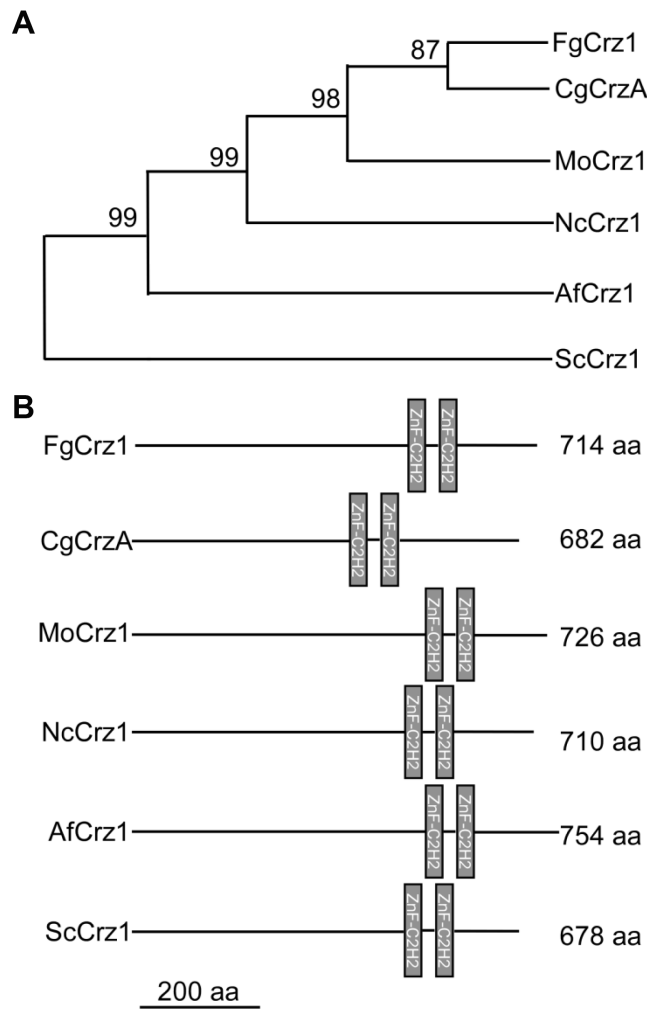


Supplementary Table 1. Primers used in this study

| Primer | Sequence (5'-3') | Application |
|---------------|--|--|
| CRZA-1F | CTAGCTGTCGCGTCCTGATC | For amplification of 5' flank region of <i>CgCRZA</i> |
| CRZA-2R | CCTCCACTAGCTCCAGCCAAGCCGTCGGTAGTCGGAAGGATG | |
| CRZA-3F | GTTGGTGTGCGATGTCAGCTCCGGAGGGTACACGGCAGGTTGCTG | For amplification of 3' flank region of <i>CgCRZA</i> |
| CRZA-4R | GGGTCTGGTAGAGACCTTG | |
| CRZA-probe-1F | GTAGCAGCAGAGGATCAGAAG | For southern blotting analysis |
| CRZA-probe-2R | GTCGGTAGTCGGAAGGATG | |
| HPH-F | GGCTTGGCTGGAGCTAGTGGAGG | For amplification of hygromycin B phosphotransferase gene cassette |
| HPH-R | CTCCGGAGCTGACATCGACACCAAC | |
| CRZA-GFP-1F | ACTCACTATAGGGCGAATTGGTACTCAAATTGGTTGATTTACG- | For <i>CgCRZA</i> -GFP fusion construct |
| CRZA-GFP-2R | GTTCTGGGCTTGCAAG CACCACCCCGGTGAACAGCTCCTCGCCCTTGCTCACCCGACCGC- CGTAGTCGC | |
| 18S-1F | GTGAGGCCCTCAAAGGTAGTGG | For qRT-PCR analysis of house-keeping gene |
| 18S-2R | GGATCCCAGTGCAGACGT | |
| CHS1-1F | CCGTAAGTGGTCTGGTCTGTTT | For qRT-PCR analysis of <i>CHS1</i> |
| CHS1-2R | GAACCACAGGAAACCGAAGA | |
| CHS2-1F | TTCCTGCAGCTCATGTTTAC | For qRT-PCR analysis of <i>CHS2</i> |
| CHS2-2R | CTGTAGGCGATCATGCTGAA | |
| CHS3-1F | GTCTTGCTGGTGCTTTCTC | For qRT-PCR analysis of <i>CHS3</i> |
| CHS3-2R | GGTGTGCGGAACATCAGTCT | |
| CHS4-1F | TCACCAGAGCCTTCCAGTCT | For qRT-PCR analysis of <i>CHS4</i> |
| CHS4-2R | CAAGACGACTGCCAGAATGA | |
| CHS5-1F | CGTCAGCATGAGTTGGATAA | For qRT-PCR analysis of <i>CHS5</i> |
| CHS5-2R | GGCTGGAGCTCATCAAAGAC | |
| CHS6-1F | TGACTCTTGCCAGAATGC | For qRT-PCR analysis of <i>CHS6</i> |
| CHS6-2R | GAAGACCTTGCCCATGTTGT | |
| CHS7-1F | GCAGAAGACTCTCCGGTCAC | For qRT-PCR analysis of <i>CHS7</i> |
| CHS7-2R | CTCTGCTGTGCCATTTTCGTA | |
| PKS-1F | ACCGCGACTTCAGCGACTG | For qRT-PCR analysis of <i>PKS</i> |
| PKS-2R | GGAGCCTTGACGGCAGCAG | |
| SCD-1F | CGACTCCTACGACTCCAAGG | For qRT-PCR analysis of <i>SCD</i> |
| SCD-2R | TGAGATTGGTCGTCGTCCTC | |
| 3HNR-1F | GTTCCAAGTACGACCGCATT | For qRT-PCR analysis of <i>3HNR</i> |
| 3HNR-2R | GGCGTAGTTGACGATGACCT | |
| 4NHR-1F | AAGACCGACATGTACGACGA | For qRT-PCR analysis of <i>4NHR</i> |
| 4NHR-2R | GGTGACCTTGATAACTTG | |

qRT-PCR, quantitative real-time PCR.



Supplementary Fig. 1. Phylogenetic tree and structural analysis of CgCrzA and its homologues. (A) Phylogenetic tree generated using Mega 5.0 program with neighbor-joining method. Bootstrap values (1,000 replications) are given at nodes. (B) Structural analysis of CgCrzA and its homologues from *Fusarium graminearum* (FgCrz1), *Magnaporthe oryzae* (MoCrz1), *Neurospora crassa* (NcCrz1), *Aspergillus fumigatus* (AfCrz1) and *Saccharomyces cerevisiae* (ScCrz1). Zinc finger domains (C₂H₂ zinc finger DNA-binding domain, IPRO007087) were indicated by gray boxes.