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Antigenotoxicity of Depsidones Isolated from Brazilian Lichens

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Tables S1-S8.

NMR (^{1}H, ^{13}C) and spectral data of compounds 1-4 (Figures S1-S9).

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Table 1S. Frequency of mutant spots in wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the standard cross (ST) after co-treatment of larvae with protocetraric acid (**1**) and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
ST		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Corr.		
mwh/flr^3																		
Negative control	20	0.70	(14)		0.05	(1)		0.05	(1)		0.80	(16)		22	2.25			
DXR (0.2)	20	4.95	(99)	+	3.75	(75)	+	4.05	(81)	+	12.75	(255)	+	251	25.71	23.46		96
1 (0.75) + DXR	20	2.05	(41)	+	1.20	(24)	+	0.70	(14)	+	3.95	(79)	+	78	8.0	5.75	75.5	100
1 (1.5) + DXR	20	3.45	(69)	+	0.80	(16)	+	1.15	(23)	+	4.20	(84)	+	84	8.6	6.35	73.0	100
1 (3.0) + DXR	20	2.25	(45)	+	0.25	(5)	+	0.35	(7)	+	2.10	(42)	+	42	4.3	2.05	91.3	100
mwh/TM^3																		
Negative control	20	0.20	(4)		0.05	(1)					0.25	(5)		5	0.51			
DXR (0.2)	20	0.65	(13)	+	0.05	(1)	+				0.70	(14)	+	15	1.54	1.01		
1 (0.75) + DXR	20	0.20	(4)	+	0.00	(0)	+				0.20	(4)	+	4	0.41	–0.10		
1 (1.5) + DXR	20	0.20	(4)	+	0.05	(1)	*i*				0.25	(5)	+	5	0.51	0.00		
1 (3.0) + DXR	20	0.05	(1)	+	0.05	(1)	*i*				0.10	(2)	*i*	2	0.20	–0.31		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.

[b] Including rare *flr*^{3} single spots.

[c] Considering *mwh* clones from *mwh* single and twin spots.

[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).

[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 2S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the high-bioactivation (HB) cross after co-treatment of larvae with protocetraric acid (**1**) acid and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (F), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
HB		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Corr.		
mwh/flr^3																		
Negative control	20	0.95	(19)		0.10	(2)		0.05	(1)		1.10	(22)		22	2.25			
DXR (0.2)	20	7.70	(154)	+	3.30	(66)	+	4.05	(81)	+	15.40	(308)	+	304	31.14	28.89		92.6
1 (0.75) + DXR	20	2.65	(53)	+	0.50	(10)	+	0.55	(11)	+	3.70	(74)	+	74	7.58	5.33	81.5	100
1 (1.5) + DXR	20	1.45	(29)	+	0.50	(10)	+	0.45	(9)	+	2.40	(48)	+	48	4.91	2.66	90.8	100
1 (3.0) + DXR	20	1.70	(34)	+	0.00	(0)	+	0.35	(7)	+	2.05	(41)	+	41	4.20	1.95	93.2	100
mwh/TM^3																		
Negative control	20	0.70	(14)		0.05	(1)					0.75	(15)		15	1.54			
DXR (0.2)	20	1.55	(31)	+	0.25	(5)	*i*				1.80	(36)	+	36	3.68	2.14		
1 (0.75) + DXR	20	0.50	(10)	+	0.05	(1)	*i*				0.55	(11)	+	11	1.13	–0.41		
1 (1.5) + DXR	20	0.50	(10)	+	0.15	(3)	*i*				0.65	(13)	+	13	1.33	–0.21		
1 (3.0) + DXR	20	0.20	(4)	+	0.05	(1)	*i*				0.25	(5)	+	5	0.51	–1.03		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.
[b] Including rare *flr*^{3} single spots.
[c] Considering *mwh* clones from *mwh* single and twin spots.
[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).
[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 3S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the standard cross (ST) after co-treatment of larvae with hypostictic acid (**2**) and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
ST		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Cor.		
mwh/flr^3																		
Negative control	20	0.70	(14)		0.05	(1)		0.05	(1)		0.80	(16)		16	1.64			
DXR (0.2)	20	4.95	(99)		3.75	(75)	+	4.05	(81)	+	12.75	(255)	+	251	25.71	24.07		96.2
2 (0.75) + DXR	20	0.55	(11)	+	0.45	(9)	+	0.75	(15)	+	1.80	(36)	+	35	3.58	1.94	91.9	100
2 (1.5) + DXR	20	0.70	(14)	+	0.25	(5)	+	0.00	(0)	+	0.95	(19)	+	19	1.95	0.31	98.7	100
2 (3.0) + DXR	20	0.40	(8)	+	0.20	(4)	+	0.10	(2)	+	0.70	(14)	+	14	1.43	–0.21	100	100
mwh/TM^3																		
Negative control	20	0.20	(4)		0.05	(1)					0.25	(5)		5	0.51			
DXR (0.2)	20	0.65	(13)	+	0.05	(1)	*i*				0.70	(14)	+	14	1.43	0.92		
2 (0.75) + DXR	20	0.20	(4)	+	0.00	(0)	*i*				0.20	(4)	+	4	0.41	–0.10		
2 (1.5) + DXR	20	0.10	(2)	+	0.05	(1)	*i*				0.15	(3)	+	3	0.30	–0.21		
2 (3.0) + DXR	20	0.25	(5)	+	0.00	(0)	*i*				0.25	(5)	+	5	0.51	0.00		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.

[b] Including rare *flr*^{3} single spots.

[c] Considering *mwh* clones from *mwh* single and twin spots.

[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).

[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 4S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the high-bioactivation (HB) cross after co-treatment of larvae with hypostictic acid (**2**) and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
HB		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Cor.		
mwh/flr^3																		
Negative control	20	0.95	(19)		0.10	(2)		0.05	(1)		1.10	(22)		22	2.25			
DXR (0.2)	20	7.70	(154)	+	3.30	(66)	+	4.05	(81)	+	15.40	(308)	+	304	31.14	28.89		91.65
2 (0.75) + DXR	20	1.55	(31)	+	0.35	(7)	+	0.60	(12)	+	2.50	(50)	+	50	5.12	2.87	90	100
2 (1.5) + DXR	20	0.40	(8)	+	0.30	(6)	+	0.30	(6)	+	1.00	(20)	+	20	2.05	–0.20	100	100
2 (3.0) + DXR	20	0.50	(10)	+	0.30	(6)	+	0.05	(1)	+	0.85	(17)	+	17	1.74	–0.51	100	100
mwh/TM^3																		
Negative control	20	0.70	(14)		0.05	(1)					0.75	(15)		15	1.54			
DXR (0.2)	20	1.55	(31)	+	0.25	(5)	*i*				1.80	(36)	+	36	3.68	2.14		
2 (0.75) + DXR	20	0.40	(8)	+	0.15	(3)	*i*				0.55	(11)	+	11	1.12	–0.42		
2 (1.5) + DXR	20	0.50	(10)	+	0.00	(0)	+				0.50	(10)	+	10	1.02	–0.52		
2 (3.0) + DXR	20	0.55	(11)	+	0.00	(0)	+				0.55	(11)	+	11	1.12	–0.42		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.

