AT2G19570	70	L	Р	L	ΗF	I S	Ι	Η	А	Е	Q	F	Ľ	V ?	Г	ΝI	Ľ	Г	1	N (	GΒ	B	R E	ΗI	Ν	F	F	А	V	S	-				-	-	-	-	-	-	- A	A	Р	С	G	Н	C R	QF		110
AT4G29570	67	L	Р	L	DH	I S	Ι	Н	А	E	Q	F	LI	LA	A I	ΝI	I	4	L I	H	F	Q	) K	κ 1	Е	С	Ι	А	I	-	-				S	Т	Ν	G	Ϋ́	Υŀ	F Q	) E	Р	С	G	Н	C	QI		113
AT4G29580	69	L	S	Р	LH	I S	Ι	Н	A	G	Q	F	Ľ	v	vī	ΗI	L	A	1	NI	N	BR	t T	Ľ	N	C	L	A	-	-	-			·F	S	S	Ν	G	S	ΥĪ	F D	) P	Р	С	Р	н	C	QI		115
AT4G29600	69	L	Р	L	ΗF	I S	Ι	Н	Р	E	Q	F	Ľ	V ?	Г	NI	L	4	1	N	SI	B	C C	βI	R	Q	L	Α	V	A	I				S	S	D	С	I	ΕI	F C	βA	Р	С	G	Ν	C F	QI	7 .	117
AT4G29610	63	L	Р	L	Ηŀ	ΗT	Ι	Н	А	E	Q	F	Ľ	V 7	Г	ΝI	I	4	1	N	S N	ЛK	K K	1	Т	Н	Ι	А	V	S	V				-	-	Т	G	Т	I	F C	βA	Р	С	G	Н	C R	QI		109
AT4G29620	90	L	Р	L	ΗH	I S	Ι	Н	А	E	Q	F	Ľ	V 7	ΓÌ	ΝI	L A	4	1	N	ΥI	B	C D	DI	C	K	L	А	V	A	Ι				S	Т	D	G	LĪ	ΕI	FC	Τ	Р	С	G	Ν	C I	QF	7 -	138
AT4G29630	68	L	Р	L	ΗF	I S	Ι	Η	А	E	Q	F	Ľ	V 1	ΓÌ	ΝI	L	4	1	N	SI	ΞK	( C	βL	Η	L	L	А	V	Т	I				S	Т	D	G	N	DI	F C	βA	Р	C	G	Ν	C F	QF	7 -	116
AT4G29640	64	L	L	P	нŦ	S	Ι	Н	A	E	Q	F	L	I	4	ΝI	L	4	1	N	SI	ΒF	, K	ΧI	Т	Н	L	А	v	S I	D				-	-	N	G	Τľ	VI	F Q	D	Р	С	Y	D	٦ C	RF		110
AT5G28050	73	K	Y	Т	DF	P T	A	Н	А	Е	V	Τź	A	IJ	R ]	ΕA	A (	CI	ΚI	K I	LN	N K	C I	E	ĒL	S	Е	С	Е	I	-				-	-	-	- 1	ΥŻ	4 3	s c	Ε	Р	С	Р	M	C F	GA	۰ ·	116
AT3G05300	4	Κ	Y	Κ	DI	P T	Α	Н	А	E	V	I	A	II	R I	ΕA	4	CI	ΚI	K I	LN	N E	ΞΙ	K	L	S	Е	С	Е	I	-				-	-	-	- '	Υ	4 3	s c	Ε	Р	С	Р	M	C F	GA	. 4	47
AT1G68720	1152	Е	L	R	D S	5 T	Α	Н	A	E	М	Ι	C	II	R I	ΕC	G	S I	K A	A ]	LF	2.5	5 W	V R	L	Α	D	-	-	-	-				-	Т	Т	L	Y	V 1	ΓL	Ε	Р	С	Р	M	CA	GA	· ·	1195
AT1G48175	51	Е	Т	R	N A	Υ	R	н	A	E	М	Εź	A	I	D	Į	Ľ	V (	G	QV	N Q	Q K	K E	o c	ιL	S	Р	s	Q	V	4 1	Εŀ	K F	7 5	S K	C	v	Ľ	Y	V 1	ГС	Ε	Р	С	I	М	CA	S A	۰ I	103
AT4G20960	114	Η	Р	K.	A (	ΞQ	P	Н	A	E	V	F /	A 1	LI	R	DA	4	GI	ΕI	LA	Α	BN	ΙA	T	A	Y	V	S	L	Е	-				-	-	-	-	-	-		-	Р	С	Ν	Н	Y C	RT		152
AT3G48540	132	Т	Κ	Y	РY	ζV	C	Н	А	E	v	N	A	I	LÌ	N 1	ΓI	N I	H A	4	S A	Ā	C C	3 Q	) K	L	-	-	-	-	-				-	-	-	- `	Y	V J	ΓN	1 F	Р	С	N	Е	CA	KJ		171
AT5G24670	293	S	Р	A	K k	C Q	K	Т	S	S	Q	S	ΡI	D	V	Q l	N	D	S I	R J	ΕI	ΞT	V	/ R	D	P	S	Μ	E	R	P 1	ΥI	. (	Т	G	Y	D	Ι	F	LI	L	.Ε	Ρ	С	Т	М	CA	MA	. :	345

