ECOMONDO
THE GREEN TECHNOLOGY EXPO

XXII Conferenza sul Compostaggio e Digestione Anaerobica
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Effect of compost against soil-borne plant pathogens and its impact on rhizosphere microbiota

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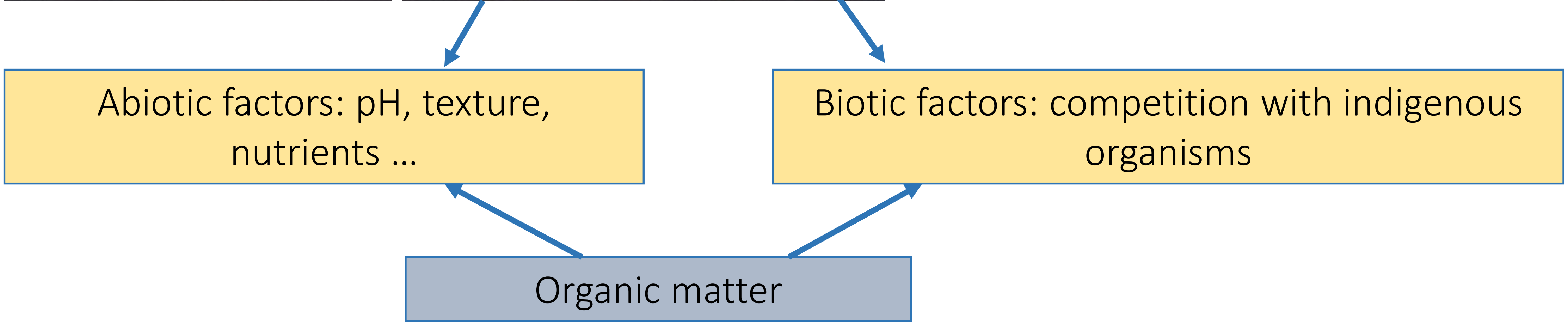
Soil-borne pathogens

Disease suppressive soil

Suppressive soil =
Soil with limited or no damage in a sensitive crop even when the pathogen is present



Abiotic factors: pH, texture, nutrients …

Biotic factors: competition with indigenous organisms

Organic matter

Fusarium wilt of lettuce

Fusarium wilt of lettuce

Protocol of the field trials on Fusarium wilt of lettuce and timing of the operations carried out in 2016 (trial 1) and 2017 (trial 2).
Two composts compared to a chemical fungicide and to biological control agents.

Treatment	**Microorganism/a.i.**	**Dosage**	**Tray treatment**	**Plot Treatment**
Serenade max - SM	*Bacillus subtilis* QST 713	2.9X10^{10} cells/L water	T5; T10; T15;T20*	-
Remedier - RM	*Trichoderma asperellum + T gamsii*	1.2X10^{6} cells/L water	T5; T10; T15;T20	-
P. putida - Pp	*P. putida* FC7B+ FC8B +FC9B	1x10^{7} cells /ml water	T5; T10; T15;T20	-
COMPOST M – CM	**Green compost + *Trichoderma* TW2**	8 g/seedling; 1kg/0.1m^{3} of soil	T0	- T20
COMPOST V – CV	**Green compost**	8 g/seedling; 1kg/0.1m^{3} of soil	T0	- T20
Trichoderma sp. - TW2	Trichoderma strain TW2	1x10^{7} cells /ml water	T5; T10; T15; T20	
Ortiva	Azoxystrobin	0.19 g a.i./L water		T20
Untreated control - C	-	-		

*Treatments: T0 at sowing; T5: 5 days after sowing; T10: 10 days after sowing; T15: 15 days after sowing; T 20: 20 days after sowing and immediately before transplanting.

Cucu, et al. 2018. Journal of Appied Microbiology, 126, 905-918.

