

Supplementary Figures

Molecular cloning of the tomato *Hairless* gene implicates actin dynamics in trichome-mediated defense and mechanical properties of stem tissue

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AtSRA1      GLLDIVLVSPVDTKRFMQTAPWLGLIPGAEGQIVNAQD-GESPLVNLLKSATSASVSSPG
SlSRA1      GLLDIVL-REVDTRQFMQTAPWLGLIPGADGQILHSQEGGDSMPVTLFKSATATMSNP
*****      ***_*****:***::*: *:*:*.*:*:*:*:*:*:*:*:*:*
AtSRA1      CLNPAAFYMSKQAEAADLLYKANMNGGSVLEYTLAFTSASLDKYCSKWSAPPKTGFVDI
SlSRA1      CTNPTSFHTISRQAEAADLLYKANINTGSVLEYALAFSAALDKYCSKWSAAPPKTGFIDI
* **::*:*:*.******:* *****:*****:*****.******:*
AtSRA1      TTSKDFYRIYGGLQIGYLEEITAPQSAQHEVLGDSIAWGGCTIIYLLGQQLHFELDFDSY
SlSRA1      TTSKDFYRIFSGLQIEYLEESIQLQSNQYEMLGDSVAWGGCTIIYLLGQQLHFELDFDSH
*****:.*** ** ** * *:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*:*
AtSRA1      QVLNVSEVETVSASHTHRNPQIHQGWEGGLEGMKKARRLNNHVFSMLKARCPLDKTACA
SlSRA1      QVLNVAEVESVAISPTQKNPNFLQIEGLEAMKKARRLNNHVFSMLKARCPLDKQACA
*****:***:*:* * *:*.***::* * *****.****** **
AtSRA1      IKQSGAPLPRVRFENTVSAFETLPQKGTVG
SlSRA1      IKQSGAPLHRIKFENTVSAFETLPQKGA--
***** *:*.******:

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Supplementary Fig. S1. Amino acid sequence comparison of Arabidopsis and tomato SRA1. Shown is a sequence alignment of Arabidopsis (*AtSRA1*) and tomato (*SlSRA1*) SRA1 proteins, which share 81% amino acid sequence identity.

