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A 150-year record of ancient DNA, lipid biomarkers and hydrogen isotopes, tracing the microbial-planktonic community succession controlled by (hydro)climatic variability in a tropical lake

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We investigated the decadal variations in phytoplankton communities, and their response to environmental and climatic conditions, from a ∼150 year long sedimentary archive of Lake Nong Thale Prong (NTP), southern Thailand. We applied a combination of analyses: lipid biomarkers, compound-specific hydrogen isotopes, bulk carbon and nitrogen concentrations and isotopes, environmental SEM, and fossil DNA using qPCR targeted to specific taxa. Past hydrological conditions were reconstructed using the hydrogen isotopic composition of leaf wax n-alkanes. Temperatures were reconstructed using the tetraether-based MBT/CBT index, measured using a new and efficient reverse-phase HPLC-MS method. The climatological data compared well with meteorological data from the last decades. Reconstructed drier and warmer conditions from ∼1857-1916 Common Era (CE) coincided with oligotrophic lake water conditions and dominance of the green algae *Botryococcus braunii* - evidenced by a combination of both fossil DNA and the occurrence of characteristic botryococcene lipids. A change to higher silica (Si) input ∼1916 CE was related to increased rainfall and lower temperatures concurring with an abrupt takeover by diatom blooms lasting for 50 years - as evidenced by ancient DNA, characteristic highly branched isoprenoid lipids, and SEM. From the 1970s onwards, more eutrophic conditions prevailed, and these were likely caused by increased levels of anthropogenic phosphate (P), aided by stronger lake stratification caused by dryer and warmer conditions. The eutrophic conditions led to increased primary productivity in the lake, consisting again of a *Botryococcus sp.,* although this time not producing botryococcene lipids. Moreover, *Cyanobacteria* became dominant – again evidenced by ancient DNA and the characteristic C_{19} alkane. Throughout the record, stratification and primary production could be linked to the intensity of methane cycling, by targeting and quantifying the *mcrA* gene that is used both by methanogens and anaerobic methane oxidizers. Our results show that a combined multi-proxy approach, especially the combination of targeted qPCR and lipid biomarker analysis, allows a highly robust reconstruction of past microbial ecosystem responses to climatic and environmental changes.