

Kinetics and new mechanism of azoxystrobin biodegradation by an *Ochrobactrum anthropi* strain SH14

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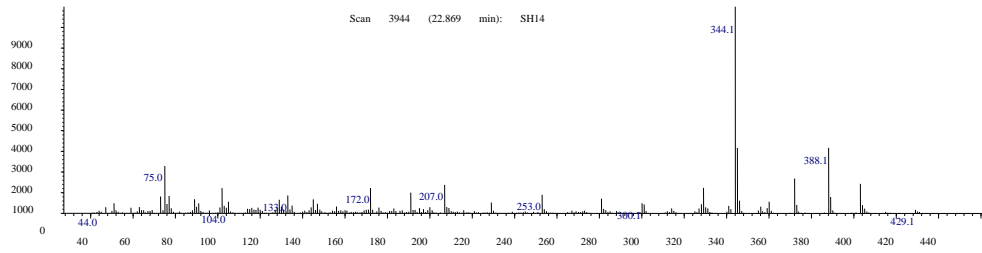
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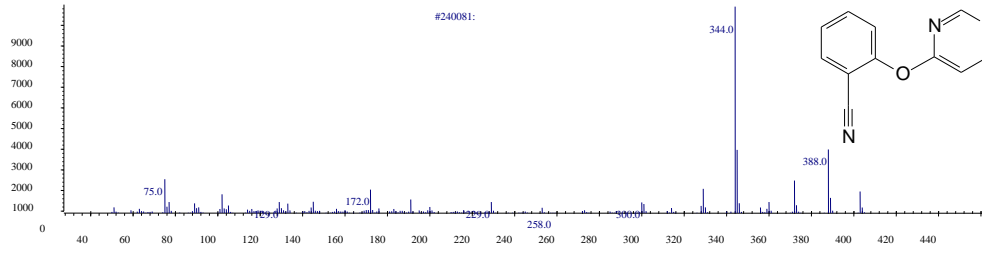
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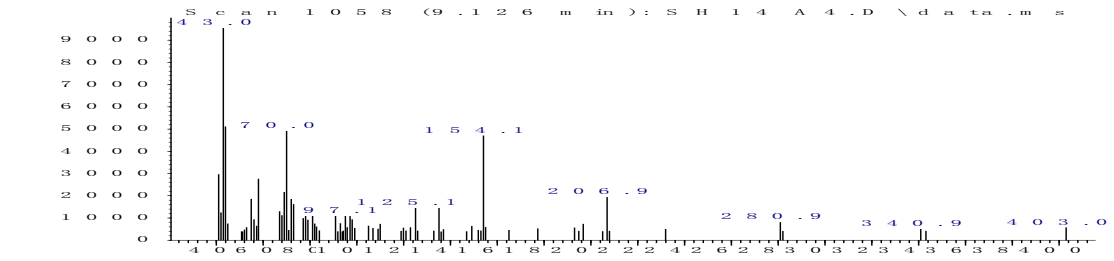
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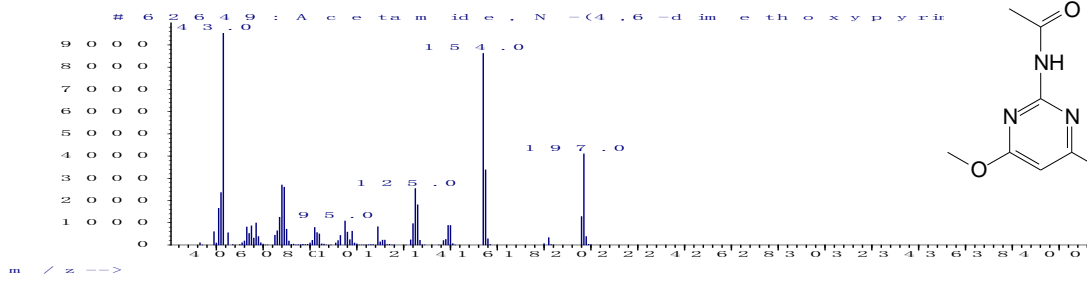
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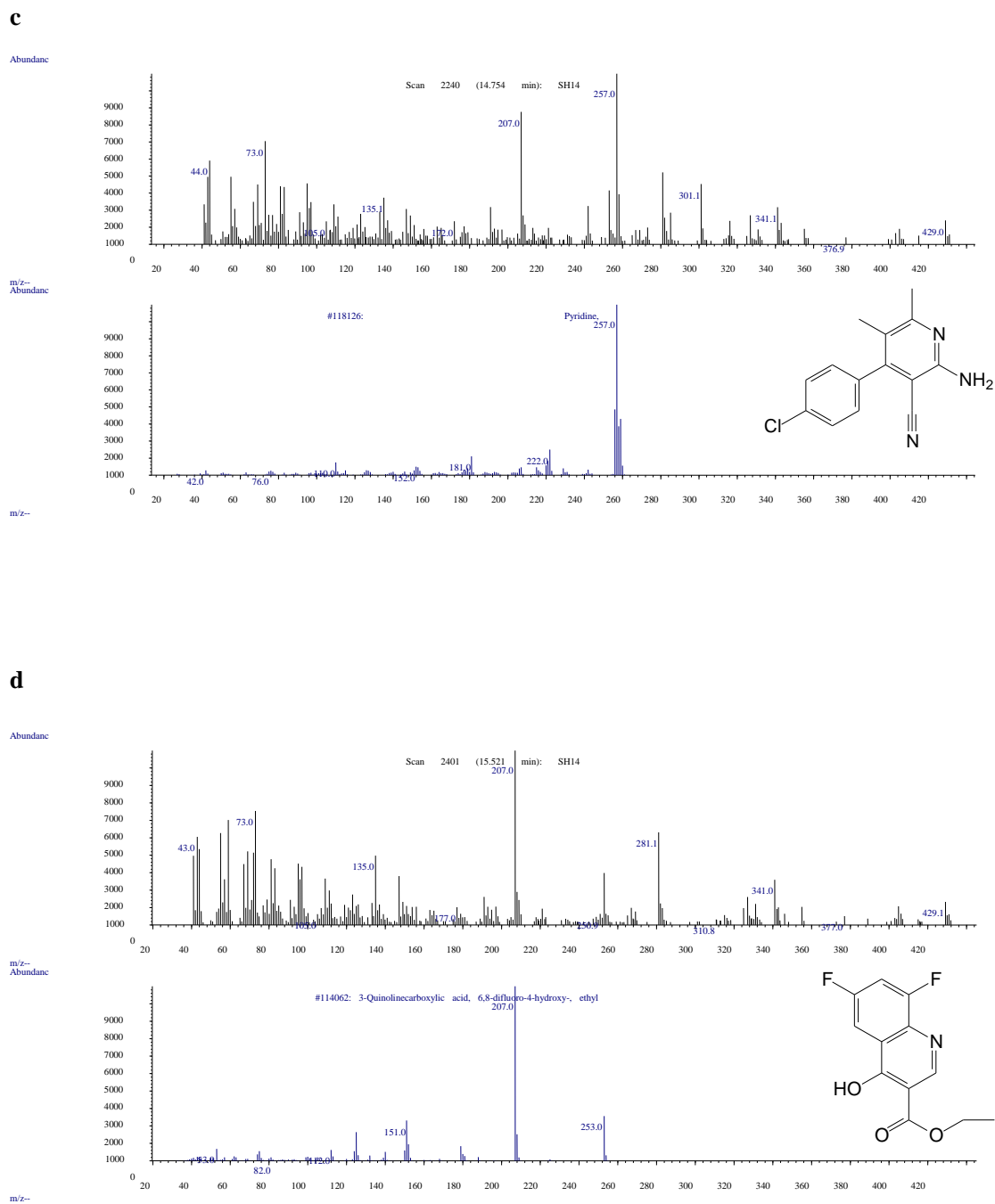