[b] Including rare *flr*^{3} single spots.

[c] Considering *mwh* clones from *mwh* single and twin spots.

[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).

[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 5S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the standard cross (ST) after co-treatment of larvae with psoromic acid (**3**) and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
ST		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Corr.		
mwh/flr^3																		
Negative control	20	0.70	(14)		0.05	(1)		0.05	(1)		0.80	(16)		16	1.64			
DXR (0.2)	20	4.95	(99)	+	3.75	(75)	+	4.05	(81)	+	12.75	(255)	+	251	25.71	24.07		94.05
3 (0.75) + DXR	20	1.00	(20)	+	0.90	(18)	+	1.00	(20)	+	2.90	(58)	+	58	5.94	4.30	82.13	88.13
3 (1.5) + DXR	20	1.40	(28)	+	0.95	(19)	+	1.10	(22)	+	3.45	(69)	+	69	7.07	5.43	77.44	92.44
3 (3.0) + DXR	20	1.45	(29)	+	0.55	(11)	+	0.70	(14)	+	2.30	(46)	+	46	4.71	3.07	87.24	86.64
mwh/TM^3																		
Negative control	20	0.20	(4)		0.05	(1)					0.25	(5)		5	0.51			
DXR (0.2)	20	0.65	(13)	+	0.05	(1)	*i*				0.70	(14)	+	14	1.43			
3 (0.75) + DXR	20	0.20	(4)	+	0.05	(1)	*i*				0.25	(5)	+	5	0.51			
3 (1.5) + DXR	20	0.15	(3)	+	0.05	(1)	*i*				0.20	(4)	+	4	0.41			
3 (3.0) + DXR	20	0.15	(3)	+	0.05	(1)	*i*				0.20	(4)	+	4	0.41			

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.

[b] Including rare *flr*^{3} single spots.

[c] Considering *mwh* clones from *mwh* single and twin spots.

[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).

[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 6S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the high-bioactivation (HB) cross after co-treatment of larvae with psoromic acid (**3**) acid and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
HB		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Corr.		
mwh/flr^3																		
Negative control	20	0.95	(19)		0.10	(2)		0.05	(1)		1.10	(22)		22	2.25			
DXR (0.2)	20	7.70	(154)	+	3.30	(66)	+	4.05	(81)	+	15.40	(308)	+	304	31.14	28.9		92.6
3 (0.75) + DXR	20	2.65	(53)	+	0.50	(10)	+	0.55	(11)	+	3.70	(74)	+	74	7.58	5.33	81.5	100
3 (1.5) + DXR	20	1.45	(29)	+	0.50	(10)	+	0.45	(9)	+	2.40	(48)	+	48	4.91	2.66	90.8	100
3 (3.0) + DXR	20	1.70	(34)	+	0.00	(0)	+	0.35	(7)	+	2.05	(41)	+	41	4.2	1.95	93.2	100
mwh/TM^3																		
Negative control	20	0.70	(14)		0.05	(1)					0.75	(15)		15	1.54			
DXR (0.2)	20	1.55	(31)	+	0.25	(5)	*i*				1.80	(36)	+	36	3.68			
3 (0.75) + DXR	20	0.50	(10)	+	0.05	(1)	*i*				0.55	(11)	+	11	1.13	–0.41		
3 (1.5) + DXR	20	0.50	(10)	+	0.15	(3)	*i*				0.65	(13)	+	13	1.33	–0.21		
3 (3.0) + DXR	20	0.20	(4)	+	0.05	(1)	*i*				0.25	(5)	+	5	0.51	–1.03		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.

[b] Including rare *flr*^{3} single spots.

[c] Considering *mwh* clones from *mwh* single and twin spots.

[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).

[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 7S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the standard cross (ST) after co-treatment of larvae with salazinic acid (**4**) and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
ST		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Corr.		
mwh/flr^3																		
Negative control	20	0.70	(14)		0.05	(1)		0.05	(1)		0.80	(16)		16	1.64			
DXR (0.2)	20	4.95	(99)	+	3.75	(75)	+	4.05	(81)	+	12.75	(255)	+	251	25.71	24.07		96.2
4 (0.75) + DXR	20	1.30	(26)	+	0.65	(13)	+	0.65	(13)	+	2.60	(52)	+	52	5.32	3.58	85.1	97.2
4 (1.5) + DXR	20	1.05	(21)	+	0.75	(15)	+	1.15	(23)	+	2.95	(59)	+	59	6.04	4.40	81.7	95.2
4 (3.0) + DXR	20	0.60	(12)	+	0.15	(3)	+	0.35	(7)	+	1.10	(22)	+	22	2.25	0.61	97.5	100
mwh/TM^3																		
Negative control	20	0.20	(4)		0.05	(1)					0.25	(5)		5	0.51			
DXR (0.2)	20	0.65	(13)	+	0.05	(1)	*i*				0.70	(14)	+	14	1.43	0.92		
4 (0.75) + DXR	20	0.30	(6)	*i*	0.00	(0)	*i*				0.30	(6)	*i*	6	0.61	0.10		
4 (1.5) + DXR	20	0.30	(6)	*i*	0.05	(1)	*i*				0.35	(7)	*i*	7	0.72	0.21		
4 (3.0) + DXR	20	0.25	(5)	+	0.00	(0)	*i*				0.25	(5)	+	5	0.51	0.00		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.
[b] Including rare *flr*^{3} single spots.
[c] Considering *mwh* clones from *mwh* single and twin spots.
[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).
[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

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Table 8S. Frequency of mutant spots in the wings of marked trans-heterozygous (*mwh/flr*^{3}) and balancer-heterozygous (*mwh/TM*^{3}) descendants of *D. melanogaster* using the high-bioactivation (HB) cross after co-treatment of larvae with salazinic acid (**4**) acid and doxorubicin (DXR).

