Dereplicating and Spatial Mapping of Secondary Metabolites from Fungal Cultures in Situ

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Figure S1. (**A**) The guttate (red circle) and mycelium (blue circle) of fungal code G100, *Clohesyomyces aquaticus*, were sampled using the droplet-LMJ-SSP. A clearer picture of the guttates from a different culture of G100 is shown on the right. (**B**) The base peak chromatogram displayed phomopsinone A in the guttate (red). (**C**) The same peak was not apparent in the mycelium (blue). The XIC for phomopsinone A (m/z 225.11 at 4.43 min) was over two orders of magnitude higher in counts per second (cps) for (**D**) the guttate (4.8x10⁵ cps) over (**E**) the mycelium (1.4x10³ cps).

Figure S2. Comparison of the MS/MS fragmentation for (A) compound 5 with (B) its standard and (C) compound 6 with its (D) standard.

Figure S3. The extracted ion chromatogram (XIC) of m/z (**A**) 381.1099 ± 5 ppm and (**B**) 399.1204 ± 5 ppm. (**C**) At 3.47 min, the accuracy for $[M + H]^+$ between the observed and calculated was 0.3 ppm (399.1204 observed vs. 399.1205 calculated for $[C_{19}H_{24}O_7Cl + H]^+$ with multiple indicators suggesting for the parent ion. The HCD fragmentation (NCE =23) of molecular ions with m/z (**D**) 381.11 and (**E**) 399.12 detected at 3.47 min. (**F**) Proposed structure based off of assumed biosynthetic route.

Figure S4. (**A**) Contaminated fungal culture coded MSX19583 with the "green" fungus indicated by the green circles and the "purple" fungus indicated by the purple circles. (**B**) Isolated fungal cultures of MSX19583 (green), *Aspergillus sydowii*, (**C**) and the contaminant (purple), *Chaetomium* sp.

Figure S5. (A) Structure of a diketopiperazine dimer (9) detected on the green fungal culture coded MSX19583 (Figure S4A). (B) A comparison of the extracted ion chromatograms (XIC) from the fungal culture (top) and the standard (bottom) for the accurate mass of compound 9. (C) A comparison of the HRMS and the MS/MS for the fungal culture and the standard for compound 9.

Figure S6. (**A**) Structure of cyclo-(L-phenylalaninyl-L-tryptophanyl) (**10**) detected on the green fungal culture coded MSX19583 (Figure S4A). (**B**) A comparison of the extracted ion chromatograms (XIC) from the fungal culture (top) and the standard (bottom) for the accurate mass of compound **10.** (**C**) A comparison of the HRMS and the MS/MS for the fungal culture and the standard for compound **10**.

Figure S7. (A) Image of pure culture MSX19583 with yellow crosshairs indicating sampled areas. (B) Heat map of compound 9 as sampling from the contaminant to the culture. (C) Heat map of compound 8 as sampling from the contaminant to the culture. (D) The color scale and diameter of spot indicate the relative amount of signal detected for the given analytes.

Figure S8. 3D model created using SketchUp Make of the custom tray designed to hold a Petri dish and a solvent vial (**A**). Photograph of the printed tray using the F306 3D printer (**B**).

Table S1. Fungal metabolites that were detected by the droplet-LMJ-SSP, recording the retention time (Rt), UV data, HRMS, and MS/MS.



Figure S1. (A) The guttate (red circle) and mycelium (blue circle) of fungal code G100, *Clohesyomyces aquaticus*, were sampled using the droplet-LMJ-SSP. A clearer picture of the guttates from a different culture of G100 is shown on the right. (B) The base peak chromatogram displayed phomopsinone A in the guttate (red). (C) The same peak was not apparent in the mycelium (blue). The XIC for phomopsinone A (m/z 225.11 at 4.43 min) was over two orders of magnitude higher in counts per second (cps) for (D) the guttate (4.8×10^5 cps) over (E) the mycelium (1.4×10^3 cps).



Figure S2. Comparison of the MS/MS fragmentation for (A) compound 5 with (B) its standard and (C) compound 6 with its (D) standard.



