Supplement

A 150-year record of phytoplankton community succession controlled by hydroclimatic variability in a tropical lake

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1 Study area

1.1 Geology

Lake Nong Thale Prong lies in a region characterized by karst topography of Permian limestone and/or dolomitic limestone, which forms part of the Ratburi Group and bounds the northern and southern directions of the lake (Raksasakulwong et al., 1989 Department of Mineral Resources of Thailand, 2007). Eastward mountain ranges consist of Jurassic-Cretaceous arkosic sandstone, claystone and siltstone (Department of Mineral Resources of Thailand, 2007). Undulating plains of Quaternary alluvial and colluvial sedimentary deposits generally surrounds the western part of NTP (Raksasakulwong et al., 1989; Department of Mineral Resources of Thailand, 2007). Vegetation is diverse, with the southern part covered by lowland tropical rainforest, dominated by Dipterocarpaceae and a significantly high diversity of Myrtaceae (Santisuk, 2006). The Nakhon Si Thammarat region also has extensive mechanized agricultural activities, consisting mainly of oil palm and natural rubber plantations.

1.2 Thailand hydroclimate

The study area is controlled by both the southwest and northeast monsoonal winds originating from the Indian Ocean and from Mongolia and China, respectively (Climatological Center, Thai Meteorological Department, 2011). The intertropical convergence zone (ITCZ) (Climatological Center, Thai Meteorological Department, 2011), El Niño southern oscillation (ENSO) (Singhrattna et al., 2005) and tropical cyclones (Climatological Center, Thai Meteorological Department, 2011), contribute substantially to annual precipitation. The mean annual temperature and rainfall averages ~27.3˚C and 2380 mm, respectively (Ministry of Communications, Thailand, 1977). Rainfall occurs almost all year round except for a short dry season of three months and <50 mm of rainfall in February (Ministry of Communications, Thailand, 1977)

2 Sediment core dating

The samples were tightly sealed and left standing for 2 to 3 weeks to achieve re-equilibration of decay products (daughter nuclei). The relative efficiency of the gamma detector system was determined by adding an externally calibrated standard (pitchblende, Stackebo, Sweden) to three of the already measured samples and analyzed again. The supported ^{210}Pb was assumed to be in equilibrium with ^{226}Ra, hence the unsupported ^{210}Pb activity was calculated

by subtracting the activity of ^{226}Ra from the activity of supported ^{210}Pb. Based on $^{210}Pb_{unsupported}$ sediment, ^{210}Pb chronology was established (see for example Cheevaporn and Mokkongpai, 1996, for a detailed description of this approach).

3 δD_{wax} of long chain *n*-alkanes biomarkers

Long chain *n*-alkanes are robust and resistant to biodegradation after burial hence widely used as biomarkers for climate reconstructions (Castañeda and Schouten, 2011). They are ubiquitous and produced by a range of organisms, for example, *n*-C_{27} to *n*-C_{35} alkanes are constituents of epicuticular waxes of higher plants (Rieley et al., 1993; Eglinton and Hamilton, 1963, 1967); *n*-C_{23} to *n*-C_{25} alkanes are a dominant component of submerged aquatic macrophytes (Ficken et al., 2000; Baas et al., 2000); and *n*-C_{17} to *n*-C_{21} alkanes are primarily produced by aquatic algae (Robinson et al., 1984; Meyers and Benson, 1988).

The dominant carbon chain length distributions and isotopic compositions of *n*-alkanes vary extensively depending on the source organism, the environments of formation and organic matter diagenesis (Chikaraishi & Naraoka, 2005). This makes it possible to track back through time their sources and the environmental conditions prevailing at the time of deposition (Pancost & Boot, 2004). Several studies have revealed that the hydrogen isotopic composition (D/H ratio or δD) of both terrestrial and aquatic biomarkers reflect that of their source water, although with an offset (Sachse et al., 2004), primarily due to biosynthetic fractionation effects (Sachse et al., 2012).

In the Thailand, δD of precipitation is primarily influenced by the amount effect and El Niño Southern Oscillation (ENSO) dynamics where El Niño leads to decreased rainfall whereas La Niña leads to increase rainfall. The δD_{wax} takes on the primary source water signal, but is in addition influenced by evaporation in soils (Smith and Freeman, 2006) and transpiration (Kahmen et al., 2013). Altogether, δD_{wax} values are thus influenced by rainfall amount – greatly connected to ENSO dynamics in the region under study – and evapotranspiration, which together cause an increase in δD_{wax} values under dryer conditions, whereas a decrease in δD_{wax} values corresponds to increased rainfall (e.g. Smittenberg et al., 2011; Konecky et al., 2012; Niedermeyer et al., 2014).

4 Methods

4.1 Meteorological rainfall data (instrumental records)

To compare the hydroclimatic conditions from our proxies to local observations, we use a time series of annual precipitation taken from the Global Precipitation Climatology Centre (GPCC Version 6.0, http://www.esrl.noaa.gov/psd/data/gridded/data.gpcc.html) (Schneider et al., 2011). The dataset has a horizontal resolution of 0.5° (~50 km) and the closest grid point to the proxy is used at 8.25° N and 99.25° W. As the proxy has a resolution of about 2-5 years, a 3 year-running mean for precipitation is used for the period 1901-2010.

4.2 Past and present processes, and methodological considerations

The biogeochemical trends suggest multiple processes control the OM input into lake NTP, which in turn play a significant role in carbon capture storage. However, in order to correctly interpret the observed patterns, the effects of diagenesis, distinctions between past (fossil) and present (active) microbial populations, as well as the limitations of the methods used must be clarified. It is immediately obvious that the coupled lipid biomarker and qPCR data allow a better resolution of key microbial trends in the lake over the last 150 years. For example, the qPCR analysis showed that the *Botryococcus sp.* were prominent in units I and III, while botryococcene lipids were detected only in the unit III. This shift between the molecular and the lipid biomarker analysis highlights the complementary nature of both methods. Phytoplanktons are not typical inhabitants of anoxic sediments deprived of light and are therefore assumed to represent fossil populations originating at various times from the water column. Indeed, SEMS imaging specifically revealed well-preserved diatoms (S1 Fig. 7) in parts of the sediments where both the lipid biomarker and qPCR data converged.

