

**The rice ERF transcription factor *OsERF922* negatively regulates  
resistance to *Magnaporthe oryzae* and salt tolerance**

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**Supplementary Material**

Supplemental Table 1. Primers used in the QRT-PCR

Primer Name	Primer Sequence (5'-3')
<i>UBQ</i> Forward:	AACCAGCTGAGGCCCAAGA
<i>UBQ</i> Reverse:	ACGATTGATTTAACCAGTCCATGA
<i>OsERF922</i> Forward:	AGGCGCTGCTCAACTTCCCG
<i>OsERF922</i> Reverse:	CACGCACTCACCGTCGCTCA
<i>Pr1a</i> Forward:	GTCTTCATCACCTGCAACTACTC
<i>Pr1a</i> Reverse:	CATGCATAAACACGTAGCATAGC
<i>rab16a</i> Forward:	CACACCACAGCAAGAGCTAAGTG
<i>rab16a</i> Reverse:	TGGTGCTCCATCCTGCTTAAG
<i>Pr1b</i> Forward:	CGATCAGCGCCCTTACTAGC
<i>Pr1b</i> Reverse:	ACACACAATCCGGCTACATAGAT
<i>Pr10</i> Forward:	GACATCGTGGATGGCTACTATGG
<i>Pr10</i> Reverse:	TCACTCACTCTAGGTGGGATATAC
<i>PAL</i> Forward:	GCGATCGGTAAGCTCATGTT
<i>PAL</i> Reverse:	CCTTGAAGCCGTAGTCCAAG
<i>OsCPS2</i> Forward:	GAATTCGCAGCAAGCACCAGC
<i>OsCPS2</i> Reverse:	GCGGCCGCCTAATTGACATCCTCGA
<i>OsCPS4</i> Forward:	GAATTCGGATGAACTAAGAGAGA
<i>OsCPS4</i> Reverse:	GCGGCCGCTTATAAGGAGTGTAG
<i>OsNCED3</i> Forward:	ACGTGATCAAGAAGCCGTACCT
<i>OsNCED3</i> Reverse:	GCTGGTCGAGCGGGATCT
<i>OsNCED4</i> Forward:	GCCGAGACACGCATTGG
<i>OsNCED4</i> Reverse:	GTGAAGGTGGCGACAGCAA

Supplemental Figure 1. *OsERF922* sequences and phylogenetic analysis

**A**

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                                     cacactgcaaaccactctctcggtctctc
1      catccatccacctctctctcgatcgtctcatgagctagcgcgccccgcggtacageccccgc
1      ATGTCTCTCTCCTTGGGGTTTAGCGCCGGCGCCGGCTCGGTGCCGATCGCCTCGCCGCC
      M S L S L G F S A G A G V G A D R L A A

