Table 1 Suppl. Primers used for *Dv-6-SFT* cloning, expression vector construction, and transgene characterization analysis.

Name	Sequence (5' to 3')
GSP1-1	ACAAGCCTTTCCGCTGTCAC
GSP1-2	CGTGATGTCATCGTGGTCCT
GSP1-3	CTCATTGAAAAGGCCTCACC
GSP2-1	GTCAGCCCGCTTGGAGTCAA
GSP2-2	ACCCCAGTCGTATCTCAGCC
GSP2-3	GTAGTCGTGCCGTTCGTCGT
GSP3-1	AGCACCGTCATAGAGCCCGA
GSP3-2	CACTCCATGCCGTCATCCCA
GSP3-3	CATCAGACCGTTGGGATCGC
GSP4-1	AAGCGGGTGATTGGGAGCAC
GSP4-2	ACTCCATCGTGCAGGGCTTC
GSP4-3	GACCACGATGACATCACGGG
Dv-6-SFT-F	TCACAATCTACCAAACTCTCTTA
Dv-6-SFT-R	CACTCTCCCAAACAACAATA
Rp6-SFT-F	TGACGGTGCTACCCAATG
Rp6-SFT-R	AGTACACCGCCGTCTGCTC
Actin-F	TGGCATCATACCTTTTACAA
Actin-R	TCCGGGCATCTGAACCTCT

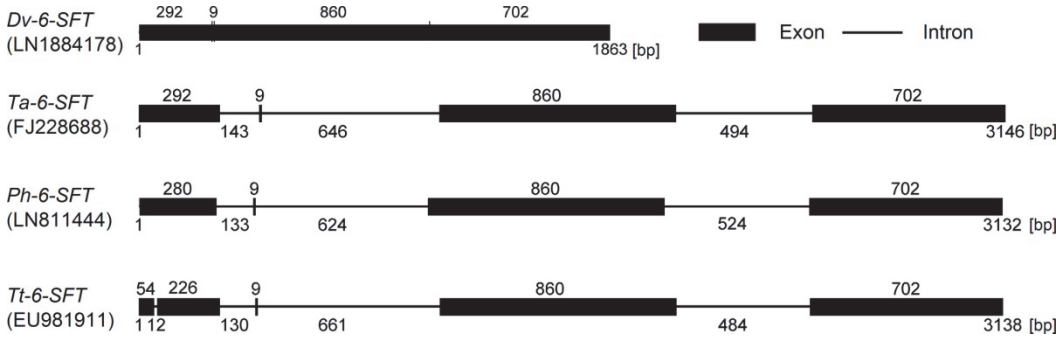
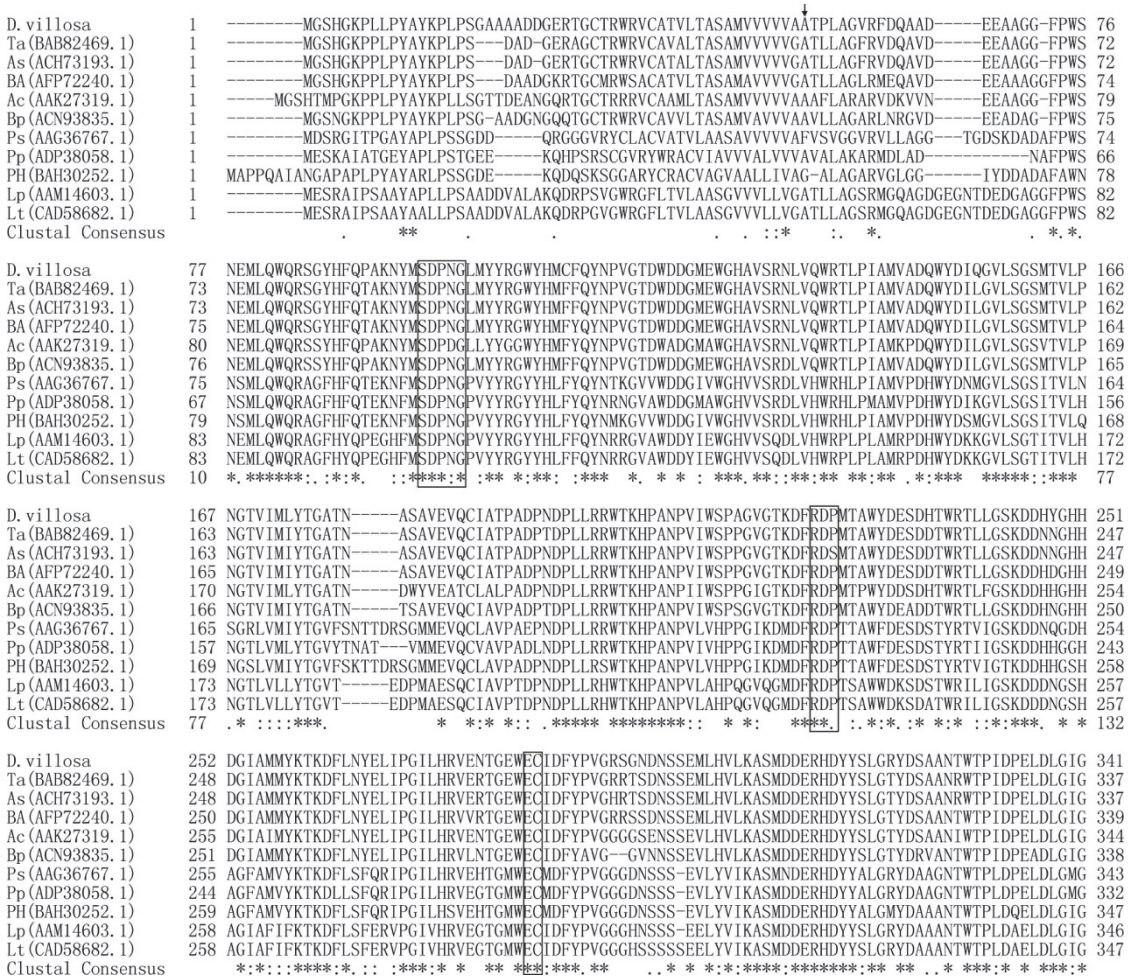


Fig. 1 Suppl. Schematic alignment of *6-SFT* genes from different organisms. *Dasypyrum villosum* (*Dv*), *Triticum aestivum* (*Ta*), *Psathyrostachys huashanica* (*Ph*), and *Triticum turgidum subsp.* (*Tt*).


D.villosa 1 --------MGSHGKPLLPYAYKPLPSGAAAADDGERTGCTRWRVCATVLTASAMVVVVVAATPLAGVRFDQAAD-----EEAAGG-FPWS 76
