

ORIGIN

```
1 atggcctctg ctgcctctgc ttcatttcct accactgtat gcttcaatac caatacgggt
61 gatgaccgaa aaccagcctt ctttgagttt aaaccacact gtacatcaaa tatggctcct
121 gcagaccctg acaaccatgc aagtgaiaaa tctactcaaa tagatggta aggaaagct
181 caaccttttg actcgtcacc attagtaaaa aatgagatgg cagtcccttc taatgaatta
241 agtctatcat cacctgttca aatggttaac tcaggagtta atgccctgtg tgaaggatg
301 ttggatgaac tgaaccctag gagcaacata acaactgggc ttccagcatc acaagttgac
361 aatagaggta gtggactttc cgttcagct gagagatg ctgctgatgg atacaactgg
421 agaaagtatg ggcagaaaca tgttaaagga agtgaatttc cacgcagtta ctacaaatgt
481 acacatccta actgcgaagt caagaaacta tttgaacgct ctcatgatgg gcaaatcact
541 gagataattht acaaggggac acatgatcac ccaaaacctc aaccaaatcg ccgttactca
601 actggaacta tcattactat gcaagaagag agatctgata aagcttcttt gactagccga
661 gatgacagag gatccaatat atgtggccag gtgtctcatc catctgagcc tgacagtact
721 ccagagctat cacctgcagc tacaatgat ggtgatcaag agggtagcagg atttttgtca
781 aaccggaata gtgatgagg tgatgatgat gatcccttct caaagcgaag aaaaatggag
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901 caaactctga gtgaggttga tatattggat gatggttacc gctggcga gtatggcgag
961 aaggtggtga gaggcaatcc taaccctagg agttattaca aatgcacaaa cacgggggtc
1021 cccgtagaa aacatgtgga aaggcatct catgatcaa aagctgtgat aaccacat
1081 gagggaaac acaatcatga tgtaccaact gcaaggaata atagttgcca tgacattgca
1141 ggaccagtaa gtgctgctgg gggacagaca agaattaggc cggagaag tgataccatc
1201 agccttgacc ttggtatggg aattagcct gctgcggaag acacaccaag cagtaaggg
1261 agaatgatgc tttccgaatt tgggacagc caagctcaca ccgcaatc caattcaag
1321 tttgtcatt cttcagcggc gccagtgtac tttggtgtc taaatacaa ctctaacca
1381 tatggctcta gagaaaatcc aagtgatagt acatcttaa accgttctgc ttatccctgc
1441 cccagaaca tgggaagaat actaatgggt ccatga
```

//

Supplementary Figure 1: Nuclotide sequence of *MuWRKY3* gene containing 1476 bp.

