Table 1 Suppl. Thermal cycling parameters for Tail-PCR.

Reaction	Cycle number	Thermal settings
Primary	1	94 °C 3 min
	5	94 °C 15 s, 60 - 68 °C 1 min, 72 °C 2.5 min
	1	94 °C 15 s, 25 °C 1 min, 0.2 °C s^{-1} to 72 °C, 72 °C 2.5 min
	15	94 °C 15 s, 60 - 68°C 1 min, 72 °C 2.5 min
		94 °C 15 s, 60 - 68 °C 1min, 72 °C 2.5 min
		94 °C 15 s, 44 °C 1 min, 72 °C 2.5 min
	1	72 °C 10 min
Secondary	1	94 °C 3 min
	15	94 °C 15 s, 60 - 68 °C 1 min, 72 °C 2.5 min
		94 °C 15s, 60 - 68 °C 1 min, 72 °C 2.5 min
		94 °C 15 s, 44 °C 1 min, 72 °C 2.5 min
	1	72 °C 10 min
Tertiary	1	94 °C 3 min
	20	94 °C 30 s, 44 °C 1 min, 72 °C 2.5 min
	1	72 °C 10 min

Table 2 Suppl. Primers used in cloning the *DcHsfA1d* gene.

Primer	Sequence (5'-3')	Usage
DcHsfA1dF1	GGWTTYAGRAARGTNGAYCCAGAYC	primers of core fragment homologous cloning
DcHsfA1dR1	GCYTTDGCHARRAANGACAT	
AD1	NTCGASTWTSGWGTT	arbitrary degenerate primers for tail-PCR
AD2	NGTCGASWGANAWGAA	
AD3	WGTGNAGWANCANAGA	
AD4	AGWGNAGWANCAWAGG	
AD5	NGTAWAASGTNTSCA A	
AD6	NGACGASWGANAWGAC	
AD7	GTNCGASWCANAWGTT	
AD8	NCAGCTWSCTNTSCTT	
DcHsfA1dSPF1	AGACCATCACTCGGCGAAAACCTGT	specific primers for 3' Tail-PCR
DcHsfA1dSPF2	ACTGAAAAGGGACAGGAATGTGCTC	
DcHsfA1dSPF3	GACAGCAACAGCAGACAACTGATAG	
DcHsfA1dF2	TCCAGYTTYGTBMGNCAG	primers of core fragment homologous cloning
DcHsfA1dR2	TTGGTGGTTTCAGAGATGCGCCTAT	
DcHsfA1dSPR1	TAGTCCGCAACGAAATAGCAACAGAT	specific primers for 5' Tail-PCR
DcHsfA1dSPR2	TTCAGCTACATTTAACAAGGCCACCG	
DcHsfA1dSPR3	CCAAAAACCGACAAAACTCAAATC	
DcHsfA1dF	GGCGAATTCATGGACTCTTCTACG	primers for full-length gene amplification
DcHsfA1dR	CGGCATCATTCAGCAAAACTTACAT	

Table 3 Suppl. Primers for real time qPCR analysis.

Primer	Gene ID	Sequence (5'-3')	Usage
DcGAPDH-F		CGGAAAGTTGACTGGTATGGC	primers for real time qPCR analysis of *DcHsfA1d*
DcGAPDH-R		CATCCTCGGTGTAGCCCAAAAT	
DcHsfA1d-qF		TGGATCAGCTTACAGAGCAAATG	
DcHsfA1d-qR		CTCCTTGCGACGGTGCTACT	
AtACTIN2 qF	AT3G18780	CTTGTTCCAGCCCTCGTTTGTG	primers for real time qPCR analysis of related genes in transgenic *Arabidopsis*
AtACTIN2 qR		CTTTGCTCATACGGTCAGCGATA	
AtHSP101 qF	AT1G74310	GCAGAGAGTTATGACCCGGTGTAT	
AtHSP101 qR		CCAGCGCCTGCATCTATGTAAAC	
AtHSP90 qF	AT5G52640	GGAAATTCTCGGGGACAAGGT	
AtHSP90 qR		CGCCTGTGCCTTCATAATCCT	
AtHSP70 qF	AT3G12580	CTGGCTGAGGCAGATGAGTTCG	
AtHSP70 qR		GTGTGTCGTCATCCATTCCTCC	
AtHSP18.2 qF	AT5G59720	AGAGGAGCAAGGAGAACGAAGAG	
AtHSP18.2 qR		CGGAACCACAACCGTAAGCAC	
AtHSFA2 qF	AT2G26150	GATGTGGGGAGGAAACGGAG	
AtHSFA2 qR		GCAGCGAACAACATTTCCATATC	
AtMBF1c qF	AT3G24500	ACGGTGTCGCGGTTCAAAC	
AtMBF1c qR		CCTCACCTCTGCTTTCACACG	

