



Miscanthus biochar promotes growth of spring barley and shifts bacterial community structures including phosphorus and sulfur mobilizing bacteria

Aaron Fox, Jacinta Gahan, Israel Ikoyi, WITOLD KWAPINSKI, Orla O'Sullivan, Paul D. Cotter, Achim Schmalenberger

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Table 1: Mean values of *Hordeum vulgare* heights (cm), dry weights (g) and soil solution pH per pot (2 plants, combined weights, averaged heights, eight replicates) under different biochar regimes. Different letters indicate significant differences ($P \leq 0.05$); \pm represents standard deviation.

Treatment	Height (cm)	\pm	Weight (g)	\pm	pH	\pm
Control	46.24 ^a	3.64	0.71 ^A	0.12	5.59 ^a	0.12
Biochar 1%	69.91 ^b	4.52	2.89 ^B	0.55	6.68 ^b	0.24
Biochar 2%	72.38 ^b	6.96	3.44 ^C	0.43	7.04 ^y	0.14

Table 2A: Spring barley shoot element analysis (mg g⁻¹ DW; composite samples)

	Control	Biochar 1 %	Biochar 2 %
Potassium	25.2	33.5	36.8
Calcium	9.5	9.2	6.8
Nitrogen	10.9	5.5	3.7
Sulfur	7.5	4.4	3.5
Magnesium	1.9	1.8	1.5
Phosphorus	0.5	0.3	0.4
Iron	0.146	0.249	0.025
Manganese	0.117	0.060	0.042
Boron	0.021	0.012	0.008
Zinc	0.011	0.006	0.004
Copper	0.009	0.005	0.002
Molybdenum	0.002	0.001	<0.001

Table 2B: Spring barley shoot element mass balance (mg pot⁻¹)

	Control	Biochar 1 %	Biochar 2 %
Potassium	17.9	96.8	126.6
Calcium	6.7	26.6	23.4
Nitrogen	7.7	15.9	12.7
Sulfur	5.3	12.7	12.0
Magnesium	1.3	5.2	5.2
Phosphorus	0.4	0.9	1.4
Iron	0.104	0.720	0.086
Manganese	0.083	0.174	0.143
Boron	0.015	0.035	0.028
Zinc	0.008	0.016	0.014
Copper	0.007	0.014	0.008
Molybdenum	0.001	0.004	<0.001

Table 3: MPN values of desulfonating (MM2TS), phytate mobilizing (MM2Phy) and phosphonoacetic acid mobilizing (MM2PAA) bacteria as well as CFU values of tri-calcium phosphate solubilizing (TCP) bacteria in the rhizosphere of *Hordeum vulgare* under different biochar regimes (control, biochar 1 and 2 %, eight replicates). Different letters indicate significant differences ($P \leq 0.05$); \pm represents standard deviation.

Treatment	MM2TS	\pm	MM2Phy	\pm	MM2PAA	\pm	TCP	\pm
Control	$2.75 \cdot 10^3$ ^A	$1.02 \cdot 10^3$	$7.68 \cdot 10^3$ ^a	$2.29 \cdot 10^3$	$2.27 \cdot 10^3$ ^x	$1.58 \cdot 10^3$	$3.86 \cdot 10^3$ ^X	$8.54 \cdot 10^2$
Biochar 1 %	$1.03 \cdot 10^4$ ^B	$4.83 \cdot 10^3$	$4.94 \cdot 10^4$ ^b	$2.88 \cdot 10^4$	$1.07 \cdot 10^4$ ^y	$6.79 \cdot 10^3$	$1.12 \cdot 10^4$ ^Y	$1.83 \cdot 10^3$
Biochar 2 %	$1.56 \cdot 10^4$ ^C	$8.82 \cdot 10^3$	$5.56 \cdot 10^4$ ^b	$3.29 \cdot 10^4$	$1.96 \cdot 10^4$ ^y	$1.62 \cdot 10^4$	$1.29 \cdot 10^5$ ^Z	$2.12 \cdot 10^4$

Table 4: Genus specific 16S rRNA gene copy numbers per ng DNA from control, 1 and 2 % biochar treatments (eight replicates). Different letters indicate significant differences ($P \leq 0.05$); \pm represents standard deviation.

	<i>Arthrobacter</i>	\pm	<i>Brevundimonas</i>	\pm	<i>Cupriavidus</i>	\pm
Control	188.1 ^A	30.0	4.1 ^a	2.0	12.5 ^{α}	2.8
Biochar 1%	149.9 ^A	16.0	17.7 ^b	8.1	24.2 ^{β}	1.1
Biochar 2%	322.7 ^B	45.7	777.9 ^c	319.3	257.4 ^{γ}	15.9

Table 5: Abundance of sulfur (S) species [%] estimated from S K-edge XANES white lines (triplicates) after Gaussian peak fitting (GS) and white line correction; \pm represents standard deviation.

	Thiols (GS1)	\pm	Sulfoxides (GS2)	\pm	Sulfonates (GS3)	\pm	Sulfate ester (GS4)	\pm
Biochar	9.22	1.34	0.85	0.09	n.d.	n.d.	90.01	0.57
Soil	30.58	5.14	5.19	0.74	36.03	1.81	28.20	2.34
<i>Miscanthus</i>	33.79	7.17	18.57	3.51	23.65	5.70	23.99	6.15

n.d. = not detected

Table 6. Multiple linear regression model**A) Initial multiple linear regression model including all predictors**

Dependent variable	Predictors	Coefficients	<i>P</i> values	VIF	Adjusted R ²
Shoot dry weight (DW)	pH	0.91	0.094	6.87	0.7631
	<i>Brevundimonas</i> (16S)	0.16	0.593	5.41	
	Phytate utilizer	0.67	0.250	3.68	
	Calcium-PO ₄ utilizer	0.12	0.763	4.11	
	Sulfonate utilizer	0.24	0.558	2.41	

B) Stepwise regression final model based on AIC with all predictors

Dependent variable	Predictor	Coefficient	<i>P</i> value	VIF	Adjusted R ²
DW	pH	1.72	p≤0.0001	n.a.	0.7745

C) Stepwise regression final model based on AIC without collinear predictors (VIF>5)

Dependent variable	Predictors	Coefficients	<i>P</i> values	VIF	Adjusted R ²
DW	Phytate utilizer	1.45	0.002	1.75	0.7408
	Calcium-PO ₄ utilizer	0.57	0.05	1.74	
	Sulfonate utilizer	0.57	0.13	1.82	

pH=soil pH, *Brevundimonas*=log of 16S rRNA gene copies of *Bevundimonas* sp., Phytate utilizer=log of phytate utilizing bacteria (MPN), Calcium-PO₄ utilizer=log of calcium phosphate solubilizing bacteria (CFU) and Sulfonate utilizer=log of toluenesulfonate utilizing bacteria (MPN); VIF=variance inflation factor; AIC= Akaike Information Criterion; n.a.=not applicable