Supplementary

Regulation of NO-Generating System Activity in Cucumber Root Response to Cold

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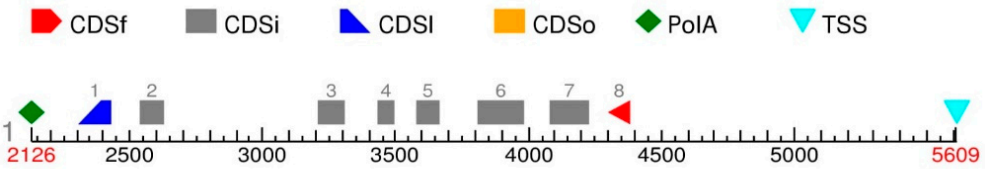
FGENESH 2.6 Prediction of potential genes in Dicot_arab genomic DNA
Seq name: ACHR02000006.1:28952665-28959378 Cucumis sativus cultivar 9930 Chr6, whole gen
Length of sequence: 6714
Number of predicted genes 1: in +chain 0, in -chain 1.
Number of predicted exons 8: in +chain 0, in -chain 8.
Positions of predicted genes and exons: Variant 1 from 1, Score:50.294348



1 -		PolA	2126		1.06			
1 -	1	CDSl	2301 -	2426	16.42	2301 -	2426	126
1 -	2	CDSi	2533 -	2625	9.76	2533 -	2625	93
1 -	3	CDSi	3203 -	3305	12.18	3203 -	3304	102
1 -	4	CDSi	3428 -	3492	-3.71	3430 -	3492	63
1 -	5	CDSi	3574 -	3662	7.91	3574 -	3660	87
1 -	6	CDSi	3804 -	3980	20.31	3805 -	3978	174
1 -	7	CDSi	4076 -	4225	4.93	4077 -	4223	147
1 -	8	CDSf	4295 -	4379	2.01	4296 -	4379	84
1 -		TSS	5609		-8.54			

Predicted protein(s):
>FGENESH:[mRNA] 1 8 exon (s) 2301 - 4379 888 bp, chain -
ATGGCGGCTGTGTCTGCAATCTTCATTTACCCAATCAAATCATGTCGCGGTATTTCAGTT
CCCCAAGCACCTCTTACCCCTACTGGATTTCGATGGGACCGTCAATGGTTGGTTGTCAAC
TCTAAAGGAAGGGCTTACACTCAGAGAGTCGAGCCTAAGCTTGCTCTCGTCCAGGTCGAC
CTCCCAAACGAAGCTTTCTTTGATGACTGGAGCCCTTCTAAATCCTCTTTTCTCGTCATT
AAAGCTCCTGGGATGGATGTCTTAAAGGTTCCCCTTACTCAACCTCCGTATAATGCTGAC
GGTGTCTCTGTCTGGGAATGGTCTGGCTCTGCACTCGATGAGGGAGATGCTCCATCAAAG
TGGTTTTCAGATTATCTTGGAAAACCCAGTCGTTTGGTTCGCTTTAATCCAGCTTCACAA
ACAAGGAAAGTAGATCCCAATTATGGTCCTGGACATCAAATCATGTTTTCGGATGAGTTC
CCCTACATGTTGATATCTCAGGGATCTTTGGATGCTTTGAATAAAGTTCTCAAAGAACCC
GTATCAATTAATCGCTTTAGACCTAACATTCTTGTTGATGGCTGCGAACCATTCTCTGAG
GATTTGTGGACTGAGATCGAAATAGACAAGTTCATATTTCAGGGTGTTAGGCTATGTGCC
CGTTGCAAGGAGACTGGAATTGCAGGACCTGAGCTGAATGAAACTCTAAAGAAAATGAGA
TCAGATACTGTCCTGCGTCCAAACCATAAACAAAAGGGAAAAATTTTCTTTGGCCAGAAT
TTGGTTTGGAAGAACATAGCAGCTGAAGGGAAGGGGAAAATCATAAAAGTGGGAGATAAA
GTCAAGGTTCTGGGGAAGGTTGCCTCTGTAGCGGAAGCAGTAGTTTGA
>FGENESH: 1 8 exon (s) 2301 - 4379 295 aa, chain -
MAAVSAIFIYPIKSCRGISVPQAPLTPTGFRWDRQWLVVNSKGRAYTQRVEPKLALVQVD
LPNEAFFDDWSPSKSSFLVIKAPGMDVLKVPLTQPPYNADGVSVWEWSGSALDEGDAPSK
WFSDYLGKPSRLVRFNPASQTRKVDPNYGPGHQIMFSDEFPYMLISQGSLDALNKVLKEP
VSINRFRPNILVDGCEPFSEDLWTEIEIDKFIFQGVRLCARCKETGIAGPELNETLKKMR
SDTVLRPNHKQKGKIFFGQNLVWKNIAAEGKGKIIKVGDKVKVLGKVASVAEAVV

