

Supplementary Materials: Transketolase is Identified as a Target of Herbicidal Substance α -Terthienyl by Proteomics

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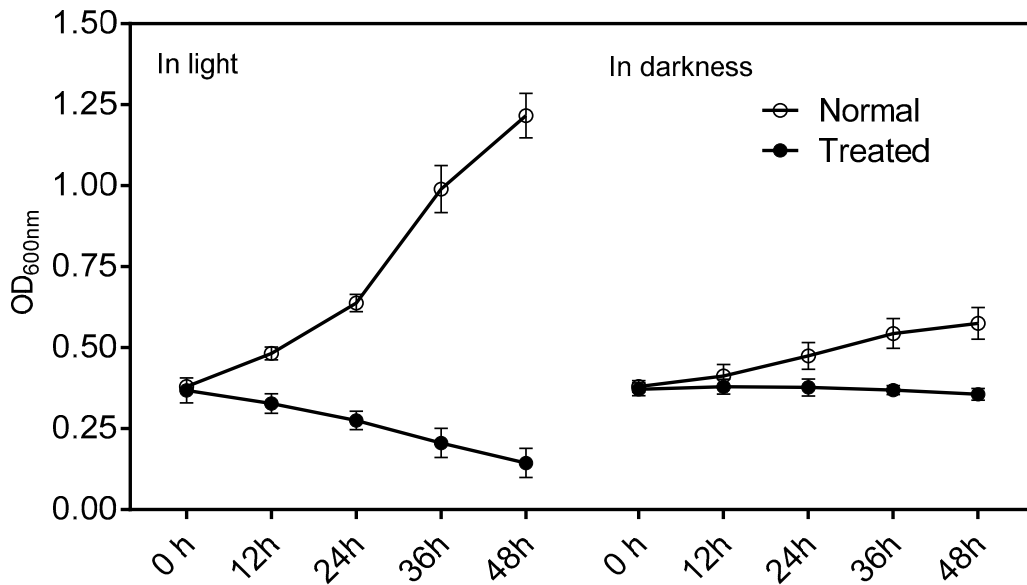


Figure S1. The bioactivity of α -terthienyl in light and darkness.

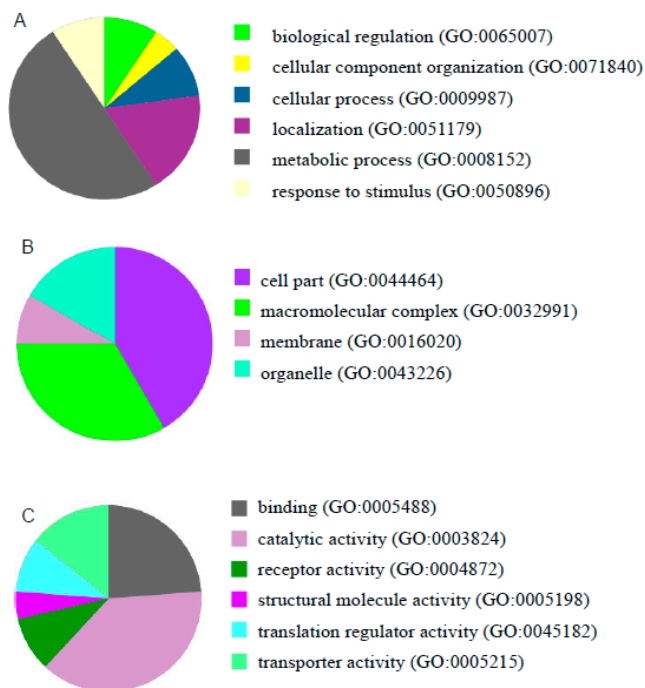


Figure S2. The GO analysis of Differential expression proteins regulated by α -terthienyl. (A) Biological processes; (B) cellular components; (C) molecular functions.