Fusarium wilt of lettuce

Effect of preventative treatments (nursery and soil-preplanting) on Fusarium wilt of lettuce in trials carried out in 2016 (trial 1) and 2017 (trial 2)

Treatment	**Disease severity %**						**Fresh weight g/12 plants**					
	2016			**2017**			**2016**			**2017**		
Serenade max - SM	26.9	±3.6	a	22.1	±3.3	ab	3135.6	±128.9	a	2727.2	±371.5	ab
Remedier - RM	27.7	±3.2	a	29.5	±7.0	ab	2731.0	±79.0	a	2868.4	±348.7	ab
P. putida - Pp	28.1	±2.9	a	35.2	±6.3	ab	3090.7	±49.6	a	1528.0	±67.2	bc
COMPOST M - CM	**25.3**	**±3.3**	**a**	**13.0**	**±4.7**	**a**	**3256.3**	**±267.6**	**a**	**3766.0**	**±481.6**	**a**
COMPOST V - CV	**32.0**	**±4.1**	**a**	**29.0**	**±5.3**	**ab**	**3323.9**	**±146.7**	**a**	**3747.6**	**±130.1**	**a**
Trichoderma sp. - TW2	32.2	±2.7	a	36.4	±3.3	b	2815.7	±78.6	a	1917.6	±134.7	bc
Azoxystrobin, Ortiva	24.8	±4.0	a	19.8	±2.3	ab	3014.0	±185.3	a	3360.4	±273.0	a
Untreated control - C	***61.0***	***±3.5***	***b***	***61.7***	***±4.1***	***c***	***1745.7***	***±93.0***	***b***	***770.8***	***±243.1***	***c***

* Tukey's HSD test ($P < 0.05$)

The two composts (CV and CM) were effective in reducing the disease in a way similar to the chemical fungicide.

Cucu, et al. 2018. Journal of Appied Microbiology, 126, 905-918.

Fusarium wilt of lettuce

Abundance of *F. oxysporum* f.sp. *lactucae* (FOL) in the rhizosphere and bulk soil after different treatments and in the untreated control at the end of trial 1 (2016) and trial 2 (2017).

Treatment	FOL (logcopy DNA^{-1})			
	Rhizosphere 2016		Rhizosphere 2017	
Serenade max - SM	6.359	a*	6.345	b
Remedier - RM	5.626	c	5.692	c
P. putida - Pp	6.034	b	6.179	b
COMPOST M - CM	**5.423**	**d**	**5.243**	**d**
COMPOST V - CV	**5.897**	**c**	**5.897**	**c**
Trichoderma sp. - TW2	6.122	b	6.292	b
Untreated control - C	6.445	a	7.635	a

* Tukey’s HSD test ($P < 0.05$)

The two composts (CV and CM) were the most effective treatments in reducing the population of the pathogen at rhizosphere level.

Cucu, et al. 2018. Journal of Appied Microbiology, 126, 905-918.

Fusarium wilt of lettuce

Abundance of *Bacillus*, *Pseudomonas*, and *Trichoderma* genes in the rhizosphere and bulk soil after different treatments and the untreated control at the end of trial 1 (2016) and trial 2 (2017).

Treatment	Bacillus (logcopy DNA-1)				Pseudomonas (logcopy DNA-1)				Trichoderma (logcopy DNA-1)			
	Rhizosphere 2016		Rhizosphere 2017		Rhizosphere 2016		Rhizosphere 2017		Rhizosphere 2016		Rhizosphere 2017	
Serenade max - SM	5.039	a*	5.087	a	4.295	b	4.337	c	3.988	d	3.936	d
Remedier - RM	4.249	bc	4.194	b	4.249	b	4.194	c	4.249	c	4.345	d
P. putida - Pp	3.989	c	3.980	c	4.599	a	4.621	b	3.989	cd	3.992	d
COMPOST M - CM	**4.702**	**b**	**4.308**	**b**	**4.781**	**a**	**4.837**	**a**	**4.905**	**b**	**5.001**	**b**
COMPOST V - CV	**3.982**	**c**	**3.990**	**c**	**4.292**	**b**	**3.880**	**d**	**4.292**	**c**	**4.775**	**c**
Trichoderma sp. - TW2	3.654	d	3.641	d	3.654	c	3.635	d	5.676	a	5.658	a
Untreated control - C	3.615	d	3.617	d	3.495	c	3.435	e	3.327	e	4.207	d