(A) WT DNA

GTTGAACCTAGAATCTGTGTGCTTTGATATCTTTGTGAAAATATCAGAGCATACAACCTCTAAGCCTAAGAGGATTGATATAATAGCCAAGGCTCTT
TATAAACCCCTATGGAAGTTCTACACAACCTCATATGAAACCCTATATAACTCAACAGTTCAGGACCTTAGCTGTTATCTGGATATATTTTAA
GCAATCACTATAGGAAGTTGGTAAACCTAGCACATGAGATTAAGCAGAATCAAAAATCTTTGGAAAGATATCATGTGTTTGTAAAGGGCTAC
AGTTATGCTCCTGAAAGCTGTTTTATGTAAAGATCTATAAAACAACAATGACAACAATGCTTTAATCCTGAACTAATAGTGGCCCTGGGCTTCTG
CTCTTCAATGTAAGAGGTGGCCAGCCATTTGTCAAGGCCAGGAATCCGGTGGACATCTCAGCGGAGGGATCTAGGCATATGAATCTTTTATG
TGTTCCACTCTATTTGCCGATTTCATCCAATGCTTAATAATGTGTCTTTAAGATAAAATGGGGGGTTTCTAACTTGGTACTTCTTTAGACC
TCACATATGTAATCTGTAAACCAACTAAAAAGACTACCAACAAGTACCAGATCTTAGTCCCGGCTAATTCATATTTGCTTACTTCGACAAC
ATGGACATTTACATCCTCTCAGTCTTACTCTCGGTTTGATAAGTAGAATTATCATATATTTGACATCCAACATTACTTTCTATCTTCAGAGT
ATTGAAGCTTTGCTAGAAGCTATGAAGAAAGCAAGGAGGCTAAATAATCATGTGTTTCAATGTTAAAAGCACGCTGTCCATTGGAAGATAAAC
AGGGCTTGTGCCATCAAAACAAGCGGTGCACCTTTGCATCGGATAAAAATTTGAGAACTACTGTGTCCGCTTTTGAACCGTTGCCACAGAAAGGTGC
CTGAGCCCTGCTTCCATTTTCATGTCAGAAGTTGTCATGTACGAACCTTCTTATCATGTATGTAATATATGTTTATCGATGACTCGTTGCTC
TGAGATTGAAGATGATGCTACCTGTTTCAAGTATAGATATAGAGATTGTAAGATGAAGTAAAACAAGTTCATTGGAATAGATGTTGAGGC
AGCAGAAATAGAATGAACATCTAATGGAGAGGTAATAGAGTACCCATAGATTTTTTCATGAAAAGTATCTTTGAGTACATGTCAGTCTTTTCTT
TTCTTTTCTATCAGATAAAACCTAATCATTAGGGTAAAACAGCTTTTGTGATTGACAAATCTAACTGGCTAAAAGCTGTAGTGTACTAAC
ACAATAGCTTTTATCCATGATTGAAGGAACATTTTTTCAACTGTTTTCGACTCACTTTTGGTTCGACTCACTTTTGGTTCGAACTTTGTCAC
GAACTACAACCTATACCCTACCTGCGTCTCATTTTATATATAACATTTCCGATCTCAAAAAGTCGAACAAGTTTAAATTTTTTCATGGATTGTAT
AGCATTTTTAAATATTAATATTTGTGATTTCATGTTCTCGCTGTTTTTCAAAAGAAATGAAGTGGTTGACTTGGCACGGAGTGAAAGAGTATAA
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TAGTGAGGAAATTCACCTAAATAATTTTTCAACCTGATTTAACTTAATTAGCAGCCAAAAAAGAGTATCTGTCTCCCTAGTGATATACA
TACATACAAACATATAAACTAATTAATAGATCCACCAAGCTTCTGTATACCAATTTCAATAACATTTCACTTAAATAATTTGTGTA
AGAGTAGCCTAATGATCAACTGTGACATTAATGTTTTTTTTTAAATAAAGAGTACAATAAAATGTGAGACACATTAATGTTGTTTGTTCAG
AAAGTTATTACATTTACCTAACCTTTATATTTGGCCCTTTTTTTTCTCTATAATAAAATGAATACATCTACACCCTCAAAAGAAATTTAATA
CAAAATAATATCCAGCTACAACCTTAAATTTGTTTGTGATCATTTACAACCTTTTTTTTTTCAAAATTTGGCAATTTCACTTTTAAAGGAAATTTGATT
TCTACACTTTGTAAGTTAGGTTTGAATGTCCTAATGTATTGAACCTATTTTAAACACTCAAGATTAATCCTATAATCCTTCTTTATGAACCTTT
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CGTAGAATGACGTAAAGAAATAAATGTAGGGTATGTAATAAGTTGAAATGAACACTAGTTAAAATTTGAAGATTTGAGCTAAATGAATAGCTC
TGAAGATAGACTGAAATAAAGTCAGCTGAGTAGTATGAAATATGATTTTTCAATTTAAAGGTTGGGAAATATT