Figure S3. The extracted ion chromatogram (XIC) of m/z (**A**) 381.1099 ± 5 ppm and (**B**) 399.1204 ± 5 ppm. (**C**) At 3.47 min, the accuracy for $[M + H]^+$ between the observed and calculated was 0.3 ppm (399.1204 observed vs. 399.1205 calculated for $[C_{19}H_{24}O_7Cl + H]^+$ with multiple indicators suggesting for the parent ion. The HCD fragmentation (NCE =23) of molecular ions with m/z (**D**) 381.11 and (**E**) 399.12 detected at 3.47 min. (**F**) The proposed structure based off of the presumed biosynthetic route, where the hydroxy group was placed at position 8 due to similar oxygenation patterns observed with related analogues.³¹



Figure S4. (**A**) Contaminated fungal culture coded MSX19583 with the "green" fungus indicated by the green circles and the "purple" fungus indicated by the purple circle. (**B**) Isolated fungal cultures of MSX19583 (green), *Aspergillus sydowii*, (**C**) and the contaminant (purple), *Chaetomium* sp.



Figure S5. (**A**) Structure of a diketopiperazine dimer (**9**) detected on the green fungal culture coded MSX19583 (Figure S4A). (**B**) A comparison of the extracted ion chromatograms (XIC) from the fungal culture (top) and the standard (bottom) for the accurate mass of compound **9.** (**C**) A comparison of the HRMS and the MS/MS for the fungal culture and the standard for compound **9**.



Figure S6. (A) Structure of cyclo-(L-phenylalaninyl-L-tryptophanyl) (10) detected on the green fungal culture coded MSX19583 (Figure S4A). (B) A comparison of the extracted ion chromatograms (XIC) from the fungal culture (top) and the standard (bottom) for the accurate mass of compound 10. (C) A comparison of the HRMS and the MS/MS for the fungal culture and the standard for compound 10.



Figure S7. (A) Image of pure culture MSX19583 with yellow crosshairs indicating sampled areas. (B) Heat map of compound 9 as sampling from the contaminant to the culture. (C) Heat map of compound 8 as sampling from the contaminant to the culture. (D) The color scale and diameter of spot indicate the relative amount of signal detected for the given analytes.



Figure S8. 3D model created using SketchUp Make of the custom tray designed to hold a Petri dish and a solvent vial (**A**). Photograph of the printed tray using the F306 3D printer (**B**).

Table S1. Fungal metabolites that were identified by the droplet-LMJ-SSP, recording the retention time (Rt), UV data, HRMS, and MS/MS.

			G100 ¹³ Clohesyomyces aquaticus GenBank # KM589854 Freshwater fungus isolated from submerged wood			
#	Chemical Structure and Chemical formula	Rt (min)	UV (nm)	Positi	ve Ionization Mode	
1	Phomopsinone A C ₁₂ H ₁₆ O ₄	4.36	205 221 284	225.1120 (-0.6)	153.0546 111.0440, 135.0440 125.0597, 97.0646 79.0178, 121.0283	
2	$\mathbf{Pyrenocine } \mathbf{M}$ $C_{12}H_{18}O_{4}$	3.62	208 221 283	227.1278 (+0.1)	209.1171 167.0703, 131.0854 93.0699, 79.0541 197.1172, 139.0390	
3	$\begin{array}{c} O \\ O \\ O \\ H \\ \hline \end{array} \\ O \\ O \\ H \\ O \\ O \\ O \\ H \\ O \\ O \\ O$	5.50	193 222 264 337	639.1713 (+0.7)	183.0651, 561.1390 193.0495, 501.1177 579.1493, 483.1071 589.1340, 377.0652 169.0495, 455.0979 543.1285, 151.0390	

