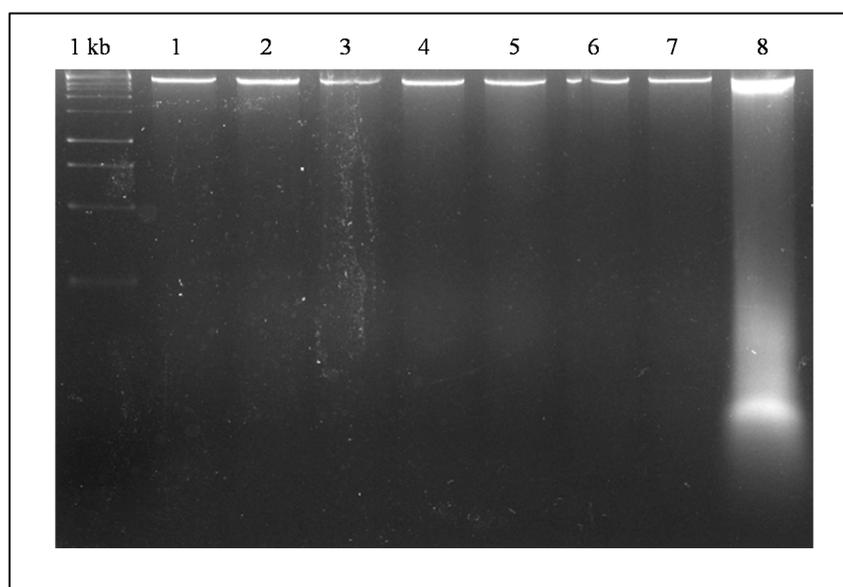
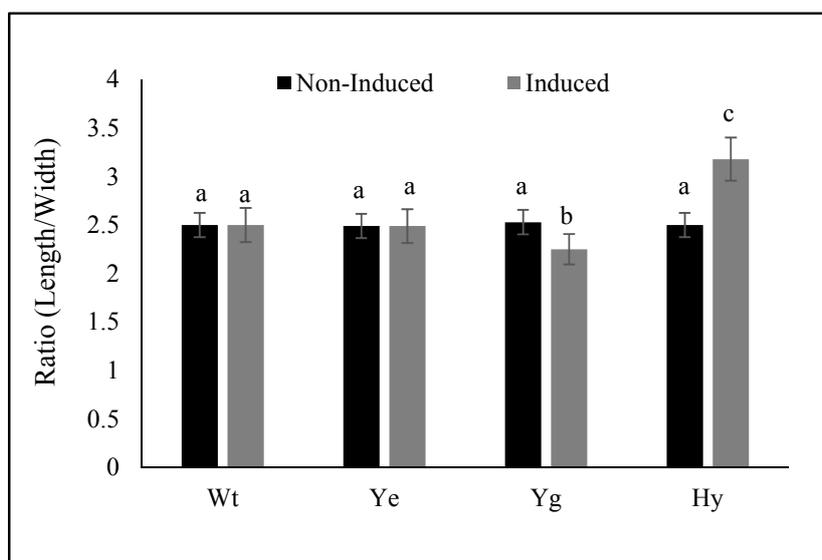


## Supplementary Material: Neutralization of *YoeB<sub>Spm</sub>* Toxicity and Enhanced Plant Growth in *Arabidopsis thaliana* via Co-Expression of Toxin-Antitoxin Genes

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**Figure S1.** Laddering of nuclear DNA from transgenic *yoeB<sub>Spm</sub>-GFP*. Lane 1: Non-induced wild-type; 2: Non-induced *yefM<sub>Spm</sub>*; 3: Non-induced *yefM<sub>Spm</sub> × yoeB<sub>Spm</sub>-GFP* hybrid; 4: Non-induced *yoeB<sub>Spm</sub>-GFP*; 5: Induced wild-type; 6: Induced *yefM<sub>Spm</sub>*; 7: Induced *yefM<sub>Spm</sub> × yoeB<sub>Spm</sub>-GFP* hybrid; 8: Induced *yoeB<sub>Spm</sub>-GFP*; 1 kb: 1 kb DNA ladder (Fermentas).