Ta(BAB82469.1) 1 --------MGSHGKPPLPYAYKPLPS---DAD-GERAGCTRWRVCAVALTASAMVVVVVGATLLAGFRVDQAVD-----EEAAGG-FPWS 72
As(ACH73193.1) 1 --------MGSHGKPPLPYAYKPLPS---DAD-GERTGCTRWRVCATALTASAMVVVVVGATLLAGFRVDQAVD-----EEAAGG-FPWS 72
BA(AFP72240.1) 1 --------MGSHGKPPLPYAYKPLPS---DAADGKRTGCMRWSACATVLTASAMAVVVVGATLLAGLRMEQAVD-----EEAAAGGFPWS 74
Ac(AAK27319.1) 1 -----MGSHTMPGKPPLPYAYKPLLSGTTDEANGQRTGCTRRRVCAAMLTASAMVVVVVAAAFLARARVDKVVN-----EEAAGG-FPWS 79
Bp(ACN93835.1) 1 --------MGSNGKPPLPYAYKPLPSG-AADGNGGQTGCTRWRVCAVVLTASAMVAVVVAAVLLAGARLNRGVD-----EEADAG-FPWS 75
Ps(AAG36767.1) 1 --------MDSRGITPGAYAPLPSSGDD-----QRGGGVRYCLACVATVLAASAVVVVVAFVSVGGVRVLLAGG---TGDSKDADAFPWS 74
Pp(ADP38058.1) 1 --------MESKAIATGEYAPLPSTGEE-----KQHPSRSCGVRYWRACVIAVVVALVVVAVALAKARMDLAD-----------NAFPWS 66
PH(BAH30252.1) 1 MAPPQAIANGAPAPLPYAYARLPSSGDE-----KQDQSKSGGARYCRACVAGVAALLIVAG-ALAGARVGLGG------IYDDADAFAWN 78
Lp(AAM14603.1) 1 --------MESRAIPSAAYAPLLPSAADDVALAKQDRPSVGWRGFLTVLAASGVVVLLVGATLLAGSRMGQAGDGEGNTDEDGAGGFPWS 82
Lt(CAD58682.1) 1 --------MESRAIPSAAYAALLPSAADDVALAKQDRPGVGWRGFLTVLAASGVVVLLVGATLLAGSRMGQAGDGEGNTDEDGAGGFPWS 82
Clustal Consensus . ** . . . . . ::* :. *. . *.*.