4	$ \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \begin{array}{c} \end{array}\\ \end{array}\\ \end{array}\\ \end{array}\\ \end{array}\\ \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \begin{array}{c} \end{array}\\ \end{array}$ \left(\begin{array}{c} \end{array}\\ \end{array}\\ \left(\begin{array}{c} \end{array}\\ \end{array}\\ \left(\begin{array}{c} \end{array}\\ \end{array}\\ \left(\begin{array}{c} \end{array}\\ \end{array} \left(\begin{array}{c} \end{array}\\ \left(\begin{array}{c} \end{array}\\ \end{array} \left(\begin{array}{c} \end{array}\\ \end{array} \left(\begin{array}{c} \end{array}\right) \left(\begin{array}{c} \end{array}) \left(\begin{array}{c} \end{array}) \left(\begin{array}{c} \end{array}) \left(\end{array}) \left(\begin{array}{c} \end{array}) \left(\end{array}) \left(\end{array}) \left(\begin{array}{c} \end{array}) \left(\end{array}) \left) \left(\end{array}) \left) \left(\end{array}) \left) \left(\end{array}) \left) \left(\end{array}) \left(\end{array}) \left(\end{array}) \left) \left(\end{array}) \left) \left(\end{array}) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left(\\) \left(\end{array}) \left) \left(\\) \left(\end{array}) \left(\\) \left() \left(\\) \left	4.98	192 216	1137.6570 (+1.4)	86.0963, 268.1651 256.1653, 228.1704 350.2066, 39.1958 377.2065, 405.2017 211.1438, 286.1754 484.2432, 155.0813 654.3506, 559.2763
		F	ungus isolate	G87 ³¹ <i>Halenospora</i> a GenBank # K ed from submer ₃	iff. <i>varia</i> J803850 ged wood in fresh water
#	Chemical Structure and Chemical formula	Rt	UV (nm)	Positi	ive Ionization Mode
		(min)		$[M+H]^+$	MS/MS
5	HO CI Greensporone A	4.03	222 294	381.1099 (0.0)	265.0259, 237.0310 241.0261, 123.0804 145.0648, 215.0102 253.0260, 263.0466 209.0364, 345.0883 363.0987, 281.0574

6	HO + CI + C	4.20	238 291	381.1099 (0.0)	265.0262, 237.0312 241.0261, 253.0261 145.0648, 209.0362 123.0805, 215.0104 289.0265, 345.0886 363.0995, 303.0793
7	HO + CI + O + O + O + O + O + O + O + O + O +	4.45	218 291	383.1256 (0.0)	265.0619, 263.0472 215.0104, 125.0961 83.0491, 171.0209 224.9948, 243.0054 253.0261, 237.0673 227.0624, 293.0577 305.0581, 329.0937 347.1045, 365.1153
8	$HO \qquad \downarrow \qquad $	4.70	217 290	383.1255 (-0.2)	241.0252, 107.0857 79.0543, 97.1014 125.0958, 211.0159 224.9953, 253.0249 265.0253, 293.0578 309.0531, 347.1031 365.1136, 329.0913
MSX19583 ³² Aspergillus sydowii GenBank # ITS: KP702233; RPB1: KP702234; RPB2: KP702231, KP702232 Fungus from MSX library					
#	Chemical Structure and Chemical formula	Rt (min)	UV (nm)	Positi [M+H] ⁺	ive Ionization Mode MS/MS

9	$\mathbf{Diketopiperazine dimer}_{C_{40}H_{36}N_6O_4}$	4.48	192 208 300	665.2877 (+0.9)	157.0763, 304.1448 332.1401, 130.0652 120.0811, 185.0715 241.0845, 433.1996 259.1226, 286.1351
10	Cyclo-(L-phenylalaninyl-L-tryptophanyl) C ₂₀ H ₁₉ N ₃ O ₂	3.46	191 218 279 289 364	334.1549 (-0.3)	130.0652, 170.0596 120.0810, 159.0914 175.0863, 234.1275 205.0968, 289.1338 261.1387, 91.0543
11	HO OH OH S-sydonic acid C ₁₅ H ₂₂ O ₄	5.07	212 240 300	[M+H-H ₂ O] ⁺ 249.1486 (+0.3)	165.0549, 151.0386 69.0699, 107.0490 121.0646, 179.0704 193.0865, 231.1387 85.1010, 213.1267
12	HOOH	4.96	198 221 278	[M+H-H ₂ O] ⁺ 235.1694 (+0.6)	151.0755, 137.0601 121.0647, 161.0956 217.1589, 107.0490 175.1121, 147.0808 205.1593, 69.0700