Figure 1S. Identification of the *CsARC* gene using the FGENESH program.
A fragment of chomosome 6 of the *Cucumis sativus* cultivar 9930, homologous to the nucleotide sequences of *Arabidopsis AtARC1* (AT1G30910) and *AtARC2* (AT5G44720) [22] acording to BLASTn, was used for the FGENESH

analysis. The predicted *CsARC* coding sequence is located on the negative strand of DNA. It consists of 8 exons with a total length of 888 bp, and the predicted protein sequence is composed of 295 aa.

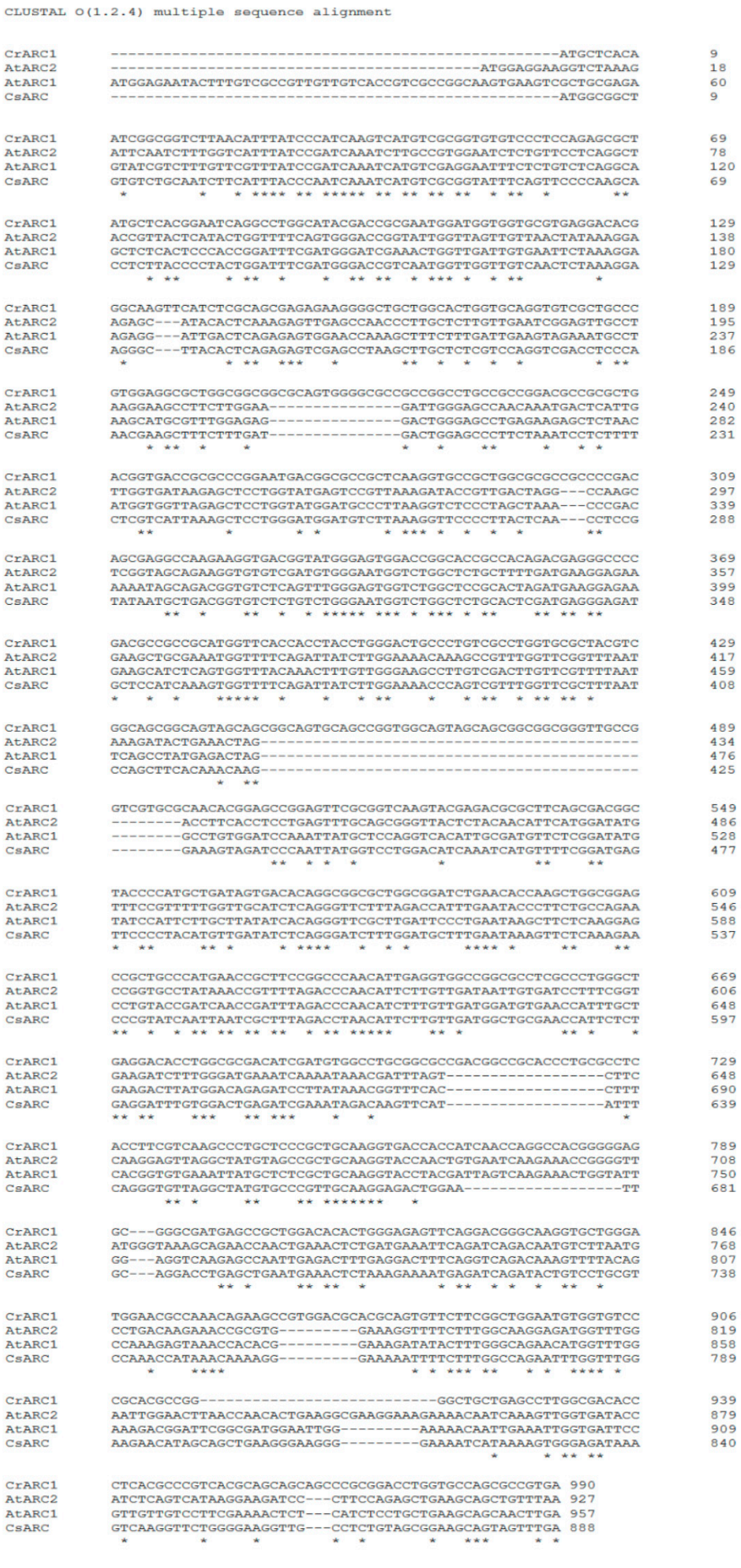


Figure 2S. Comparison of *AtARC1* (AT1G30910), *AtARC2* (AT5G44720), *CrARC1* (JF940524) from *Chlamydomonas reinhardtii*, and predicted *CsARC* CDS sequences using Clustal Omega (http://clustal.org/omega/). Asterisks indicate positions with a single, fully conserved nucleotide in all aligned sequences.