Genotypes and treatments (mmol L^{-1})	Number of flies (*N*)	Spots per fly (*F*), number of spots (*N*), and statistical diagnosis (*D*)[a]												Spots with *mwh* clone[c] (*n*)	Frequency of clone formation per 10^5 cells per cell division (*n*/*NC*)[d]		%*I*[e]	%*R*
		Small single spots (1-2 cells)[b] *m* = 2			Large single spots (>2 cells)[b] *m* = 5			Twin spots *m* = 5			Total spots *m* = 2							
HB		*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*	*F*	*N*	*D*		Obs.	Corr.		
mwh/flr^3																		
Negative control	20	0.95	(19)		0.10	(2)		0.05	(1)		1.10	(22)		22	2.25			
DXR (0.2)	20	7.70	(154)	+	3.30	(66)	+	4.05	(81)	+	15.40	(308)	+	304	31.14	28.89		92.52
4 (0.75) + DXR	20	2.10	(42)	+	1.50	(30)	+	1.35	(27)	+	4.95	(99)	+	97	9.94	7.69	73.4	100
4 (1.5) + DXR	20	3.35	(67)	+	1.00	(20)	+	0.70	(14)	+	5.05	(101)	+	100	10.24	7.99	72.4	100
4 (3.0) + DXR	20	1.20	(24)	+	0.75	(15)	+	0.35	(7)	+	2.30	(46)	+	46	4.71	2.46	91.5	100
mwh/TM^3																		
Negative control	20	0.70	(14)		0.05	(1)					0.75	(15)		15	1.54			
DXR (0.2)	20	1.55	(31)	+	0.25	(5)	*i*				1.80	(36)	+	36	3.7	2.16		
4 (0.75) + DXR	20	0.30	(6)	+	0.00	(0)	+				0.30	(6)	+	6	0.61	–0.93		
4 (1.5) + DXR	20	0.35	(7)	+	0.00	(0)	+				0.35	(7)	+	7	0.71	–0.83		
4 (3.0) + DXR	20	0.35	(7)	+	0.00	(0)	+				0.35	(7)	+	7	0.71	–0.83		

[a] Statistical diagnoses according to Frei and Würgler (1988, 1995). U-test, two-sided; probability levels: +, positive; *i*, inconclusive; $p \leq 0.05$ *vs*. untreated control; $p \leq 0.05$ *vs*. DXR only.

[b] Including rare *flr*^{3} single spots.

[c] Considering *mwh* clones from *mwh* single and twin spots.

[d] Frequency of clone formation: clones per fly per 48 800 cells (without size correction).

[e] Balancer chromosome TM^3 does not carry the *flr*^{3} mutation and recombination is suppressed owing to the multiply inverted region in this chromosome. %*I*: inhibition; %*R*: recombination.

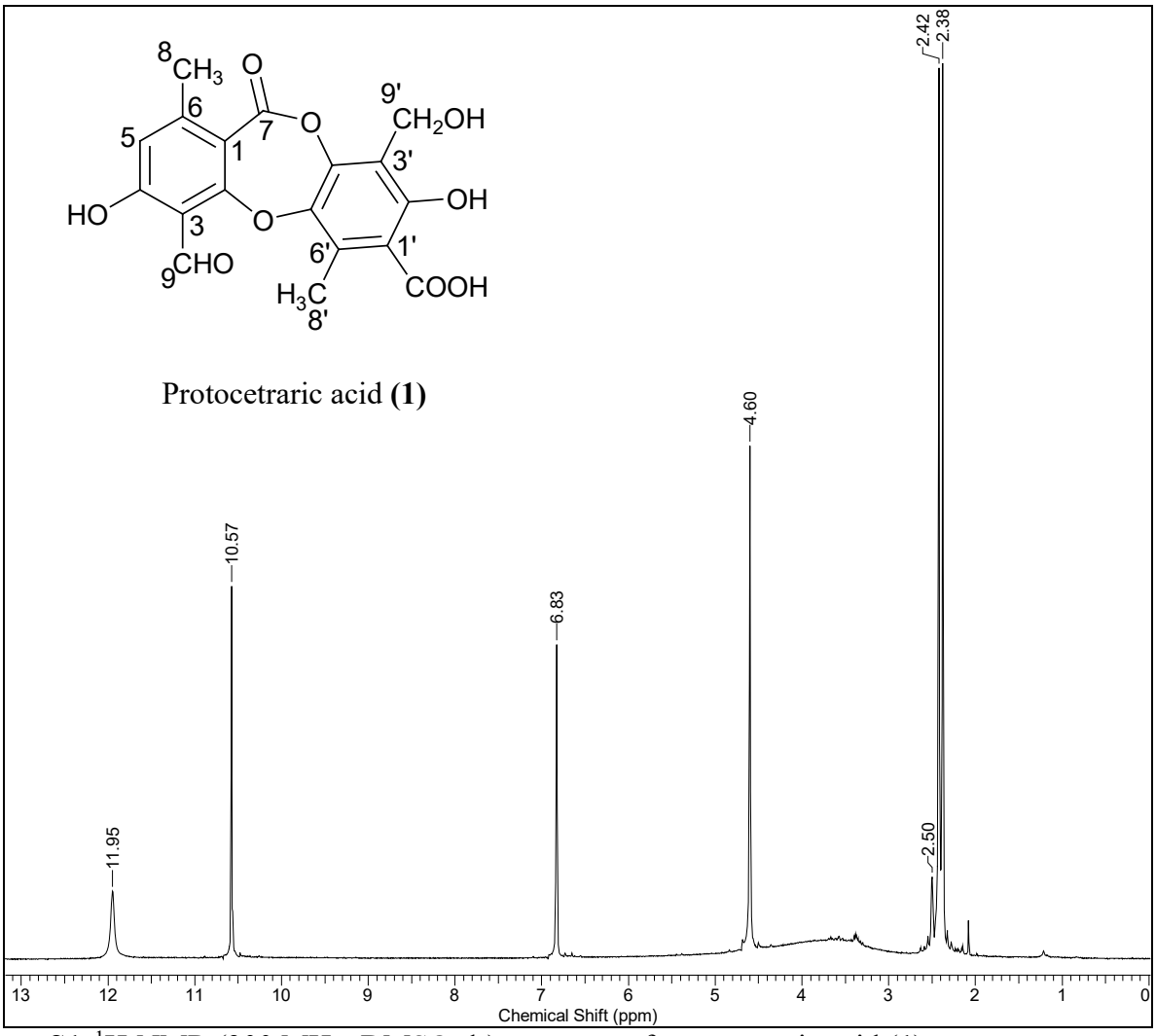


Figure S1. ^{1}H-NMR (300 MHz, DMSO-d_6) spectrum of protocetraric acid (**1**).

