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**Agro-wastes as feedstock for the production of endo- $\beta$ -xylanase from *Cohnella* sp. strain AR92**

**Online supplementary table headings**

**Online supplementary table 1.** Plackett-Burman design matrix and the response variables evaluated

**Online supplementary table 2.** Estimated effects for xylanase production and growth of *Cohnella* sp. strain AR92 from the Plackett-Burman design

**Online supplementary table 3.** Box-Behnken matrix for the three selected factors and their experimental and predicted values of xylanase activity

**Online supplementary table 4.** Estimated effects and statistical analysis for xylanase production from the results of the Box-Behnken design

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**Online supplementary fig. 1.** Maximum-likelihood (**a**) and maximum-parsimony (**b**) phylogenetic trees based on 16S rRNA gene sequences, showing the position of strain AR92 and related taxa. Bootstrap values are shown as percentages of 100 replicates; only values above 70% are shown. The four species of the genus *Paenibacillus* were used as outgroup. Bar, 0.02 substitutions per nucleotide position. Accession numbers are shown after names

**Online supplementary fig. 2.** Effect of different nitrogen sources on the *Cohnella* sp. AR92 growth (**●**, biomass at 96 h) and xylanase production at (**■**) 48 h; (**▨**) 96 h and (**▨**) 192 h. Error bars represent the standard deviation from at least three independent experiments

**Online supplementary fig. 3.** Response surface and contour plots of the combined effects on xylanase production (**a**) of yeast extract and phosphor concentrations, and (**b**) of yeast extract and carbon (OH-SCB) concentrations

**Online supplementary table 1.** Plackett-Burman design matrix and the response variables evaluated

Run	Coded values*						Xylanase Activity [IU/ml]	Biomass [CFU/ml]
	C	N	Ca <sup>2+</sup>	Mg <sup>2+</sup>	YE	P		
1	-1	+1	+1	+1	+1	+1	11.2	7.0·10 <sup>7</sup>
2	+1	-1	-1	+1	+1	-1	4.3	1.2·10 <sup>7</sup>
3	-1	-1	-1	-1	+1	-1	5.2	9.0·10 <sup>6</sup>
4	+1	+1	+1	+1	-1	-1	0.9	3.0·10 <sup>6</sup>
5	+1	-1	+1	-1	+1	+1	4.9	4.5·10 <sup>7</sup>
6	+1	-1	-1	-1	-1	+1	0.9	5.0·10 <sup>6</sup>
7	+1	+1	-1	-1	+1	+1	5.3	2.5·10 <sup>8</sup>
8	+1	-1	+1	+1	-1	+1	4.8	2.0·10 <sup>6</sup>
9	+1	+1	+1	-1	-1	-1	0.5	2.3·10 <sup>6</sup>
10	-1	-1	-1	-1	-1	-1	0.8	7.2·10 <sup>5</sup>
11	+1	-1	+1	+1	+1	+1	8.1	7.0·10 <sup>7</sup>
12	-1	+1	+1	-1	-1	+1	3.3	2.0·10 <sup>7</sup>
13	-1	-1	+1	+1	-1	-1	3.1	8.8·10 <sup>5</sup>
14	-1	-1	-1	+1	-1	+1	3.5	2.5·10 <sup>6</sup>
15	+1	+1	-1	+1	-1	+1	2.5	7.0·10 <sup>6</sup>
16	+1	+1	+1	+1	+1	-1	4.4	2.0·10 <sup>7</sup>
17	+1	+1	-1	-1	-1	-1	0.2	7.5·10 <sup>5</sup>
18	+1	-1	-1	+1	+1	-1	4.1	1.5·10 <sup>7</sup>
19	-1	+1	-1	+1	-1	-1	3.7	8.5·10 <sup>5</sup>
20	-1	+1	-1	+1	+1	+1	13.7	5.5·10 <sup>7</sup>
21	-1	+1	-1	-1	+1	+1	7.9	2.5·10 <sup>7</sup>
22	+1	-1	+1	-1	-1	+1	0.9	9.5·10 <sup>6</sup>
23	-1	-1	+1	-1	+1	-1	5.4	7.5·10 <sup>6</sup>
24	-1	+1	+1	-1	+1	-1	4.2	6.0·10 <sup>6</sup>

\* Coded value (-1) represented the low levels of the studied factors (g/l): OH-SCB (C) 5.0; (NH4)<sub>2</sub>SO<sub>4</sub> (N) 0.5; CaCl<sub>2</sub>·2H<sub>2</sub>O (Ca<sup>2+</sup>) 0.0; MgCl<sub>2</sub>·6H<sub>2</sub>O (Mg<sup>2+</sup>) 0.0; yeast extract (YE) 0.1 and Na<sub>2</sub>HPO<sub>4</sub>/KH<sub>2</sub>PO<sub>4</sub> (P) 0.35/0.1. Coded value (+1) denoted the high levels of the independent variables: C 10.0; N 1.0; Ca<sup>2+</sup> 0.1; Mg<sup>2+</sup> 0.5; YE 1.0 and P 3.5/1.0.