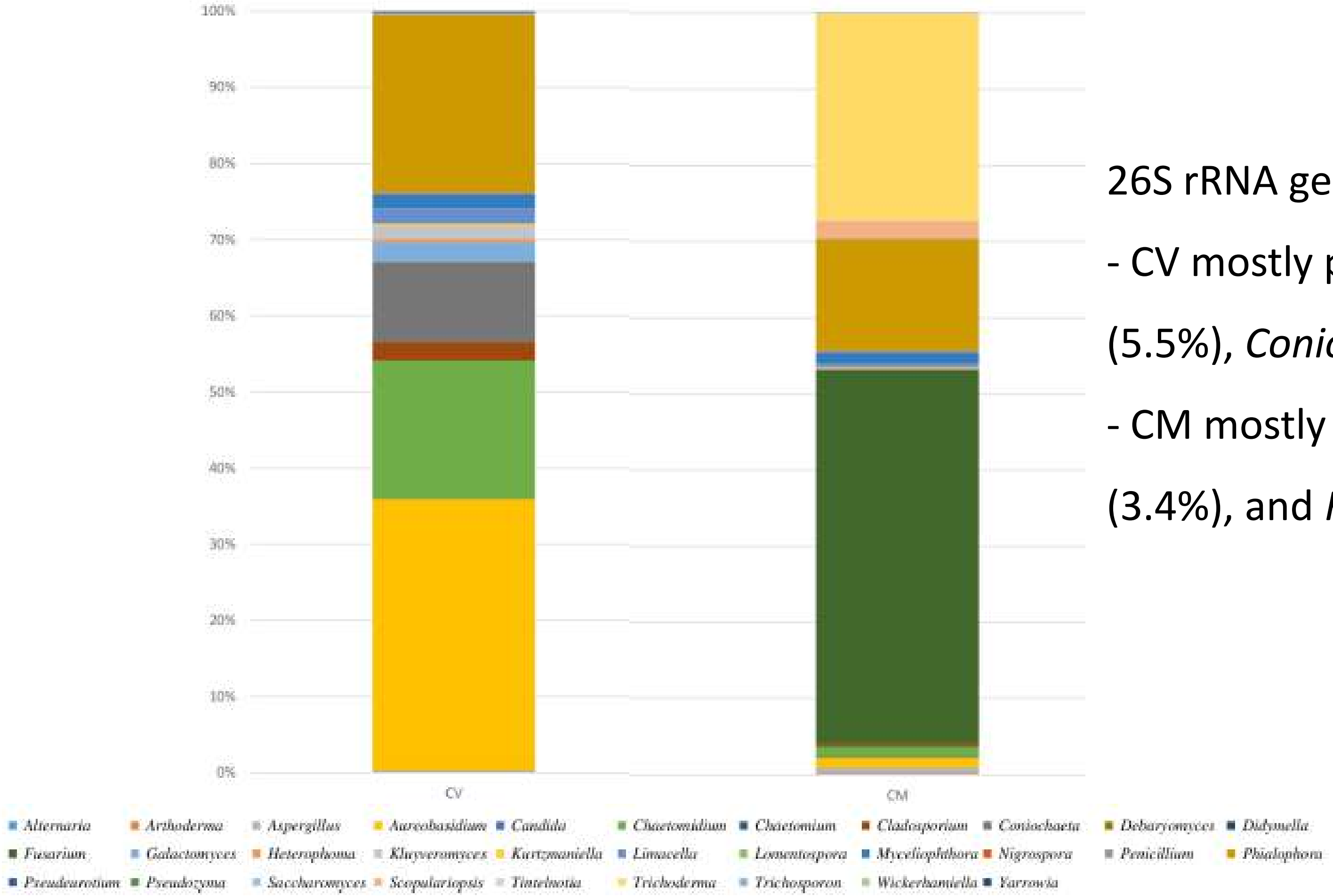
* Tukey's HSD test ($P < 0.05$)

The two composts (CV and CM) increased the population of key beneficial microorganisms (*Bacillus*, *Pseudomonas*, *Trichoderma*) at rhizosphere level.

Cucu, et al. 2018. Journal of Appied Microbiology, 126, 905-918.