D.villosa 77 NEMLQWQRSGYHFQPAKNYMSDPNGLMYYRGWYHMCFQYNPVGTDWDDGMEWGHAVSRNLVQWRTLPIAMVADQWYDIQGVLSGSMTVLP 166
Ta(BAB82469.1) 73 NEMLQWQRSGYHFQTAKNYMSDPNGLMYYRGWYHMFFQYNPVGTDWDDGMEWGHAVSRNLVQWRTLPIAMVADQWYDILGVLSGSMTVLP 162
As(ACH73193.1) 73 NEMLQWQRSGYHFQTAKNYMSDPNGLMYYRGWYHMFFQYNPVGTDWDDGMEWGHAVSRNLVQWRTLPIAMVADQWYDILGVLSGSMTVLP 162
BA(AFP72240.1) 75 NEMLQWQRSGYHFQTAKNYMSDPNGLMYYRGWYHMFYQYNPVGTDWDDGMEWGHAVSRNLVQWRTLPIAMVADQWYDILGVLSGSMTVLP 164
Ac(AAK27319.1) 80 NEMLQWQRSSYHFQPAKNYMSDPDGLLYYGGWYHMFYQYNPVGTDWADGMAWGHAVSRNLVQWRTLPIAMKPDQWYDILGVLSGSVTVLP 169
Bp(ACN93835.1) 76 NEMLQWQRSSYHFQPAKNYMSDPNGLMYYRGWYHMFFQYNPVGTDWDDGMEWGHAVSRDLVQWRTLPIAMVADQWYDILGVLSGSMTVLP 165
Ps(AAG36767.1) 75 NSMLQWQRAGFHFQTEKNFMSDPNGPVYYRGYYHLFYQYNTKGVVWDDGIVWGHVVSRDLVHWRHLPIAMVPDHWYDNMGVLSGSITVLN 164
Pp(ADP38058.1) 67 NSMLQWQRAGFHFQTEKNFMSDPNGPVYYRGYYHLFYQYNRNGVAWDDGMAWGHVVSRDLVHWRHLPMAMVPDHWYDIKGVLSGSITVLH 156
PH(BAH30252.1) 79 NSMLQWQRAGFHFQTEKNFMSDPNGPVYYRGYYHLFYQYNMKGVVWDDGIVWGHVVSRDLVHWRHLPIAMVPDHWYDSMGVLSGSITVLQ 168
Lp(AAM14603.1) 83 NEMLQWQRAGFHYQPEGHFMSDPNGPVYYRGYYHLFFQYNRRGVAWDDYIEWGHVVSQDLVHWRPLPLAMRPDHWYDKKGVLSGTITVLH 172
Lt(CAD58682.1) 83 NEMLQWQRAGFHYQPEGHFMSDPNGPVYYRGYYHLFFQYNRRGVAWDDYIEWGHVVSQDLVHWRPLPLAMRPDHWYDKKGVLSGTITVLH 172
Clustal Consensus 10 *.******:.:*:*. ::****:* :** *:**: :*** *. * * : ***.**::**:** **:** .*:*** *****::*** 77
D.villosa 167 NGTVIMLYTGATN-----ASAVEVQCIATPADPNDPLLRRWTKHPANPVIWSPAGVGTKDFRDPMTAWYDESDHTWRTLLGSKDDHYGHH 251
Ta(BAB82469.1) 163 NGTVIMIYTGATN-----ASAVEVQCIATPADPTDPLLRRWTKHPANPVIWSPPGVGTKDFRDPMTAWYDESDDTWRTLLGSKDDNNGHH 247
As(ACH73193.1) 163 NGTVIMIYTGATN-----ASAVEVQCIATPADPNDPLLRRWTKHPANPVIWSPPGVGTKDFRDSMTAWYDESDDTWRTLLGSKDDNNGHH 247
