

Genome-wide Identification, Expression Profiling and Evolutionary Analysis of Auxin Response Factor Gene Family in Potato (*Solanum tuberosum* Group Phureja)

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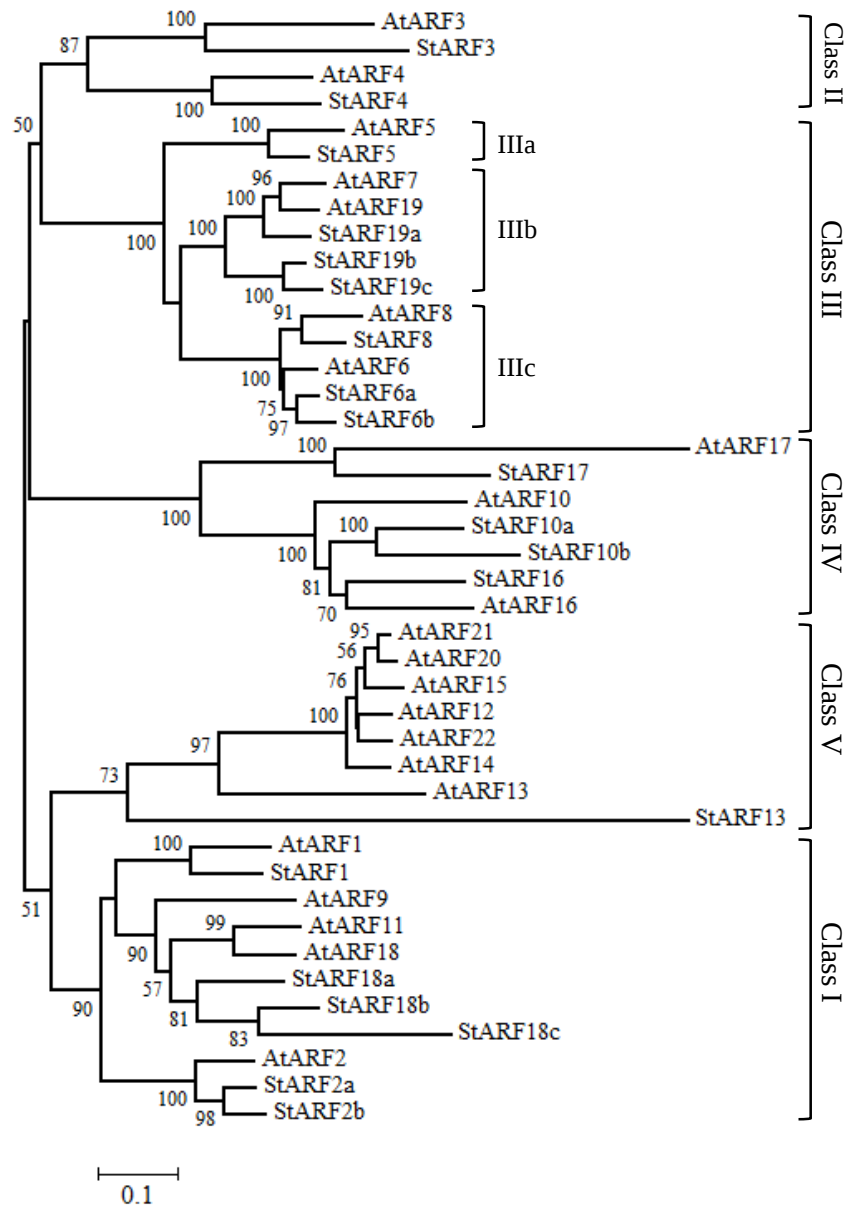
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Supplementary Figure S1. Phylogenetic analysis of ARFs from *Arabidopsis* and *potato*. With the aid of MEGA program (version 10), Amino sequences of full-length putative StARF and AtARF proteins were aligned, and neighbor-joining tree was generated with 500 bootstrap replications. Bootstrap values are shown on branches.