However, the same cannot be said for the *mcrA* genes, since the microorganisms associated with the anaerobic methane cycle typically dwell in anoxic sediments (e.g. Knittel and Boetius 2009; Conrad et al., 2010). During methanogenesis, organic matter degradation proceeds *via* a complex microbial community consisting of hydrolytic, fermenting, acetogenic and methanogenic microorganisms (Rudd and Taylor, 1980; Conrad et al., 2010; Zinder 1993; Knittel and Boetius 2009). In anoxic sediments of freshwater systems, organic matter is routinely degraded to CO_2 and CH_4 by aceticlastic methanogens (Rudd and Taylor, 1980; Conrad et al., 2010). The CH_4 is then consumed by anaerobic CH_4 oxidizing consortium, which consist of sulfate reducers that oxidizes organic carbon and a syntrophic

methanotrophic archaeal population (Knittel and Boetius 2009). The rate of anaerobic CH_4 oxidation by the anaerobic CH_4 oxidizers in lake sediments is estimated to be 0.0001 to 1.0 nmol cm^{-3} day^{-1} (Knittel and Boetius 2009).

Several studies have used qPCR methods to quantify and screen microbial population dynamics and functional gene abundance in an ecosystem. However, its sensitivity has been challenged due to method biases including sample preservation, efficiency of DNA extraction (Alain et al 2011, Luna et al 2006, Miller et al 1999, Webster et al 2003, Zhou et al 1996) and specificity of selected primers (Lloyd et al 2013, Smith and Osborn 2009, Teske and Sorensen 2007, Wintzingerode et al 1997). Additionally, this method cannot distinguish between the DNA from living and dead cells and also environmental DNA (eDNA). Thus, while the phytoplankton populations are likely from fossils DNA or eDNA, which lived in the water column at various times, the methane cyclers are not considered as such.

4.3 Comparison between δD_{wax}, instrumental data and ESEM analysis

A general coherent trend is observed between proxy data δD_{wax} and the instrumental data of the annual mean precipitation up until 1901, beyond which there are no recorded instrumental data. General increase in precipitation inferred from decreasing δD_{wax} values from ~1900-1960 relative to a general decreasing precipitation from ~1960 to present corresponds to relatively increase in annual mean precipitation from ~1900 -1960 relative to a general decrease in annual mean precipitation. The seeming coherence between δD_{wax} and the instrumental data is an indication of the ability of δD_{wax} proxy to track precipitation. This is further substantiated when compared to the images taken during the ESEM analysis. Increase and decrease in precipitation inferred from the δD_{wax} corresponded with increase and decrease in fluvial deposits, respectively, as observed from the image scans of the sediments. Increase in precipitation also coincided with increase in diatom diversity and bloom as was observed both in picture scan and also the abundance of HBIs concentration, a proxy for diatoms.

Table S1. Geochemistry data showing Age, Depth, $\delta^{13}C_{org}$, C_{org}, $\delta^{15}N$, N, C/N, S, O_2 and P

Age	**Depth**	**$\delta^{13}C_{org}$ (‰)**	**% C_{org}**	**δ^{15} N(‰)**	**% N**	**C/N**	**S**	**O_2**	**P**
2010	0,5	-26,55	34,13	0,44	3,80	8,98	5,20	45,93	0,77
1997	6,5	-26,56	36,68	0,64	3,81	9,62			
1988	10,5	-26,81	36,08	0,67	3,77	9,56	6,17	47,80	0,90
1982	13,5	-26,76	35,93	0,71	3,77	9,53	5,17	46,53	0,73
1974	17,5	-26,86	35,88	0,81	3,72	9,65	5,27	47,17	0,83
1957	25,5	-27,73	34,96	0,63	3,47	10,09	5,07	47,10	0,70
1948	29,5	-27,94	35,94	0,52	3,22	11,17	4,77	47,57	0,47
1935	35,5	-27,99	35,61	0,49	3,36	10,61	5,67	48,27	0,53
1920	42,5	-28,14	36,25	0,38	3,33	10,87			
1912	46,5	-28,24	37,00	0,34	3,15	11,75	5,10	48,60	0,73
1901	51,5	-29,35	37,37	0,23	3,50	10,69	6,10	48,20	0,50
1882	60,5	-29,84	38,82	0,08	3,31	11,71	5,47	47,53	0,47
1871	65,5	-33,03	39,74	-0,70	3,09	12,87	6,77	48,07	0,60
1861	70,5	-30,52	31,55	-0,51	2,33	13,55	4,10	48,73	0,37
1855	73,5	-31,28	31,17	-0,47	2,56	12,16			

Table S2. Biomarker data (µg/g dry sample) and hydrogen isotopes of C_{27}-C_{31} *n*-alkanes (VSMOW ‰.). n.d. = not detected; < 0.1 µg/g dry sample. Estimated standard error for the biomarker based on prior results is 5% and the average standard deviation for hydrogen isotopes is 4‰.