**Online supplementary table 2.** Estimated effects for xylanase production and growth of *Cohnella* sp. strain AR92 from the Plackett-Burman design

Factor	Xylanase Activity			Biomass		
	[IU/ml]			[CFU/ml]		
	Effect	Standard error	p- value	Effect	Standard error	p- value
C	-2.482	0.498	0.000	0.292	0.099	0.009
N	0.988	0.498	0.063	0.192	0.099	0.071
P	2.512	0.498	0.000	0.708	0.099	0.000
YE	4.467	0.498	0.000	1.008	0.099	0.000
Mg <sup>2+</sup>	2.068	0.498	0.001	-0.058	0.099	0.565
Ca <sup>2+</sup>	-0.012	0.498	0.982	0.108	0.099	0.291

**Online supplementary table 3.** Box-Behnken matrix for the three selected factors and their experimental and predicted values of xylanase activity

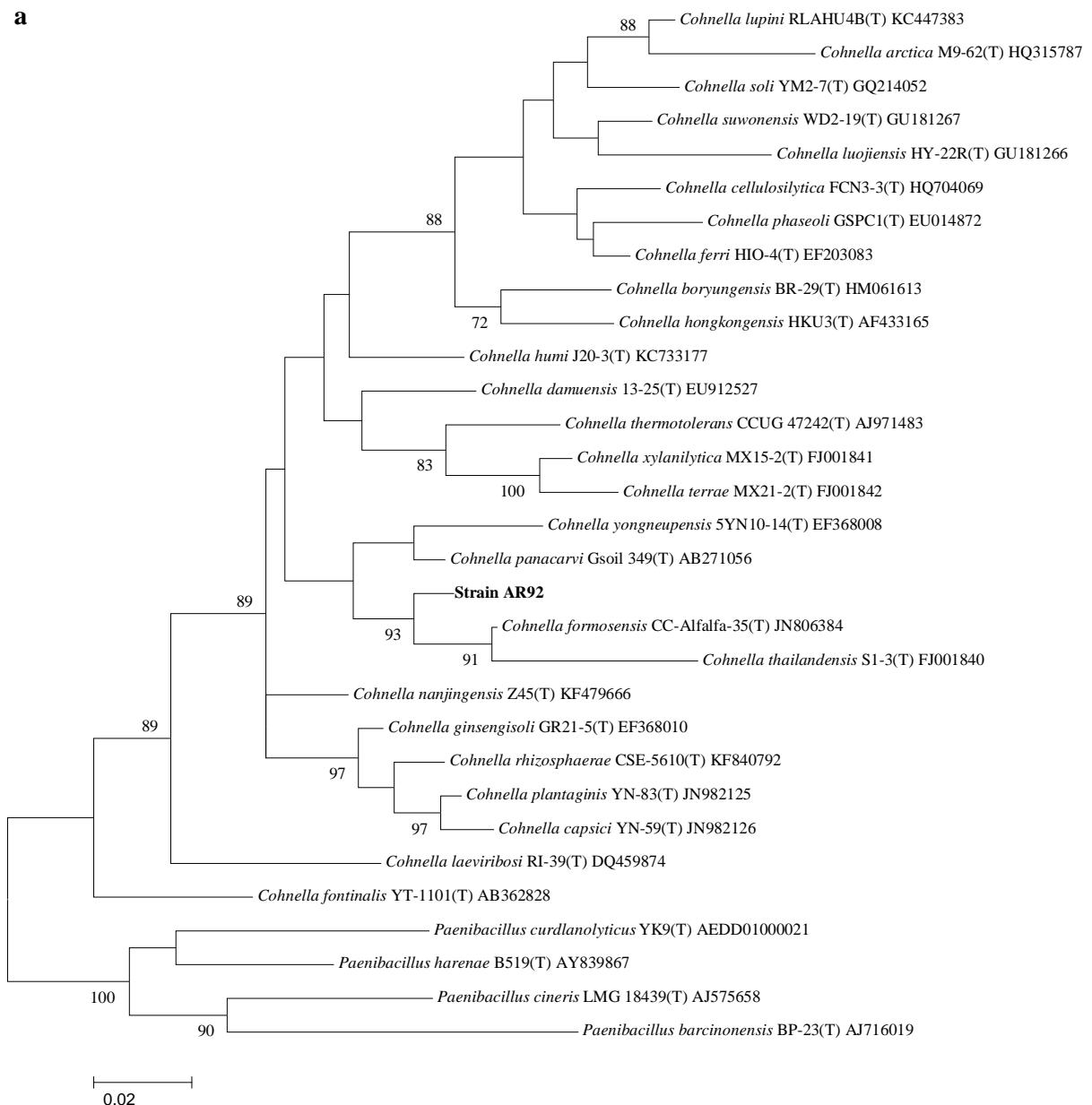
Run	Values (g/l)			Produced EA [IU/ml]	Predicted EA [IU/ml]
	C	YE	P		
1	6.0	1.5	5.25/1.50	14.2	14.5
2	10.0	1.0	1.75/0.50	12.4	12.2
3	6.0	1.0	3.50/1.00	13.9	14.5
