

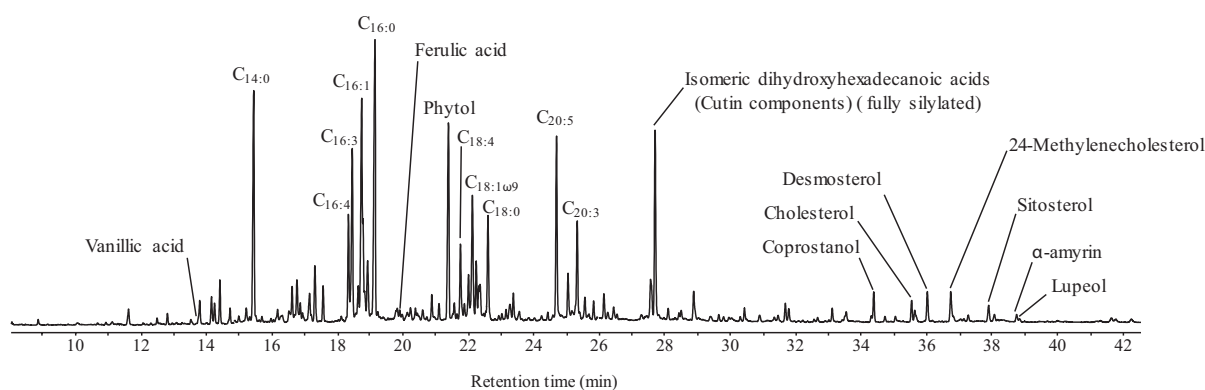
Enhanced biotic degradation of terrestrial POM in an estuarine salinity gradient: interactive effects of organic matter pools and changes of bacterial communities

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A



B

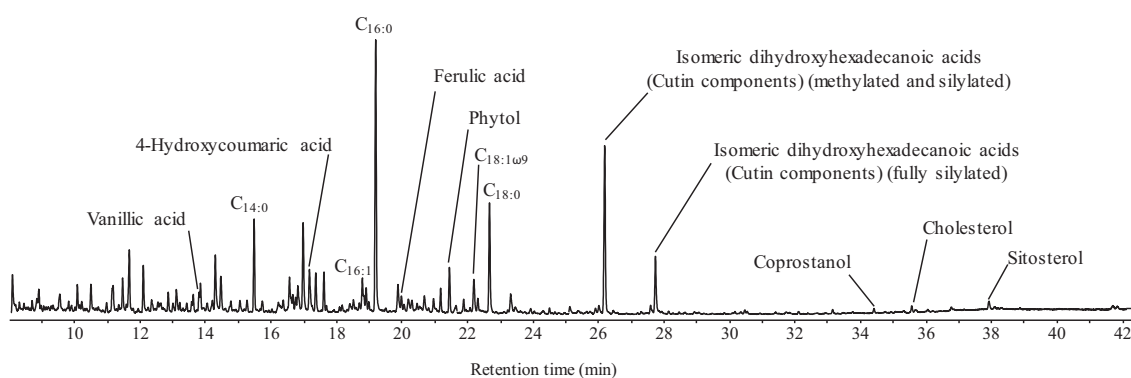


Figure S1: TOF mass chromatograms of the silylated total lipid extract of SPM collected in the Rhône River at the Arles station during (the 24/01/2017) (A) and after (the 30/03/2017) (B) the potamoplankton bloom event.