Age	Depth	C_{17} *n*-alkanes	Total Botryococcenes	C_{25} HBI	δD of C_{27}-C_{31} *n*-alkanes
2008	1,5				
2006	2,5	53,8	1,3	73,8	
2001	4,5	49,7	0,9	59,7	-172
1999	5,5	2,0	1,1	59,0	-168
1995	7,5	39,4	1,4	64,3	-174
1993	8,5	43,2	2,2	92,7	-171
1991	9,5	36,3	1,8	71,5	-171
1986	11,5	31,5	2,0	79,9	-178
1984	12,5	31,1	1,9	69,0	-175
1980	14,5	31,8	2,4	96,5	-171
1978	15,5	28,4	2,3	139,5	-177
1976	16,5	7,0	n.d	n.d	-176
1972	18,5	20,5	1,7	73,3	-177
1969	19,5	17,5	1,8	68,9	-165
1967	20,5	17,6	1,5	76,7	-171
1963	22,5	16,7	2,4	143,5	-168
1961	23,5	12,7	2,5	159,4	
1959	24,5	13,2	3,2	201,1	-166
1955	26,5	6,8	3,3	215,7	-181
1952	27,5	4,1	2,8	177,5	-180
1950	28,5	4,0	3,1	179,7	-179
1946	30,5	2,6	3,1	180,5	-179
1944	31,5	2,4	3,0	177,4	-180
1942	32,5	2,5	4,0	213,8	-178
1940	33,5	2,2	2,9	n.d	-181
1938	34,5	1,7	2,9	165,4	-179
1933	36,5	1,6	3,6	89,6	-179
1931	37,5	1,5	3,6	151,3	-168
1929	38,5	2,0	4,8	n.d	-176
1927	39,5	1,9	4,5	147,8	-177
1925	40,5	1,7	4,8	147,3	-170
1923	41,5	1,5	3,9	160,1	-177
1918	43,5	0,3	2,7	21,5	-180
1916	44,5	0,6	4,1	28,2	-177
1914	45,5	0,5	3,7	25,5	
1910	47,5	0,5	4,2	25,0	-176
1908	48,5	0,6	5,7	24,5	-172
1906	49,5	0,5	6,3	17,5	-175
1903	50,5	0,6	7,3	16,4	-178
1899	52,5	0,5	8,7	12,7	-176
1897	53,5	0,3	4,9	6,2	-168
1895	54,5	0,3	6,3	5,9	-176
1893	55,5	0,4	8,4	8,7	-173
1889	57,5	0,7	8,5	9,8	-170
1886	58,5	0,5	6,3	8,2	-172
1884	59,5	0,5	7,6	9,2	-166
1880	61,5	0,4	8,5	4,7	-174
1878	62,5	0,4	10,5	5,0	-171
1876	63,5	0,4	7,8	6,0	-175
1874	64,5	0,4	5,2	5,5	-172
1869	66,5	0,6	8,4	8,0	-177
1867	67,5	0,6	7,0	8,7	-177
1865	68,5	0,4	5,1	10,6	-184
1861	70,5	0,3	4,4	12,2	-168
1859	71,5	0,3	4,5	11,2	-169
1857	72,5	0,3	5,3	11,1	-178

Table S3. QPCR data showing Archaea, Bacteria, Cyanobacteria, Eukarya, Diatoms, Botryococcus and *mcrA* genes abundance.

	Archaea		**Bacteria**		**Cyanobacteria**		**Eukarya**		**Diatoms**		**Botryococcus**		**mcrA**	
Age	abundance cells g-1	Standard error	abundance cells g-1	Standard error	abundance cells g-1	Standard error	absolute abundance cells g-1	Standard error	absolute abundance cells g-1	Standard error	absolute abundance cells g-1	Standard error	absolute abundance cells g-1	Standard error
2010	7,14E+09	7,56E+08	2,97E+11	3,22E+10	7,94E+10	1,64E+10	1,55E+10	3,86E+09	1,68E+08	2,69E+07	1,16E+11	6,39E+09	6,10E+08	3,91E+07
1997	6,18E+09	2,26E+08	2,35E+11	1,28E+10	5,23E+10	3,81E+09	8,96E+09	2,49E+09	9,01E+07	1,76E+07	9,14E+10	1,42E+10	3,39E+08	1,86E+07
1988	1,16E+10	1,00E+09	3,25E+11	3,53E+10	3,58E+10	2,07E+09	1,15E+10	1,71E+09	1,62E+08	1,73E+07	2,88E+10	2,94E+09	4,79E+08	1,85E+07
1982	6,18E+09	6,85E+08	2,03E+11	1,92E+10	1,05E+10	4,47E+08	3,90E+09	6,26E+08	4,22E+07	6,92E+06	7,03E+09	7,99E+08	1,40E+08	4,70E+07
1974	7,39E+09	1,30E+09	2,25E+11	1,07E+11	1,85E+10	4,46E+09	1,00E+10	1,00E+09	1,59E+08	1,99E+07	3,01E+10	4,85E+08	4,04E+08	8,33E+07
1957	4,30E+08	4,00E+07	7,67E+09	7,30E+08	2,95E+08	4,00E+06	2,49E+08	5,38E+07	5,11E+06	1,24E+06	2,98E+08	8,72E+07	1,22E+07	1,31E+06
1948	1,69E+10	3,29E+09	5,73E+11	1,48E+10	7,54E+09	6,24E+08	1,32E+10	9,16E+08	1,15E+08	2,25E+07	2,41E+09	2,69E+08	4,74E+08	1,52E+07
1935	6,72E+08	3,53E+07	1,80E+10	8,31E+08	2,21E+08	9,64E+06	1,68E+08	1,78E+07	2,27E+06	3,08E+04	1,40E+08	6,24E+07	9,73E+06	1,21E+06
1920	3,20E+07	2,27E+06	3,61E+08	1,60E+08	5,26E+06	1,81E+06	8,85E+06	9,86E+05	ND		1,78E+07	3,08E+07	5,25E+05	1,54E+05
1912	6,91E+09	2,29E+09	1,54E+11	2,95E+10	2,72E+09	1,18E+08	4,11E+09	3,24E+08	5,58E+07	5,18E+06	1,36E+09	6,93E+07	1,82E+08	7,43E+07
1901	4,51E+08	9,32E+07	8,10E+09	3,76E+08	2,08E+08	2,02E+07	1,20E+08	3,17E+07	8,21E+05	5,43E+04	6,96E+07	4,37E+07	4,62E+06	1,24E+06
1882	4,48E+09	3,37E+08	1,03E+11	1,38E+10	1,01E+09	1,51E+08	3,57E+09	7,96E+08	1,57E+07	3,67E+06	2,07E+09	3,21E+08	1,39E+08	1,89E+07
1871	2,34E+10	1,79E+09	2,86E+11	4,66E+09	3,84E+09	2,73E+08	6,57E+09	3,87E+09	4,96E+07	7,55E+06	6,77E+09	9,98E+08	5,26E+08	1,01E+08
1861	5,51E+09	5,52E+08	8,37E+10	1,98E+09	6,51E+08	4,74E+07	3,05E+09	2,26E+08	2,73E+07	3,08E+06	2,49E+10	3,35E+09	1,62E+08	1,26E+07
1855	1,13E+10	3,45E+08	2,33E+11	1,14E+10	7,41E+08	1,53E+08	1,12E+10	6,92E+08	5,18E+07	3,69E+06	1,08E+11	1,17E+10	3,09E+08	1,55E+07