Mycobiota in compost

Relative abundance of the fungal community in the two composts: CV (green compost) and CM (green compost + *Trichoderma*).



26S rRNA gene sequencing:

- CV mostly populated by *Phialophora* (5.5%), *Coniochaeta* (4.2%), and *Aureobasidium* (8.5%);
- CM mostly populated by *Trichoderma* (6.4%), *Phialophora* (3.4%), and *Fusarium* (11.5%).

Bellini, et al. 2020. Frontiers in Plant Science, 11, 885.

Basal rot (*Phytophthora capsici)* on zucchini

Basal rot (*Phytophthora capsici)* on zucchini

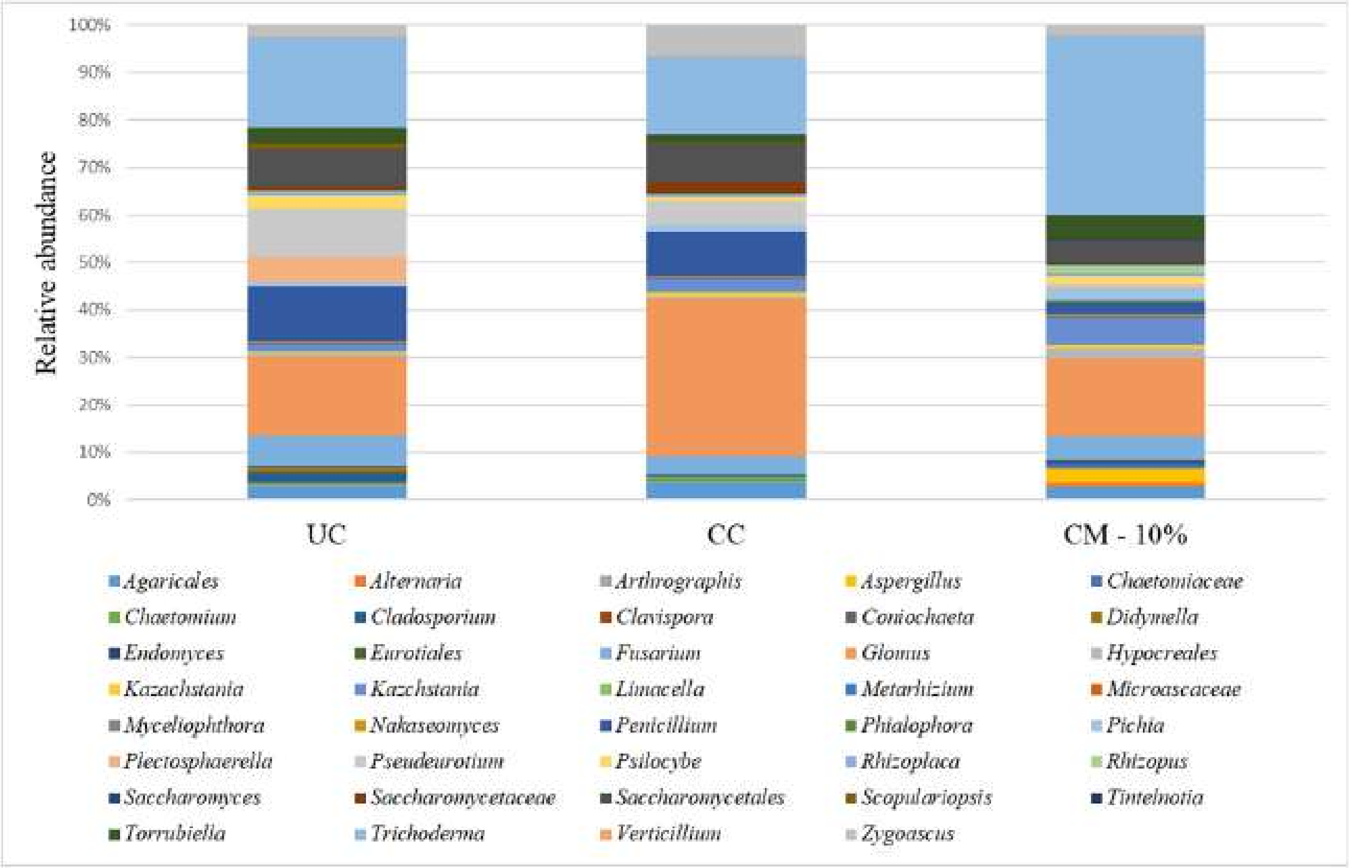
Treatment	Disease incidence		AUDPC	
Non-inoculated control	0	c*	0.0	a
Untreated control	90	a	351.3	c
Chemical control	0	c	0.0	a
COMPOST CM (10% v/v)	45	**b**	**137.1**	**ab**