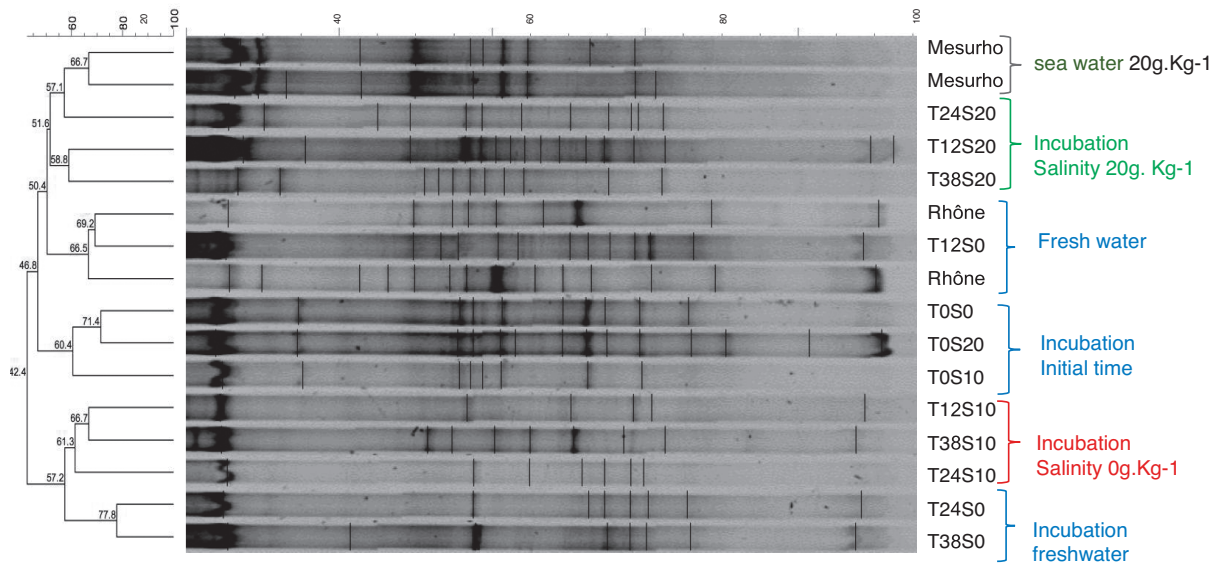


Figure S2: Dendrogram from DGGE analyses of the evolution of the bacterial community according to Jaccard's indexes and the classification algorithm hierarchy UPGMA (Unweighted Pair Group Method with Arithmetic mean) samples according to time incubation (0 (T0), 12 (T1), 24 (T2) or 38 (T3) days of incubation) and the water salinity (0 g kg⁻¹ (S0), 10 g kg⁻¹ (S10) or 20 g kg⁻¹ (S20)).