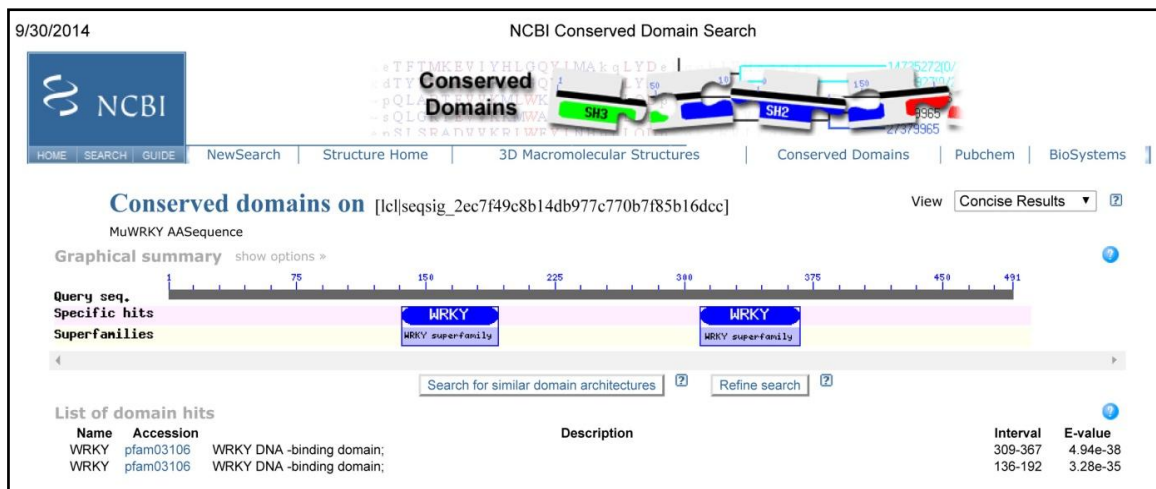
Compute pI/Mw

Theoretical pI/Mw (average) for the user-entered sequence:

```
10 20 30 40 50 60
MASAASASFP TTVCFNNTV DDRKPSFFEF KPHCTSNMAP ADPDNHASEK STQIDGQGKA
70 80 90 100 110 120
QPFDS SPLVK NEMAVPSNEL SLSSPVQMVN SGVNARVEGD LDELNPRSNI TTGLPASQVD
130 140 150 160 170 180
NRGSGLSVAA ERVSADGYNW RKYGQKHVKG SEFPRSYYKC THPNCEVKKL FERSHDGQIT
190 200 210 220 230 240
EIIYKGTHDH PKQPNNRRYS TGTIITMQEE RSDKASLTSR DDRGSNICGQ VSHPSEPDS
250 260 270 280 290 300
PELSPAATND GDQEGTGFLS NRNSDEVDDD DPFSKRRKME LGNADITPVV KPIREPRVVV
310 320 330 340 350 360
QTLSEVDILD DGYRWRKYGQ KVRGNPNPR SYKCTNTGC PVRKHVERAS HDPKAVITTY
370 380 390 400 410 420
EGKHNHDVPT ARNNSCHDIA GPVSAAGGQT RIRPEESDTI SLDLGMGISP AAEDTPSSQG
430 440 450 460 470 480
RMMLSEFGDS QAHTGNSNFK FVHSSTAPVY FGLVNNNSNP YGSRENPSDS TSLNRSAYPC
490
PQNMGRILMG P
```

Theoretical pI/Mw: 6.12 / 53740.10

Supplementary Figure 2: Deduced amino acid sequence of *MuWRKY3* protein showing predicted *pI* and molecular weight.



Supplementary Figure 3: Conserved domain analysis of *MuWRKY3* protein showing two domains. One towards N-terminal and another at the C-terminal region.

Plant-mPLOC: Predicting subcellular localization of plant proteins including those with multiple sites

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Your input sequence (491aa) is:

```
>MuWRKY3
MASAASASFPPTVCFNTNTVDDRKPSFFFEFKPHCTSNMAPADPDNHASEKSTQIDGQGKA
QPFDSPLVKNEMAVPSNELSLSSPVQMVNSGVNARVEGDLDLNPNSNITGLPASQVD
NRGSGLSVAAERVSADGYNWRKYGQKHVKGSEFPRSYKCTHPNCEVKKLFERSHDGQIT
EIIYKGTDHHPKPQPNRRYSTGTIITMQEERSDKASLTSRDDRGSNICGQVSHPSEPST
PELSPAATNDGDQEGTGFLSNRNSDEVDDDDPFSKRRKMELGNADITPVVKPIREPRVVV
QTLSEVDILDDGYRWRKYGQKVVRGNPNRPSYKCTNTGCPVRKHVERASHDPKAVITTY
EGKHNHDVPTARNNSCHDIAGPVSAAGGQTRIRPEESDTISLDLGMGISPAAEDTPSSQG
RMMLSEFGDSQAHTGNSNFKFVHSSTAPVYFGVLNNNSNPYGSRENPSDSTSLNRSAYPC
PQNMGRILMGP
```

----- Plant-mPLOC Computation Result -----

Query protein	Predicted location(s)
MuWRKY3	Nucleus.

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Supplementary Figure 4: Predicted sub-cellular localization of *MuWRKY3* gene showing the localization in the nucleus.

