

# Supplementary Materials: Toxicity of Recombinant Necrosis and Ethylene-Inducing Proteins (NLPs) from *Neofusicoccum parvum*

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A

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**B**

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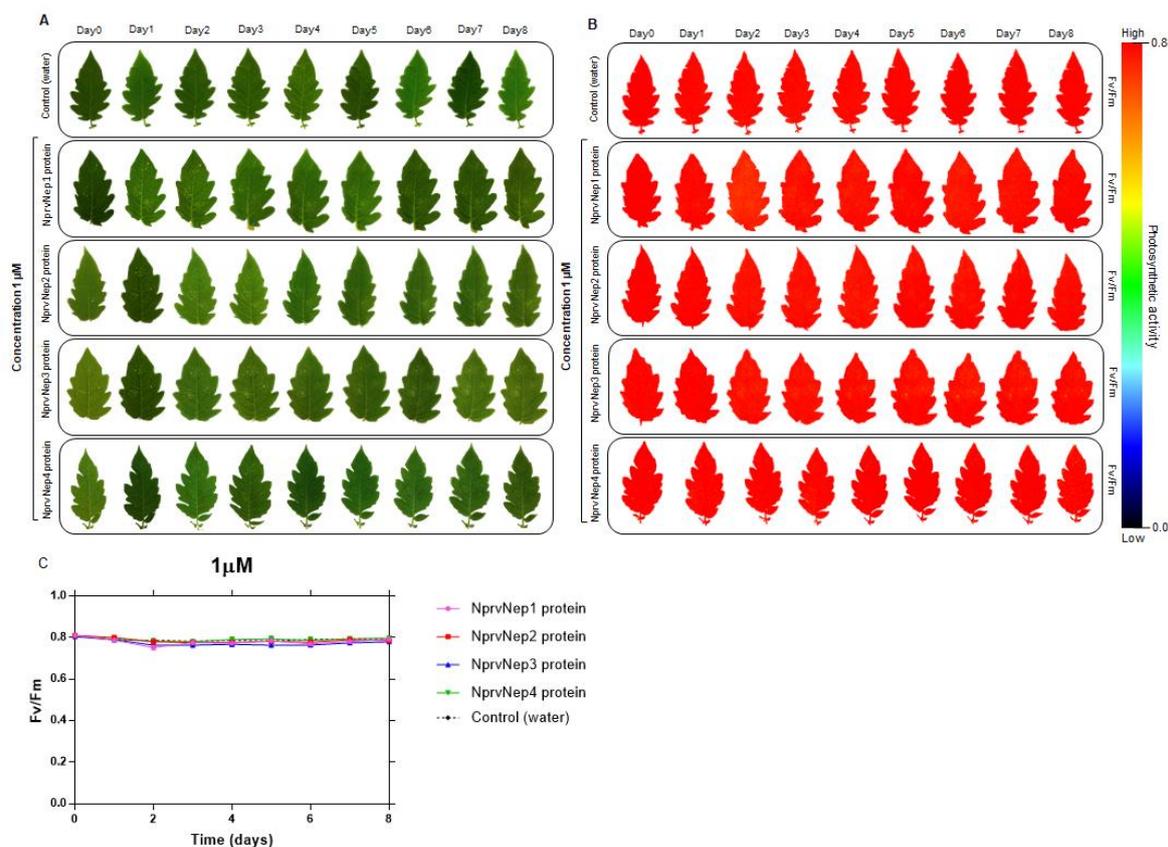
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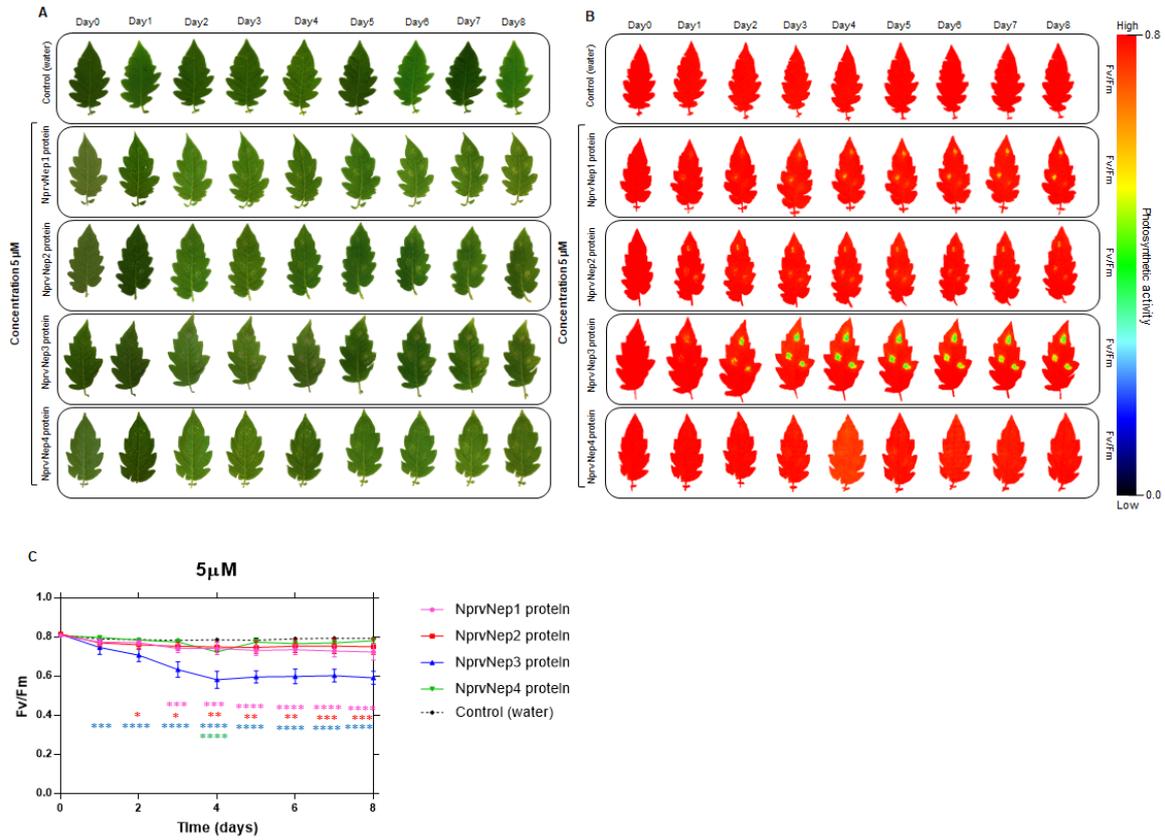
