Supplemental Figure 1: Alignment of the five Arabidopsis and two rice SERK proteins

Multiple alignments of the five Arabidopsis SERKs and two rice SERKs using MUSCLE.

<table>
<thead>
<tr>
<th>Consensus Identity</th>
<th>1. AtSERK1 (At1g71830)</th>
<th>2. AtSERK2 (At1g34210)</th>
<th>3. OsSERK1 (Os08g07760)</th>
<th>4. OsSERK2 (Os04g38480)</th>
<th>5. AtSERK3 (At4g33430)</th>
<th>6. AtSERK4 (At2g13790)</th>
<th>7. AtSERK5 (At2g13790)</th>
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Supplemental Figure 2. Identification of \textit{XO}\textit{Serk2Ri} transgenic lines with reduced expression of \textit{OsSerk2}

The relative expression level of \textit{OsSerk1}, \textit{OsSerk2} and \textit{Xa21} was determined by quantitative RT-PCR using RNA extracted from rice leaves of three independently transformed \textit{XO}\textit{Serk2Ri} lines (\textit{B-1}, \textit{B-2}, and \textit{B-3}) and \textit{Xa21} transgenic plants. The expression of each gene was normalized to the \textit{actin} reference gene expression level. The expression level of each gene is shown as percentage expression relative to the \textit{Xa21} control plants. Data shown represent average expression level of one out three biological experiments with error bars indicating standard deviation (SD) of three technical replicates.
Supplemental Figure 3. Identification of a ProAXO\textit{OsSerk2}Ri transgenic line with reduced expression of \textit{OsSerk2}

The relative expression level of \textit{OsSerk1}, \textit{OsSerk2} and \textit{Xa21} was determined by quantitative RT-PCR using RNA extracted from rice leaves of \textit{ProAXO}\textit{OsSerk2}Ri (\textit{ProAXa21/X-B-1}), and \textit{Xa21} transgenic plants. The expression of each gene was normalized to the \textit{actin} reference gene expression level. The expression level of each gene is shown as a percentage expression relative to the \textit{Xa21} control plants. Data shown represent average expression level of one out three biological experiments with error bars indicating SD of three technical replicates.
Supplemental Figure 4. Average lesion length in the T1 generation of \textit{XOsSerk2Ri2} plants

Lesion length was measured 14 days post inoculation with \textit{Xoo} strain PXO99AZ. “\textit{Ri}(+)” indicates T1 plants (\textit{A814} derived from \textit{B-1}) carrying the transgene \textit{OsSerk2Ri} whereas “\textit{Ri}(-)” indicates T1 plants without \textit{OsSerk2Ri} transgene. This experiment was repeated three times with similar results.
Supplemental Figure 5. Average lesion length in the T1 generation of ProAXOsSerk2Ri plants

Disease lesion length was measured 14 days post inoculation with Xoo strain PXO99AZ. “Ri(+)” indicates T1 plants (A804 derived from ProAXa21/X-B-1) carrying the transgene OsSerk2Ri whereas “Ri(-)” indicates T1 plants not carrying the OsSerk2 transgene. This experiment was repeated three times with similar results.
Supplemental Figure 6. Silencing of OsSerk2 abolishes XA21-mediated immunity in ProAXa21 plants

Six week-old plants of ProAXOsSerk2Ri1 (A804), ProAXa21 (resistant control) and Kit (susceptible control) were inoculated with Xoo PXO99AZ. (A) A804 plants in the presence of OsSerk2Ri develop long water-soaking lesions. Photograph depicts representative symptom development in leaves 14 days post inoculation. “+” and “-” indicate absence or presence of the Xa21 and OsSerkRi transgene, respectively. (B) ProAXOsSerk2Ri plants (A804-55 homozygous for OsSerkRi) develop long water-soaking lesions. Lesion length was measured 0, 5, 10, and 15 days post inoculation. Graph shows average lesion length ± SD of at least 21 leaves from 7 independent plants. Statistical significance comparing A804-55 with Xa21 plants is indicated by asterisks (**P≤0.05, ANOVA analysis, Tukey’s test). (C) A804-55 plants display susceptibility to Xoo PXO99AZ. Bacterial populations were counted 0, 5, 10, and 15 days post-inoculation. Each data point represents the average ± SD of six leaves from two independent plants. The statistical significance between A804-55 with Xa21 plants is indicated by asterisk (**P≤0.05, ANOVA analysis, Tukey’s test). These experiments were repeated at least three times with similar results.
Supplemental Figure 7. Identification of one OsSerk2Ri transgenic Kitaake rice line with reduced expression level of OsSerk2

The relative expression level of OsSerk1 and OsSerk2 and Xa21 was determined by quantitative RT-PCR using RNA extracted from rice leaves of Kit-OsSerk2Ri-4 (X-B-4) and Kitaake plants. The expression of each gene was normalized to the actin reference gene expression level. The expression level of each gene is shown as percentage expression relative to the Kitaake control plants. Data shown represent average expression level of one out three biological experiments with error bars indicating standard deviation (SD) of three technical replicates.
Supplemental Figure 8: Silencing of OsSERK2 does not interfere with chitin induced defense gene expression in rice