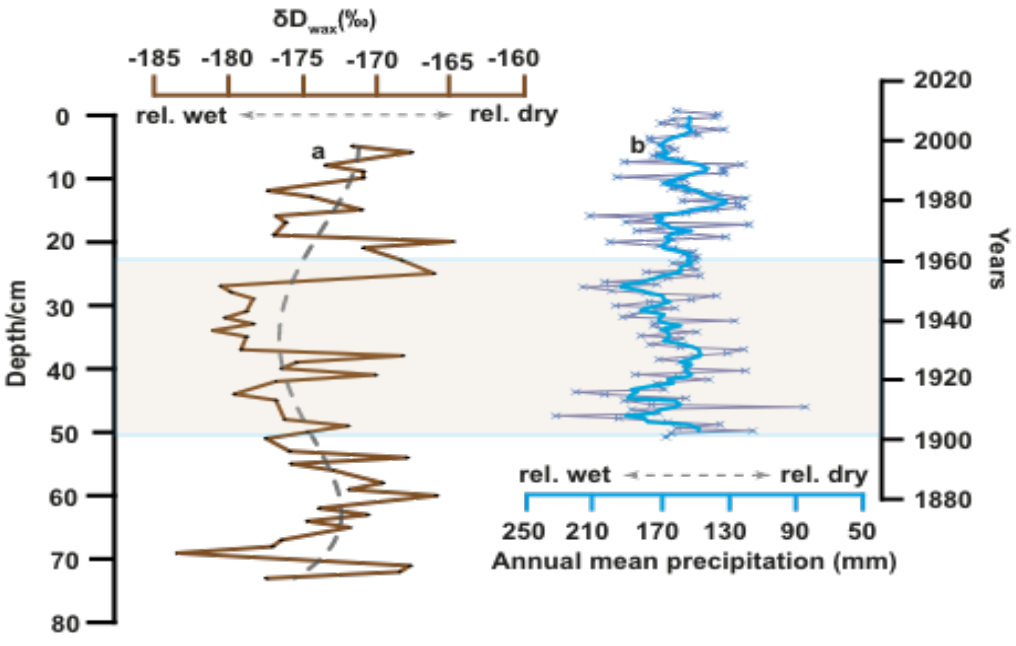

Figure S1. A comparison between proxy data (a) δD_{wax} and instrumental data (b) Annual mean precipitation. The dashed line represents the polynomial fit.

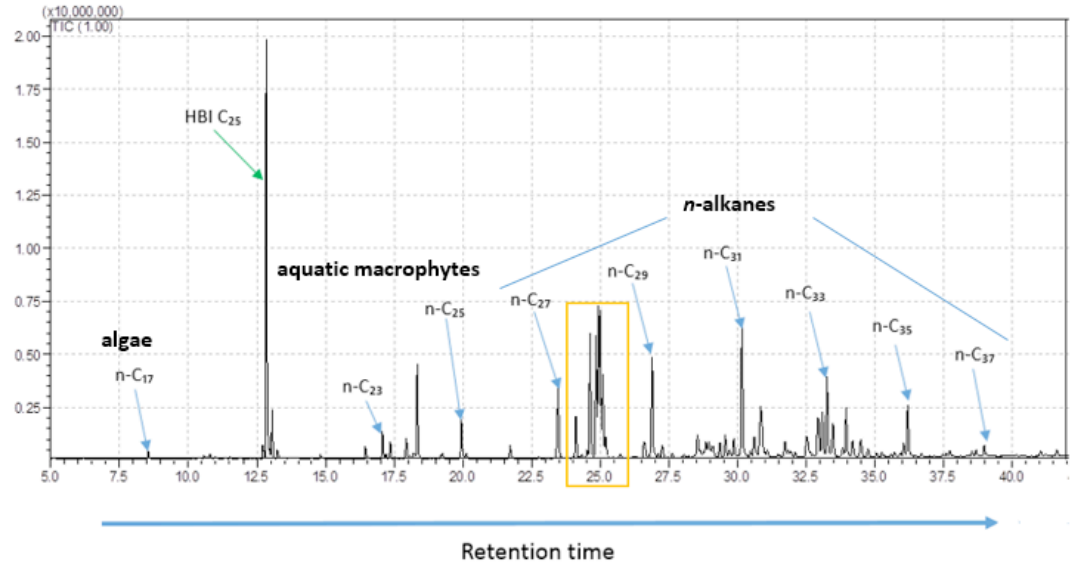

Figure S2. A GC-MS chromatogram of Nong Thale Pron sample, depth 70.5 cm. X-axis= retention time [min] and y-axis= abundance of compound. Chromatograms in yellow box represent botryococcenes (details below).