BA(AFP72240.1) 165 NGTVIMIYTGATN-----ASAVEVQCIATPADPNDPLLRRWTKHPANPVIWSPPGVGTKDFRDPMTAWYDESDDTWRTLLGSKDDHDGHH 249
Ac(AAK27319.1) 170 NGTVIMLYTGATN-----DWYVEATCLALPADPNDPLLRRWTKHPANPIIWSPPGIGTKDFRDPMTPWYDDSDHTWRTLFGSKDDHHGHH 254
Bp(ACN93835.1) 166 NGTVIMIYTGATN-----TSAVEVQCIAVPADPTDPLLRRWTKHPANPVIWSPSGVGTKDFRDPMTAWYDEADDTWRTLLGSKDDHNGHH 250
Ps(AAG36767.1) 165 SGRLVMIYTGVFSNTTDRSGMMEVQCLAVPAEPNDPLLRRWTKHPANPVLVHPPGIKDMDFRDPTTAWFDESDSTYRTVIGSKDDNQGDH 254
Pp(ADP38058.1) 157 NGTLVMLYTGVYTNAT---VMMEVQCVAVPADLNDPLLRRWTKHPANPVIVHPPGIKDMDFRDPTTAWFDESDSTYRTIIGSKDDHHGGH 243
PH(BAH30252.1) 169 NGSLVMIYTGVFSKTTDRSGMMEVQCLAVPADPNDPLLRSWTKHPANPVLVHPPGIKDMDFRDPTTAWFDESDSTYRTVIGTKDDHHGSH 258
Lp(AAM14603.1) 173 NGTLVLLYTGVT-----EDPMAESQCIAVPTDPNDPLLRHWTKHPANPVLAHPQGVQGMDFRDPTSAWWDKSDSTWRILIGSKDDDNGSH 257
Lt(CAD58682.1) 173 NGTLVLLYTGVT-----EDPMAESQCIAVPTDPNDPLLRHWTKHPANPVLAHPQGVQGMDFRDPTSAWWDKSDATWRILIGSKDDDNGSH 257
Clustal Consensus 77 .* ::::***. * *:* *:: .***** ********:: * *: ****. :.*:*.:* *:* ::*:***. * * 132
D.villosa 252 DGIAMMYKTKDFLNYELIPGILHRVENTGEWECIDFYPVGRSGNDNSSEMLHVLKASMDDERHDYYSLGRYDSAANTWTPIDPELDLGIG 341
Ta(BAB82469.1) 248 DGIAMMYKTKDFLNYELIPGILHRVERTGEWECIDFYPVGRRTSDNSSEMLHVLKASMDDERHDYYSLGTYDSAANRWTPIDPELDLGIG 337
As(ACH73193.1) 248 DGIAMMYKTKDFLNYELIPGILHRVERTGEWECIDFYPVGHRTSDNSSEMLHVLKASMDDERHDYYSLGTYDSAANRWTPIDPELDLGIG 337
BA(AFP72240.1) 250 DGIAMMYKTKDFLNYELIPGILHRVVRTGEWECIDFYPVGRRSSDNSSEMLHVLKASMDDERHDYYSLGTYDSAANTWTPIDPELDLGIG 339
Ac(AAK27319.1) 255 DGIAIMYKTKDFLNYELIPGILHRVENTGEWECIDFYPVGGGGSENSSEVLHVLKASMDDERHDYYSLGTYDSAANIWTPIDPELDLGIG 344