**Supplemental figure 1.** Cytidine/deoxycytidylate deaminase motif found in several Arabidopsis predicted proteins.

Arabidopsis Rice	MYSSYSAN	10 / A L A L R A A K P	20 9 S S C A H S T Y H H	30 М І Н Н Н Н Н Н Н G D G C	40 7 N T Y T N S <mark>L</mark> Q W G D C H Q Q E <b>L</b> L L	50 P I R S <mark>R N Q Q D Y 9</mark> P L N P R A A A A P 1	60 C S L <mark>L</mark> P E R S E S R F M <mark>L</mark> D G Y L L R	70 3 Y K L S K A Y T S S H S A H F L L L S A	80 R	90 100 - C Y C V S S R S S C C C C C H R R R R V A A R C C
Arabidopsis Rice	С С S Т Р S S S С С G G G G S V	110 SSFV / AGHVSWRLC	120 Y K P K V L I N P G F D P P R V C R C S G H	130 V L Y G V R Q S T L   G A G R S S D L G A V	140 I Q W P S F Q R <mark>R</mark> L / Y R R R L E C <mark>R</mark> C	150 L V <mark>G G G R L</mark> M G - ( G G <mark>G G G R L</mark> D L G /	160 C E V Y S S C <mark>D</mark> G I A G C G P R R <b>D</b> A P	170 R R K N R S F K L R R L V G R A V R Q E	180 C L <mark>E</mark> E S D E C C G V W <b>E</b> Y E G G E W P	190 200 G R <mark>S C S</mark> D H T <mark>S C S</mark> M E C H T DW G
Arabidopsis Rice	DV <mark>E</mark> AMISF DEEEDCGI	210 <sup>7</sup> L S E <mark>E</mark> L I D E E I A QW <mark>E</mark> A P P R F	220 R K W N L V S R V K R L S R R R S E E D	230 <b>B</b> K K K V G N V R K V <b>B</b> G D R C R D C H R F	240 / S V E G <mark>S</mark> N S <mark>Y</mark> G R K DA E <mark>S</mark> D Y <mark>Y</mark> D	250 N G R V S Q R V K K E D E Y S G R Q R E I	260 P E G F G R <mark>R</mark> K E I R R N M N E <mark>R H</mark> G R	270 K E D V K L N E R Y F T D S N Q R R R D	280 D C E H C G Q R D Y H D D D D Y	290 300 R R K <mark>K</mark> S S E L E S L E F <mark>R R W K</mark> E R R E R R
Arabidopsis Rice	E <mark>S</mark> R R G S K L D S E F D D A V	310 . V T G E Y I G K S / A R R G I E D R R	320 Y R G D E E R E V R Y S E D D R K Y D R	330 P R R R K S S R R E R K D F G Y E C	340 S C S G A V D V R R G A S	350 S Y Y S L A S S G E R Y T D N N Q R S D	360 F E S D T E D Q E E W R T E D R D Y E V	370 D V E I Y R E N V R D V R R E G K H R R	380 S S E K K V V D Q S . N D D Q R Y <mark>V</mark> T R H	390 400 A K <mark>R</mark> L K S R K <mark>E</mark> A S Q M Q Q <b>R</b> T D G T E <mark>E</mark> D V S L
Arabidopsis Rice	H S L E S Y R W H I	410 DEEYDYDDRC	420 9 I A E R R Y Y S G R	430 T Q K SA R A SA L F	440 Hedesnrass	450 S R N I V D T R V A I	460 R N K E N S A S R V	470 	400 D E S S T G V D S R E Q T S E E R N Q R	490 500 Y Q K Q I F E Y S S S V V Q S F D E K K
Arabidopsis Rice	H D H D D A Q L	510 JSVRDSRIG	520 TRDVRVITED	530 E G E N <mark>S</mark> N Q A N D A N L A S S S K N 1	510 / T L N Q R R R K K F M I S K H H N T V	550 F S Q T E N <mark>R V S E</mark> D Q K S T T <mark>R</mark> K D D	560 S T G N Y E E D M E S R N R S Q K I M E	570 IHEVHVNDAE LSEVRGTNTE	580 T S S Q N Q H D S R T Q S Y H Q	590 600 K L F N E R E D Y R E D R R R Y I E N R A S S
Arabidopsis Rice	V H <mark>S</mark> I R N D S L Q <b>S</b> S V K T T	610 S G N E N I E S S C S D T R T Q V D C	620 H Q L K E R L E T R H D E V D Q Q V V A	630 Y S S E D <mark>R V S E</mark> MF L T D S R <b>R R S E</b> K I	640 R R R T K Y S S S Q L T D I K M D S T S	650 NVSRTSLKQR	660 NSDEVNQMDI	670 E E G I N V L Q N F D D R S N S V H N I	680 P E V T N N Q Q P L T H I T R D K K R Y	690 700 V E E R I S K Q A G T R R V N Q Q V I H E T D I D V
Arabidopsis Rice	Т Т Е Н І S Е S Q N V T H V D V	710 5 5 E I H D I D I R 7 5 K V R A S D I S	720 N T Y V <mark>S Q</mark> R E D Q V S R N <mark>S Q</mark> K A S E	730   R N	740 Q E V H A G L E Q I H A S N S S M	750 V S G L Q S E R K Q ( V R G P Q S Y L E A A	760 Q D Y H I E H N P L A L H N R V Y S T S	770 Q T T Q S D R T S V A T D I V N T T A E	780 S V S H T S D A V R K H G Q V E A S T N	790 800 Y T E I Q R K <mark>S E</mark> K R L I N A A I A S T <mark>S E</mark> S H I Q