Protocetraric acid (**1**): ^{1}H-NMR (300 MHz, DMSO-d_6) δ 2.38 (s, 3H, CH_3-8'), 2.42 (s, 3H, CH_3-8), 4.60 (s, 2H, CH_2OH-9'), 6.83 (s, 1H, H-5), 10.57 (s, 1H, CHO), 11.95 (sl, 1H, OH-4).

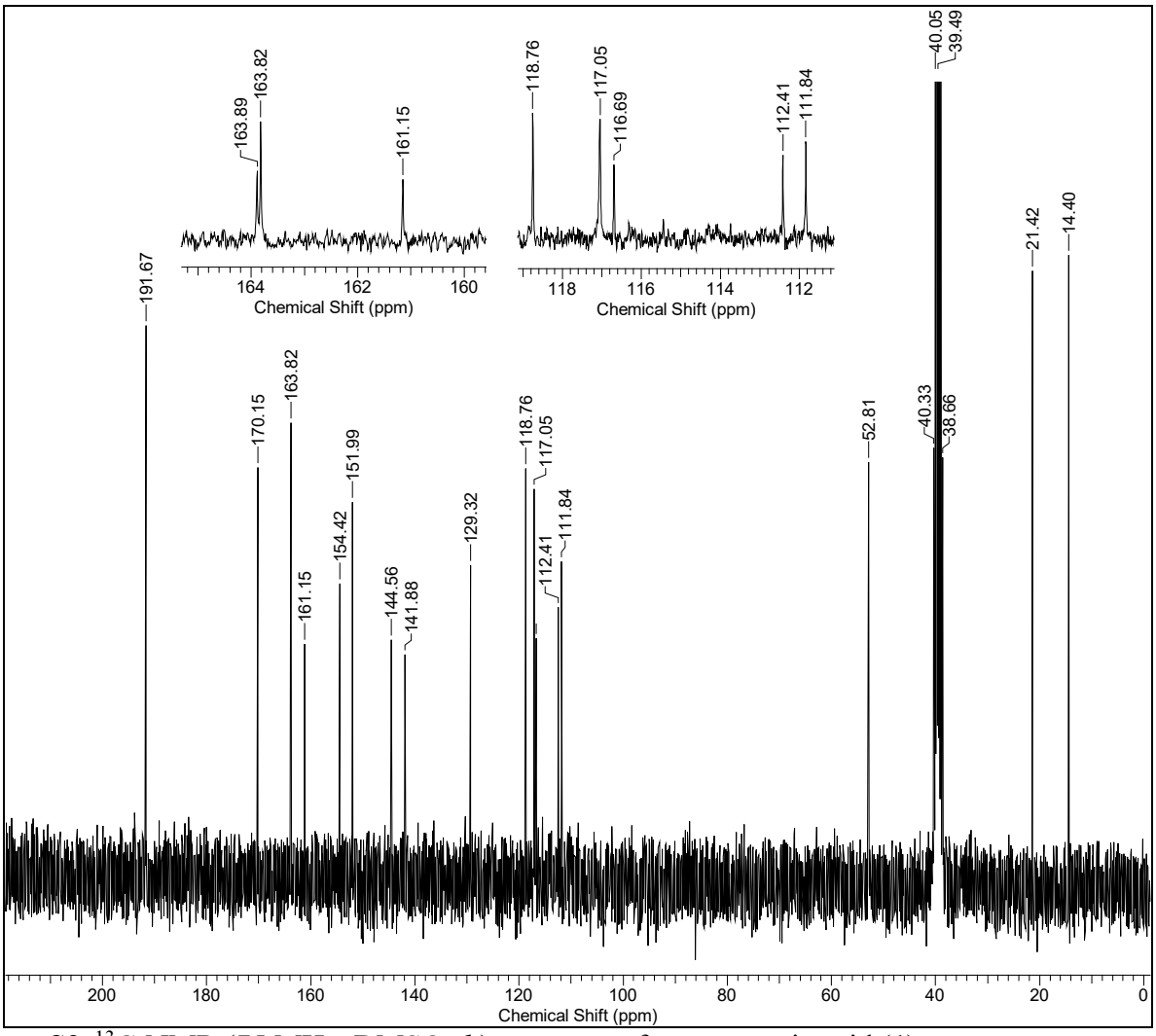
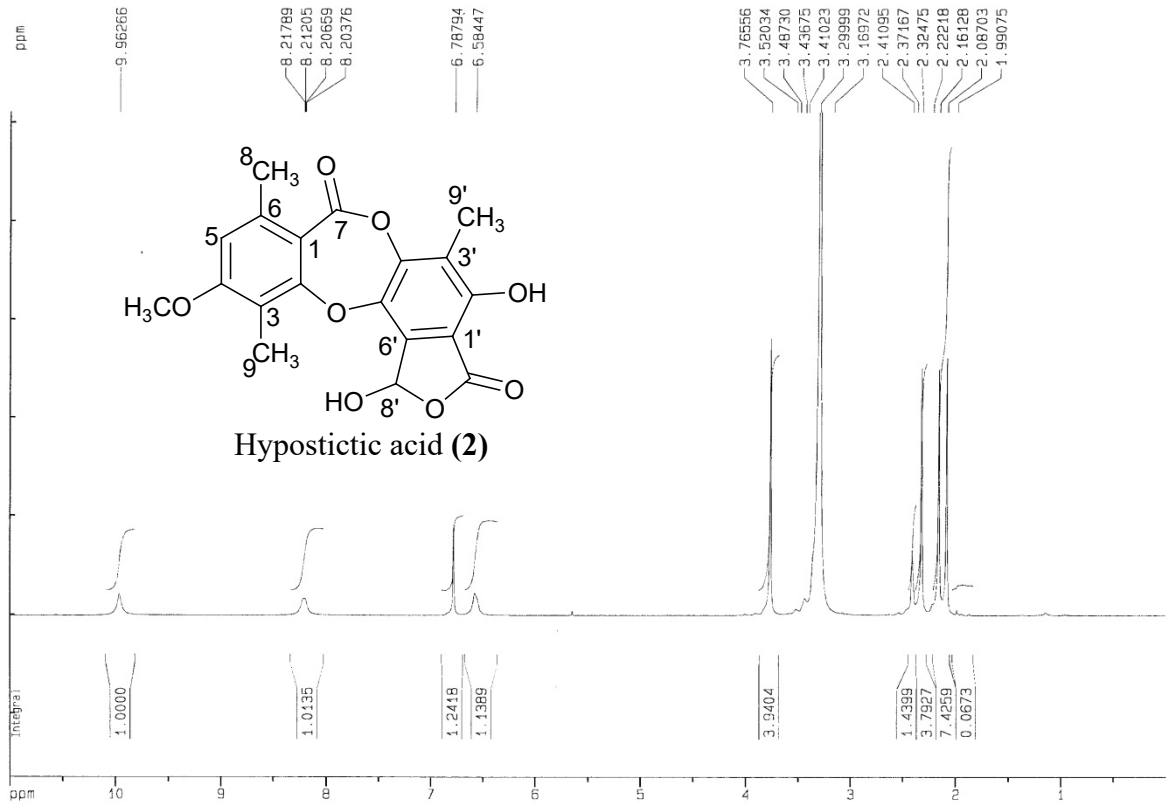


Figure S2. ^{13}C-NMR (75 MHz, DMSO-d_6) spectrum of protocetraric acid (**1**).