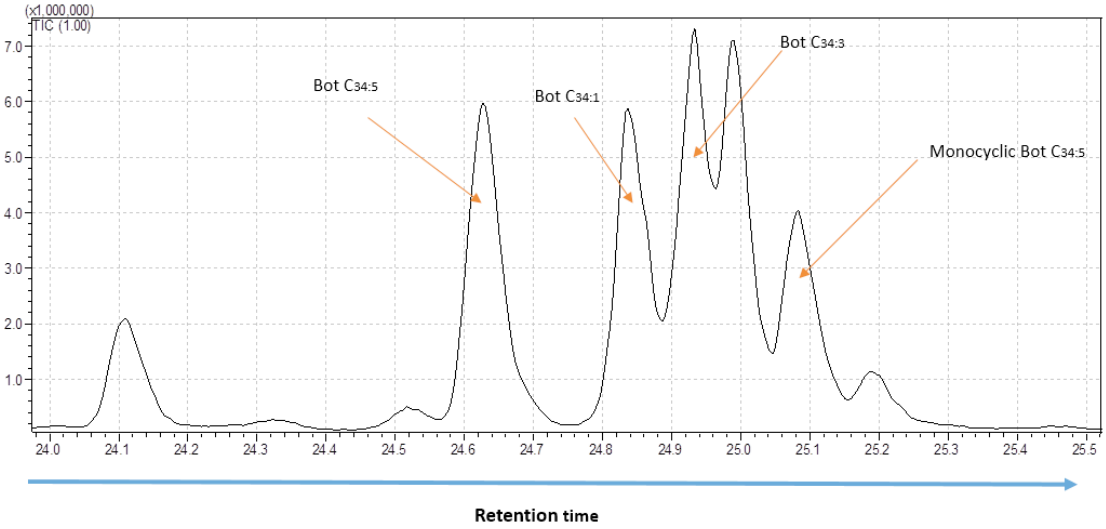

Figure S3. An enhancement of the marked area in Figure 2 showing the botryococcenes with their retention times and corresponding peak heights/areas. X-axis= retention time [min] and y-axis= abundance of compound.

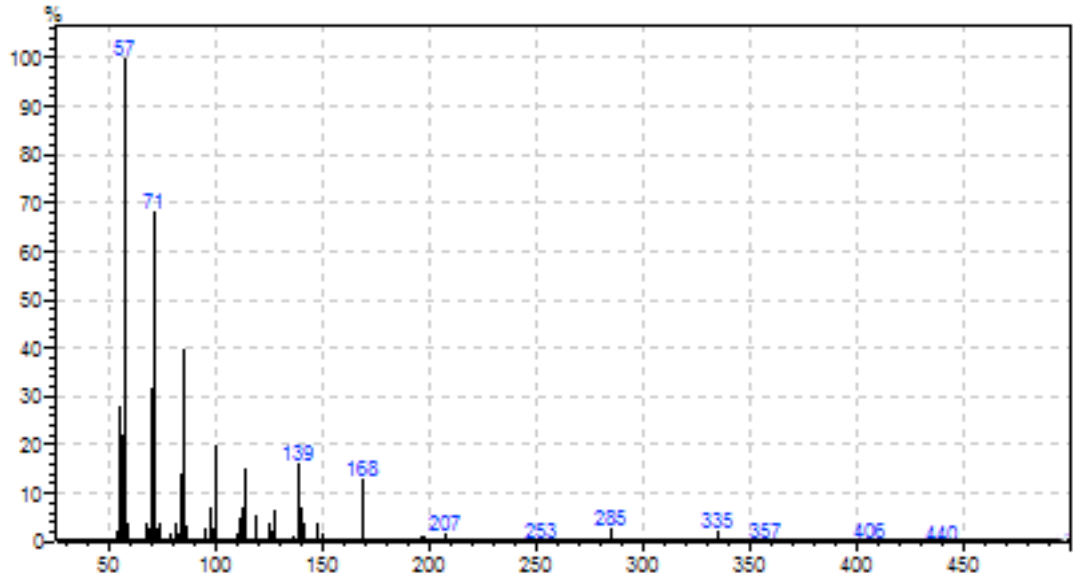

Figure S4. Spectrum showing the C_{17} *n*-alkane, the x-axis= molecular mass while the y-axis= the ratio of intensity of abundance in the molecule.

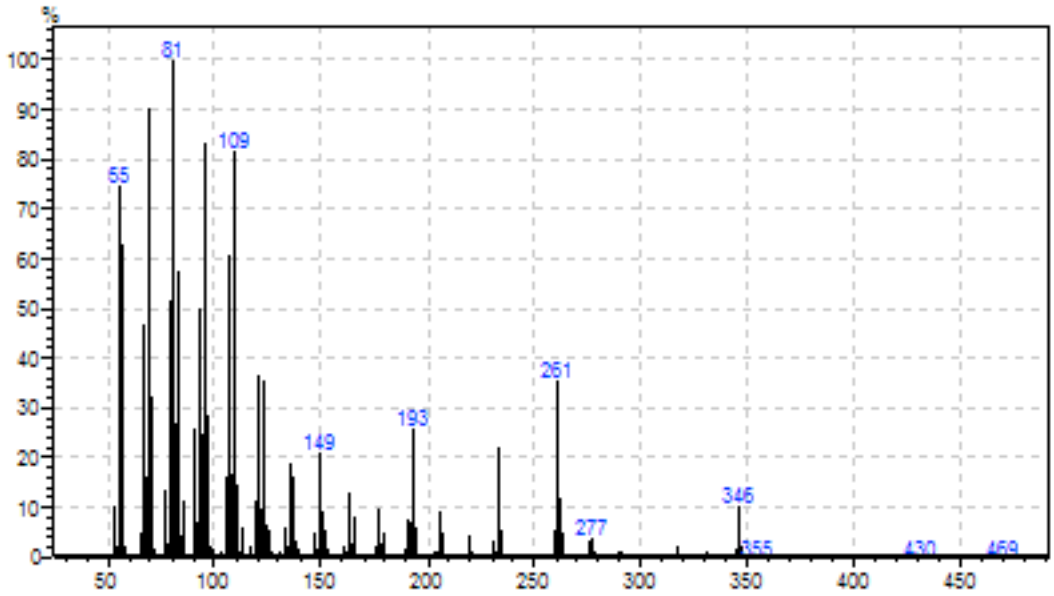

Figure S5. Spectrum showing the C_{25} Highly branched Isoprenoid (HBI). The x-axis= molecular mass while the y-axis= the ratio of intensity of abundance in the molecule.