* Tukey's HSD test ($P < 0.05$)

The compost CM significantly reduced the disease on zucchini.

Bellini, et al. 2020. Frontiers in Plant Science, 11, 885.

Basal rot (*Phytophthora capsici)* on zucchini



Relative abundance of the mycobiota in the rhizosphere samples at the end of the trials: untreated control (UC), chemical control (CC), and CM – 10% treatment.

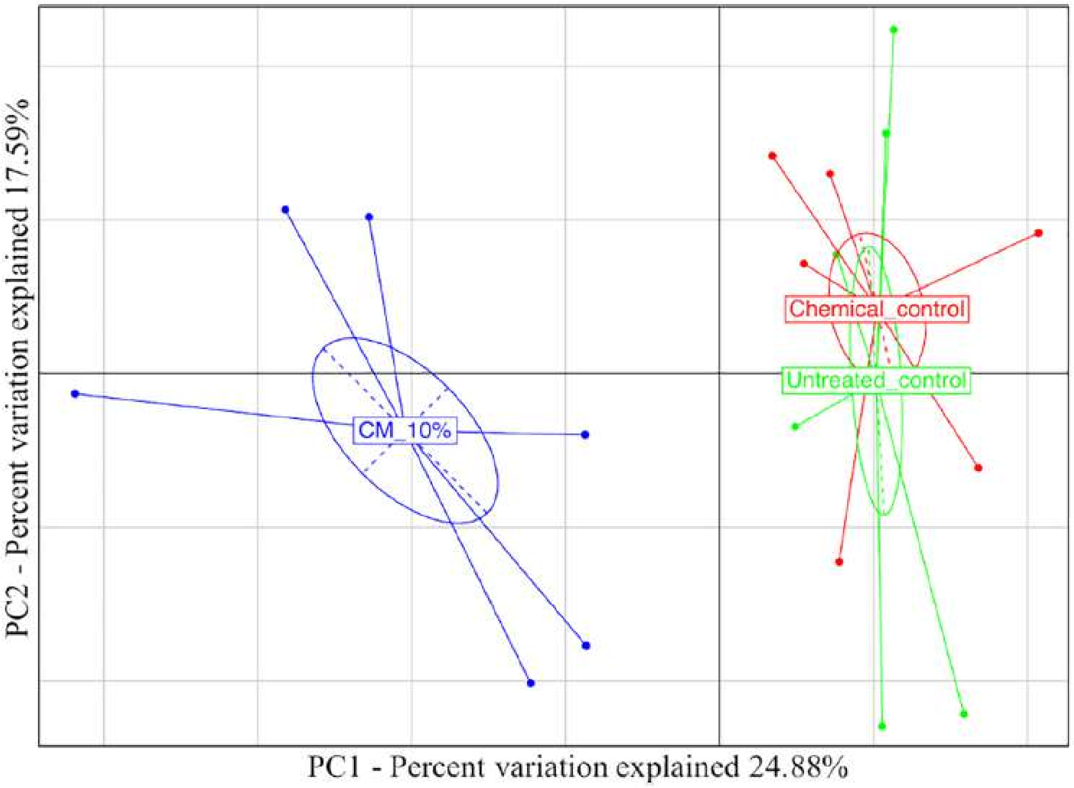
Core mycobiota, composed of:

- *Fusarium,* which reaches about 3% of the relative abundance in the control samples (UC), 1% in the compost (CM–10%) and 2% in the chemical treatment (CC);
- *Glomus,* which reaches 9, 5, and 15% in UC, CM-10%, and CC;
- *Penicillium*, which reaches 6, 1, and 4% of the relative abundance in UC, CM – 10%, and CC;
- *Saccharomycetales,* which reaches 4, 1, and 3%;
- *Torrubiella,* which reaches 2, 2, and 1%;
- *Trichoderma*, which reaches 10, 12, and 7%;
- *Zygoascus,* which reaches 1, 1, and 3%.