Bp(ACN93835.1) 251 DGIAMMYKTKDFLNYELIPGILHRVLNTGEWECIDFYAVG--GVNNSSEVLHVLKASMDDERHDYYSLGTYDRVANTWTPIDPEADLGIG 338
Ps(AAG36767.1) 255 AGFAMVYKTKDFLSFQRIPGILHRVEHTGMWECMDFYPVGGGDNSSS-EVLYVIKASMNDERHDYYALGRYDAAGNTWTPLDPELDLGMG 343
Pp(ADP38058.1) 244 AGFAMVYKTKDLLSFQRIPGILHRVEGTGMWECMDFYPVGGGDNSSS-EVLYVIKASMDDERHDYYALGRYDAAGNTWTPLDPELDLGMG 332
PH(BAH30252.1) 259 AGFAMVYKTKDFLSFQRIPGILHSVEHTGMWECMDFYPVGGGDNSSS-EVLYVIKASMDDERHDYYALGMYDAAANTWTPLDQELDLGIG 347
Lp(AAM14603.1) 258 AGIAFIFKTKDFLSFERVPGIVHRVEGTGMWECIDFYPVGGGHNSSS-EELYVIKASMDDERHDYYSLGRYDAAANTWTPLDAELDLGIG 346
Lt(CAD58682.1) 258 AGIAFIFKTKDFLSFERVPGIVHRVEGTGMWECIDFYPVGGGHSSSSSEELYVIKASMDDERHDYYSLGRYDAAANTWTPLDAELDLGIG 347
Clustal Consensus *:*:::****:*.:: :***:* * ** ***:***.** ..* * *:*:****:*******:** ** ..* ***:* * ***:*

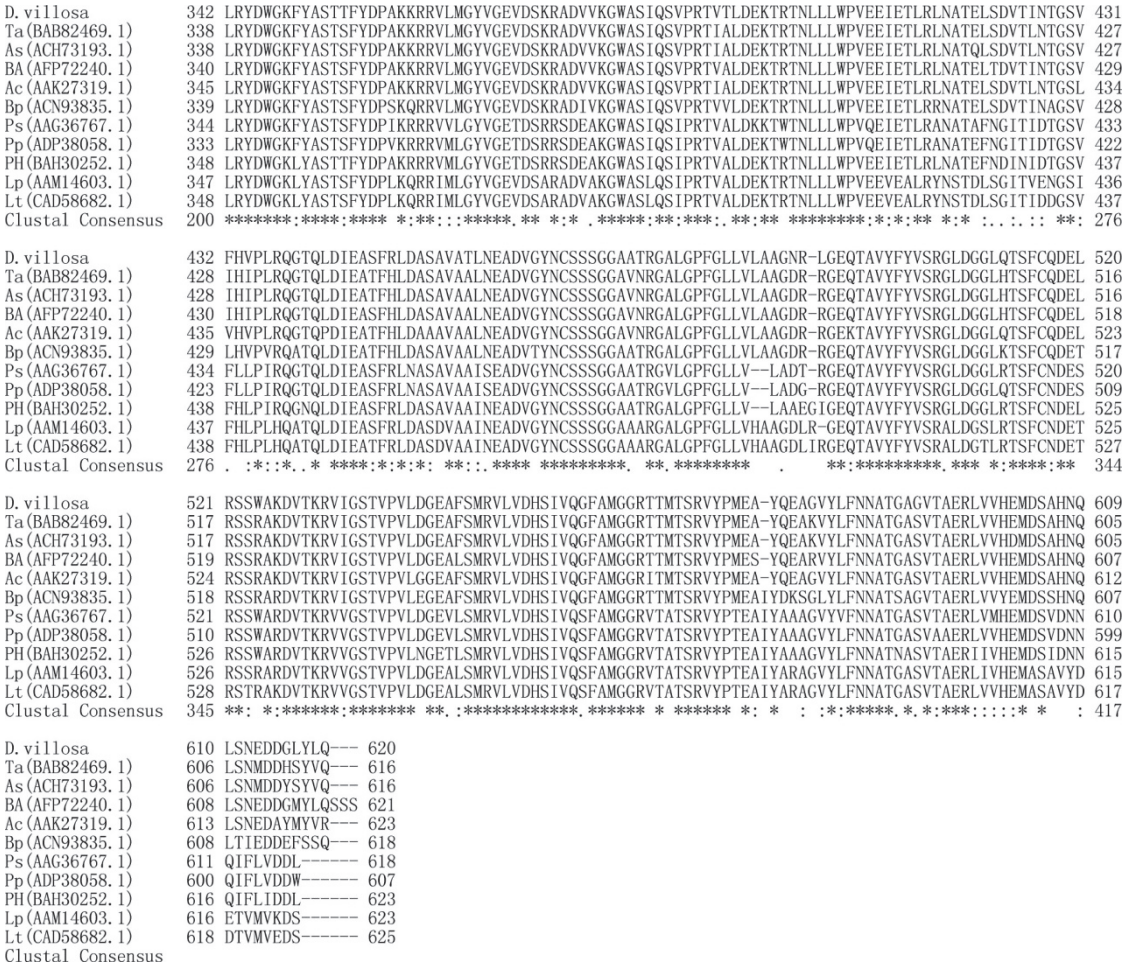


Fig. 2 Suppl. Alignment of the amino acid sequences of various *6-SFTs* and the putative *6-SFT* from *Dasypyrum villosum*. The motifs indicated are crucial for β-fructosidase catalysis. Conserved regions are *boxed*. The consensus symbols are as follows: *asterisks* - identical residues, *colons* - conserved substitutions; *periods* - semiconserved substitutions. The *arrow* indicates the putative N-terminus of the mature protein in *D. villosum.* The conserved domains among 6-SFTs are *boxed*, *i.e.*, SDPNG (sucrose-binding box), the RDP motif, and the EC domain. The other sequences were derived from *Triticum aestivum* (Ta), *Aegilops searsii* (As), *Hordeum vulgare* subsp. *vulgare* (BA), *Agropyron cristatum* (Ac), *Bromus pictus* (Bp), *Phleum pratense* (PH), *Poa secunda* (Ps), *Poa pratensis* (Pp), *Lolium temulentum* (Lt), and *Lolium perenne* (Lp).