Percent Identity Matrix - created by Clustal2.1

	CrARC1	AtARC2	AtARC1	CsARC
1: CrARC1	100.00	47.30	47.41	47.24
2: AtARC2	47.30	100.00	65.68	65.20
3: AtARC1	47.41	65.68	100.00	67.45
4: CsARC	47.24	65.20	67.45	100.00

Figure 3S. Estimation of sequence identity of *AtARC1*, *AtARC2*, *CrARC1*, and *CsARC* CDS using Clustal Omega. Values presented are expressed as percentages.

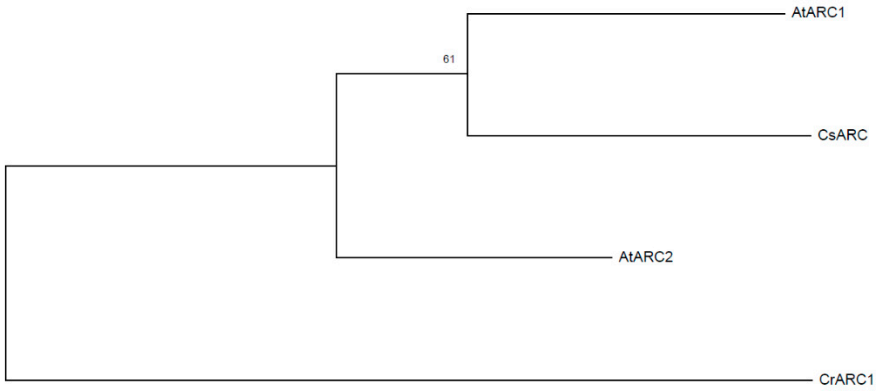


Figure 4S. Phylogenetic tree of AtARC1, AtARC2, CrARC1, and predicted CsARC aa sequences. Multiple alignments were performed using ClustalOmega. The tree was constructed using MEGAX software (https://www.megasoftware.net/) by the maximum likelihood method with 1000 bootstrap replicates.