61     GCGCCCGCGCTCCAGGCCGCCGGTGCTCTGCCGCCACGCGTGGACGTGTCTCTGTCTGCTG
21     A P A L Q A A G A L P P R V D V S L S L

121    GCGCGCGCGCCAACGGGCAGCCGTCGTCGTACCTCCCGCTCAACGAGAACGACTCGCTG
41     A R A A N G Q P S S Y L P L N E N D S L

181    GACATGGTCCTCTTCGACGTCCTCCGCGAGGCCCTCCGCGGTGGCGGCGCTGTCTGTCGTCG
61     D M V L F D V L R E A S A V A A L S S S

241    TCGTCGTCGTCGCCGAGCTGGGCGCGCGGACGACGGCGCCGGTGGTCGCCGCCACCCC
81     S S S S P E L G A R T T A P V V A G H P

301    GCCGGGCGCAAGGGTGGCGGGCGGAGGCCGAGGCAGGGGAGCGGCGGAGGGGCGGC
101    A G R K G G G G G G R G A A A R G G

361    GCCGCTGGCGGGCGGCACTACCGCGGTGTGAGGCGGCGCCGTGGGGGAAGTACGCCGCG
121    A A G G R H Y R G V R R R P W G K Y A A

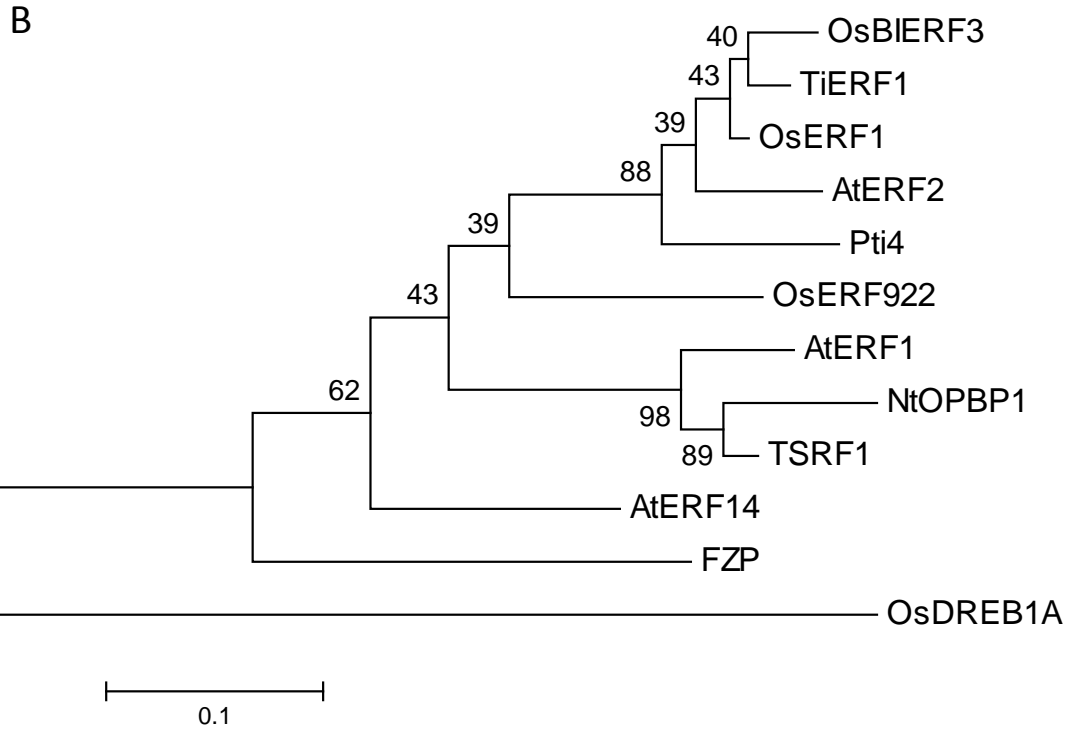
421    GAGATCCGTGACCCGACGCGGCACGGCGCGCGGCTGTGGCTCGGCACCTTCGGCACGGCC
141    E I R D P T R H G A R L W L G T F G T A

481    GAGGAGCCGCCGCGGCGTACGACCGCGCCGTTCCGCATGCGGGGCGCCAAGGCGCTG
161    E E A A A A Y D R A A F R M R G A K A L

541    CTCAACTTCCCGCCGGCTGTCTGCCGGTACGGCGCCCGTCCGCGGCGCCGCCGCGGCGCG
181    L N F P P A V A G D G A R R G A A A A A

601    AAGCAGGTCGGCATGAGCGACGGTGAGTGCGTGATATAG
201    K Q V G M S D G E C V I *

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Supplemental Figure 1. *OsERF922* sequences and phylogenetic analysis

(A) The nucleotide sequence of *OsERF922* cDNA and its deduced amino-acid sequence. The 5'-untranslated region is italicized. The residues forming the ERF domain are in bold and shaded, including the conserved amino-acid residues.

(B) The phylogenetic tree of *OsERF922* with close homologs from a BLAST search. The deduced amino-acid sequence of *OsERF922* was aligned with some of the published members of ERF using the CLUSTAL W program and the phylogenetic tree was drawn using the TREEVIEW program to produce a neighbor-joining tree of the full-length amino-acid sequences from ERF proteins. The GenBank accession numbers are listed in brackets for each of the following ERF proteins: *OsBIERF3*(AAV98702), *AtERF1*(AY086078), *AtERF2*(BAA32419), *Pti4*(T07686), *TSRF1*(AF49420), *OsERF1*(ABK34954), *OsERF922* (BAB67922), *NtOPBP1* (U81157), *TiERF1*(ABQ52686), *AtERF14*(P93822), *FZP*(BAJ09616), *OsDREB1A*(AAN02486).