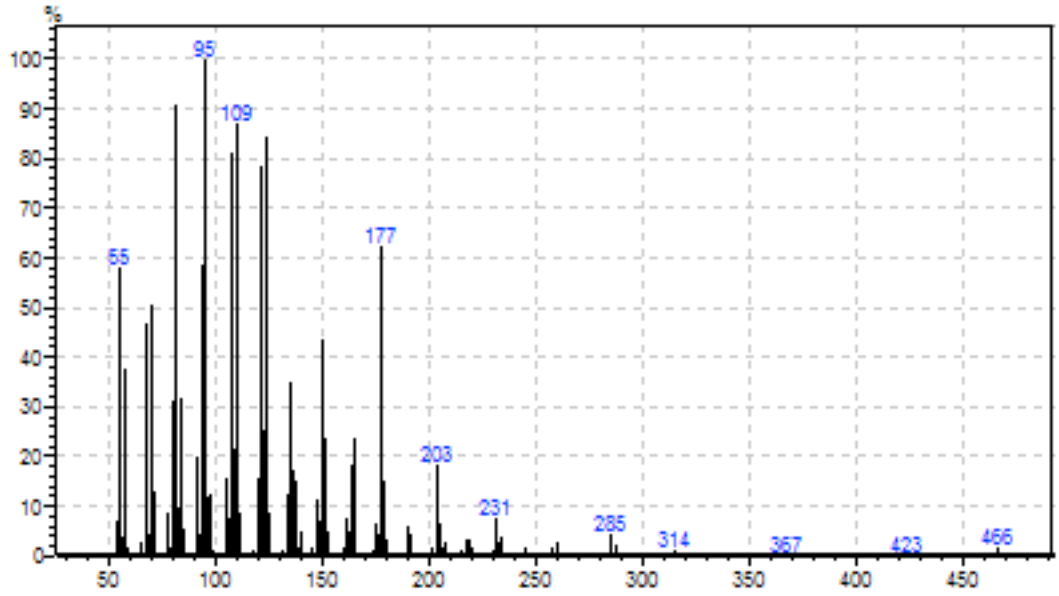

Figure S6. Spectrum showing the C34:5 monocyclic Botryococcene, with x-axis= molecular mass while the y-axis= the ratio of intensity of abundance in the molecule.

