Supplementary table

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|  | Table S1. Gene expression analysis studies performed on sunflower during 2004-2022 | | | | | | |
|  |  | | | | | | |
| No. | Experiment type | Tissue | Treatment | No. of target gene evaluated | No of Genotypes for real-time PCR | Reference gene | Reference |
| 1 | RNAseq-Field condition | Leaf | Anthesis and 12 days after anthesis | 16 | one | *EF-1α* | (1) |
| 2 | Field experiment | Leaves n. 10 and 20 | With accumulation of degree days from emergence (°Cd) between 432 to 861 and 670 to 1180, for leaves 10 and 20 respectively | 12 | 1 | *EF-1α* | (2) |
| 3 | RNAseq-Green house | root | Inoculation with Verticillium vs Control | 18 | one | *18S rRNA* | (3) |
| 4 | RNAseq-Field condition | Disc florets and bracts | Inoculation with Sclerotinia vs control | 47 | three | *Actin* | (4) |
|  |  |  |  |  |  |  |  |
| 5 | Greenhouse | leaves | Salt stress | 1 | 2 | *Actin* | (5) |
| 6 | RNAseq-Greenhouse | leaves and roots | under drought stress | 5 | 1 | *Actin* | (6) |
| 7 | cDNA microarray-Greenhouse | Whole plant | Drought and salt tolerance | 9 | 3 | No reference gene-used | (7) |
| 8 | cDNA microarray-Greenhouse | Leaves and stem at two- and four-leaf stages | Cold stress | 11 | 2 | *b-Actin* | (8) |
| 9 | Field experiment | Seed | Developmental stages | 8 | 1 | *β-tubulin* | (9) |
| 10 | Green house | sprouts | Different germination time points and tissues. | 5 | 1 | *ETIF5A* and *Actin 7* | (10) et al., 2019 |
| 11 | Normal conditions | Pistil-stamen-leaves root-seed | Developmental stages | 8 | 1 | Actin7 | (11) |
| 12 | Greenhouse | Leaves | Dehydration stress | 3 | 2 | NA | (12) |
| 13 | Green house | Leaves | Salt and drought stress | 55 | 1 | *Actin* | (13) |
| 14 | Greenhouse | Cotyledons | - | 1 | 1 | *Actin* | (14) |
| 15 | RNAseq-greenhouse | root, young leaf, mature leaf, shoot, stamen, pistil, seed, ligule | Drought stress, Salt stress-GA3-ABA | 13 | 1 | *Actin* | (15) |
| 16 | Greenhous | Leaves | UV-Heavy metal stresses | 1 | 1 | *Actin* | (16) |
| 17 | Greenhouse | Leaves | Gene transformation | 4 | 1 | *Actin2/8* | (17) |
| 18 | Greenhouse | leaves | Drought-Crowding. Simulated herbivory | 23 | 1 | *Actin* and *60S* *ribosomal RNA* | (18) |
| 19 | Greenhouse | Leaves | Water stress | 4 | 6 | *Actin* | (19) |
| 20 | Greenhouse | Leaves | Inoculation with sclerotinia | 1 | 2 | *Actin* | (20) |
| 21 | Greenhouse-RNAseq | Leaves | Salinity stress | 1 | 11 | *Actin* | (21) |
| 22 | RNAseq | root | arbuscular mycorrhizal fungi | 2 | 1 | E3 ubiquitin-ligase BRE1-like 1  mitochondrial ubiquitin ligase activator of NFKB 1 | (22) |

Rafarances

1. Moschen S, Marino J, Nicosia S, Higgins J, Alseekh S, Astigueta F, et al. Exploring gene networks in two sunflower lines with contrasting leaf senescence phenotype using a system biology approach. BMC Plant Biology. 2019;19(1):1-15.

2. Moschen S, Bengoa Luoni S, Paniego NB, Hopp HE, Dosio GA, Fernandez P, et al. Identification of candidate genes associated with leaf senescence in cultivated sunflower (Helianthus annuus L.). PloS one. 2014;9(8):e104379.

3. Guo S, Zuo Y, Zhang Y, Wu C, Su W, Jin W, et al. Large-scale transcriptome comparison of sunflower genes responsive to Verticillium dahliae. BMC genomics. 2017;18(1):1-13.

4. Fass MI, Rivarola M, Ehrenbolger GF, Maringolo CA, Montecchia JF, Quiroz F, et al. Exploring sunflower responses to Sclerotinia head rot at early stages of infection using RNA-seq analysis. Scientific reports. 2020;10(1):1-14.

