Supplementary Information: The *Sclerotinia sclerotiorum* ADP-ribosylation factor 6 plays an essential role in abiotic stress response and fungal virulence to host plants

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**Figure S1.** Knockout of *SsArf6* in *S. sclerotiorum.* **(A)** The schematic diagram of the strategy used for knockout of *SsArf6*. The *SsArf6* gene, Hygromycin phosphotransferase gene (hph), and G418 resistance gene *NEO* were denoted by yellow, red, and green rectangles, respectively. The labeled primers in the diagram were used for amplifying flanking sequences of *SsArf6* or facilitating mutant screening. **(B)** The verification of knockout of *SsArf6* by PCR. Genomic DNA obtained from WT, knockout mutant *ΔSsarf6* were utilized as templates for PCR. A total of six primer pairs were employed to detect the insertion of *hph* and its upstream and down-stream fragments, as well as to confirm the knockout of *SsArf6*. The sizes of the amplified bands were indicated within brackets. The lanes labeled as M represent the DNA marker.

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**Figure S2.** Complementation of *SsArf6* in *ΔSsarf6* mutants of *S. sclerotiorum.* **(A)** The schematic diagram of the strategy used for the complementation of *ΔSsarf6*. The *SsArf6* gene, *Hygromycin phosphotransferase* gene (hph), and G418 resistance gene *NEO* were denoted by yellow, red, and green rectangles, respectively. The labeled primers in the diagram were used for amplifying full-length genomic DNA of *SsArf6* or facilitating transformant screening. **(B)** The verification of complementation of *SsArf6* by PCR. Genomic DNA obtained from the deletion mutant *ΔSsarf6*, and complemented mutant *SsArf6-C* were utilized as templates for PCR. A total of six primer pairs were employed to confirm the complementation of *SsArf6*. The sizes of the amplified bands were indicated within brackets. The lanes labeled as M represent the DNA marker.

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**Figure S3.** The semi-quantitative RT-PCR analysis of the WT, *ΔSsarf6* and *SsArf6-C* strains. Semi-quantitative RT-PCR was performed using cDNA templates from WT, *ΔSsarf6* and *SsArf6-C* for 28 cycles. *SsTub* (β-tubulin) was used as an internal reference.

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| **Table S1.** Primers used in study | | |
| Primer name | Primer sequence | Primer function |
| UF | GACAATCCGAGCACTCAA | Amplification of upstream sequence of *SsArf6*. The red part presents homologous sequences from HY fragment using for homologous recombination. |
| UR | GTGCTCCTTCAATATCATCTTCTGT CGAGATATGCGTGTGTATG |
| DF | AGGTACACTTGTTTAGAGGTAATCCGCTCCAATCTACCTTCTCG | Amplification of upstream sequence of *SsArf6.* The red part presents homologous sequences from YG fragment using for homologous recombination. |
| DR | GGAATTGGAAAATGGGGT |
| HYGF | ACAGAAGATGATATTGAAGGAGCAC | Amplification of HY and YG fragment |
| HYR | GCATCATCGAAATTGCCGTCAACC |
| YGF | TCTCGGAGGGCGAAGAATCTCGTGC |
| HYGR | GGATTACCTCTAAACAAGTGTACCT |
| UF1 | GACTCTTACCTCGCAATGAA | Check if the position of homologous substitution is correct |
| HYR1 | CGTTCCTGTCTGCTAATAAG |
| YGF1 | TAGTGAATGCTCCGTAACA |
| DR1 | CTCGGTCATTGATTGTGTATAG |
| Arf6F | GACTCTTACCTCGCAATGAA | Amplification of upstream and full-length sequences of *SsArf6*.The lowercase part presents homologous sequences from NEO fragment using for  homologous recombination. |
| Arf6R | agtgctccttcaatatcatcttctgCTTTGCTTGTGGAGCAGG |
| NEOF | CAGAAGATGATATTGAAGGAGCAC | Amplification of NEO sequence of G418 resistance gene |
| NEOR | GGATTACCTCTAAACAAGTGTACCT |
| checkF | GTAGAGACGGTGACATATAAGA | Knockout transformants identification |
| checkR | CATACCAATCCTTCCATTAACC |
| checkF | GTAGAGACGGTGACATATAAGA | Complementation transformants identification |
| NER | CGTCAAGAAGGCGATAGAA |
| EOF | TCTCCTGTCATCTCACCTT |
| DR | GGAATTGGAAAATGGGGT |
| SsTubqF | ACCTCCATCCAAGAACTC | Amplification of reference gene |
| SsTubqR | GAACTCCATCTCGTCCAT |