Arabidopsis Rice	G Q G S T T A N A R I E D SA N	810 / Q S D / N T I G S V Q E Q	820 I D L T R I C A S D	830 S T V V S S S H G L I	840 S K V E K N D T R S G Q V S R T	850 G <mark>A Q K E D S R</mark> L D I S A T N L V D R T R I	860 H A N S <mark>K K D</mark> G Q T E T R D K S D Q Q I	870 TLGLQ TQASNIDRND	880 9 S Y Q <mark>S K</mark> L S <mark>E</mark> E A 9 H V T <mark>S K</mark> F Y <b>E</b> S S	890 900 S S S Q S S L MA S R T K Q D S R Q S L A R L K DA
Arabidopsis Rice	L Q L V D L V S G R L M E H N V	910 S E E M Q G S <mark>E</mark> T T / G L N W Q Q E E S	920 L I P P S S Q L V S R R V S N DM D I A	930 R R S G <mark>Q S</mark> Y R T <b>G</b> C T L E M <mark>Q S</mark> T E D <mark>G</mark> S	940 G V S I Q E I S H G S S M V P V D E E K	950 T S E S G Y T T A F R P M I T G S S E Q	960 HPRAGASVN VRSETTAGS	970 S Q S A <b>G</b> E L M G F S I P S <b>G</b> S S A R Q	980 T S H E D A M G S A P V N E S L L E S A	990 1000 H <b>R L E</b> Q A <b>S</b> E K Y <b>V G</b> E A <b>R L E</b> K S <b>S</b> T F H <b>V G</b> Q
Arabidopsis Rice	F	1010 5 V I N P E T E E Q 5 V S DA DT T L T	1020 R A E S N Q L K R R R K N D K S I M E G	1030 D S R <mark>R S S</mark> G G S G A - I A R S S S R S R N	1040 X K <mark>G P S D E M W</mark> V 4 G G P S D E M W D	1050 T D <mark>S A</mark> Q G T P V Q <mark>S A</mark> T S Q E T F I	1060 - H P G A T <mark>E G</mark> N A K T A D K E <b>E G</b> S S	1070 AVG VDG GTT ST SL	1080 NAIFK T PKNETALAR	1090 1100 R N G R S L W N V I A D I K V H K S L W A Y V A D I
Arabidopsis Rice	A R L R W G S R V R L G W I Q R	1110 R A G S P D S - S A R G E S L D S N S N	1120 K P A G R <mark>S S</mark> P N E R S V K K <mark>S S</mark> S S N	1130 S V S S A T W F S G F S Q N T E G W I S S (	1140 R E H D G S S D D N Q E R D N E G I Q K	1150 T K G D K V S P Q E 7 K T E S S K P K D H	1160 A P S L H Q V E V G L M K S H T G E S L	1170 Q T S P R S K K E S L P T G S Q	1180 Q <mark>SE</mark> YPGT DLLI <mark>SE</mark> SGNV	1190 1200 T K L K Q R S E R H E G V P Q I N T S K G D F I S R
Arabidopsis Rice	V <mark>S</mark> S P S S T I T <mark>S</mark> K E DA HM	1210 L E G G S V S N R I T G E K A K Q S K	1220 M S S T S G N Q I V V A A S P K Q N T V	1230 G V D E E E G G N F I G G F S E D S T P T I	1240 5 F R L P E T A L T L V D V A K K H F P	1250 EVPMKLPSRN EHEASTSSMIT	1260 L I R S P P I K E S T T K G F A D N D T	1270 S E S S G E G V I A G T S S	1280 L T E A S S D Q N F M P I S T E G V G W	1290 1300 T V G E G R R Y P R M DA T A G S D E W R Y D P S G
Arabidopsis Rice E.coli	G Q N P L L F H A M T P Y R H H	1310 <sup>9</sup> G R N L R S <del>P</del> A V <sup>9</sup> H T Q V M M <del>P</del> H E	1320 MEPPVPRPRM DTPAILESAE	1330 V S G S S <mark>S L R E Q V L P T V</mark> G S T F	1340 / E Q Q Q P L S A K R F E E K I V V Q E	1350 S Q E E T G S V S A T P E V I R T D G K	1360 D S A L I Q R K L Q D A E L K R R K F Q M R R A F I	1370 R N K Q V V R D S F R N K Q V M K E T F T G V F	1380 E EWEEAYKVE D EWEEAYQRD F L S EVEFS	1390 1400 A E R R T V D E I F M R E A E Q R K T D E L F M R E H E Y W M R H
Arabidopsis Rice E.coli	A L V E A K K A A L H E A Q R A A L T L A K R A	1410 A A DT W E V P V G A A DL W E V P V G W D E R E V P V G	1420 3 A V L V H D G K I I 3 A V L V Q N G E I I 3 A V L V H N N R V I	1430 A R G Y N L V E E L F A R G C N L V E D L F G E G W N R P I G R F	1440 R D S T A H A E M I R D S T A H A E I V I D P T A H A E I M	1450 CIREGSKALR CIREASNKLK ALRQGGLVMQ1	1460 S W R L A D T T L Y T W R L A D T T L Y N Y R L I D <mark>A</mark> T L Y	1470 VTLEPCPMCA VTLEPCAMCA VTLEPCVMCA	1480 GAILQARVNT GAILQARVDT GAMIHS <mark>RI</mark> GR	1490 1500 L VWGA PNKLLGA D VVWGA PNKLLGA D VVFGA RDAKTGA A
Arabidopsis Rice E.coli	G SW I R L F F G SW V R L F F G S L M D V L F	1510 PGGEGNG <mark>S</mark> PGDGQTSSLE HHPG	1520 - E A S E K P P P S A N T N Q G A G P	1530 V H P F H P K M T I F V H P F H P K I S I F M N H R V E I T	1540 R R G V L E S E C A R R G I L S A E C S F E G I L A D E C A	1550 Q T <mark>M Q Q F F Q</mark> L R E I M Q Q F F H L R A L L S D F F R M R	1560 R K K K D K N S D P R K K Q K P E S P P R Q E I K A Q K K A	1570 P T P T D H H H H H A H P Q G R N H P Q S S T D	1580 L P K L L N K M H Q V K F F S K M H H M	1590 1600 V L P F F C L F G T 1 F C L