**Figure S2.** Ratio of length to width of leaf (7th position) of induced and non-induced plants. Wt: wild-type *A. thaliana*; Ye: transgenic *A. thaliana* (*yefM<sub>Spm</sub>*); Yg: transgenic *A. thaliana* (*yoeB<sub>Spm</sub>-GFP*); Hy: transgenic *A. thaliana* (*yefM<sub>Spm</sub> × yoeB<sub>Spm</sub>-GFP*) hybrid. Data are presented as the mean  $\pm$  standard deviation ( $n = 20$ ); significance values (with significant differences between samples indicated by the letters a, b and c) were determined by one-way ANOVA (Tukey used as the *post hoc* test with  $p < 0.05$ ).

**Table S1.** Possible binding sites for the YefM-YoeB<sub>Spn</sub>-GFP complex in the *Arabidopsis thaliana* genome based on the 27-nucleotides binding site for YefM-YoeB<sub>Spn</sub> in *S. pneumoniae* as determined by DNaseI footprinting by Chan *et al.* [18].

Accession No.	Chromosome No.	Identities (Out of 27 Nucleotides)	Gene	Features	Possible Molecular Function(s)
GI/240256243 ref/NC_003075.7	4	21	<i>ARPC5</i>	Actin related protein 2/3 complex, subunit 5A	Regulation of actin polymerization and together with an activating nucleation—promoter factor (NPF)
GI/240255695 ref/NC_003074.8	3	20	Representative gene model—At3g31051.1	Hypothetical protein	Involved in transcription or purifying selection
GI/2402544121 ref/NC_003070.9	1	20	<i>UBP13</i>	Ubiquitin carboxyl terminal hydrolase related protein	Cystein type peptidase activity; Ubiquitin—dependent protein catabolic process
GI/240256493 ref/NC_003076.8	5	19	1. MATE (Multidrug and toxic compound extrusion) 2. Representative gene model—At2g16870	1. MATE efflux family protein 2. TIR-NBS-LRR class disease resistance protein	1. Citrate exudation into the rhizosphere, drug transmembrane transporter activity. 2. ADP/ATP binding
GI/240256243 ref/NC_003075.7	4	19	Representative gene model—At4g37095.1	Hypothetical protein	Gene codes for small protein either involved in transcription or purifying selection
GI/240255695 ref/NC_003074.8	3	19	<i>T21J18-100</i>	Polynucleotide adenylyltransferase domain and RNA recognition motif containing protein	Nucleotide binding nucleotidyltransferase activity
GI/240254678 ref/NC_003071.7	2	19	<i>TT12/DTX14</i> Representative gene model—At3g59030	MATE efflux family protein (F3L12.8)	Citrate exudation into the rhizosphere, drug transmembrane transporter activity
GI/240254678 ref/NC_003071.7	2	19	<i>TT12/DTX14</i> Representative gene model—At3g59030	MATE efflux family protein	Citrate exudation into the rhizosphere, drug transmembrane transporter activity
GI/240254421 ref/NC_003070.9	1	19	1. Representative gene model—At1g34930 2. <i>LAX3</i>	1. Plant thionin family protein 2. Auxin influx carrier <i>LAX3</i>	1. Cystein rich protein with toxic and antimicrobial properties involved in plant defense mechanism. 2. Promotes lateral root emergence and is involved in phototaxis arrangement of leaves and stem
GI/240254678 ref/NC_003071.7	2	18	<i>APC2</i> Representative gene model—At2g04660.1	Anaphase promoting complex subunit—2	A highly conserved ubiquitin protein ligase involved in cell cycle regulation and also promotes protein binding