Protocetraric acid **(1)**: ^{13}C-NMR (75 MHz, DMSO-d$_6$) δ 14.4 (C- 8'), 21.4 (C-8), 52.8 (C-9'), 111.8 (C-3), 112.4 (C-1), 116.7 (C-1'), 117.1 (C-5), 118.7 (C-3'), 129.3 (C-6'), 141.8 (C-5'), 144.5 (C-4'), 152.0 (C-6), 154.4 (C-2'), 161.1 (C-7), 163.8 (C-2), 163.9 (C-4), 170.1 (C-7'), 191.7 (C-9).



Hypostictic acid (**2**)

Figure S3. ^{1}H-NMR (300 MHz, DMSO-d_6) spectrum of hypostictic acid (**2**)**.**

Hypostictic acid (**2**): ^{1}H-NMR (300 MHz, DMSO-d_6) δ 2.08 (s, 3H, CH_3-8), 2.22 (s, 3H, CH_3-9'), 2.32 (s, 3H, CH_3-9), 3.76 (s, 3H, -OCH_3), 6.58 (sl, 1H, lactol), 6.70 (s, 1H, H-5), 8.20 (1H, OH lactol), 9.9 (s, 1H, OH).

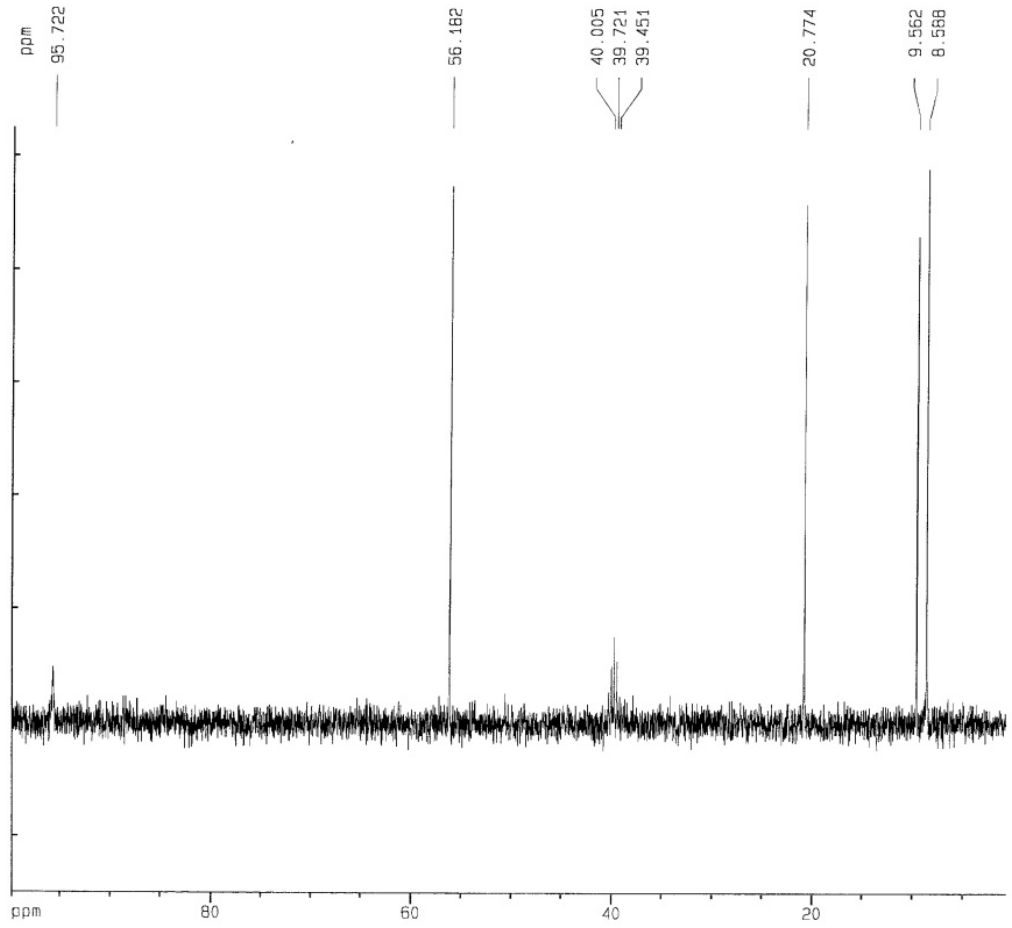


Figure S4.[13]C-NMR (75 MHz, DMSO-d_6) spectrum of hypostictic acid **(2)** 0-100 ppm**.**