**Supplemental figure 2.** Alignment of the Arabidopsis, rice and *E. coli* tadA proteins highlights the poor conservation of the large N-terminal domains of the plant TADA

E.coli A. aeolicus S. aureus Chlamydomonas Phiscomytrella Arabidopsis Populus Potato Soybean Cotton Aquilegia Rice Wheat	1 1 196 1091 55 1 952 13 76 1371 523	- M R  	R A F   E E W D E W D E W D E W D E W D E W D E W		V F F  L Y T Y K V Y L R Y Q C Y K L Y Q R Y Q H		V E F - M T - R R T L R K Q Q R K Q R K Q R K	S H E I G K I N D V D E X T D I X I D E X I D E	YW YF GF IF MF MF LF	H V L L E E E E E E E E E E E E E E E E E			<pre> </pre>	W       D       E       K         F       Q       A       A       A         A       A       A       D       N       T         A       A       A       D       T       S       N         A       A       A       D       T       S       N       T       S       N       T       S       N       T       S       N       T       S       N       T       S       N       T       S       N       T       S       N       T       S	R G G D G W W W W W W W W W W W W W W W W		GAV GAU GAV GAV GAV GAV GAV GAV GAV GAV		$\begin{array}{c} H N N N \\ E G \\ C D D \\ C \\ A A D C \\ C \\$	R V E V G A T V K I K I K I K I K I K I K I 	$\begin{bmatrix} G \\ G \\ S \\ K \\ A \\ A \\ C \\ C$		57 41 42 37 249 1148 112 37 1009 70 133 1428 580
															d	d						a	
E.coli A. aeolicus S. aureus Chlamydomonas Phiscomytrella Arabidopsis Populus Potato Soybean Cotton Aquilegia Rice Wheat	58 42 43 38 250 1149 113 38 1010 71 134 1429 581	R P I S V E R V H C V E L V E	G R H E L K T L Q R L R E L R E L R E L R E L R D L R D L R D L R	DPT OPT OPT SPL DST DST DST DST DST DST	A A A A A A A A A A A A A A A A A A A	E   M   L E   H   L E   H   L E   M   L E   M   L E   M   L E   M   L E   M   L E   M   L E   V		Q G ( E A ( A G A E A G A E A G E A S E A	S L V R V R Q A K N S K S K S K S K S K S K S K S K S K	M Q N T G S R A G G S L R R T T L R S S L R T T L R S L R T L K T L K T	YRL WRL WRL WRL WRL WRL WRL WRL WRL WRL W	I D E G E G L G T D A D S D A D A D A D A D A D		Y V T Y V T				GA GA GA GA GA GA GA GA GA GA GA GA GA G	$ \begin{array}{c} M \mid H \\ L \lor V \\ L \lor M \\ Q \\ M \\ Q \\ M \\ M \\ Q \\ M \\ M \\ L \\ Q \\ M \\ M \\ M \\ L \\ Q \\ M \\ \mathsf$	S       R       I       G         S       R       I       E         S       R       I       P         S       R       I       P         S       R       V       G         S       R       V       S         S       R       V       G         S       R       V       N         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D         S       R       V       D			117 101 102 97 309 1208 172 97 1069 130 193 1488 640
		а			aa						b	b			а					b			
E.coli A. aeolicus S. aureus Chlamydomonas Phiscomytrella Arabidopsis Populus Potato Soybean Cotton Aquilegia Rice Wheat	118 102 103 98 310 1209 173 98 1070 131 194 1489 641	R DA L D K D D P P S R N K P N K R P N K K R P N K K R P N K K R P N K K R R R N K K R R N K K R R N K K R N K K K R N K K K K K K K K K K K K K K K K K K K	KTG KHG RLG LLG LLG LLG LLG LLG LLG LLG	$A A G$ $G \lor V$ $C S G$ $A D G G$	S L M S V F S L M S W I S W I S W I S W I S W V S W V S W V S W V S W V		- H - D - Q - P P - P P Q - P Q  - P Q  - P P  - P P 	G E C G E C G E C G C E G C C G C C G C C G C C C G C C C G C C C C C	G NG E NG E NG E NV G XG G XG G S T S T	 S S G S E L L E P S E Q S E X S S D S L D S L D P	EQ E SEN T NE T NE T D NT S NC	E P K (P P) (P P) (P A) (P A)	   	E Q Q H P V H P V H	P G M   P T L   S N F   P - F		R V E R V H R V H T T T T M T T M T T M T M T M T M T M T	U E V E V R I R I R I R I R I R I R V R	EGI YYP GGC RGV RGV RGV RGV RGV RGV RGV RGV RGV RGV	L A D E L E E A L E E A L E E S L E S E L E S E L A T E L A T E L A S T E L S A E L S A E L S T E	CAAL S-EL CSTL CADV CGDI CAQT CAQT CADA CADA CADA CADA CSEI CSEI	L S S T R Q Q Q Q Q Q Q Q V V Q Q Q Q Q Q Q Q Q Q	157 140 142 137 363 1264 229 154 1125 187 251 1547 699