Supplementary Table 1. Primers used in qRT-PCR experiments

Name	Sequences (5'→3')
StARF1-F	TAAAAGGGGCTCAAGCAGGC
StARF1-R	ACTGTTCTTGCTCTTCTTCAACA
StARF2a-F	ATCCAAGTCTTTGGGCAGA
StARF2a-R	ATGGACAGGCCAATGACCAA
StARF2b-F	TTAATCTCCATCCTCCGCC
StARF2b-R	TGGGACAATAAACACATTTCACAA
StARF3-F	TGCACAAGTCTCACTAGTTCCT
StARF3-R	CGAGGGACAGAGAAACCACC
StARF4-F	TACTGGACGGCCATTTTGCT
StARF4-R	GGGCGGACTGGTTTATCACA
StARF5-F	AGCATATTGAACTTTGCCTTCC
StARF5-R	GCAGCTCTCGCAAACAGAT
StARF6a-F	CTCAGCAAGAGGAAGCAGGG
StARF6a-R	GTTGAGGCGGTAAACCAGGA
StARF6b-F	TGGGGTCAAGTCTCATTTGAA
StARF6b-R	TGAGCACAAGAGCTTGTAAGT
StARF8-F	AGGCTCAGGACACATGTGATTTA
StARF8-R	TGGTTCTGGAGAAACCTTTTCG
StARF10a-F	GTTCCCTACTGCGATGGTGCT
StARF10a-R	TGACGAACATGTCCATGTCAA
StARF10b-F	TTGCGTTAGGGCCTCTTCTG
StARF10b-R	GATGGGGTCAGCAACCTGAA
StARF13-F	ACTTCGACTCTGTTCCCTGC
StARF13-R	TGGCTATCCAACCTTTTCACCT
StARF16-F	CATAAAAAGCTCGTCGCGGG
StARF16-R	CAGGTCCACCTCCAATTCCC
StARF17-F	TGAAGGCACAAGCGGTAGAG
StARF17-R	ACTTGTCGGTCCTGAAGCAT
StARF18a-F	TGTTGACAACTTTTGGTGGGG
StARF18a-R	TCGCTCTTTTCCACTCAGCG
StARF18b-F	TCTATTCGCGCGTTAACCTGT
StARF18b-R	ACAAGTCTCACAGAAAGGGCA
StARF18c-F	ATCTCATGCTGTGACGACCC
StARF18c-R	CCAAGGCTCCCCTTGACATC
StARF19a-F	TGCTTCCAAAATTGCGACCT
StARF19a-R	CTTCATTGGTTGCGGCAGTG
StARF19b-F	TCCCGCCTCTGGATTACTCA
StARF19b-R	GAGTCACCAGCAAAGAGCCT
StARF19c-F	GCGGAATTTGCAGGTTGGTT
StARF19c-R	TCCTCTTGAACATGCCGTCC
StEF1 α -F	AGGTTCTAGTTCTCTGCCTTGTATGTC
StEF1 α -R	CGCCACCGCCTATCAAGTAC

Supplementary data. Alignment of deduced amino acid sequences of *StARF* genes.

Alignment was generated using ClustalW program. The conserved N-terminal DNA-binding domain (DBD) and C-terminal domain (CTD) is underlined in blue and red, respectively.

1. *Marchantia polymorpha* ARFs

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>StARF19b

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>StARF19c

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>StARF5

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>StarF3

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>StarF4

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>StarF13

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>StarF17

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>StarF16

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>StarF10a

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>StarF10b

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>StarF18a

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>StarF18b

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>StARF18c

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>StARF1

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>StARF2b

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>StARF2a

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6. *Arabidopsis thaliana* ARFs

>AtARF19

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>AtARF5

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>AtARF6

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>AtARF13

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>AtARF12

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>AtARF22

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>AtARF21

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>AtARF20

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>AtARF15

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>AtARF14

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>AtARF1

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>AtARF17

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>AtARF10

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>AtARF3

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>AtARF11

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>AtARF18

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>AtARF9

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>AtARF16

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>AtARF7

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>AtARF8

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>AtARF4

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>AtARF2

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7. *Chlamydomonas reinhardtii* ARF-like protein

>Cre13.g562400

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