(B) *hl* DNA

GTTGAACCTAGAATCTGTGTGCTTTGATATCTTTGTGAAAATATCAGAGCATACAACCTCTAAGCCTAAGAGGATTGATATAATAGCCAAGGCTCTT
TATAAACCCCTATGGAAGTTCTACACAACCTCATATGAAACCCTATATAACTCAACAGTTCAGGACCTTAGCTGTTATCTGGATATATTTTAA
GCAATCACTATAGGAAGTTGGTAAACCTAGCACATGAGATTAAGCAGAATCAAAAATCTTTGGAAAGATATCATGTGTTTGTAAAGGGCTAC
AGTTATGCTCCTGAAAGCTGTTTTATGTAAAGATCTATAAAACAACAATGACAACAATGCTTTAATCCTGAACTAATAGTGGCCCTGGGCTTCTG
CTCTTCAATGTAAGAGGTGGCCAGCCATTTGTCAAGGCCAGGAATCCGGTGGACATCTCAGCGGAGGGATCTAGGCATATGAATCTTTTATG
TGTTCCACTCTATTTGCCGATTTCATCCAATGCTTAATAATGTGTCTTTAAGATAAAATGGGGGGTTTCTAACTTGGTACTTCTTTAGACC
TCACATATGTAATCTGTAAACCAACTAAAAAGACTACCAACAAGTACCAGATCTTAGTCCCGGCTAATTCATATTTGCTTACTTCGACAAC
ATGGACATTTACATCCTCTCAGTCTTACTCTCGGTTTGATAAGTAGAATTATCATATATTTGACATCCAACATTACTTTCTATCTTCAGAGT
ATTGAAGCTTTGCTAGAAGCTATGAAGAAAGCAAGGAGGCTAAATAATCATGTGTTTCAATGTTAAAAGCACGCTGTCCATTGGAAGATAAAC
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AATTTACTAATACTCAAGATAAATTTAGAGCCCTTCAAAGTAAAGGAGGTCTCATCATATTTGGTTAAACATGATCCAAATGATGTGTATGTCGTC
CATCTGAAATATCCGAGTCTACATTTATAAAGATGAAGCGTAGAATGACGTAAGAAATAAATTTAGGGTATGTAATAAGTTGAAATGAAACA
CTAGTTAAAATTTGAAGATTTCTGAGCTAAATGAATAGCTCTGAAGATAGACTGAAATAAAGTCAGCTGAGTAGTATGAAATATGATTTTCAATTT
AAAGGTTGGGAAATATT

Supplementary Fig. S2. Genomic sequence of the affected region in WT and *hl* plants.

(A) Sequence of WT *SR1* genomic DNA. The red highlighted sequence denotes the last exon of the gene. Sequences that are present or absent (3187 bp) in *hl* are indicated by the black and gray letters, respectively. Sequences that are present but rearranged in *hl* are underlined in red (56 bp), dark blue (66 bp), and green (46 bp). (B) Sequence of *SR1* genomic DNA in the *hl* mutant. WT sequences that are retained in *hl* are underlined in red (56 bp), dark blue (66 bp), and green (46 bp), and correspond to the underlined sequences in panel A. The orientation of sequences underlined in green is reversed in WT. In addition, two nucleotides (highlighted with red) appear to be inserted in *hl*.

WT MAVP IEEA IAAALSTFSLEDDQPEVQGPFWVSAEGGATISPIEYSDVAAYRSLSEDTKA
h1 MAVP IEEA IAAALSTFSLEDDQPEVQGPFWVSAEGGATISPIEYSDVAAYRSLSEDTKA

WT INQLNTLIQEGKEMGSVLYTYRSCVKALPQLPDSMKQSQADLYLETYQVLDLEMSRLREI
h1 INQLNTLIQEGKEMGSVLYTYRSCVKALPQLPDSMKQSQADLYLETYQVLDLEMSRLREI

WT QRWQASAASKLAADMQRFSRPERRINGPTVTHLWSMLKLLDVLIQLDHLKNAKASIPNDF
h1 QRWQASAASKLAADMQRFSRPERRINGPTVTHLWSMLKLLDVLIQLDHLKNAKASIPNDF

WT SWYKRTFTQVSVQWQDTSMDREELDDLQIFLSTRWAILLNLHVEMFRVNNVEDILQVLIV
h1 SWYKRTFTQVSVQWQDTSMDREELDDLQIFLSTRWAILLNLHVEMFRVNNVEDILQVLIV

WT FIVESLELNFALLFPERHTLLRVLPLVLAASSEKDESESLYKRVKINRLMNIKNDPVV
h1 FIVESLELNFALLFPERHTLLRVLPLVLAASSEKDESESLYKRVKINRLMNIKNDPVV

WT PAFPDHLSPAAILKELSTYFPKFSQTRLLTLPAPHELPLREAQDYQRQYLIVNHIGAI
h1 PAFPDHLSPAAILKELSTYFPKFSQTRLLTLPAPHELPLREAQDYQRQYLIVNHIGAI

