

Table S1. Identification of bacterial strain Kol B3 based on the similarity of the *tuf* gene sequence to the sequences stored in the NCBI database.

Bacterial strain	Sequence length [bp]	The genus/species of bacteria with the greatest similarity to the NCBI sequence	NCBI Sequence No.	Degree of Similarity [%]	Identification
Kol B3	720	<i>B. velezensis</i>	CP031694.1	100	<i>Bacillus</i> sp.
		<i>B. amyloliquefaciens</i>	CP014700.1	100	
		<i>B. methylotrophicus</i>	LN999829.1	100	

Table S2. The influence of AZ on *Bacillus* sp. Kol B3 bacteria growth.

Cultivation variant	Dried biomass [mg]	Bacterial CFU
Kol B3 (control)	21 ± 2	10.03 ± 5.95 × 10 ⁸
Kol B3 + AZ	22 ± 2	11.53 ± 7.01 × 10 ⁸

Kol B3 (control) – biotic control of *Bacillus* sp. Kol B3; Kol B3 + AZ – cultivation of *Bacillus* sp. Kol B3 amended with azoxystrobin.

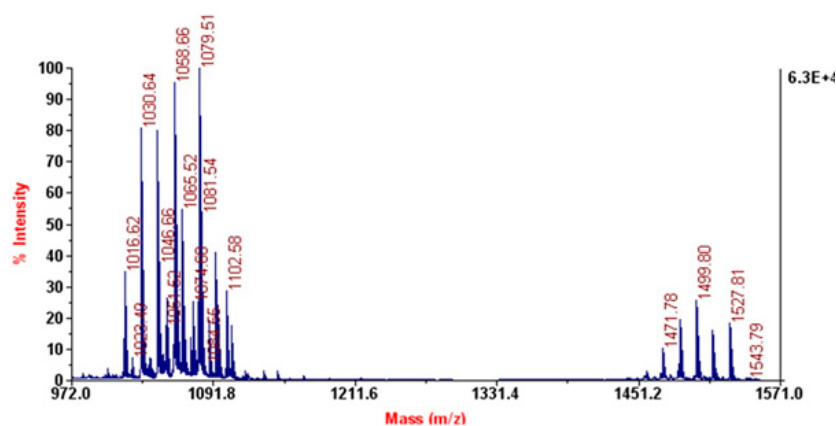


Figure S1. MALDI-TOF/TOF mass spectrum of the lipopeptide mixture presented in an extract prepared by a modified QuEChERS procedure from the culture supernatant of *Bacillus* sp. Kol B3.