E.coli A. aeolicus S. aureus Chlamydomonas Phiscomytrella Arabidopsis Populus Potato Soybean Cotton Aquilegia	158 141 143 364 1265 230 155 1126 188	D F F F F F F F F F F F F F F F F F F F	R M R K K N L R R R R Q L R Q L R Q L R Q L R	R Q G R N N Q K K K K R R R K K R R R K R R R R R R R R R	I KA I I G K K S P K C K E K K E K K K K K K K K K K		(AQ R DDPC D SD NG 	S S T I  2 I G P I S I S P P I Q	D    P T P P P Q P P P P L S S	  G L W T D H P S C S C L S S L S S S	   	S P T V S P T V S H H T N P R H - H - S	   N S P H L P P Q L H H P S C L P	  LA F K L L K I L K F L K L L I T T		  1 H - ( 1 H G H D H D	  V V R Q V L F F H V F H	         	F C L F C L F C L F C L	178 156 143 413 1307 275 204 1169 218			

**Supplemental figure 3.** Alignment of the C-terminal active domains of plant TADA sequences found in genomic and EST databases, as compared to bacterial proteins of known structure. Histidine and cysteines involved in the coordination of a zinc ion are in red, and an essential glutamic acid residue that is directly responsible for the hydrolytic reaction is in green. Amino acids directly involved in tRNA binding in the reference structures are indicated, respectively by <u>a</u> and <u>b</u>, according to which monomer of the homodimer enzyme they belong.



**Supplemental figure 4.** RNAi plants deficient in TADA expression are also affected in cp-tRNA<sup>Arg</sup> editing. (A) Phenotypes of slow growth of several individual plants of the RNAi line that expresses a *TADA*-specific RNA stem-loop. Plants that were further analyzed are numbered. (B) RT-PCR analysis of *TADA* gene mRNA accumulation in the selected plants. C is negative control. (C) Analysis of tRNA anticodon editing in selected plants shows that editing deficiency correlates with *TADA* silencing.



**Supplemental figure 5.** TADA is not involved in chloroplast C-to-U editing. Regions of several chloroplast gene transcripts comprising known editing sites were amplified by RT-PCR and sequenced. No difference could be found between *tada-1* and wild-type Col-0 plants.



**Supplemental figure 6.** TADA is not involved in mitochondrial C-to-U editing. Regions of several mitochondrial gene transcripts comprising editing sites were amplified by RT-PCR and sequenced. All 82 sites analyzed on 6 different genes are edited in *tada-1*. Only a few examples are shown.

![](_page_6_Figure_0.jpeg)

**Supplemental figure 7.** *tada-1* plants have normal leaf structure and equivalent number of chloroplasts per cell as wild type plants.

(A and B) Confocal microscope image of mesophyll cells of wild type (A) and *tada-1* (B) leaves (adaxial side) observed under visible light.

(C and D) Confocal images of the fluorescence of chlorophyll in leafs of wild type (C) and *tada-1* (D) plants suggest that there are no significant differences in the number of chloroplasts per cell in tada-1.

(E and F) The same as in C and D, in cross sections of wild type (E) and tada-l (F) leaves.