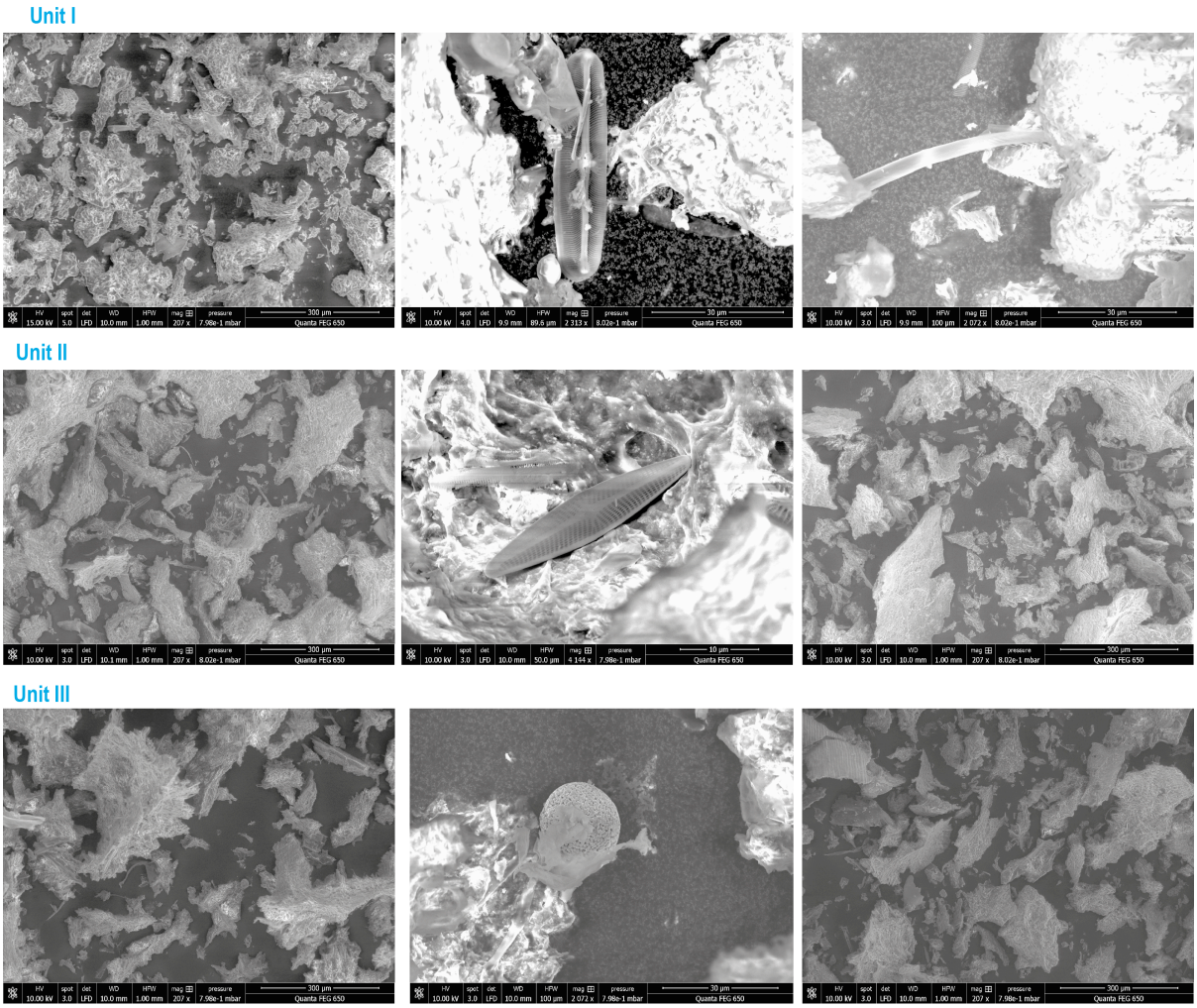

Figure S7. Examples of electron scan images of the sediment samples showing different morphologies' or tests of diatoms

References

Al-Samarrai, T. and Schmid, J. A.: Simple method for extraction of fungal genomic DNA, Lett. Appl. Microbiol., 30, 53-56, 2000.

Alain, K., Callac, N., Ciobanu, M-C., Reynaud, Y., Duthoit, F. and Jebbar, M.: DNA extractions from deep subsea floor sediments: Novel cryogenic-mill-based procedure and comparison to existing protocols, J. Microbiol. Meth., 87, 355-362, 2011.

Baas, M., Pancost, R., Van Geel, B. and Sinninghe Damsté. J. S.: A comparative study of lipids in Sphagnum species, Org. Geochem., 31, 535-541, 2000.

Castañeda, I. and Schouten, S.: A review of molecular organic proxies for examining modern and ancient lacustrine environments, Quat. Sci. Rev., 30, 2851-2891, 2011.

Cheevaporn, V. and Mokkongpai, P.: Pb-210 radiometric dating of estuarine sediments from the eastern coast of Thailand. Journal of Science Society, Thailand, 22, 313-324, 1996.

Chikaraishi, Y. and Naraoka, H.: $\delta^{13}C$ and δD identification of sources of lipid biomarkers in sediments of Lake Haruna (Japan), Geochim. Cosmochim. Acta, 69, 3285–3297, 2005.

Climatological Center.: Tropical cyclones in Thailand historical data 1951-2010. Meteorological Development Bureau Thai Meteorological Department, http://www.ptcwmoescap.org/AdhocGroupAttachments/26_TROPICAL%20CYCLONES%20IN%20THAILAND.pdf, 2011.

Conrad, R., Calus, P. and Casper, P.: Stable isotope fractionation during the methanogenic degradation of organic matter in the sediment of an acidic bog lake, Lake Grosse Fuchskuhle, Limnol. Oceanogr., 55, 1932–1942, 2010.

Crépeau. V, Cambon, B. M-A., Lesongeur, F., Randrianalivelo, H., Sarradin, P-M., Sarrazin, J. and Godfroy, A. : Diversity and function in microbial mats from the Lucky Strike hydrothermal vent field, FEMS Microbiol. Ecol., 76, 524-540, 2011.

Department of Mineral Resources of Thailand: Geological map of Nakhon Si Thammarat, Thailand, Scale 1:50,000, (in Thai), 2007.

Dilworth, E. and Frey, J. E.: A rapid method for high throughput DNA extraction from plant material for PCR amplification, Plant Mol. Biol. Rep., 18, 61-64, 2000.

Dong, H., Jiang, H., Yu, B., Liu, X. and Zhang, C.: Impacts of environmental change and human activity on microbial ecosystems on the Tibetan Plateau, NW China, GSA Today, 20, 4–10, 2010.

Eglinton, G. and Hamilton, R. J.: Leaf epicuticular waxes, Science, 156, 1322–1335, 1967.

Eglinton, G., Hamilton, R. J.: The distribution of alkanes, in: Swain, T. (Ed.), Chemical Plant Taxonomy, Academic Press, 187–217, 1963.

Felder, M., Poli, P., and Joiner, J.: Errors induced by ozone field horizontal inhomogeneities into simulated nadir-viewing orbital backscatter UV measurements, J. Geophys. Res., 112, D01303, doi:10.1029/2005JD006769, 2007.

Ficken, K. J., Li, B., Swain, D. L. and Eglinton, G.: An n-alkane proxy for the sedimentary input of submerged/floating freshwater aquatic macrophytes, Org. Geochem., 31, 745–749, 2000.

Knittel, K, and Boetius, A.: Anaerobic oxidation of methane: progress with an unknown process, Annu. Rev. Microbiol., 63, 311-334, 2009.

Konecky, B. L., Russell, J. M., Rodysill, J. R., Vuille, M., Bijaksana, S. and Huang, Y.: Intensification of southwestern Indonesian rainfall over the past millennium, Geophys. Res. Lett., 40, 386–391, 2013.

Lloyd, K. G., May, M. K., Kevorkian, R. T and Steen, A. D.: A meta-analysis of quantification methods shows that archaea and bacteria have similar abundances in the subseafloor, Appl. Environ. Microbiol., 79, 7790-7799, 2013.

Luna, G. M., Dell'Anno, A. and Danovaro, R.: DNA extraction procedure: a critical issue for bacterial diversity assessment in marine sediments, Environ. Microbiol., 8, 308-320, doi: 10.1111/j.1462-2920.2005.00896.x, 2006.

Mayhew, P. J., Jenkins, G. B. and Benton, T. G.,: A long-term association between global temperature and biodiversity, origination and extinction in the fossil record, Proc. Royal Soc. B., **275,** 47–53, 2008.