Figure S1. Gas chromatography–mass spectrometry (GC-MS) analysis of the metabolites produced during azoxystrobin degradation by strain SH14. (a–d) Characteristic ions of compounds (A–D). Retention time of each compound was noted as 22.869, 9.126, 14.754 and 15.521 min, respectively and were identified as (a) azoxystrobin; (b) *N*-(4,6-dimethoxypyrimidin-2-yl)-acetamide; (c) 2-amino-4-(4-chlorophenyl)-3-cyano-5,6-dimethyl-pyridine; (d) 3-quinolinecarboxylic acid, 6,8-difluoro-4-hydroxy-, ethyl ester, respectively

Table S1. Analysis of variance (ANOVA) for the fitted quadratic polynomial model of azoxystrobin degradation by strain SH14.

Source	DF	SS	MS	F Value	P Level*
X ₁	1	35.2795	35.2795	10.0001	0.0074
X ₂	1	45.7476	45.7476	12.9681	0.0032
X ₃	1	8.305	8.305	2.3542	0.0416
X ₁ X ₁	1	2010.88	2010.88	570.0243	0.0001
X ₁ X ₂	1	9.245	9.245	2.62068	0.0455
X ₁ X ₃	1	0	0	0	1
X ₂ X ₂	1	168.7994	168.7994	47.8496	0.0001
X ₂ X ₃	1	3.38	3.38	0.9581	0.3455
X ₃ X ₃	1	52.0429	52.0429	14.7526	0.002
Model	9	2320.06	257.7955	73.0773	0.0001
Error	13	45.8602	3.5277		
Total	22	2366.02			

Note: $R^2=0.9806$, $adj.R^2=0.9672$. DF refers to degrees of freedom; SS refers to sum of sequences; MS refers to mean square. *P Level less than 0.05 indicates that the model terms are significant.