WT RAEHDDFTVRFASAMSQVLVLLKSIDGVDVEWVKEVKGNTYDMVVEGFQLLSRWTARVWEQ
h1 RAEHDDFTVRFASAMSQVLVLLKSIDGVDVEWVKEVKGNTYDMVVEGFQLLSRWTARVWEQ

WT CAWKFSRPCKDPVPMESHDMPASFSDEYKVVRYNYNAEERKALVELVSYIKSIGSMQKV
h1 CAWKFSRPCKDPVPMESHDMPASFSDEYKVVRYNYNAEERKALVELVSYIKSIGSMQKV

WT DTSVTDALWETIHAEVQDFVQNTLATMLRRTTFRKKKDLSRILSDMRTLSADWMANASKPE
h1 DTSVTDALWETIHAEVQDFVQNTLATMLRRTTFRKKKDLSRILSDMRTLSADWMANASKPE

WT TEMQSYPHSGEESRGTLYFPRPVAPTSAQVHCLQFLIYEVVSGGNMRKPGGIFGNSGSEI
h1 TEMQSYPHSGEESRGTLYFPRPVAPTSAQVHCLQFLIYEVVSGGNMRKPGGIFGNSGSEI

WT PINDLKQLETFFYKLGFFLHVLDYATLGLTLDLGLFWREFYLESSRVIQFPIECSLPW
h1 PINDLKQLETFFYKLGFFLHVLDYATLGLTLDLGLFWREFYLESSRVIQFPIECSLPW

WT MLVDHVIESPIIGLLESALMSFDIYNDAAQQALVILKQRFYDEIEAEVDNCFDIFVLKL
h1 MLVDHVIESPIIGLLESALMSFDIYNDAAQQALVILKQRFYDEIEAEVDNCFDIFVLKL

WT CETIFTYYKSWAASELLDPSFLFAIDIGEKFVQPMRFVALLKTTRVKLLGRTINLRSLI
h1 CETIFTYYKSWAASELLDPSFLFAIDIGEKFVQPMRFVALLKTTRVKLLGRTINLRSLI

WT ADRMNMFRDNLEFLFDRFESQDLCAIVELEMLLDILQLTHELLSKDLTIDSFNLMLNEM
h1 ADRMNMFRDNLEFLFDRFESQDLCAIVELEMLLDILQLTHELLSKDLTIDSFNLMLNEM

WT QENVSLVSYSSRLASQIWTEMQNDFLNFILCNTTQRVRSARVPPVPVQKPSVPYAKPN
h1 QENVSLVSYSSRLASQIWTEMQNDFLNFILCNTTQRVRSARVPPVPVQKPSVPYAKPN

WT FYCGTPDLNSAYQS FARLYCGFFGVP HMFSLVKLLGSRSLPWLIRALLDNISNKITTVEP
h1 FYCGTPDLNSAYQS FARLYCGFFGVP HMFSLVKLLGSRSLPWLIRALLDNISNKITTVEP

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WT      MITGLQEALPKSIGLLPFDGGISGCMRLAKEHLSCWHSKSELKAEVLCGIKEIGSILYWM
hl      MITGLQEALPKSIGLLPFDGGISGCMRLAKEHLSCWHSKSELKAEVLCGIKEIGSILYWM
*****

WT      GLLDIVLREVDTRQFMQTAPWLGLIPGADGQILHSQEGGDSPMVTLFKSATTATMSNPNC
hl      GLLDIVLREVDTRQFMQTAPWLGLIPGADGQILHSQEGGDSPMVTLFKSATTATMSNPNC
*****

WT      TNPTSFHTISRQAEAADLKYKANINTGSVLEYALAFSAALDKYCSKWSAAPKTGFIDIT
hl      TNPTSFHTISRQAEAADLKYKANINTGSVLEYALAFSAALDKYCSKWSAAPKTGFIDIT
*****