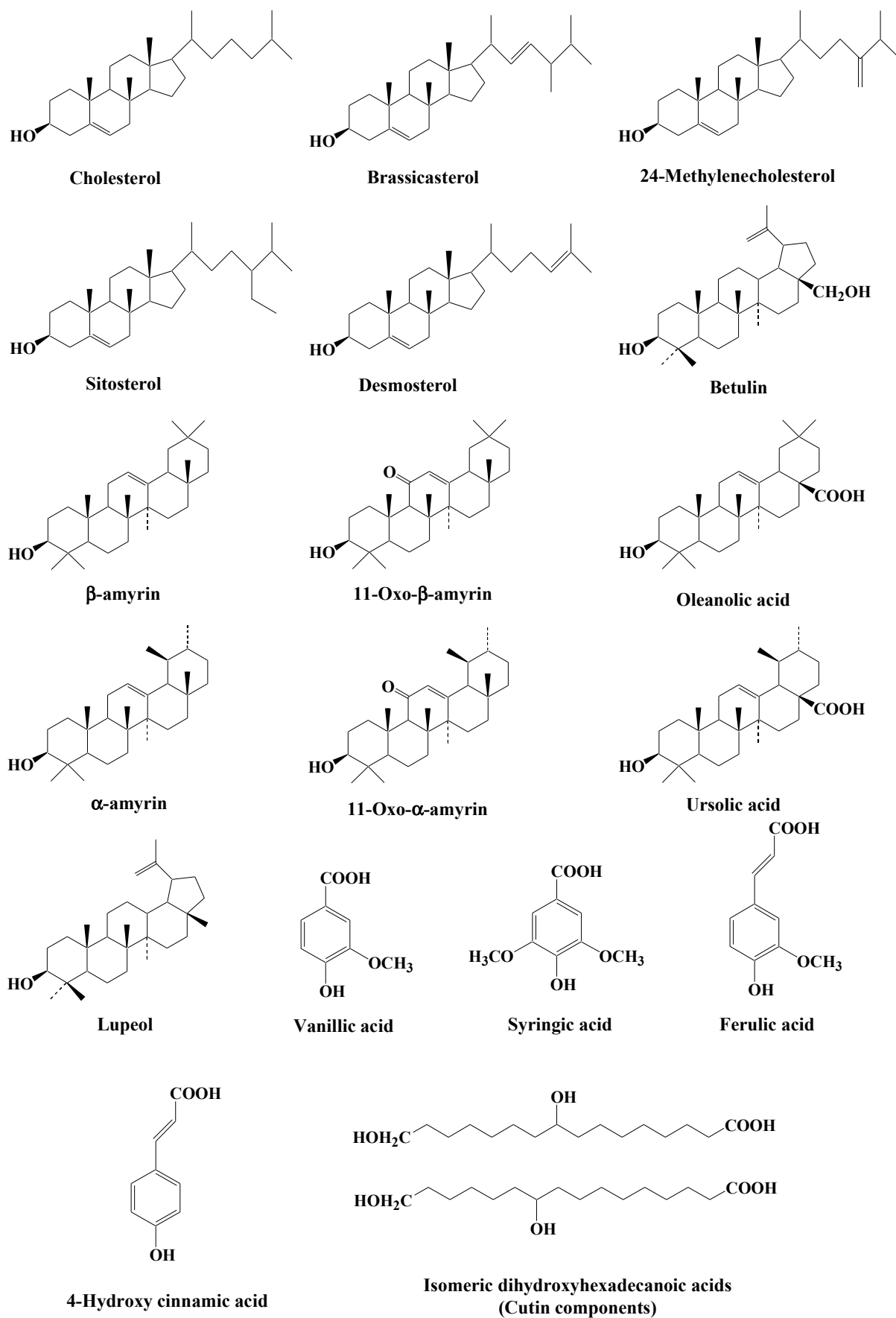


Figure S3: Structures of the main compounds described in this study

Table S1: Evolution of the concentration (ng mg^{-1}) of vascular plant components during incubations at different salinity conditions

	Sample ^a	a-Amyrin	b-Amyrin	Lupeol	Isomeric dihydroxy C _{16:0} acids ^b
Rhône SPM (Bloom samples)	T0S0	0.7	0.8	0.8	30.1
	T0S0	0.5	0.9	1.0	44.6
	T12S0	0.3	0.5	0.9	24.5
	T12S0	0.2	0.3	0.3	48.5
	T24S0	0.4	0.3	0.8	75.3
	T24S0	0.2	0.2	0.2	11.7
	T38S0	0.2	0.2	0.3	15.8
	T38S0	0.6	0.7	0.8	4.1
	T0S10	0.5	0.6	0.5	24.6
	T0S10	0.2	0.3	0.3	15.5
	T12S10	0.5	0.5	0.6	30.3
	T12S10	0.5	0.6	0.6	10.5
	T24S10	0.2	0.2	0.3	5.2
	T24S10	0.5	0.6	0.7	16.1
	T38S10	0.4	0.6	0.8	4.0
	T38S10	0.4	0.5	0.7	4.9
Rhône SPM (Post-bloom samples)	T0S20	1.1	1.4	1.3	22.0
	T0S20	1.1	1.3	1.5	63.2
	T12S20	1.0	1.1	1.0	36.8
	T12S20	3.7	1.5	1.9	17.2
	T24S20	0.4	0.4	0.4	8.3
	T24S20	0.2	0.3	0.2	12.6
	T38S20	0.3	0.4	0.4	8.9
	T38S20	0.3	0.5	0.5	11.4
Rhône SPM (Post-bloom samples)	T0S20	0.1	0.2	0.2	7.3
	T0S20	0.3	0.3	0.6	7.3
	T12S20	0.2	0.4	0.3	8.6
	T12S20	0.3	0.5	0.5	1.5
	T24S20	0.2	0.3	0.3	6.4
	T24S20	0.2	0.3	0.3	5.4
	T38S20	0.1	0.2	0.3	4.7
	T38S20	0.1	0.2	0.3	6.2