Table 4 Suppl. Primers for reverse transcription PCR analysis of transgenic *Arabidopsis.*

Primer	Sequence (5'-3')
DcHsfA1d RT-F	CTGGCAACTGAGACAGGAGATG
DcHsfA1d RT-R	CTCCTTGCGACGGTGCTACT
AtACTIN2 RT-F	GGTAACATTGTGCTCAGTGGTGG
AtACTIN2 RT-R	GCATCAATTCGATCACTCAGAG

Table 5 Suppl. Primers for yeast fusion expression vector construction.

Primer	Sequence (5'-3')
DcHsfA1d-ADF	CACATCGATACATGGACTCTTCTACGACC
DcHsfA1d-ADR	GACGAGCTCTTATGCTAGTTTGTCTGAAT
DcHsp70-BDF	CAGCATATGATGGCGGGTAAAGGAGAAG
DcHsp70-BDR	GACGGATCCAATTCAACAGTAAAACGGC

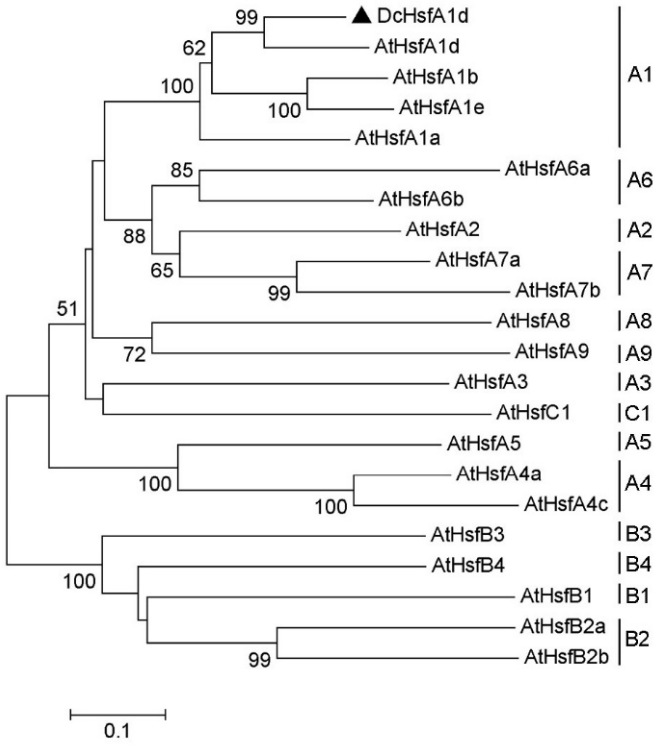

Fig. 1 Suppl. Phylogenetic analysis of DcHsfA1d and AtHsfs based on amino acid sequences. The amino acid sequences of AtHsfs for phylogenetic analysis were obtained from web page: https://www.arabidopsis.org/. The phylogenetic tree was obtained using the *MEGA 5* software. Bootstrap values > 50 were shown.