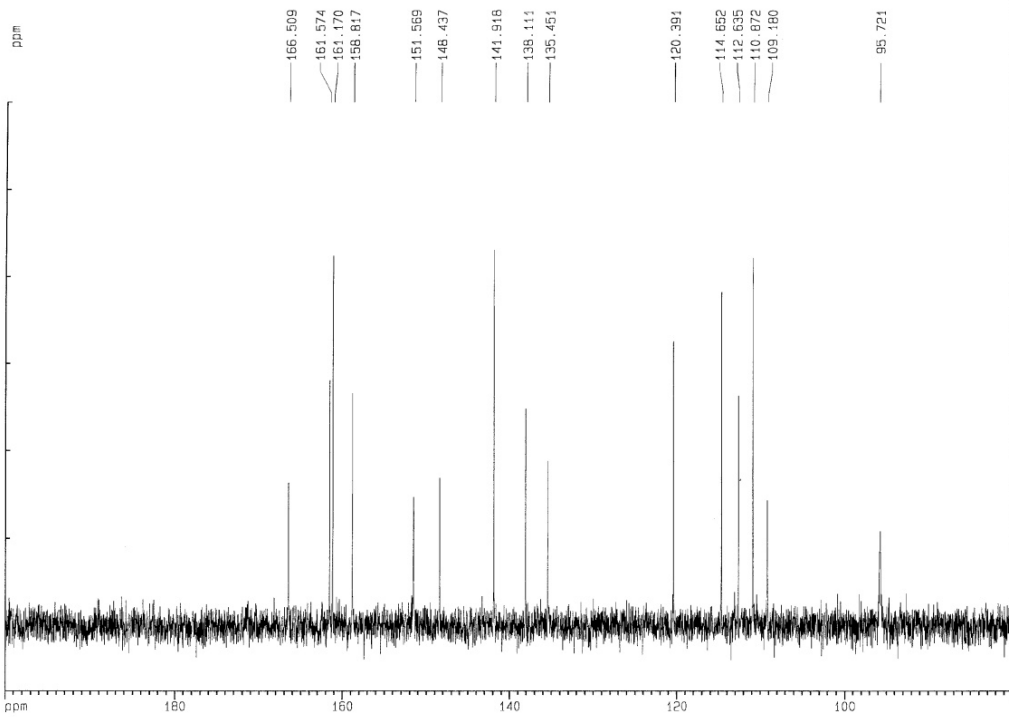


Figure S5. [13]C-NMR (75 MHz, DMSO-d_6) spectrum of hypostictic acid (**2**), 80-200 ppm**.**

Hypostictic acid (**2**): ^{13}C-NMR (75 MHz, DMSO-d$_6$) δ 8.5 (C-8), 9.5 (C-9'), 20.7 (C-9), 56.1 (OCH_3), 95.7 (C-8'), 109.1 (C-1'), 110.8 (C-3), 112.6 (C-1), 114.6 (C- 5), 120.3 (C-3'), 135.4 (C-6'), 138.1 (C-5'), 141.9 (C-6), 148.4 (C-4'), 151.5 (C-2'), 158.8 (C-7), 161.1 (C-7'), 161.5 (C-4), 166.5 (C-2).

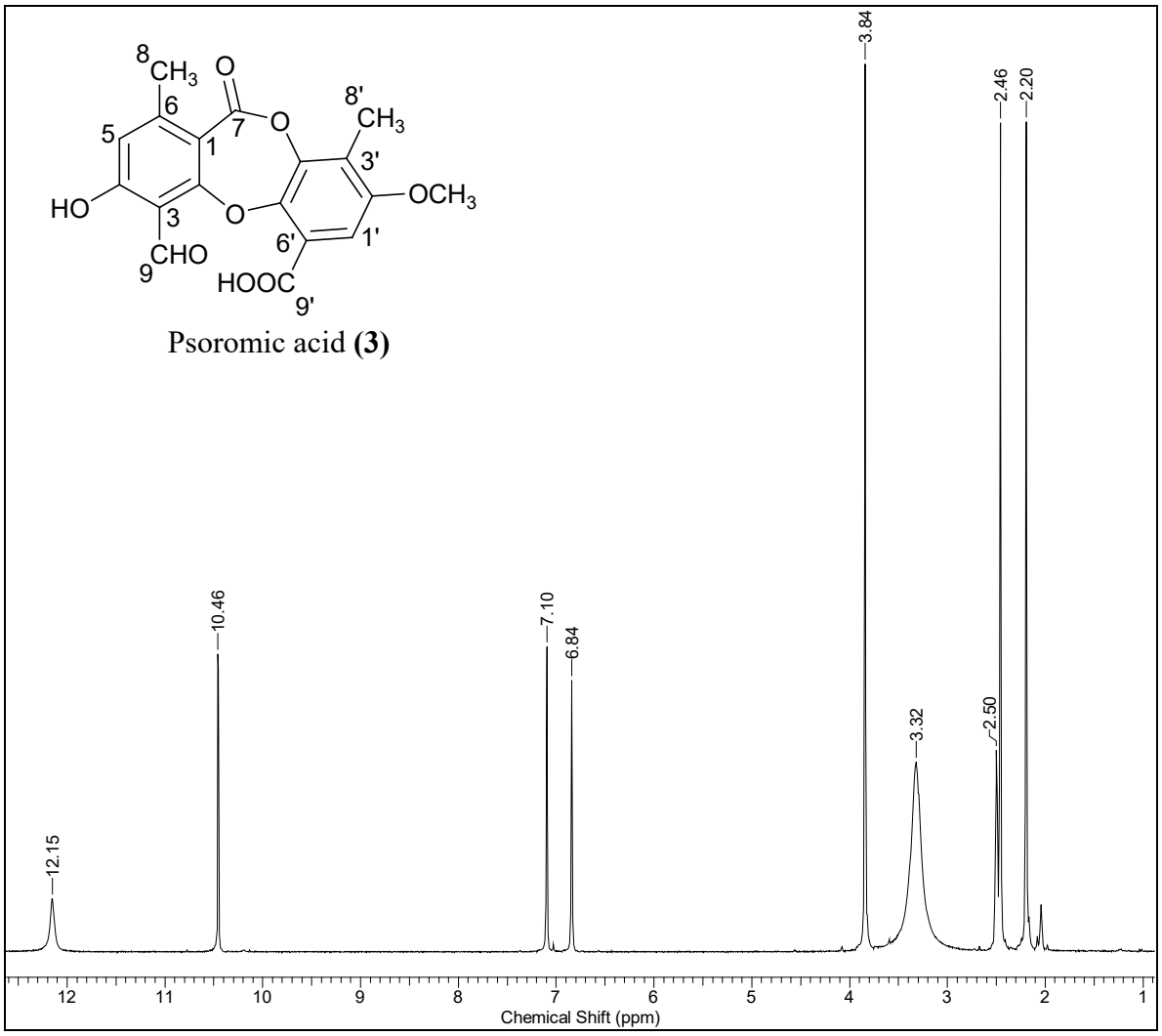


Figure S6. ^{1}H-NMR (300 MHz, DMSO-d$_6$) spectrum of psoromic acid (**3**).

Psoromic acid (**3**): ^{1}H-NMR (300 MHz, DMSO-d$_6$) δ 2.20 (s, 3H, CH_3-8'), 2.46 (s, 3H, CH_3-8), 3.84 (s, 3H, OCH_3), 6.84 (s, 1H, H-5), 7.10 (s, 1H, H-1'), 10.46 (s, 1H, CHO), 12.15 (s, 1H, OH).

