Table S1. Statistical parameters of each compared OPLS-DA models and the result of cross-validation ANOVA (CV-ANOVA)

<table>
<thead>
<tr>
<th>Stagea</th>
<th>Model</th>
<th>R$<em>2$X$</em>{\text{(cum)}}$b</th>
<th>Q$<em>2$X$</em>{\text{(cum)}}$</th>
<th>CV-ANOVA (p)c</th>
<th>Significanced</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pre</td>
<td>SS vs RR</td>
<td>0.694</td>
<td>0.588</td>
<td>0.113</td>
<td>ns</td>
</tr>
<tr>
<td></td>
<td>SS vs SR</td>
<td>0.575</td>
<td>0.218</td>
<td>0.888</td>
<td>ns</td>
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<tr>
<td></td>
<td>RR vs SR</td>
<td>0.580</td>
<td>0.748</td>
<td>&lt; 0.001</td>
<td>**</td>
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<tr>
<td>Post 1</td>
<td>SS vs RR</td>
<td>0.569</td>
<td>0.620</td>
<td>0.078</td>
<td>ns</td>
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<tr>
<td></td>
<td>SS vs SR</td>
<td>0.643</td>
<td>0.800</td>
<td>0.007</td>
<td>**</td>
</tr>
<tr>
<td></td>
<td>RR vs SR</td>
<td>0.546</td>
<td>0.721</td>
<td>0.010</td>
<td>*</td>
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<tr>
<td>Post 2</td>
<td>SS vs RR</td>
<td>0.680</td>
<td>0.767</td>
<td>0.016</td>
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<tr>
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<td>SS vs SR</td>
<td>0.610</td>
<td>0.521</td>
<td>0.262</td>
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<tr>
<td></td>
<td>RR vs SR</td>
<td>0.645</td>
<td>0.708</td>
<td>0.009</td>
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<tr>
<td>Post 3</td>
<td>SS vs RR</td>
<td>0.620</td>
<td>0.587</td>
<td>0.114</td>
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<tr>
<td></td>
<td>SS vs SR</td>
<td>0.683</td>
<td>0.281</td>
<td>0.861</td>
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</tr>
<tr>
<td></td>
<td>RR vs SR</td>
<td>0.589</td>
<td>0.662</td>
<td>0.030</td>
<td>*</td>
</tr>
</tbody>
</table>

aTwo days before inoculation (pre), and 2 d (post 1), 7 d (post 2) and 30 d post inoculation (post 3).

bR$_2$X$_{\text{(cum)}}$: the cumulative sum of squares (SS) of the entire X explained by all extracted components (Explanation power); Q$_2$X$_{\text{(cum)}}$: the cumulative Q$^2$ for all the X-variables (PC) and y-variables (PLS) for the extracted components (Prediction power). This parameter was acquired from Simca-P (ver. 12.0).

cANOVA of cross-validated predictive residuals of OPLS analysis.

d**; Correlation is significant at $P \leq 0.01$ (2-tailed), *; significant at $P \leq 0.01$ (2-tailed), ns: not significant.
Figure S1. OPLS-DA sample scatter plots (A to F) and their metabolite S-Plots (G to L) of different response types (RR; resistant, SR; moderately resistant, SS; susceptible). In scatter plot, Black dots represent RR, red dots SR, and blue dots SS. The short dashed circle is shown Hotelling's T-squared distribution (0.95). In S-plot, metabolites marking red dots are selected by VIP score (>1, PLS-DA) and $p(corr)$ value [0.5 < $p(corr)$, OPLS-DA]. Collected metabolites are shown in Table 3.