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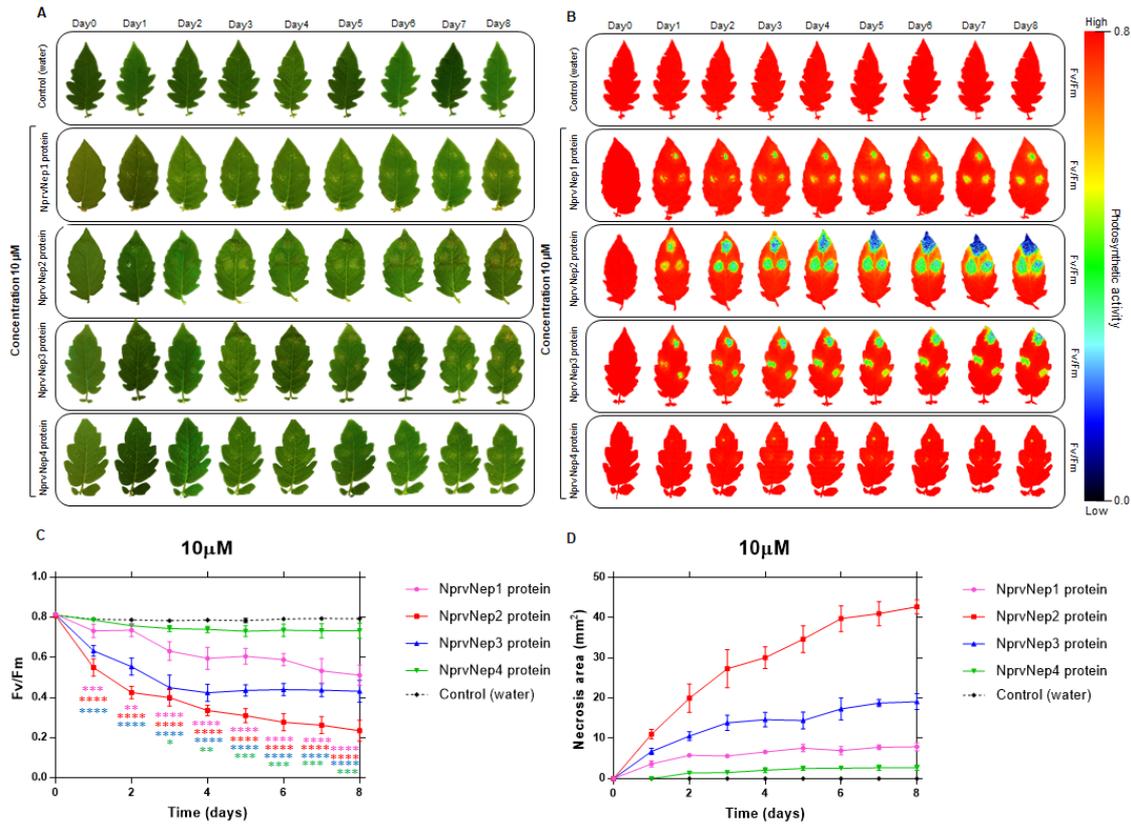
**Figure 1.** Alignment of the DNA and cDNA sequence of *Neofusicoccum parvum* NLPs; **A:** NprvNep1, **B:** NprvNep2, **C:** NprvNep3, **D:** NprvNep4, and **E:** NprvNep5. Red boxes indicate the absence and presence of the introns in cDNA and DNA, respectively.