	S-sydonol C ₁₅ H ₂₄ O ₃						
		End	G77 ³³ Aspergillus iizukae GenBank # AB859956 Endophytic fungus isolated from surface sterilized leaves of Silybum marianum				
#	Chemical Structure and Chemical formula	Rt (min)	UV (nm)	$\frac{\text{Posit}}{[M+H]^+}$	ive Ionization Mode MS/MS		
13	HO = O = O = O = O = O = O = O = O = O =	4.06	218 284	331.0810 (-0.7)	272.0681, 299.0535 275.0446, 284.0308 287.0917, 255.0649 244.0726, 228.0408		
14	$\begin{array}{c} \begin{array}{c} & & & \\ & & & \\ & & & \\ & & & \\ & & & \\ \end{array}$ Antibiotic SS 19508D; SS 19508D $C_{17}H_{13}O_{7}Cl$	4.52	214 284	365.0423 (+0.1)	306.0286, 333.0149 291.0060, 317.9919 321.0529, 286.0828 263.0098, 277.0258 286.0844, 271.0587		
15	$CI \rightarrow O \rightarrow $	5.15	220 284 352	399.0034 (+0.3)	339.9913, 324.9667 366.9775, 351.9529 296.9696, 310.9878 268.9758, 295.9627 355.0136, 320.0448		

16	$\begin{array}{c} OH & O & O \\ CI & & & \\ & & & \\ & & & \\ OHO & & OH \\ & & \\ OHO & & OH \\ & & \\ OHO & OHO \\ & & \\ OHO$	5.26	220 281 347	401.0190 (+0.2)	209.0444, 237.0391 277.0262, 341.9870 219.0286, 151.0389 326.9632, 368.9863 179.0337, 86.9995 305.0213, 297.9612		
		G324 <i>Penicillium</i> sp. GenBank # KM215636 Endophytic fungus isolated from surface sterilized leaves of <i>Silybum marianum</i>					
#	Chamical Structure and Chamical formula	Rt	UV (nm)	Positi	ve Ionization Mode		
П		(min)	C V (IIII)	$[M+H]^+$	MS/MS		
17	10, 20-dehydro[12,13-dehydroprolyl-2-(1,1- dimethylallyl) tryptophyl] diketopiperazine] C ₂₁ H ₂₁ N ₃ O ₂	3.56	222 270	348.1708 (+0.4)	196.1120, 292.1077 182.0964, 264.1128 237.1020, 306.1232 331.1448, 280.1080 169.0759, 130.0652		
18		4.09	217 288 437	350.1864 (+0.3)	130.0651, 198.1276 153.0657, 69.0700 238.1338, 294.1234 282.1232, 144.0807 221.1075, 183.1042 170.0598, 151.0500		



4	Chamical Structure and Chamical formula	Rt	Rt nin) UV (nm)	Positive Ionization Mode	
#	Chemical Structure and Chemical formula	(min)		$[M+H]^+$	MS/MS
20	HO HO HO HO HO HO HO HO HO HO HO HO HO H	7.08	224 295	374.2328 (+0.6)	175.1475, 71.0700 119.0853, 188.0562 105.0701, 83.0855 133.1012, 147.1166 170.0806, 200.0913 302.1758, 356.2210
G168 <i>Fusarium</i> sp. GenBank # KP897159 Endophytic fungus isolated from surface sterilized stems of <i>Hedera helix</i>					
#	Chamical Structure and Chamical formula	Rt	IW (nm)	Positi	ive Ionization Mode
π	Chemical Structure and Chemical for mula	(min)		$[M+H]^+$	MS/MS
21	$ \begin{array}{c} $	7.87	210	654.4301 (-3.5)	196.1325, 214.1431 86.0962, 100.1117 186.1486, 314.1964 210.1487, 228.1586 328.2092, 414.2442

