continued…

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **First Author****[year]** | **Study****population** | **Highest gene expressions reported** | **Proposed mechanism** **of action**  | **Conclusions** |
| Upregulated genes[number] | Downregulated genes[number] |
| Kawakami[2013] | Healthy adults23 years (mean age) | White Rice: *APP, E1F1, JDP2,9-sep, SLC4A7, SLC39A1*Barley:*CLDN19, GRAP2, LRRC37A3, SETD8, SUV420H2, ZFY* | White rice & barley:*PDK4, CPT1A, SL25A20*White rice: *TNNT3, MBLAC1, ATP67VIA, ATP2A3, CR1**AGBL5, BCAS4*Barley: *ATF7, TRABD, MAFIP* | -*PDK4* regulates glucose to fatty acid conversion in postprandial state-*CPT1A & SL25A20* involved in β-oxidation  | - WBC gene expression profile alters in postprandial state -Gene expressions are affected at different time points.  |
| Gasper[2007] | Healthy adults18-46 years | Broccoli:*HSD11B2* [1]HG broccoli:*GCLM, TXNRD1, Tr1,* *HSPA1A, HSPH1,* *AKR1C1, AKR1C2,* *SLC7A11* | Broccoli:[17]HG broccoli:*NR1D2, MXD1, TEF**BHLHB2* | GCLM and *SLC7A11* both involved in Glutathione biosynthesis | -Several xenobiotic metabolizing genes are activated after intake of HG broccoli, -Only one gene is found to be upregulated after broccoli intake-gene expressions involved in transcription & metal ion binding are reported to significantly change after intake of standard broccoli |

\*Gene expression changed only in women

\*\*These genes were expressed in both proximal parts of the small intestine (jejunum and duodenum)

\*\*\*These three genes were related to glucose metabolism

§ Genes: Red= significant expression; Blue= common genes among some of the studies

**Abbreviations:** ACADM, acyl-CoA dehydrogenase; ACAT1, acetyl-CoA acetyltransferase 1; RXRβ; RXRs, Retinoid X receptor beta; HSPA1A, heat shock 70 kDa protein 1A; PRDX3, peroxiredoxin 3; SCDS, sterol-C5-desaturase; IRAK3, interleukin-1 receptor-associated kinase 3; Interleukin-8; CXCR4, chemokine CXC motif chemokine receptor; CCNK, cyclin K; HIF1A, hypoxia inducible factor1 alpha subunit; CRY2, cryptochrome 2 photolyase-like; AGO2, Argonaute RISC catalytic component 2; NR1D2 nuclear receptor subfamily 1 group D2, MXD1, MAX dimerization protein 1; TEF, Thyrotrophic embryonic factor, BLHLB2, Basic helix-loop-helix domain class B2; HSD11B2 hydroxysteroid (11-b dehydrogenase 2); PRKAA1 = Protein kinase, AMP-activated, alpha 1 catalytic subunit; STK11 = serine/threonine kinase 11; AKT2 = v-akt murine thymoma viral oncogene; IRS2 = insulin receptor substrate 2; PRKAG2 =protein kinase AMP-activated, gamma 2 noncatalytic subunit; CPT1A = carnitine palmitoyltransferase 1A (liver); PRKAG1 = protein kinase AMP-activated, gamma 1 noncatalytic subunit; CPT2 = carnitine palmitoyltransferase 2; CAB39 = calcium binding protein 39.