4	6.0	1.5	1.75/0.50	11.4	11.9
5	2.0	0.5	3.50/1.00	6.5	6.3
6	2.0	1.0	1.75/0.50	7.2	7.1
7	2.0	1.0	5.25/1.50	8.1	8.6
8	6.0	1.0	3.50/1.00	14.6	14.5
9	6.0	0.5	1.75/0.50	9.9	9.4
10	10.0	0.5	3.50/1.00	9.7	10.3
11	6.0	1.0	3.50/1.00	14.6	14.5
12	6.0	0.5	5.25/1.50	11.3	10.3
13	10.0	1.5	3.50/1.00	14.7	14.8
14	10.0	1.0	5.25/1.50	14.2	14.1
15	2.0	1.5	3.50/1.00	8.9	8.4
16	6.0	1.0	3.50/1.00	14.5	14.5
17	6.0	1.0	3.50/1.00	14.6	15.0
18	2.0	1.5	3.50/1.00	9.7	8.9
19	6.0	1.5	1.75/0.50	12.4	12.5
20	2.0	0.5	3.50/1.00	6.8	6.7
21	10.0	1.0	1.75/0.50	13.4	12.7
22	2.0	1.0	5.25/1.50	8.7	9.1
23	2.0	1.0	1.75/0.50	6.9	7.6
24	6.0	0.5	1.75/0.50	9.7	9.9
25	10.0	0.5	3.50/1.00	10.2	10.8
26	6.0	1.0	3.50/1.00	15.5	15.0
27	6.0	0.5	5.25/1.50	10.6	10.8
28	10.0	1.5	3.50/1.00	15.2	15.4
29	6.0	1.0	3.50/1.00	15.1	15.0
30	10.0	1.0	5.25/1.50	15.1	14.6
31	6.0	1.0	3.50/1.00	15.4	15.0
32	6.0	1.5	5.25/1.50	15.1	15.0