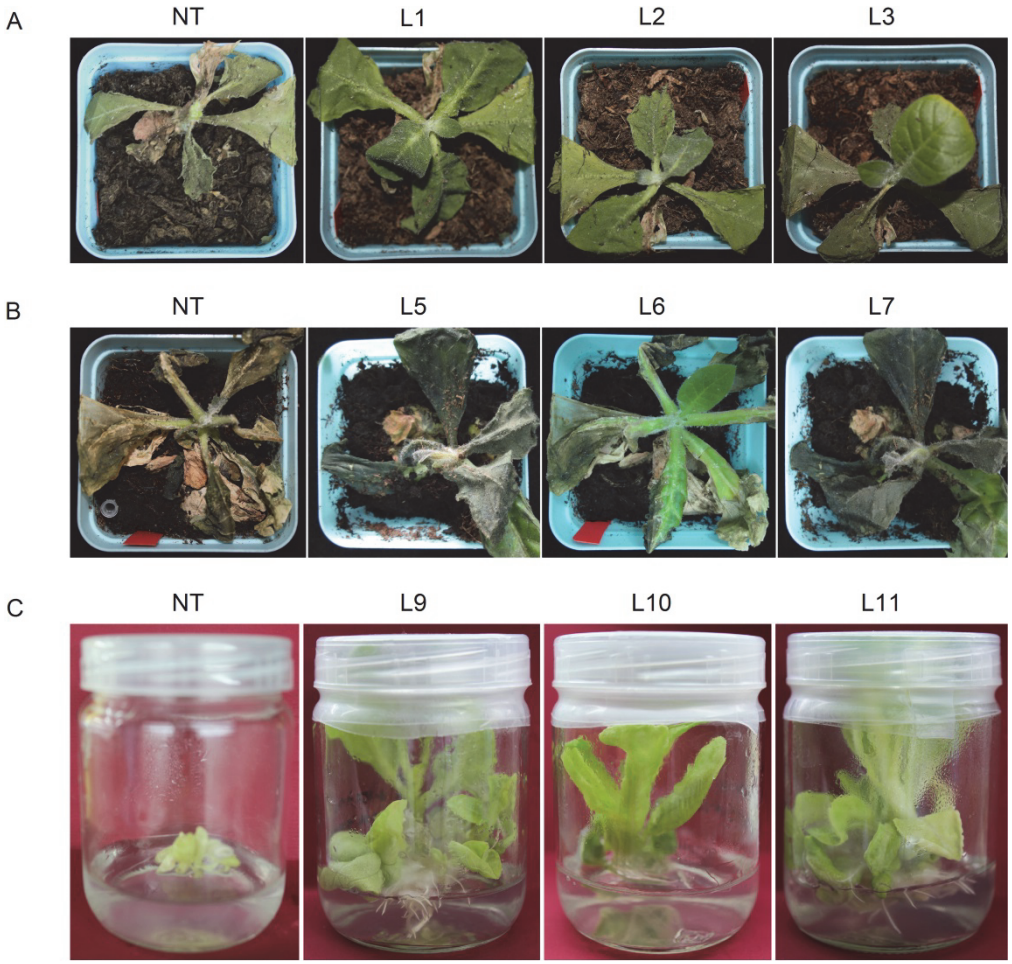


Fig. 3 Suppl. Phenotypes of tobacco plants transformed with the *Dasypyrum villosum Dv-6-SFT* gene under different stresses. *A* - Performance of *Dv-6-SFT* transgenic (L1 - L3) and non-transgenic (NT) tobacco plants at 40 d after drought stress. *B* - Transgenic (L5 - L7) and NT tobacco plants recovered under room temperature for 9 d after cold stress (10°C for 10 d and -20°C for 35 min). *C* - Growth status of transgenic (L9 - L 11) and NT tobacco plants stressed with 200 mM NaCl for 35 d.