22	$ \begin{array}{c} $	8.24	210	668.4458 (-3.4)	210.1489, 100.1117 228.1586, 196.1325 86.0962, 328.2093 200.1639, 217.1433 186.1487, 314.1956 441.2947, 598.7202
23	$\begin{array}{c} 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 \\ 0 $	5.05	223	571.0860 (-2.6)	485.0493, 556.0576 541.0351, 528.0696 496.0432, 456.0803 441.0589, 571.0832 513.0442, 511.0640 231.0291, 297.0352
]	MSX5955 Hypocreal GenBank # J(Fungus from MS	53 ³⁵ es sp. Q749725 SX library
#	Chemical Structure and Chemical formula	Rt (min)	UV (nm)	Positi [M+H] ⁺	ive Ionization Mode MS/MS

24	HO^{N}	5.63	212 303	697.1026 (0.0)	169.0603, 383.1494 232.0990, 615.1462 284.1017, 551.2020 401.1592, 266.0911 465.1022, 348.0461
25	$\begin{array}{c} & & OH \\ & & O \\ & & O \\ & & S \\ & & S \\ & & H \\ & H \\ & & H \\ $	5.44	210 300	727.11334 (0.3)	169.0671, 199.0712 232.0991, 284.1025 268.1075, 296.1021 314.1130, 383.1498 413.1608, 266.0918
MSX70741 ³⁶ Hypocreales sp. GenBank # JN377382 Fungus from MSX library					

		(min)		$[M+H]^+$	MS/MS	
26	$\begin{array}{c} ^{n} ^{n}$	6.38	217	1963.13428 (-1.6)	931.5340, 750.4118 849.4814, 466.2643 537.3010, 1189.6916 991.5539, 623.3485 381.2119, 744.4483	
		MSX57715 ³⁶ Hypocreales sp. GenBank # JN377381 Fungus from MSX library				
#	Chemical Structure and Chemical formula	Rt	LIV (nm)	m) Positive Ionization Mode		
	Chemical Structure and Chemical formula	(min)		$[M+H]^+$	MS/MS	
27	$\frac{\mathcal{F}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}}_{\mathcal{A}}^{\mathcal{A}}\mathcal{A}_{$	6.09	222	1937.12146 (-0.2)	908.5174, 724.3960 823.4647, 440.2488 511.2867, 774.4476 1163.6768, 335.1964 639.3439, 965.5388 1078.6225, 284.1588	
G169 G169 Alternaria sp. GenBank # KP897160 Endophytic fungus isolated from surface sterilized stems of Hedera helix					<i>a</i> sp. P897160 n surface sterilized stems of <i>eelix</i>	
#	Chamical Structure and Chamical formula	D t (min)	IIV (nm)	Nega	tive Ionization Mode	
#	Chemical Structure and Chemical Iormula			[M-H] ⁻	MS/MS	

28	HO HO Alternariol monomethyl ether C ₁₅ H ₁₂ O ₅	5.03	222 255 287 298 332 341	271.06070	256.0372, 250.9916 210.9987, 190.9926 231.0053, 204.9888 59.0135, 154.9923
29	$\begin{array}{c} OH \\ \hline \\ O \\ HO \\ HO \\ \hline \\ C_{20}H_{14}O_{6} \end{array} OH \\ OH$	3.89	216 257 285 356	349.0708 (+0.4)	303.0653, 261.0557 331.0616, 285.0551 313.0494, 275.0694 287.0371, 317.0466 301.0532, 338.3737
30	$\begin{array}{c} OH \\ \hline \\ \bullet \\ HO \\ HO \\ \hline \\ OH \\ \hline \\ OH \\ \hline \\ OH \\ OH$	3.81	218 258 283 356	351.0863 (0.0)	315.0647, 333.0765 305.0819, 263.0714 301.0494, 289.0500 285.0555, 298.0639 297.0555, 287.0700