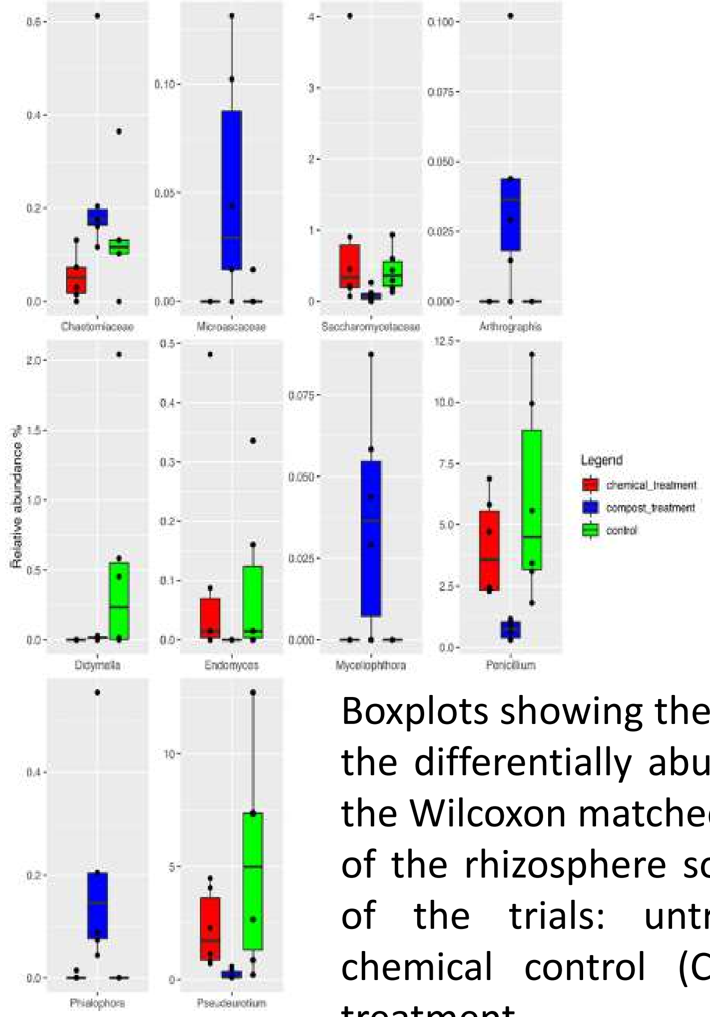
Bellini, et al. 2020. Frontiers in Plant Science, 11, 885.

Basal rot (*Phytophthora capsici)* on zucchini

It was possible to observe a clear separation of the samples treated with compost, while the chemical treatment and control ones clustered together.



Principal component analysis based on the mycobiota composition referred to the rhizosphere samples at the end of the trials: untreated control (UC), chemical control (CC), and CM – 10% treatment.



Boxplots showing the relative abundance of the differentially abundant OTUs based on the Wilcoxon matched pairs test (FDR 0.05) of the rhizosphere soil samples at the end of the trials: untreated control (UC), chemical control (CC), and CM – 10% treatment.

Bellini, et al. 2020. Frontiers in Plant Science, 11, 885.

Conclusion

- The application of suppressive composts helps to control soil-borne diseases by 50-70% compared to the untreated controls, thus reducing the abundance of the pathogens in the compost treated soils.
- An increase in the abundance of beneficial microorganisms such as *Trichoderma* and *Bacillus* was also observed in the rizhosphere of plants treated with compost.
- The core mycobiota of the suppressive composts was mainly composed of 31 genera with a clear predominance of the same few taxa.
- The suppressive activity of a compost is strictly influenced by its microbiota, which may induce a shape in the rhizosphere microbial composition of treated plants.

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