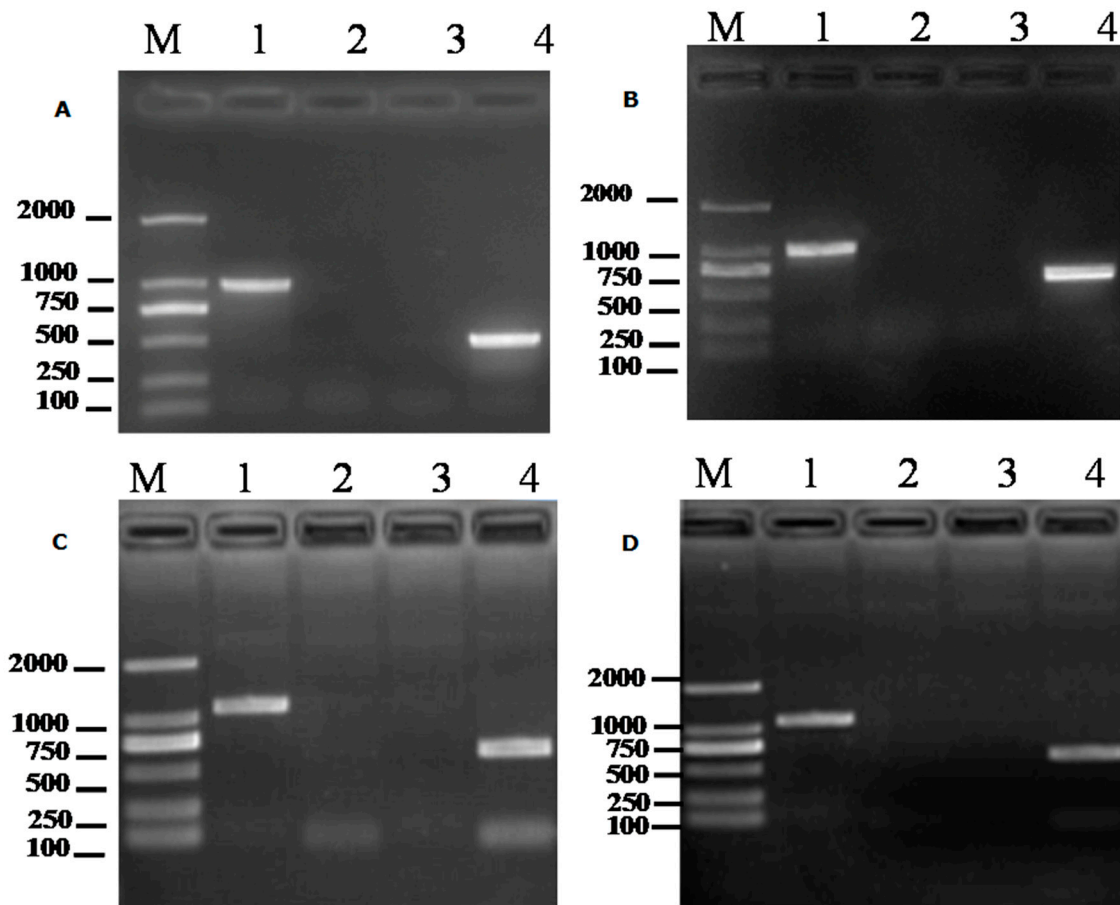


Figure S3. Homozygous mutant identification. The homozygous mutant was amplified by using primers LP and RP, wild type strains can be amplified by the corresponding bands, but not amplified in the mutant; gene amplified by using the primers of LP or RP and LBb1 primers on T-DNA, mutant strains can be amplified by the corresponding bands, but not in the wild type was obtained. *Chli1* homozygous mutant (amplified band size of 996 BP, LP and RP primers BP and RP primers amplified band size was about 500 BP, **A**), *atvha-c* homozygous mutant (amplified band size is 1071 BP, LP and RP primers BP and RP primers amplified bands of size 700 BP, **B**), *atkl1* homozygous mutant, (the size of amplified bands was 996 BP, LP and RP primers BP and RP primers amplified band size was about 500 BP, **C**), *prk* homozygous mutant (amplified band size is 1048 BP, LP and RP primers BP and RP primers amplified band size is about 700 BP, **D**). 1. Col-0, LP+RP; 2. Col-0, BP+RP/LP; 3. homozygote, LP+RP; 4. homozygote, BP+RP/LP; M, DL2000.

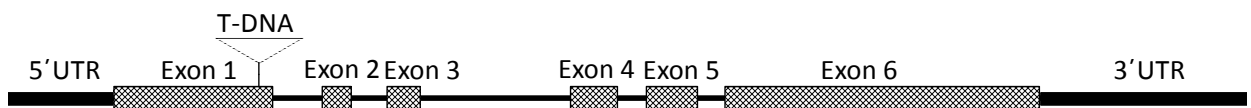


Figure S4. The gene structure of SAIL_58_D02.