5. Teymouri M, Shahri MPK, Darvishzadeh R. Salt-Induced Differences During the Gene Expression of Telomerase Enzyme in Sunflower. Iranian Journal of Biotechnology. 2021;19(1):e2579.

6. Liang C, Wang W, Wang J, Ma J, Li C, Zhou F, et al. Identification of differentially expressed genes in sunflower (Helianthus annuus) leaves and roots under drought stress by RNA sequencing. Botanical studies. 2017;58(1):1-11.

7. Lai Z, Gross BL, Zou Y, Andrews J, Rieseberg LH. Microarray analysis reveals differential gene expression in hybrid sunflower species. Molecular ecology. 2006;15(5):1213-27.

8. Hewezi T, Léger M, El Kayal W, Gentzbittel L. Transcriptional profiling of sunflower plants growing under low temperatures reveals an extensive down-regulation of gene expression associated with chilling sensitivity. Journal of Experimental Botany. 2006;57(12):3109-22.

9. Castillo FM, Canales J, Claude A, Calderini DF. Expansin genes expression in growing ovaries and grains of sunflower are tissue-specific and associate with final grain weight. BMC plant biology. 2018;18(1):1-14.

10. Cheevarungnapakul K, Khaksar G, Panpetch P, Boonjing P, Sirikantaramas S. Identification and functional characterization of genes involved in the biosynthesis of caffeoylquinic acids in sunflower (Helianthus annuus L.). Frontiers in plant science. 2019:968.

11. Lim AR, Kong Q, Singh SK, Guo L, Yuan L, Ma W. Sunflower WRINKLED1 Plays a Key Role in Transcriptional Regulation of Oil Biosynthesis. International journal of molecular sciences. 2022;23(6):3054.

12. Ahmad HM, Wang X, Fiaz S, Nadeem MA, Khan SA, Ahmar S, et al. Comprehensive genomics and expression analysis of eceriferum (CER) genes in sunflower (Helianthus annuus). Saudi journal of biological sciences. 2021;28(12):6884-96.

13. Li W, Zeng Y, Yin F, Wei R, Mao X. Genome-wide identification and comprehensive analysis of the NAC transcription factor family in sunflower during salt and drought stress. Scientific reports. 2021;11(1):1-12.

14. Fambrini M, Salvini M, Conti A, Michelotti V, Pugliesi C. Expression of the?-carotene desaturase gene in sunflower. Plant Biosystems. 2004;138(3):203-6.

15. Bing J, Xiao E, Li C, Wang Z. Genome-Wide Identification and Expression Analysis of Growth-Regulating Factor Family Genes in Sunflower (Helianthus annuus L.). 2019.

16. Büyük İ, ArAS S, CAnSArAn-DumAn D. Varied expression pattern of the small heat shock protein gene encoding HSP17. 7 against UVA, UVB, Cu2+ and Zn2+ stresses in sunflower. Plant Protection Science. 2016;52(2):99-106.

17. Manavella PA, Chan RL. Transient transformation of sunflower leaf discs via an Agrobacterium-mediated method: applications for gene expression and silencing studies. nature protocols. 2009;4(11):1699-707.

18. Mayrose M, Kane NC, Mayrose I, Dlugosch KM, Rieseberg LH. Increased growth in sunflower correlates with reduced defences and altered gene expression in response to biotic and abiotic stress. Molecular ecology. 2011;20(22):4683-94.

19. Poormohammad Kiani S, Grieu P, Maury P, Hewezi T, Gentzbittel L, Sarrafi A. Genetic variability for physiological traits under drought conditions and differential expression of water stress-associated genes in sunflower (Helianthus annuus L.). Theoretical and applied genetics. 2007;114(2):193-207.

20. Jamshidi E, Parvini Kohneh Shahri M, Darvishzadeh R. Transcript analysis of telomerase enzyme gene in sunflower infected by sclerotinia stem rot disease. Journal of Plant Molecular Breeding. 2019;7(1):31-6.

21. Sharifi Alishah M, Darvishzadeh R, Ahmadabadi M, Piri Kashtiban Y, Hasanpur K. Identification of differentially expressed genes in salt-tolerant oilseed sunflower (Helianthus annuus L.) genotype by RNA sequencing. Molecular Biology Reports. 2022:1-14.

22. Vangelisti A, Natali L, Bernardi R, Sbrana C, Turrini A, Hassani-Pak K, et al. Transcriptome changes induced by arbuscular mycorrhizal fungi in sunflower (Helianthus annuus L.) roots. Scientific reports. 2018;8(1):1-14.