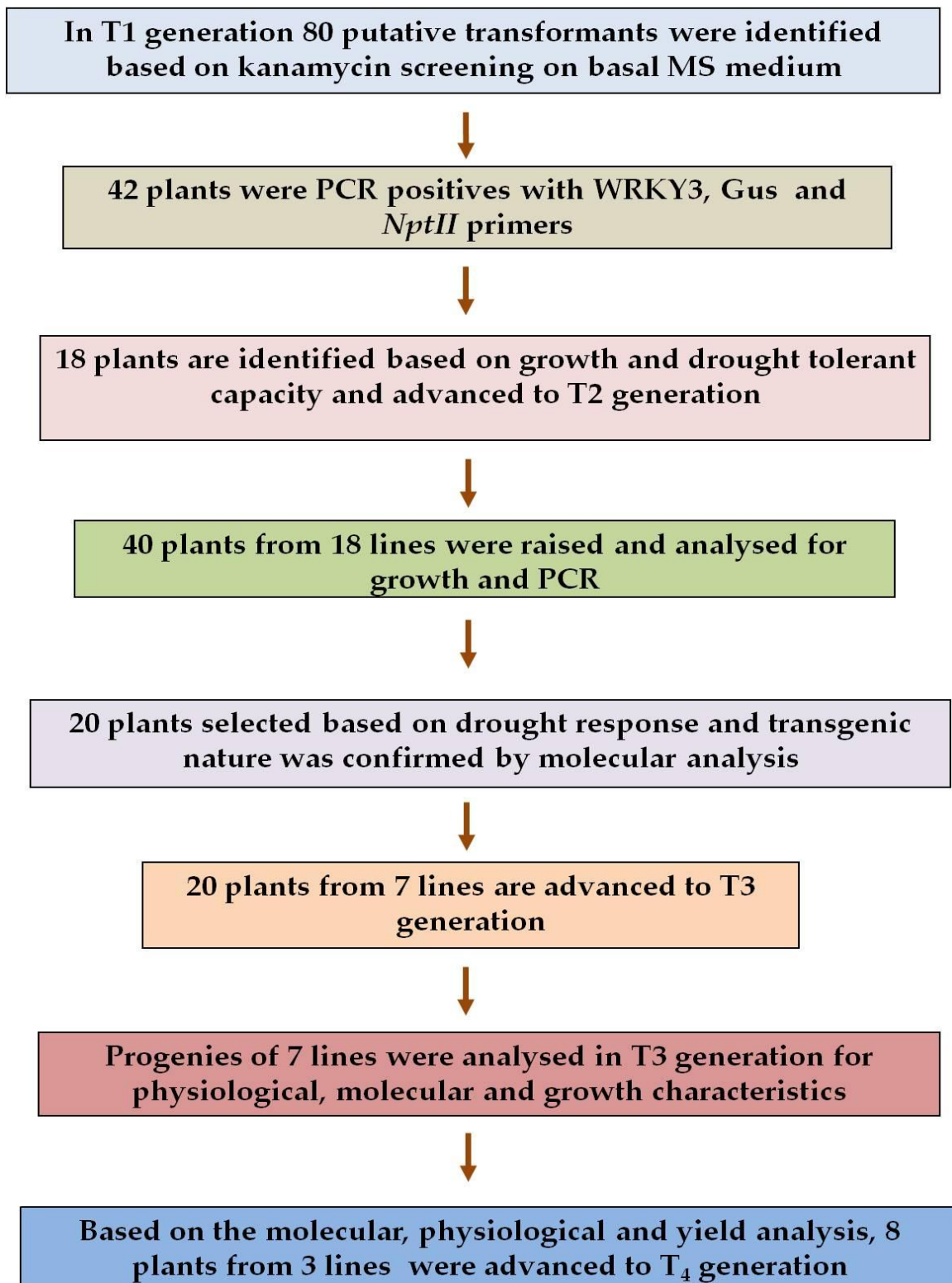
```

      10      20      30      40      50      60      70      80
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NBWRKY3 -----
NTWRKY3 -----MKKPLVHENPRKNRVIKELVDG
SMWRKY3 -----MDNSSDDLNRRAIEGLIRG
CMWRKY  -----METGQKWPLIKELTQG
GMWRKY3 -----MASAASATFPVTTACFN-----TNTVDARKSSFFEFKPLNRS
MuWRKY3 -----MASAASAFP-TTVCFN-----TNTVDDRKPSFFEFKPHCTS
NAWRKY3 -----MQSLK
ATWRKY3 MAEKKE-----KEPSKLSSTGV-SRPTISLPPRPFGEFFSGGVGFS--PGPMTLVSNLFSDDP-EFKSFSQLLAG
BPWRKY3 MADKEEQVEVHQKQPSTLKSSTGAPSRPTISLPPRPFGEFFSGGLGFS--PGPMTLVSNLFSDDP-ELKTFSSQLLAG
BRWRKY3 MAENEEE---QKQSLTSKSSTGGASRPTISLPPRPFGEFFSGGVGFSFGSPGPMTLVSNMFSDDP-EFKSFSQVLVAG
GHWRKY3 MAEQGK-----RSKLSAPTYPTITLPPRPIDGLFQSGSGLS--PGPMTLVSAFFSDDPSTNRSFSQLLAG
OSWRKY3 --MGGEPRARAEAWAAALPAALVALVRDTATYTRMMHRLRMETPRGPTCQLDPCCCCTAHVIPPPPPVSRTHATRDA
TAWRKY3 -----
ASWRKY3 -----MMTMDLMGRY
ZMWRKY3 -----MEEVEVANRAAVESCHRVLALL
AAWRKY3 -----
VPWRKY3 -----
BOWRKY3 -----
HVWRKY3 -----

      90      100     110     120     130     140     150     160
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NBWRKY3 -----
NTWRKY3 KRFBT-----QLQTLQQPFIADHGVPVSADELLLLKIWRSFSEAITELNTWGLA
SMWRKY3 REFTR-----RLKQIIKISGGEVENIMAEIDLVAKILDSFSETLVSINNS---
CMWRKY  KEYTY-----QLKNHLDNP---MSTETCEFLVEKILNSYENAIMLNRAAI
GMWRKY3 NKVPA-----DFNNHVSQSTQVEGPGKAQSFASSPLVESEITVPSNELSLS
MuWRKY3 NMAPA-----DPDNHASEKSTQIDGQKQPFDSPLVKNEMAVPSNELSLS
NAWRKY3 NNAQS-----NGGNQYNNQSSQ-----
ATWRKY3 AMASPAAAAVAAAVVATAHHQTPVSSVGGGGGGDVPREFKQSRPTGLMITQPPGMFTVPPGLSPATLLDSPSFFGLF
BPWRKY3 AMASP-AAAVAAAVVATAH-QTPVSSVG---GGGDVDPREFKQNRPTGLMIAQPPAMFTVPPGLSPATLLDSPSFFGLF