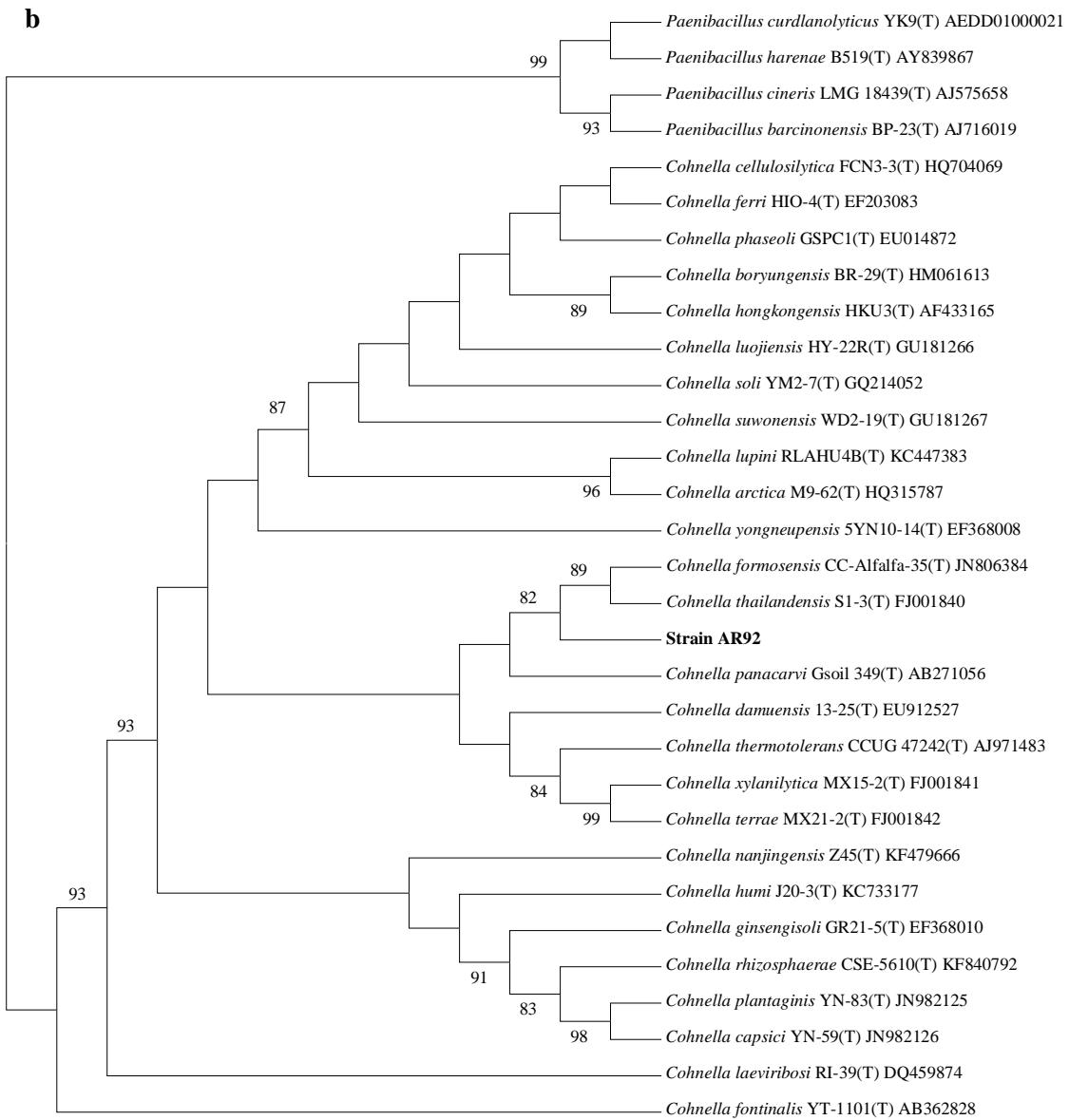
**Online supplementary table 4.** Estimated effects and statistical analysis for xylanase production from the results of the Box-Behnken design

