

## **Supplementary material**

### **Construction of a nontoxic nano-pesticide toward natural predator for perfect cooperative pest management: An innovative strategy for pesticide reduction**

Shangyuan Wu <sup>a,#</sup>, Qinhong Jiang <sup>a,#</sup>, Chunyang Huang <sup>b,#</sup>, Hailin Yang <sup>c</sup>, Changhua Zhang <sup>b</sup>, Meizhen Yin <sup>d</sup>, Jie Shen <sup>a</sup>, Shuo Yan <sup>a,\*</sup>, Hu Li <sup>a,\*</sup>

<sup>a</sup> *College of Plant Protection, China Agricultural University, Beijing 100193, P. R. China*

<sup>b</sup> *Guizhou Tobacco Company, Zunyi Branch, Zunyi 563000, P. R. China*

<sup>c</sup> *Yunnan Tobacco Company, Yuxi Branch, Yuxi 653100, P. R. China*

<sup>d</sup> *State Key Laboratory of Chemical Resource Engineering, Beijing Lab of Biomedical Materials, Beijing University of Chemical Technology, Beijing 100029, P. R. China*

# These authors have contributed equally to this work.

\* Corresponding authors. College of Plant Protection, China Agricultural University, Beijing 100193, P. R. China.

E-mail addresses: yanshuo2011@foxmail.com (S. Yan) and tigerleecau@hotmail.com (H. Li).

## Supplementary Figure

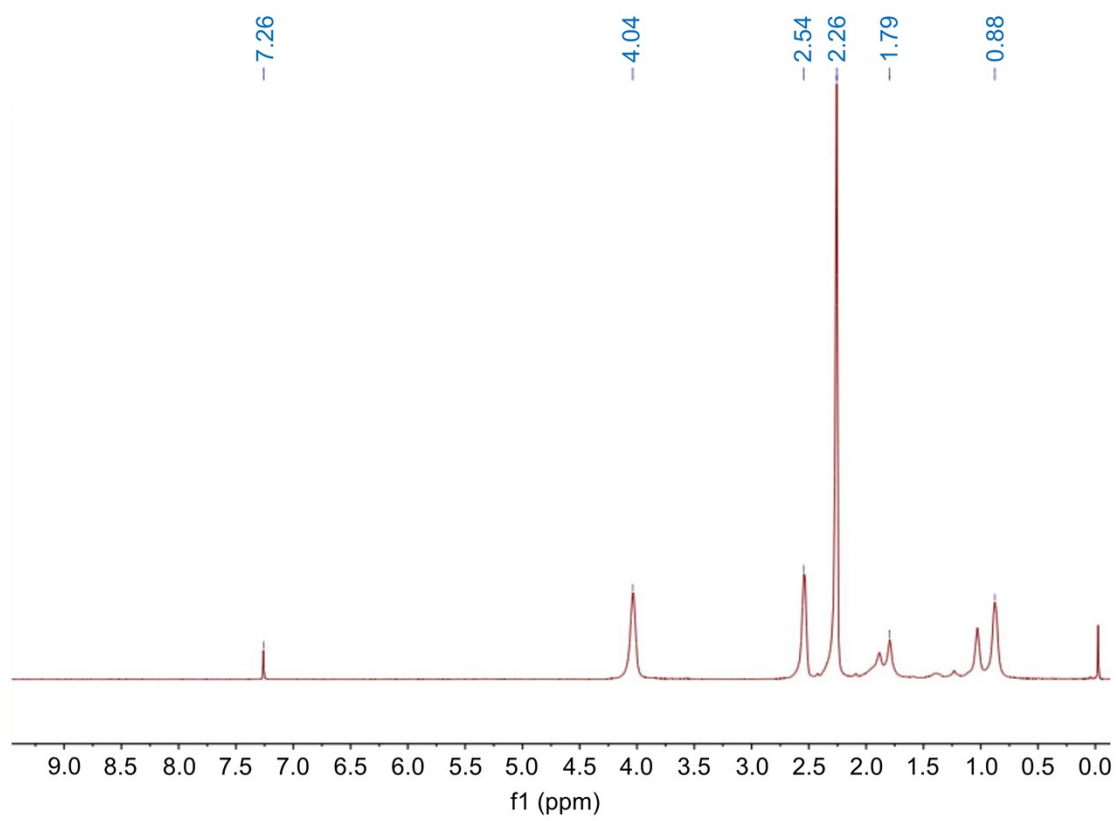


Figure S1. <sup>1</sup>H NMR spectrum of SPc in CDCl<sub>3</sub>.

## Supplementary Tables

Table S1. Primers for quantitative real-time PCR.

Gene name	Primer	Sequence
<i>Vacuolar protein sorting-associated protein 4A</i>	VPS4A-F	TGGCTTGGTGAGTCTGAGAG
	VPS4A-R	CCCACGGTATGTTGGTAGCT
<i>Rab11 family-interacting protein 1</i>	RAB11FIP1-F	AGGTGAAGCAGATCCAGGTG
	RAB11FIP1-R	TAGGTGGTTTTGCAGGAGGA
<i>ADP-ribosylation factor 1</i>	ARF1-F	GCGCCACCAATATTCAGGAG
	ARF1-R	AATACAACCTTGAGCCGTCGC
<i>Trehalase</i>	TREH-F	ACACTGGGGAACAATGGGAT
	TREH-R	CCGCCTGTCTTTCCAACCTC
<i>Phosphoenolpyruvate carboxykinase [GTP]</i>	PckG-F	GGAGGTAATTCGCTGCTTGG
	PckG-R	GCCAACACACTCCACTTTGT
<i>Folate-binding protein 1</i>	FBP1-F	GGATGTAGACTGTGCTGGGT
	FBP1-R	TATTTTCCCCTTTTGCGGCA
<i>Acetyl-CoA carboxylase 1</i>	ACC1-F	GACCCTGACTGCTTCTGAGT
	ACC1 -R	GATAGTGGGCATGCTTGTGG
<i>Beta-actin</i>	Beta-actin-F	CACCTTCTACAACGAGCTGC
	Beta-actin-R	AGGCGTAGAGGGAGAGTACA

Table S2. Sequencing quality and genome mapping.

Sample	Total clean reads (M)	Q20	GC percent	Percentage of mapped reads
SPc-1	69.43	97.71%	34.30%	87.36%
SPc-2	67.47	97.62%	33.98%	88.38%
SPc-3	67.3	97.75%	34.04%	88.63%
Control-1	67.53	97.63%	34.30%	89.35%
Control-2	70.32	97.65%	34.30%	88.57%
Control-3	67.22	97.66%	34.45%	89.12%