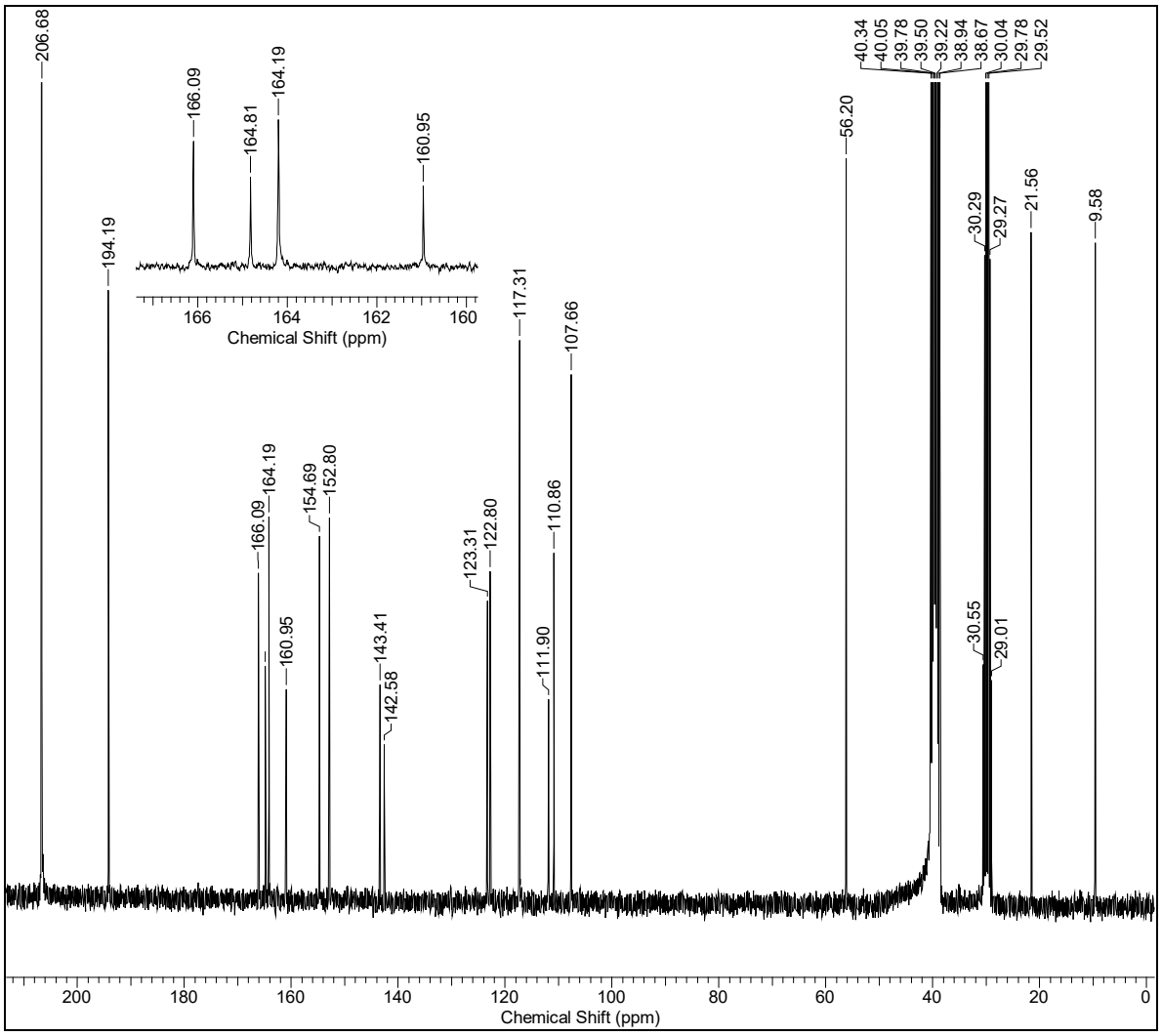


Figure S7. ^{13}C-NMR (75 MHz, DMSO-d_6) spectrum of psoromic acid (**3**).

Psoromic acid (**3**): ^{13}C-NMR (75 MHz, DMSO-d_6) δ 9.5 (C- 8'), 21.5 (C-8), 56.2 (OCH_3), 107.8 (C-1') 110.9 (C-3), 111.9 (C-1), 117.3 (C-5), 122.8 (C-3'), 123.3 (C-6'), 142.5 (C-5'), 143.4 (C-4'), 152.8 (C-6'), 154.6 (C-2'), 160.9 (C-7), 164.1 (C-4), 164.8 (C-2), 166.0 (C-7'), 194.1 (C-9).