^aT = incubation time (0; 12; 24 or 38 days), S = Salinity (0; 10 or 20 g kg⁻¹)

^bCuticular wax components

Table S2: Evolution of the concentration (ng mg⁻¹) of phenolic acids during the different incubations

	Sample ^a	Vanillic acid	Syringic acid	4-Hydroxycoumaric acid	
Rhône SPM (Bloom samples)	T0S0	3.5	2.4	6.6	
	T0S0	4.9	3.1	8.4	
	T12S0	2.5	2.5	6.6	
	T12S0	1.6	1.6	5.5	
	T24S0	2.5	2.0	5.3	
	T24S0	1.6	1.0	2.9	
	T38S0	1.5	1.0	4.8	
	T38S0	1.3	0.9	1.9	
	T0S10	4.4	1.9	4.8	
	T0S10	2.7	1.7	4.0	
	T12S10	1.2	1.0	4.2	
	T12S10	0.5	0.7	1.6	
	T24S10	1.5	0.9	3.3	
	T24S10	1.8	1.7	3.3	
	T38S10	1.1	1.3	2.2	
	T38S10	2.1	1.2	6.6	
	T0S20	3.9	2.1	6.6	
	T0S20	3.6	2.1	6.8	
	T12S20	1.9	1.7	5.1	
	T12S20	1.1	1.2	2.9	
	T24S20	1.1	0.9	2.3	
	T24S20	1.2	0.8	4.6	
	T38S20	1.9	1.2	4.5	
	T38S20	2.3	1.6	5.2	
	Rhône SPM (Post-bloom samples)	T0S20	2.9	0.8	2.9
		T0S20	4.0	2.3	7.1
		T12S20	1.5	0.9	3.4
		T12S20	1.1	0.9	2.1
T24S20		1.4	1.2	3.2	
T24S20		1.3	0.9	2.7	
T38S20		1.2	1.0	3.8	
T38S20		1.1	0.9	2.5	

^aT = incubation time (0, 12, 24 or 38 day), S = Salinity (0, 10 or 20 g kg⁻¹)

Table S3: (Brassicasterol + 24-methylenecholesterol)/sitosterol ratio and sitostanol % (relative to the parent sitosterol) measured in SPM samples collected in the Rhône salinity gradient

(Brassicasterol + 24-methylenecholesterol) / sitosterol	Sitostanol (%)
0.012	0.432
0.054	1.697
0.167	5.978
0.121	4.734
0.114	3.573
0.411	6.656
0.135	3.183
0.722	6.652
0.492	10.025
0.078	6.951
0.601	10.128
0.579	11.803
0.548	11.619
1.947	8.133
2.486	13.043
2.994	12.149
1.746	9.017
2.926	15.393
2.250	11.376

Table S4: The average percentage of bacteria and archaea at the phylum level between the different stations