Chlorophyll	content	of tada-1	plants
	,		

			mol/mol				
	chla	chlb	chl a+b	a/b			
WT	1.29 + 0.12	0.41 + 0.05	1.70 + 0.16	3.25 + 0.30			
tada-1	0.54 + 0.09	0.17 + 0.04	0.71 + 0.12	3.27 + 0.27			

# Similarities between the N-terminal and C-terminal domains of plant TADA proteins

		Full lenght prot	ein		
		IdentityScores(	%)		
	Arabidopsis	Phiscomytrella	Rice	Soybean	
Arabidopsis	100.0	10.7	18.4	33.1	
Phiscomytrella	14.5	100.0	7.9	11.9	Similarity Scores (%)
Rice	32.5	11.7	100.0	18.2	
Soybean	47.5	16.1	30.3	100.0	

		IdentityScores(	%)		_
	Arabidopsis	Phiscomytrella	Rice	Soybean	
Arabidopsis	100.0	51.2	64.9	75.4	
Phiscomytrella	61.0	100.0	48.1	50.2	Similarity Scores (%)
Rice	78.2	62.0	100.0	66.3	
Soybean	81.4	60.5	80.7	100.0	

		IdentityScores(	%)		
	Arabidopsis	Phiscomytrella	Rice	Soybean	
Arabidopsis	100.0	2.7	13.7	24.1	
Phiscomytrella	6.1	100.0	2.0	3.5	Similarity Scores (%)
Rice	28.8	4.7	100.0	12.5	
Soybean	39.8	6.8	25.9	100.0	

Accumulation of chloroplast transcripts in tada-1 and tada-1 complemented with AN-TADA compared to Col-0

ΔN-TADA

log2(mut/WT)

-0,2243 -0,1046 -0,4446 0,1190

0,3544 -0,3166 0,1782 -0,0650 -0,1895 0,2034 0,1208 0,1828 0,1747 0,1008 0,2985 0,1111 0,2469 0,1292 0,1292 0,1127 0,2613

0,0595 -0,2576 0,1418 -0,0088 1,0360 0,4700 0,5855 -0,0615 0,2204 0,20411 0,0446 0,1128 0,3119

0,1077 0,1773 0,2818 0,0527 -0,1760

-0,0954 -0,0264

0,2592

 Std

 deviation

 0,0764

 0,0365

 0,0466

 0,0214

 0,0532

 0,0542

 0,0573

 0,0671

 0,0103

 0,0103

0,0103 0,0447 0,0776 0,0522 0,0844 0,0170

0,0170 0,0677 0,2123 0,2021 0,0429 0,0299

0,0528 0,0420

0,0845 0,0251 0,0301 0,2508 0,0332 0,0477 0,0920 0,0742 0,1402 0,0742 0,1466 0,0342 0,0572 0,2123 0,2123 0,2150 0,2767