BRWRKY3 AMASP----AAAVVAGAH-QTPVSSVG---GGDSLLDPRFKQNRPTGLMITQPPGMFTVPPGLSPATLLDSPSFFGLF
GHWRKY3 AMASP-----GAKLPYNPMDDSFMEVG---FENGGEKNSGFKQNRPLNLGVGNP-WFTVPPGLSPSGLLNSPGLFCLS
OSWRKY3 EASVP-----PPPASAAVSSRSDGTGQMAAGVTLACAAPPPLRAPRASDGGRRRGVV
TAWRKY3 -----
ASWRKY3 GRADE-----QVAIQEAAAAGLRGMEHLILQLSRTGTGTGTSES-----SLA
ZMWRKY3 SQQRD-----PALLKSVASETAFAKAKFRKVAALLGSGVGHARGFRSRRVRPLGLV
AAWRKY3 -----
VPWRKY3 -----
BOWRKY3 -----
HVWRKY3 -----

      170     180     190     200     210     220     230     240
.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|.....|
NBWRKY3 -----
NTWRKY3 FQIEEVDQADSGDRKSKDSTSELKKKKDKQGK-----DRR
SMWRKY3 ---DVVVATAVEVKSPEDYSSGCKSS-----DRR
CMWRKY  HETHTFDEISPSVEVSDPEESNSPHNSHKNVFK-----KRK
GMWRKY3 SPVQMVSSASAPVDVLDLDEINHKGNT-----A
MuWRKY3 SPVQMVNSGVNARVEGDLDELNPRSN-----T
NAWRKY3 -----
ATWRKY3 SPLQGTFGMTHQQALAQVTAQAVQGNN-VHMQQSQSQSEYPSSTQQQQQQQASLTIIPSFSSAPRSQIRASVQETSQGG
BPWRKY3 SPIQGAFGMTHQQALAQVTAQAVQNG-VQIQS---QSEYPSSTQQQET-----SSEPMSQLPA-----LAQ
BRWRKY3 SPIQGSFGMTHQQALAQVTAQAVQNS-IQMOS-----ESSTQQQTL-----LTEVPSLPAP-----AQ
GHWRKY3 P--QSEFGISHQQALAQVTAQALVQSHVHAQPEYQTLAAGSLEPSIP-----PSSGNPEETSQQLMLSSDPQSSA
OSWRKY3 KGGAGTDTCRSPQRLNVRPRERERVACVRARAKN-----HEHGQ
TAWRKY3 -----
ASWRKY3 GASEPAAQGGQQQQQVDCREITDMTVS-----KFK
ZMWRKY3 GHKSPVGGGNNPVEMLPSSAAVTSPS-----PST
AAWRKY3 -----
VPWRKY3 -----
BOWRKY3 -----
HVWRKY3 -----

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Supplementary Figure 6: Image showing the flow of events in generation of transgenic plants, analysis and advancement to next generation.