Mayhew, P. J., Jenkins, G. B. and Benton, T. G.: A long-term association between global temperature and biodiversity, origination and extinction in the fossil record. Proc. Royal. Soc. B., 275, 47–53, 2008.

Meyers, P. and Benson, L. V.: Sedimentary biomarker and isotopic indicators of the paleoclimatic history of the Walker Lake basin, western Nevada. Org. Geochem., 13, 807–813, 1988.

Miller, D. N., Bryant, J. E., Madsen, E. L. and Ghiorse, W. C. : Evaluation and optimization of DNA extraction and purification procedures for soil and sediment samples, Appl. Environ. Microbiol., 65, 4715-4724, 1999.

Ministry of Communications, Thailand: Climatological Data of Thailand, 25 Year Period (1951–1975), Meteorological Department, Ministry of Communications, Bangkok, 1977.

Niedermeyer, E. M., Sessions, A. L., Feakins, S. J. and Mohtadi, M.: Hydroclimate of the Indo-Pacific Warm Pool during the past 24,000 years, PNAS, 111, 9402-9406, 2014.

Pancost, R. D. and Boot, C. S.: The palaeoclimatic utility of terrestrial biomarkers in marine sediments, Mar Chem, 92, 239–261, 2004.

Rahalkar, M., Deutzmann, J., Schink, B. and Bussmann, I.: Abundance and activity of methanotrophic bacteria in littoral and profundal sediments of Lake Constance (Germany), Appl. Environ. Microbiol., 75, 119-126, 2009.

Raksasakulwong, L., Teerarungsigu, N., Tunpisit, P., Jungsamran, S.: Report of geological map of Amphoe Thung Yai, Ban Thang Luang, and Ban Nua Klong, scale 1:50,000. Meeting of Bureau of Geological Survey. Department of Mineral Resources of Thailand, 161-166, (in Thai), 1989.

Rieley, G., Collister, J. W., Stern, B. and Eglinton, G.: Gas chromatography/Isotope ratio mass spectrometry of leaf wax *n*-alkanes from plants with differing carbon dioxide metabolisms, Rapid Commun. Mass Spectrom., 7, 488–491, 1993.

Robinson, N., Cranwell, P. A., Finlay, B. J. and Eglinton G.: Lipids of aquatic organisms as potential contributors to lacustrine sediments, Org. Geochem. 6, 143–152, 1984.

Rozanski, K., Araguas-Araguas, L., and Gonfiantini, R.: Isotopic patterns in modern global precipitation. In: Climate change in continental isotopic records (Swart, P. K., Lohmann, K. C.; McKenzie, J. A.; Savin, S., editors), AGU Monograph, 78, 1-36, 1993.

Rudd, J. W. M. and Taylor, C. D.: Methane cycling in aquatic environments, Adv. Aquat. Microbiol., 2, 77–150, 1980.

Sachse, D., Billault, I., Bowen, G. J., Chikaraishi, Y., Dawson, T. E., Feakins, S. J., Freeman, K. H., Magill, C. R., McInerney, F.A., van der Meer, M. T. J., Polissar, P., Robins, R. J., Sachs, J. P., Schmidt, H.-L., Sessions, A. L., White, J. W. C., West, J. B. and Kahmen, A.: Molecular paleohydrology: Interpreting the hydrogen-isotopic composition of lipid biomarkers from photosynthesizing organisms, Annu. Rev. Earth Planet. Sci., 40, 221 – 249, 2012.

Sachse, D., Radke, J. and Gleixner, G.: Hydrogen isotope ratios of recent lacustrine sedimentary n-alkanes record modern climate variability, Geochim. Cosmochim. Acta, 68, 4877–4889, 2004.

Santisuk, T.: Forests of Thailand, The Forest Herbarium, http://www.dnp.go.th/Botany/pdf/, 2006.

Schneider, U., Andreas, B., Peter, F., Anja, M-C., Bruno, R. and Markus, Z.: GPCC Full Data Reanalysis Version 6.0 at 0.5°: Monthly Land-Surface Precipitation from Rain-Gauges built on GTS-based and Historic Data. DOI: 10.5676/DWD_GPCC/FD_M_V6_050, 2011.

Smith, C. J. and Osborn, A. M.: Advantages and limitations of quantitative PCR (Q-PCR)-based approaches in microbial ecology, FEMS Microbiol. Ecol., 67, 6-20, 2009.

Smittenberg, R. H., Baas, M., Schouten, S. and Sinninghe Damsté, J. S., The demise of the alga Botryococcus braunii from a Norwegian fjord was due to early eutrophication, The Holocene, 15, 133-140, 2005.

Teske, A. and Sorensen, K. B.: Uncultured archaea in deep marine subsurface sediments: have we caught them all?, The ISME J., 2, 3-18, 2007.

Thomson, J. A.: An improved non-cryogenic transport and storage preservative facilitating DNA extraction from ‘difficult’ plants collected at remote sites, Telopea, 9, 755-760, 2002.

Tierney, J. E., Oppo, D. W., Rosenthal, Y., Russell, J. M. and Linsley, B. K.: Coordinated hydrological regimes in the Indo-Pacific region during the past two millennia, Paleoceanography, 25, PA1102, doi:10.1029/2009PA001871, 2010.

1 Webster, G., Newberry, C. J., Fry, J. C. and Weightman, A. J.: Assessment of bacterial
2 community structure in the deep sub-seafloor biosphere by 16S rDNA-based techniques:
3 a cautionary tale, J. Microbiol. Meth., 55, 155-164, 2003.

4 Wintzingerode, F., Göbel, U. B. and Stackebrandt, E.: Determination of microbial diversity in
5 environmental samples: pitfalls of PCR-based rRNA analysis, FEMS Microbiology
6 Reviews, 21, 213-229, 1997.