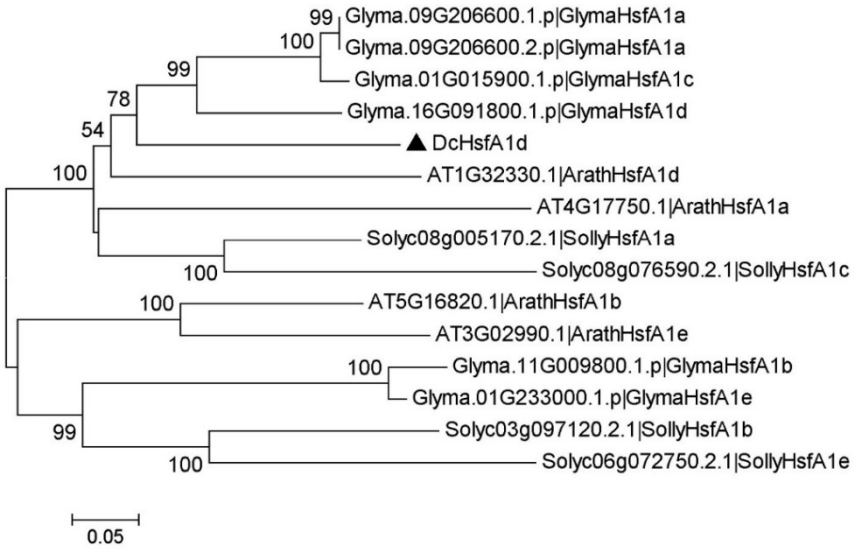

Fig. 2 Suppl. Phylogenetic analysis of DcHsfA1d and HsfA1s from other species based on amino acid sequences. The amino acid sequences of HsfA1s from other species were obtained from *HEATSTER* platform (https://applbio.biologie.uni-frankfurt.de/hsf/heatster/). The phylogenetic tree was obtained using the *MEGA 5* software. Bootstrap values > 50 were shown.

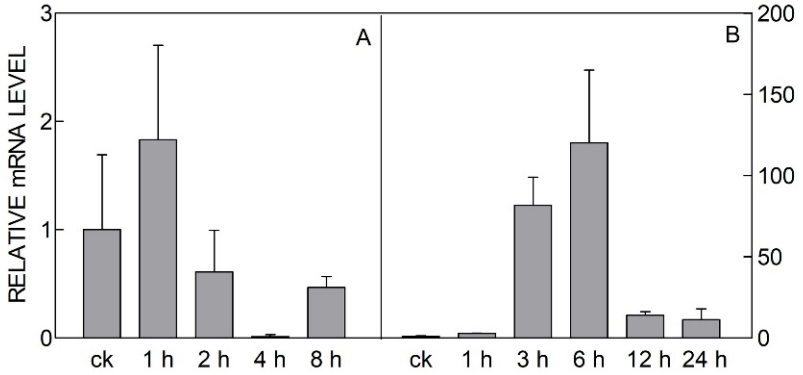

Fig. 3 Suppl. Transcript analysis of *DcHsfA1d* in carnation under heat stress or ABA treatment. *A* - Transcript analysis of *DcHsfA1d* in carnation under heat stress treatment. 40-d-old carnation seedlings were treated at 42 °C for 0, 1, 2, 4, and 8 h. *B* - Transcript analysis of *DcHsfA1d* in carnation under ABA treatment. 40-d-old carnation seedlings were sprayed with distilled water containing 100 µM ABA and leaves were collected after 0, 1, 3, 6, 12, and 24 h. The *DcGAPDH* gene was used as an internal control. Error bars represent standard deviation of three independent biological replications.

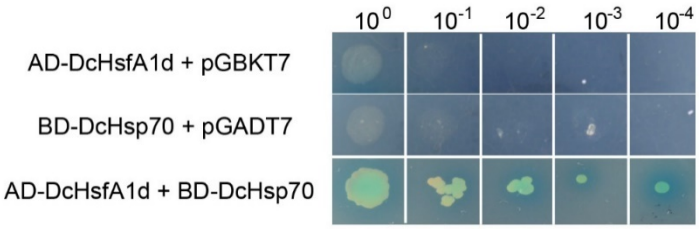

Fig. 4 Suppl. Yeast two-hybrid interaction of DcHsfA1d and DcHsp70. Yeast cultures of 10^0, 10^{-1}, 10^{-2}, 10^{-3} and 10^{-4} were plated onto a selective medium SD/-Trp/-Leu/-His/-Ade within X-α-gal. The survival and blue coloration represented interaction.

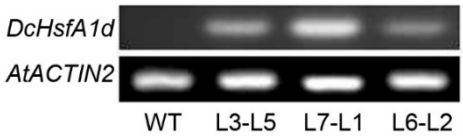

Fig. 5 Suppl. Reverse transcription PCR analysis of *DcHsfA1d* in transgenic *Arabidopsis*. The *AtACTIN2* gene is shown as an internal reference gene. WT - wild type. L3-L5, L7-L1, L6-L2, three independent T3 lines.