Phylum	StA	StB	StC	StD	StrE
Other	0.082	0.085	1.343	0.930	0.467
Crenarchaeota	0.045	0.209	1.519	0.992	3.838
Euryarchaeota	0.004	0.068	1.184	0.577	3.467
[Parvarchaeota]	0.000	0.000	0.000	0.000	0.000
Acidobacteria	3.272	0.029	0.144	0.011	0.000
Actinobacteria	3.920	10.050	6.766	3.182	5.261
Armatimonadetes	0.074	0.000	0.000	0.000	0.000
BRC1	0.078	0.000	0.000	0.000	0.000
Bacteroidetes	6.664	24.997	20.023	23.266	15.031
Chlamydiae	0.000	0.005	0.000	0.000	0.000
Chlorobi	0.349	0.017	0.000	0.003	0.000
Chloroflexi	0.472	0.201	0.539	0.304	1.004
Cyanobacteria	0.000	0.000	0.000	0.000	0.000
Elusimicrobia	0.008	0.000	0.000	0.000	0.000
FCPU426	0.000	0.000	0.000	0.000	0.000
Fibrobacteres	0.000	0.000	0.079	0.000	0.000
Firmicutes	2.122	0.121	1.364	0.057	0.146
Fusobacteria	0.161	0.024	0.053	0.022	0.000
GN04	0.000	0.000	0.000	0.000	0.000
Gemmatimonadetes	0.377	0.041	0.238	0.121	0.326
Lentisphaerae	0.000	0.000	0.036	0.005	0.020
NC10	0.008	0.000	0.000	0.000	0.000
Nitrospirae	0.511	0.012	0.098	0.000	0.000
OP3	0.000	0.000	0.000	0.000	0.000
PAUC34f	0.000	0.000	0.089	0.019	0.080
Planctomycetes	0.348	0.073	0.136	0.084	0.600
Proteobacteria	77.619	63.525	63.894	69.312	65.715
SAR406	0.000	0.085	0.851	0.571	1.915
SBR1093	0.004	0.058	0.717	0.396	1.401
Spirochaetes	0.012	0.000	0.070	0.000	0.000
TM6	0.000	0.000	0.000	0.000	0.000
TM7	0.072	0.000	0.000	0.000	0.000
Tenericutes	0.006	0.000	0.000	0.000	0.000
Verrucomicrobia	3.668	0.398	0.660	0.143	0.718
WS3	0.128	0.002	0.079	0.003	0.000
ZB3	0.000	0.000	0.119	0.005	0.010

Table S5 : The average percentage of predominant bacteria et the family level between the different sampling sites.

Phylum	Class	Order	Family	StA	StB	StC	StD	StE
Actinobacteria	Actinobacteria	Actinomycetales	ACK-M1	0,000	3,309	1,484	0,136	0,000
Bacteroidetes	Bacteroidia	Bacteroidales	Porphyromonadaceae	0,359	0,048	0,231	0,005	0,000
Bacteroidetes	Cytophagia	Cytophagales	Cytophagaceae	0,148	7,343	3,217	0,313	0,000
Bacteroidetes	Flavobacteriia	Flavobacteriales	Cryomorphaceae	0,000	0,445	3,052	9,539	0,255
Bacteroidetes	Flavobacteriia	Flavobacteriales	Flavobacteriaceae	1,751	15,935	12,657	11,783	12,877
Crenarchaeota	Thaumarchaeota	Cenarchaeales	Cenarchaeaceae	0,011	0,153	1,903	1,028	6,780
Proteobacteria	Alphaproteobacteria	Rickettsiales	Pelagibacteraceae	0,179	2,240	20,627	11,960	60,728
Proteobacteria	Alphaproteobacteria	Rhodobacterales	Rhodobacteraceae	29,662	3,405	17,895	31,328	3,772
Proteobacteria	Betaproteobacteria	Burkholderiales	Comamonadaceae	16,487	58,260	20,236	3,734	0,082
Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	2,015	6,142	3,999	0,369	0,016
Proteobacteria	Betaproteobacteria	Methylophilales	Methylophilaceae	2,384	0,423	0,212	0,033	0,049
Proteobacteria	Betaproteobacteria	Rhodocyclales	Rhodocyclaceae	14,283	0,044	0,240	0,056	0,000
Proteobacteria	Gammaproteobacteria	Alteromonadales	Alteromonadaceae	0,000	1,393	9,153	23,855	1,496
Proteobacteria	Gammaproteobacteria	Alteromonadales	Colwelliaceae	0,021	0,170	0,113	0,023	0,000
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Halomonadaceae	0,021	0,432	4,546	5,674	13,888
Proteobacteria	Gammaproteobacteria	Oceanospirillales	Oceanospirillaceae	0,000	0,052	0,000	0,000	0,000
Proteobacteria	Gammaproteobacteria	Vibrionales	Pseudoalteromonadaceae	0,169	0,065	0,188	0,070	0,058
Proteobacteria	Gammaproteobacteria	Xanthomonadales	Sinobacteraceae	32,511	0,140	0,245	0,093	0,000