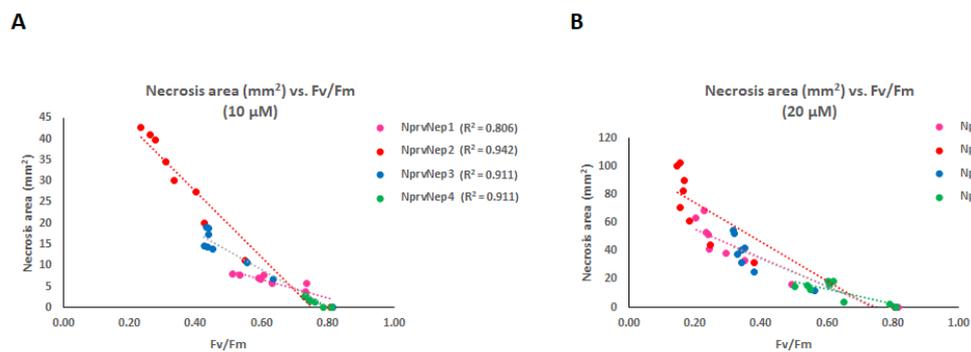
**Figure 2.** Effect of 1 μM recombinant NprvNeps on detached tomato leaves symptoms development. (A), chlorophyll fluorescence (B), and  $F_v/F_m$  (C). Ultra-pure water was used as a control. The color scale bar indicates the  $F_v/F_m$  intensity of the leaf pixels given in false colors from high (red) to low (black) values. All measurements were performed in biological triplicates and error bars show the standard deviation. Two-way ANOVA, followed by a Dunnett's multiple comparison test was used to determine the statistical significance of phytotoxicity of each protein within the same concentration against the control (C).



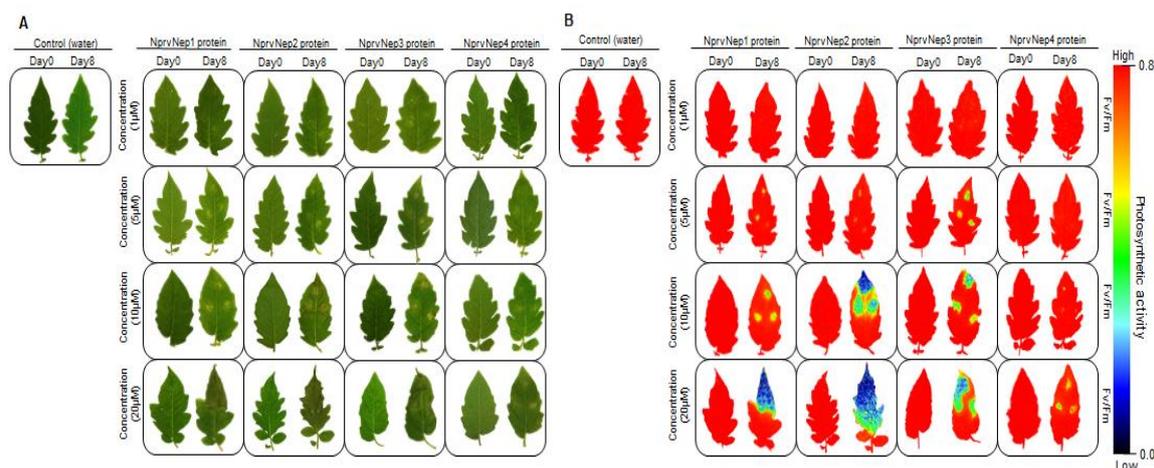
**Figure S3.** Effect of 5  $\mu\text{M}$  recombinant NprvNeps on detached tomato leaves symptoms development. (A), chlorophyll fluorescence (B), and  $F_v/F_m$  (C). Ultra-pure water was used as a control. The color scale bar indicates the  $F_v/F_m$  intensity of the leaf pixels given in false colors from high (red) to low (black) values. All measurements were performed in biological triplicates and error bars show the standard deviation. Two-way ANOVA, followed by a Dunnett's multiple comparison test was used to determine the statistical significance of phytotoxicity of each protein within the same concentration against the control (C) (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ ).