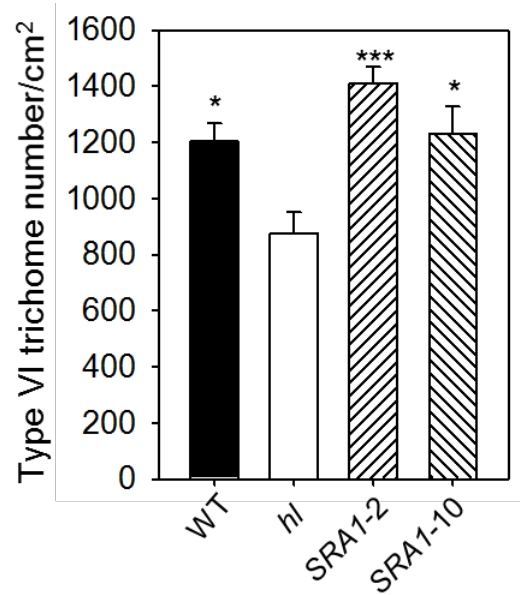
WT      TSKDFYRIFSGLQIEYLEESIQLQSNQTYEMLGDSVAWGGCTIIYLLGQQLHFELDFDSHQ
hl      TSKDFYRIFSGLQIEYLEESIQLQSNQTYEMLGDSVAWGGCTIIYLLGQQLHFELDFDSHQ
*****

WT      VLNVAEVESVAISPTQKNPNFLQIEGLEAMKKARLNNHVFMSLKARCPLEDKQACAI
hl      VLNVAEVESVAISPTQKNPNFLQV-----
*****

WT      KQSGAPLHRIKFENTVSAFETLPQKGA
hl      -----

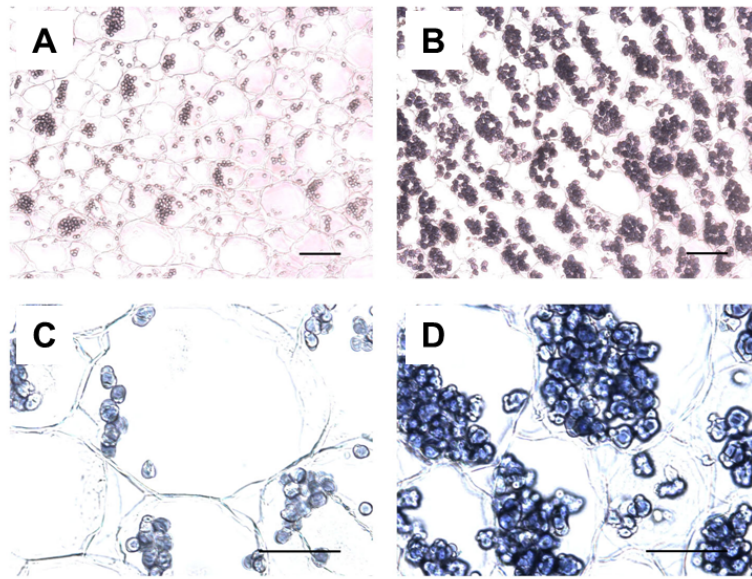
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Supplementary Fig. S3. Comparison of the predicted amino acid sequence of SRA1 in WT and *hl* plants. The *hl* mutant form of SRA1 is predicted to lack 63 amino acids at the C-terminus of the protein.



Supplementary Fig. S4. Density of type VI trichomes on leaves from WT, *hl*, and *SRA1*-complemented transgenic lines.

Light microscopy was used to determine the density of type VI trichomes on leaves of 4-week-old WT, *hl*, and complemented transgenic lines (*SRA1-2* and *SRA1-10*). Each data point represents the mean \pm SE of five independent plants per line. Asterisks represent significant differences between *hl* and other genotypes (unpaired *t* test: * $P < 0.05$; *** < 0.001).



Supplementary Fig. S5. Iodine staining of pith cells from WT and *hl* stems.

WT (A) and *hl* (B) pith cells at low magnification (scale bar: 100 μm). WT (C) and *hl* (D) pith cells at high magnification (scale bar: 50 μm). Iodine-stained granules show characteristic purple-black color.