Estimated effects			ANOVA			
Factor	Effect	Standard error	Sum of squares	Degree of freedom	F-value	p-value
C	5.418	0.262	106.245	1	428.56	0.000
YE	3.194	0.262	36.926	1	148.95	0.000
P	1.735	0.249	12.041	1	48.57	0.000
CC	-5.797	0.361	63.849	1	257.55	0.000
C:YE	1.471	0.387	3.5772	1	14.43	0.001
C:P	0.210	0.352	0.088	1	0.36	0.558
YE:YE	-3.667	0.361	25.548	1	103.06	0.000
YE:P	0.845	0.352	1.428	1	5.76	0.026
P:P	-2.280	0.361	9.881	1	39.86	0.000

**Online supplementary figure 1**

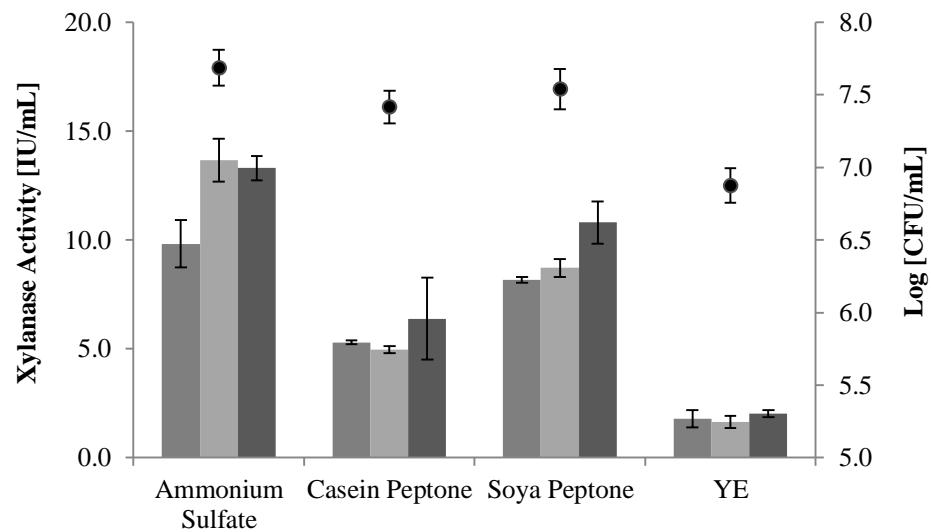
a



**b**

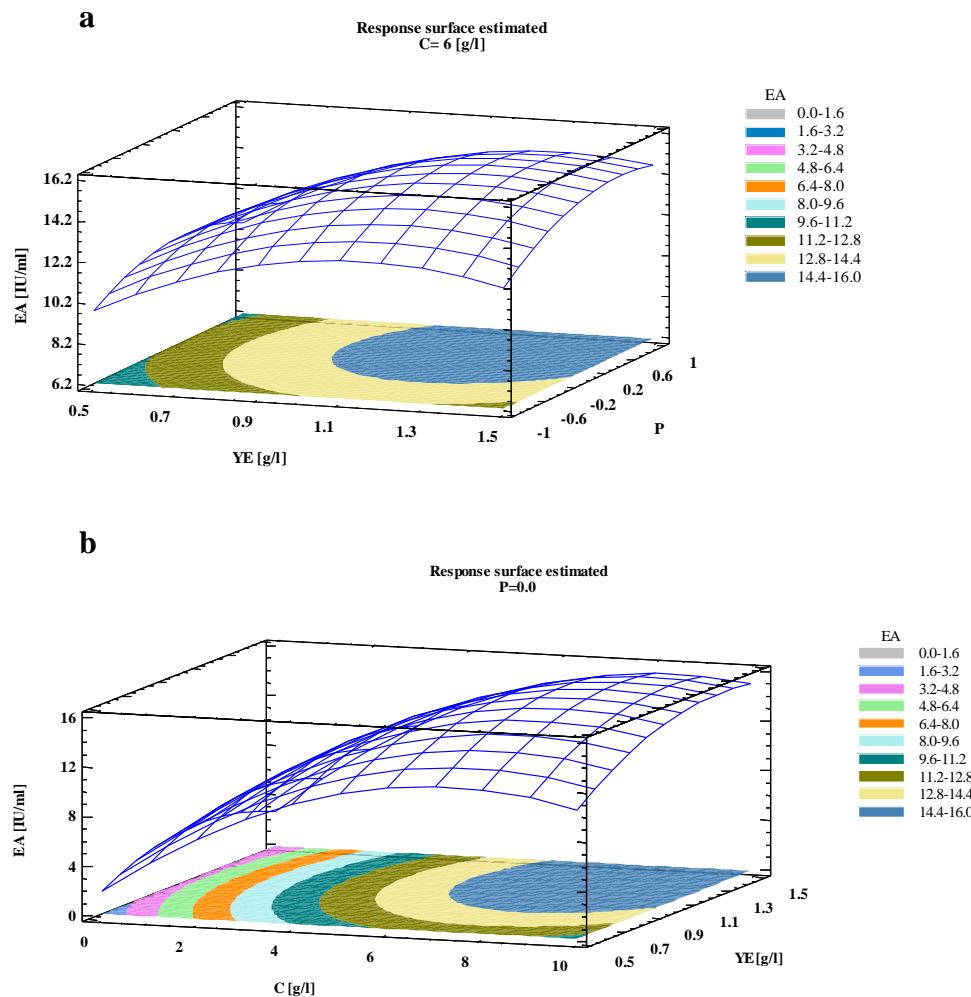
**Online supplementary fig. 1.** Maximum-likelihood (a) and maximum-parsimony (b) phylogenetic trees based on 16S rRNA gene sequences, showing the position of strain AR92 and related taxa. Bootstrap values are shown as percentages of 100 replicates; only values above 70% are shown. The four species of the genus *Paenibacillus* were used as outgroup. Bar, 0.02 substitutions per nucleotide position. Accession numbers are shown after names.

**Online supplementary figure 2**



**Online supplementary fig. 2.** Effect of different nitrogen sources on the *Cohnella* sp. AR92 growth (●, biomass at 96 h) and xylanase production at (■) 48 h; (▨) 96 h and (■) 192 h. Error bars represent the standard deviation from at least three independent experiments.

**Online supplementary figure 3**



**Online supplementary fig. 3.** Response surface and contour plots of the combined effects on xylanase production **(a)** of yeast extract and phosphor concentrations, and **(b)** of yeast extract and carbon (OH-SCB) concentrations.