0,1092

		tada-	1	ΔΝ-ΤΑ	DA			tada-	1
AGI number	name	log2(mut/WT)	std deviation	log2(mut/WT)	std deviation	AGI number	gene name	log2(mut/WT)	std deviation
AtCq00020	psbA	0,8054	0,0491	-0,1595	0,0442	AtCq00650	rpS18	1,9344	0.2780
AtCq00040	matK	2,3189	0,1101	0,5093	0,0480	AtCq00660	rpL20	2,2311	0,0343
AtCq00065	rpS12A	1,3696	0,3918	-0,0344	0,0403	AtCq00670	clpP1	1,3675	0,2835
AtCq00070	psbK	0,9578	0,1955	0,2535	0,1647	AtCq00680	psbB	0,8433	0,1387
AtCq00080	psbl	1,2850	0,0902	0,2482	0,0267	AtCq00690	psbT	1,0385	0,1910
AtCg00120	atpA	-0,1907	0,2887	-0,0109	0,0442	AtCg00700	psbN	0,9276	0,1431
AtCg00130	atpF	0,0510	0,3267	0,1497	0,0347	AtCg00710	psbH	1,2012	0,1858
AtCq00140	atpH	1,0965	0,1554	0,1458	0,0485	AtCq00720	petB	1,3280	0,1569
AtCg00150	atpl	1,2991	0,0879	0,3405	0,0765	AtCg00730	petD	1,4878	0,0986
AtCg00160	rpS2	2,1155	0,0213	0,1483	0,0891	AtCg00740	rpoA	1,8270	0,0805
AtCg00170	rpoC2	1,7943	0,0804	-0,0408	0,0462	AtCg00750	rpS11	1,6219	0,1498
AtCg00180	rpoC1	2,3223	0,3357	0,0172	0,0819	AtCg00760	rpL36	1,6840	0,0868
AtCg00190	rpoB	2,0063	0,1816	0,0638	0,2947	AtCg00770	rpS8	1,8282	0,1574
AtCg00210	petN	0,5397	0,1392	0,2790	0,0429	AtCg00780	rpL14	2,0004	0,1015
AtCg00220	psbM	1,2521	0,1890	0,1488	0,0643	AtCg00790	rpL16	2,2788	0,2590
AtCg00270	psbD	0,1718	0,3309	-0,3185	0,0345	AtCg00800	rpS3	2,2956	0,0504
AtCg00280	psbC	0,3961	0,2312	-0,0289	0,0080	AtCg00810	rpL22	2,4849	0,1794
AtCg00300	psbZ	0,5647	0,1839	-0,3080	0,0267	AtCg00820	rpS19	2,1272	0,1741
AtCg00330	rps14	1,2863	0,1106	-0,1024	0,0121	AtCg00830	rpL2	1,9490	0,3350
AtCg00340	psaB	0,5365	0,1639	0,0621	0,0494	AtCg00840	rpL23	1,5826	0,2384
AtCg00350	psaA	0,4837	0,2721	0,2099	0,0715	AtCg00860	ycf2.1	2,2036	0,2554
AtCg00360	ycf3	2,3968	0,2409	0,3084	0,0205	AtCg00870	ycf15	2,1766	0,2122
AtCg00380	rps4	0,9036	0,1102	-0,0262	0,0381	AtCg00890	ndhB	2,1289	0,3321
AtCg00420	ndhJ	1,1838	0,0364	0,0333	0,0604	AtCg00900	rpS7	1,6901	0,2161
AtCg00430	ndhK	1,1638	0,1312	0,0712	0,0474	AtCg01000	ycf1	1,8017	0,0899
AtCg00440	ndhC	1,2007	0,1800	0,0883	0,0377	AtCg01010	ndhF	1,6878	0,1986
AtCg00470	atpE	1,3050	0,3040	0,1823	0,0312	AtCg01020	rpL32	1,4453	0,1131
AtCg00480	atpB	0,6658	0,1833	0,2143	0,0243	AtCg01040	ccsA	1,2967	0,1533
AtCg00490	rbcL	-0,0113	0,2145	0,4040	0,0365	AtCg01050	ndhD	1,5050	0,4549
AtCg00500	accD	1,8685	0,6108	-0,3235	0,0984	AtCg01060	psaC	1,0875	0,3100
AtCg00510	psal	1,0765	0,2086	0,0628	0,0176	AtCg01070	ndhE	1,6530	0,2138
AtCg00520	ycf4	1,5718	0,1285	0,1478	0,0344	AtCg01080	ndhG	2,1465	0,1331
AtCg00530	cemA	1,7827	0,3528	-0,1010	0,0484	AtCg01090	ndhl	1,6501	0,0897
AtCg00540	petA	1,8801	0,0684	-0,0745	0,0203	AtCg01100	ndhA	1,2454	0,2785
AtCg00550	psbJ	2,2268	0,2562	0,0380	0,0620	AtCg01110	ndhH	1,4940	0,2229
AtCg00560	psbL	1,4054	0,1798	0,2330	0,0409	AtCg01120	rpS15	2,1629	0,1058
AtCg00570	psbF	1,4384	0,1856	0,2257	0,0386	AtCg00920	rrn16S	0,9788	0,2123
AtCg00580	psbE	1,3913	0,1572	0,1761	0,1059	AtCg00950	rrn23S	3,1049	0,1752
AtCg00590	petL	1,6698	0,1699	0,1909	0,0140	18S rRNA	nuc18S	0,4364	0,2150
AtCg00600	petG	1,7946	0,1898	0,2499	0,0376	At5g25760	UBC	-0,2292	0,2230
AtCg00630	psaJ	1,5379	0,1534	0,6279	0,0287	At5g08290	YLS8	-0,1251	0,1547
AtCg00640	rpL33	1,5574	0,1316	0,1686	0,1864	At3g18780 & At1g49240	actin2.8	0,0390	0,1198

	cp-coded proteins			ns	ribosomal proteins					rpo			Ps	a			
	162	CDS 's	(41837	codons)	29	CDS's	(4008	codons)	4	CDS's	(3461	codons)	5	CDS's	(1651	codor	ıs)
Codon		#	%Total	%CGN		#	%Total	8CGN		#	%Tota	1		#	%Tota	1	%CGN
CGG		192	0,5	14,3		28	0,7	11,0		27	Ο,	8 18,1		1	Ο,	1	2,7
CGA		461	1,1	34 <b>,</b> 5		99	2,5	39,0		66	1,	9 44,3		12	Ο,	7	32,4
CGU		516	1,2	38,6		103	2,6	40,6		32	Ο,	9 21,5		19	1,	2	51,4
CGC		169	0,4	12,6		24	0,6	9,4		24	Ο,	7 16,1		5	Ο,	3	13,5
Total	-	1338				254				149				37			

Frequencies of CGN codons in Arabidopsis chloroplast-encoded protein genes

		Psb			Rbcl				PetA				PetB					
		15	CDS's	(2407	codons)	1 CDS	(480	) codons)		1	CDS	(32	1 codons)		1 CDS	(21)	5 codons)	)
	Codon		#	%Total	. %CGN		# %	Total	%CGN			#	%Total	%CGN		# %	Total	%CGN
	CGG		5	0,2	6,6		0	0,0	0,0			0	0,0	0,0		0	0,0	0,0
	CGA		18	0,7	23,7		6	1,3	30,0			3	0,9	33,3		2	0,9	22,2
	CGU		43	1,8	56,6	1	2	2,5	60,0			4	1,2	44,4		5	2,3	55,6
	CGC		10	0,4	13,2		2	0,4	10,0			2	0,6	22,2		2	0,9	22,2
Γ	Total		76			2	0					9				9		