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10      20      30      40      50      60
MASTSSLALS QALLARAISH HGSDQRGSLP AFSGLKSTGS RASASSRRRI AQSMTKNRSL
70      80      90      100     110     120
RPLVRAAAVE TVEPTDSSI VDKSVNSIRF LAIDAVEKAK SGHPGLPMGC APMAHILYDE
                                     *
                                     #

130     140     150     160     170     180
VMRYNPKNPY WFNDRDFVLS AGHGCMMLLYA LLHLAGYDSV QEEDLKQFRQ WGSKTPGHPE
                                     *

190     200     210     220     230     240
NFETPGIEVT TGPLGGIAN AVGLALAEKH LAARFNKPPA EVVDHYTYAI LGDGCQMEGI
                                     +*

250     260     270     280     290     300
SNEACSLAGH WGLGKLIIFY DDNHISIDGD TEIAFTENVD QRFEALGWHV IWVKNNGTGY
                                     *
                                     + +

310     320     330     340     350     360
DEIRAAIKEA KVTVDKPTLI KVTITIGYGS PNKANSYSVH GAALGEKEVE ATRNNLGPY
                                     *
                                     #

370     380     390     400     410     420
EPFQVDDVK SHWSRHTPEG ATLESDWSAK FAAYEKKYPE EASELKSIIIT GELPAGWEKA

430     440     450     460     470     480
LPTYTPESPG DATRNLSQC LNALAKVVPV FLGGSADLAS SNMTLLKAFG DFQKATPEER
                                     *

490     500     510     520     530     540
NLRFGVREHG MGAICNGIAL HSPGLIPYCA TFFVFTDYMR GAMRISALSE AGVIYVMTHD
*                                     *

550     560     570     580     590     600
SIGLGEDGPT HQPIEHIASF RAMPNTLMFR PADGNETAGA YKIAVTKRKT PSILALSROK
*                                     *

610     620     630     640     650     660
LPHLPGTSIE GVEKGGYTIS DDSSGNKPDV ILIGTGSELE IAAQAAEVLK KDGKTVRVVS
670     680     690     700     710     720
FVCWELFDEQ SDEYKESVLP SDVSARVSI E AASTFGWGKI VGGGKKSIGI NSFGASAPAP
730     740
LLYKEFGITV EAVVDAAKSF F

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Figure S5. The analysis of key amino acid sites. Metal binding: +; Binding site: *; Important for catalytic activity site: #.

Table S1. The primers for identification.

Spot ID	Gene Name	Gene No.	Seeds Salk No.	Primers for TP-PCR identification	Primers for Q-PCR identification
435	<i>PRK</i>	AT1G32060	SAIL_881_A12	LP 5'-GCAAACACCATGACTCGAGAG-3' RP 5'-AAAACAGATGGCAATTTGCAG-3'	F 5'-ACCATCTCGTGGATTCCCTTGC-3' R 5'-CTCGTCCAGTCTATCAAATTGTCC-3'
619	<i>ATTKL1</i>	AT3G60750	SAIL_58D02	LP 5'-TCCAACGGTCATATTTGATCC-3' RP 5'-GATTCCTTGCCAAGAGGACC-3'	F 5'-TACCTGAGAAAGCACCACCG-3' R 5'-CACCCCTTTTCCACTCCTTCG-3'
431	<i>CHLI1</i>	AT4G18480	SALK_132265	LP 5'-AAATGGGTGGTTTACCAATCC-3' RP 5'-TCTGGTTGGAATACGGTTGAG-3'	F 5'-TAGGGACGGTTAGAGATGCTGATT-3' R 5'-TCCTGCTCGGTTTTGTAAGTGT-3'
26	<i>ATVHA-C</i>	AT1G12840	SALK_072056	LP 5'-CTGCGAAATTGAAACCAAAAAC-3' RP 5'-ATCCTCTTGCTCCTCTTCAGC-3'	F 5'-GCTTCTTCGTTATGGAATCG-3' R 5'-CTCCTTCAGAGGTGACATTGT-3'
146	<i>VPS25</i>	AT4G19003	SALK_010439C	--	F 5'-CGTGCGGAGTGGTTAGATA-3' R 5'-AGACAGAGAACTTGACGCCT-3'
11	<i>ADK2</i>	AT5G03300	SALK_000565C	--	F 5'-TGAGTCGGCACCTACTGGAA-3' R 5'-TCAGGCGATACTGTGAGGAAGA-3'
108	<i>ATELF5A-2</i>	AT1G26630	SALK_020969C	--	F 5'-ACCTATCCTCAATCAGCCG-3' R 5'-CGAATCCAAGCCTCATCT-3'
192	<i>DHAR2</i>	AT1G75270	SALK_026089C	--	F 5'-TTCTCGGCGACTGTCCGTTTA-3' R 5'-AGCCACCCATTGCCATCA-3'
--	<i>Lb1</i>	--	--	5'-GCGTGGACCGCTTGCTGCAACT-3'	--
--	<i>LB2</i>	--	--	5'- GCCTTTTCAGAAATGGATAAATAGCCTTG CTTCC-3'	--
--	<i>ACTIN</i>	AT2G37620	--	--	F 5'-GAATCGCCGACAGAATGA-3' R 5'-TACTGAGGGAGGCCAAGA-3'