Leaf strips of four-week old Kitaake control or OsSerk2Ri(X-B-4-2) plants were treated or not with 50 ug/ml of chitin for 2 or 12 hours. Expression levels of the two defense marker genes PR10b (A) and Os04g10010 (B) were measured by quantitative RT-PCR. Expression levels for each gene were normalized to actin reference gene expression. Data shown is normalized to Kitaake mock control at 2h or 12h, respectively. Bars depict average expression level ± standard error of two biological replicates with two technical replicates each. This experiment was repeated three times with similar results.
Supplemental Figure 9. Silencing of OsSerk2 impairs BR signaling
The “X” axis represents different concentrations of 24-epiBL (Sigma). The “Y” axis stands for the length of coleoptiles. Transgenic plants of Xa21-OsSerk2Ri-2 (A814-178 and A814-186) with stable reduced expression of OsSerk2 were used for analyses. Xa21 plants were used for control. This experiment was repeated three times with similar results.
Supplemental Figure 10. Determination of the interaction between catalytically inactive OsSKERK2 and XA21 mutant variants

HA-OsSERK2JK (OsSERK2JK), HA-OsSERK2JMK (OsSERK2JMK), HA-OsSERK2TJK (OsSERK2TJK), and their catalytically inactive variants, HA-OsSERK2JK\textsuperscript{D433N} (OsSERK2JK\textsuperscript{DN}), HA-OsSERK2JMK\textsuperscript{D433N} (OsSERK2JMK\textsuperscript{DN}), HA-OsSERK2TJK\textsuperscript{D433N} (OsSERK2TJK\textsuperscript{DN}) and empty vector pB42AD were co-transformed with LexA-XA21JK (XA21JK), LexA-XA21K668 (XA21K668) and their catalytically inactive variants, LexA-XA21JK\textsuperscript{D841N} (XA21JK\textsuperscript{DN}), LexA-XA21K668\textsuperscript{K736E} (XA21K668\textsuperscript{KE}), LexA-XA21K668\textsuperscript{D841N} (XA21K668\textsuperscript{DN}) and the empty vector pLexA, respectively. The Matchmaker LexA two-hybrid system (Clontech) was used for the yeast two-hybrid experiments. The blue color indicates nuclear interaction between the two co-expressed proteins. This experiment was three times with similar result.
Supplemental Figure 11. GST-OsSERK2 is hyperphosphorylated when heterologously expressed in *E.coli*

GST-fused OsSERK2JMK proteins (GST-OsSERK2JMK) were incubated with 1 X Protein MetalloPhosphatases (PMP) buffer in the presence (+) or absences (-) of Lambda Protein Phosphatase (1000U) for 1 hour at 30°C. Proteins were separated by SDS-PAGE and stained with CBB.
Supplemental Figure 12. OsSERK2JK and OsSERK2JMK transphosphorylates XA21K668 in vitro but not vice versa.

(A) Depiction of protein domain architecture used for trans-phosphorylation assays. OsSERK2JMK, XA21K668 and their respective kinase inactive variants, OsSERK2JMK$^{K334E}$ (OsSERK2JMK$^{KE}$), and XA21K668$^{D841N}$ (XA21K668$^{DN}$) proteins contain part of the TM domain, full JM and kinase domain. OsSERK2JK and its kinase catalytically inactive variant, OsSERK2JK$^{D433N}$ (OsSERK2JK$^{DN}$), contain full JM and kinase domains but lack part of the TM domain. (B) In vitro trans-phosphorylation assay between OsSERK2JK and XA21K668. The assay was performed by incubating GST-OsSERK2JMK (abbreviated as OsSERK2JMK), GST-OsSERK2JMK$^{K334E}$ (abbreviated as OsSERK2JMK$^{KE}$), GST-OsSERK2JK (abbreviated as OsSERK2JK) and GST-OsSERK2JK$^{D433N}$ (abbreviated as OsSERK2JK$^{DN}$) in presence or absence of His-Nus-XA21K668 (abbreviated as XA21JK) or His-Nus-XA21K668$^{D841N}$ (abbreviated as XA21JK$^{DN}$) using radioactive labeled $[^{32}P]$$\gamma$-ATP. Proteins were separated by SDS/PAGE and analyzed by autoradiography in the top panel and the protein loading control is shown by CBB in lower panel. This experiment was repeated twice with similar results.
Supplemental Figure 13. MS2 spectra for all peptides given in Table 1
The complete MSMS analyses can be found in Supplemental Data 1.
Supplemental Figure 14A. Phylogenetic analysis was performed on the two rice, five Arabidopsis SERK proteins and its next 10 closest rice homologs as determined by blastp.

Rice SERK1 and SERK2 were grouped with their five Arabidopsis counterparts. Full-length amino acid sequences of all SERK proteins and their ten closest rice homologs were analyzed using Geneious Tree builder. The phylogenetic tree was generated using a bootstrap neighbor-joining tree applying 1,000 replicates. For all SERK proteins identifiers are given in brackets.
Supplemental Figure 14B. Multiple alignments of the five *Arabidopsis* SERKs, two rice SERKs and their then closest rice homologs using Muscle.