Primers used in this study

Name	Purpose	Sequence
P1	Genotyping	CGAGTTTATCTGAAGAAGCCC
P2	GFP construction	CAAGGTACCTCTTCTAATTCAAC
P3	Genotyping	TCCACCCACAAGTAACCTCC
P4	GFP construction	CTTGGATCCACTTCTTCTTC
P5	Genotyping	GGAGACTCGTTATAGCAGTGAG
P6	Genotyping	GCCICIICAGAIAGCIIIGACIG
P7		AGGIGGAAACIIIGAGIICC
P8		
P9 D10	IADA RI-PCR	
P10 D11		
P11 012	cp-trnR editing test	
P12 D13	trnA editing test	
P13 D14	trnA editing test	TGTTGAGATGCGGGGTATC
P15	trnV editing test	GGTTTCGTGGTGTAGTTGG
P16	trnV editing test	TGGTGGCTTCGCCCGGGTTC
P17	trnT editing test	GCTTTCATAGCTCAGTTGG
P18	trnT editing test	TGGTGCTTTCGTTGAGAGTTG
P19	trnL editing test	GTTGATATGGCCGAGTTGG
P20	trnL editing test	TGGTGTTGACAGTGGGATTTG
P21	trnI editing test	GGCCCATTAGCTCAGTTGG
P22	trnI editing test	TGGTGGCCCATGCAGG
P23	trnR editing test	GACTCCATGGCCCAATG
P24	trnR editing test	TGGCTGGGGATCGAACC
P25	ndhB RT-PCR	CAACTCTCTGTATTCCTCTATCC
P26	ndhB RT-PCR	AGCTAGGATTTCCAGAAGAAGATGC
P27	ndhD RT-PCR	GCGGCTTTTCCAGTTACTCGGGATTC
P28	ndhD RT-PCR	CAGGATCCGTTATAGAACTAATACC
P29	rps12 RI-PCR	
P30	rps12 RT-PCR	
P31	rps14 RT-PCR	
P32	rps14 RT-PCR	
P34	nad3 RT-PCR	TGCCCTATCACTTTACTCCC
P35	nad5 RT-PCR	GGTTACATCCATAAGTAGCTTGGTCC
P36	nad5 RT-PCR	GCGATGACCCTCTTTAGATCG
P37	cox3 RT-PCR	ATACCATGTTCGTATGGTGG
P38	cox3 RT-PCR	AAACCATGAAAGCCTGTTGC
P39	ccb206 RT-PCR	CTCGTATATCGTCGTAACGC
P40	ccb206 RT-PCR	TGGATTTTGCGAGCTGTTCC
P41	ccmC RT-PCR	TCAAAGACCAGAAGCTACGC
P42	ccmC RT-PCR	CAAGATACGGGTTGAGAAGG
P43	ccmFc RT-PCR	TTTATGGTCGTGCCTTGTGG
P44	ccmFc RT-PCR	TTTCGTCGTTGCTCATTCCC
P45	rps12 RT-PCR	GGAAAGAGAATAATGCCCACG
P46	rps12 RT-PCR	GAGGCATCTTCCATTCATATCG
P47	AN-IADA construction	GGGGACAAGTTIGTACAAAAAAGCAGGCTTACGGTCTCCTGCTGTAATGG
P48	AN-IADA construction	GGGGACCACITIGTACAAGAAAGCTGGGTCTTCCATTGTGTGTGGAGGA
P49	AN-IADA genotyping	GTICGAAGGTGAAGGTGACG
P50	AN-IADA genotyping	
P51	AN-IADA genotyping	
P52	AN-IADA genotyping	
P53	cp-trnR in vitro synthesis	
	cp-trnk in vitro synthesis	
P55 P56	trnR in vitro synthesis	
P50	trnA in vitro synthesis	GAGTAATACGACTCACTATAGGGGGATGTAGCTCAGATGG
P58	trnA in vitro synthesis	CTGGATCCTGGTGGAGAGATGCGGGGGTATCG
actin2.8F	aRT-PCR	GGTAACATTGTGCTCAGTGGTGG
actin2.8R	aRT-PCR	AACGACCTTAATCTTCATGCTGC
Q18SF	gRT-PCR	AAACGGCTACCACATCCAAG
Q18SR	qRT-PCR	ACTCGAAAGAGCCCGGTATT
UBC-1	qRT-PCR	TTCGTTCTCTTTGGGAAATTAGA
UBC-2	qRT-PCR	CTCGCTGTACCTCTTTGTATTCTTT
YLS8-1	qRT-PCR	GGGATGAGACCTGTATGCAGATGGA
YLS8-2	qRT-PCR	GCTCGTACATGGTGTTGAAGTCTGG