**Figure S4.** Effect of 10 μM recombinant NprvNeps on detached tomato leaves symptoms development (A), chlorophyll fluorescence (B), and Fv/Fm (C) and necrosis area (D). Ultra-pure water was used as a control. The color scale bar indicates the Fv/Fm intensity of the leaf pixels given in false colors from high (red) to low (black) values. All measurements were performed in biological triplicates and error bars show the standard deviation. Two-way ANOVA, followed by a Dunnett's multiple comparison test was used to determine the statistical significance of phytotoxicity of each protein within the same concentration against the control (C) (\* $p < 0.05$ , \*\* $p < 0.01$ , \*\*\* $p < 0.001$ , \*\*\*\* $p < 0.0001$ ).



**Figure S5.** Scatter plot of necrosis area vs. Fv/Fm values for 8 days. The correlation between necrosis area and Fv/Fm values of detached tomato leaves treated with 10 μM (A) and 20 μM (B) recombinant NprvNeps (1-4) for 8 days is shown. Each point is the mean of biological triplicates.



**Figure S6.** Toxicity of recombinant NprvNeps to detached tomato leaves evaluated by chlorophyll fluorescence. Effect of 1, 5, 10, and 20  $\mu\text{M}$  recombinant NprvNeps on symptoms development (A), and chlorophyll fluorescence (B) at 0 and 8 dpi. Ultra-pure water was used as a control. The color scale bar indicates the  $F_v/F_m$  intensity of the leaf pixels given in false colors from high (red) to low (black) values. All experiments were performed in biological triplicates.

**Table S1.** Primers used for cloning and amplification.

Gene Name	Sequences (5' to 3')
<i>NprvNep1</i>	F: GCCCCGGTCGAGAAGCGC
	R: CTACAACGCCGCTAACGCTAGGTTG
<i>NprvNep2</i>	F: GCGGTTGTTCAACGCCGCGG
	R: TCACAACGACAGGCACAGGGG
<i>NprvNep3</i>	F: GCTGCCATCCAACGCCGC
	R: TCAGACCTCAGCCTTGGCGAGG
<i>NprvNep4</i>	F: GCTCCCACGCAGAAGCTGAACG
	R: TTAGACCCAAGCCTCCTCAATCTTG
<i>NprvNep5</i>	F: GAGCAGATCGAGAAGCGCGCTG
	R: TTAGATCCAGGCCCTTGCCGAGGTTG

**Table S2.** The data of 6 *NprvNep* genes.

Genes	GenBank No	Extracellular protein /signal peptide	Signal peptide length	Protein molecular weight (kDa)
<i>NprvNep1</i> *	gi 615425645	Y	18	26.5
<i>NprvNep2</i> *	gi 485922125	Y	21	27.6
<i>NprvNep3</i> *	gi 485923842	Y	21	25.8
<i>NprvNep4</i> *	gi 485928552	Y	18	26.2
<i>NprvNep5</i> *	gi 485917230	Y	28	27.3
<i>NprvNep6</i>	gi 615411409	N	0	17.9

A signal peptide of the NprvNep was predicted with the tool SignalP4.0. The SignalP Network predicted cleavage sites between 17 and 29 amino acid residues. \* The *NprvNep* genes were selected for functional analysis. 'Y' has a signal peptide. 'N' has no a signal peptide.