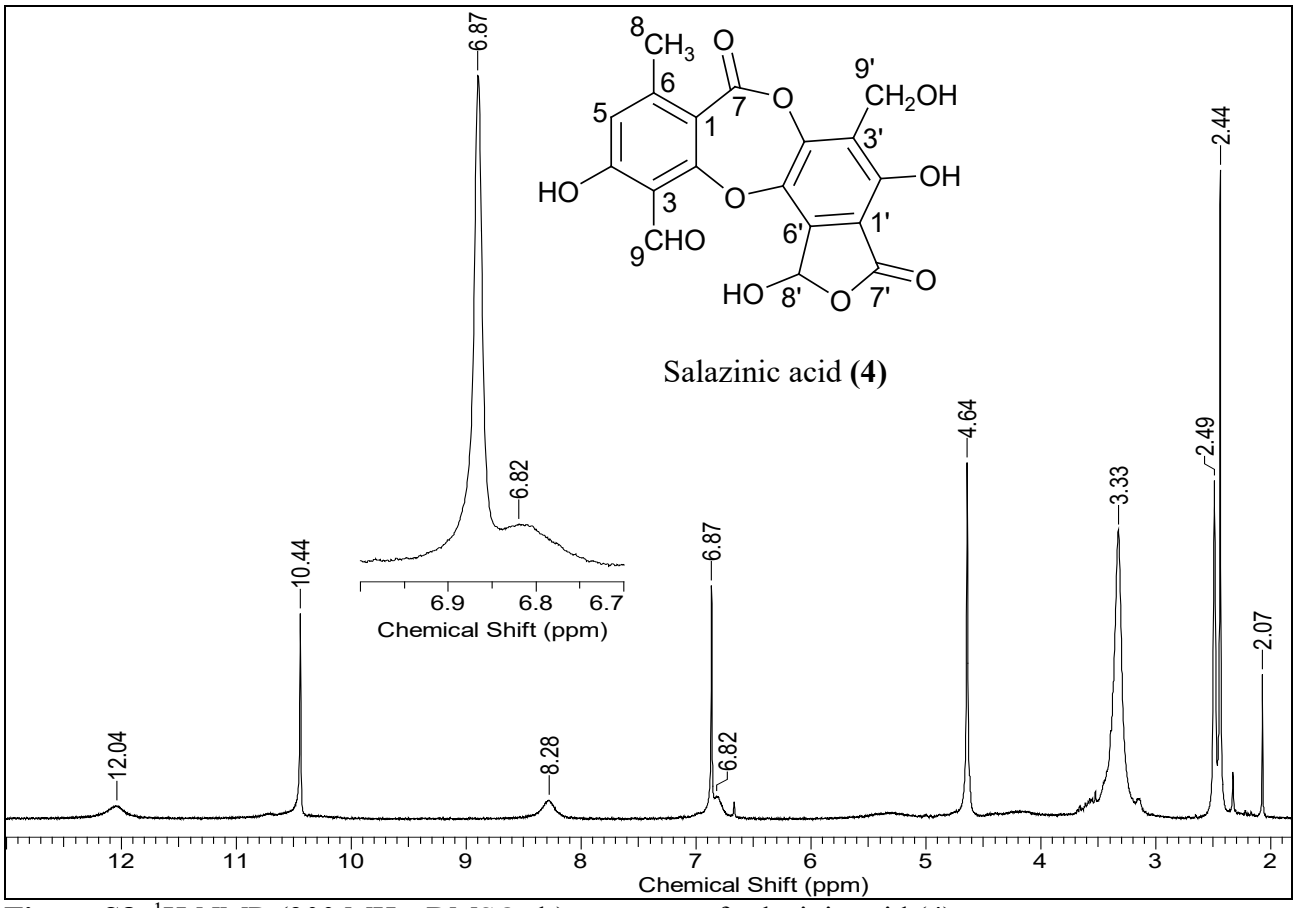


Figure S8. ^{1}H-NMR (300 MHz, DMSO-d_6) spectrum of salazinic acid (**4**).

Salazinic acid (**4**): ^{1}H-NMR (300 MHz, DMSO-d_6) δ 2.44 (s, 3 H, CH_3-8), 4.64 (s, 2H, CH_2OH), 6.82 (sl, 1H, H-5), 6.87 (s, 1H, lactol), 8.28 (sl, 1H, OH lactol), 10.44 (s, 1H, CHO), 12.04 (sl, 1H, OH-4).

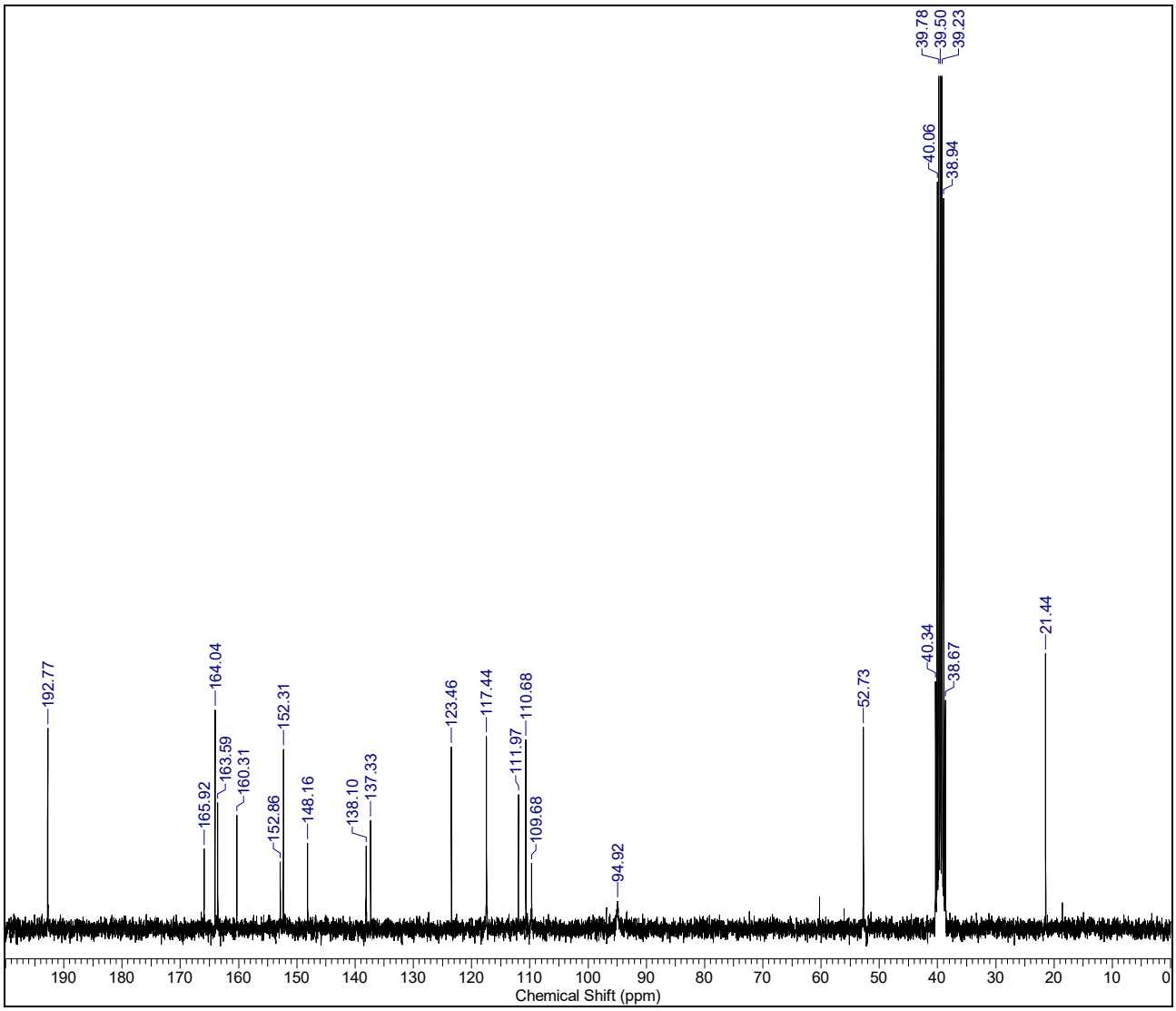


Figure S9. ^{13}C-NMR (75 MHz, DMSO-d_6) of salazinic acid (**4**).

Salazinic acid (**4**): ^{13}C-NMR (75 MHz, DMSO-d_6) δ 21.4 (C-8), 52.7 (C-9'), 94.9 (C-8'), 109.7 (C-1'), 110.7 (C-3), 112.0 (C-1), 117.4 (C-5) 123.5 (C-3'), 137.3 (C-6'), 138.1 (C-5'), 148.2 (C-4'), 152.3 (C-2'), 152.9 (C-6), 160.3 (C-7), 163.6 (C-7'), 164.0 (C-2), 165.9 (C- 4), 192.8 (C-9).