S1 File. Supplementary Methods. Detailed description of the criteria used for dataset inclusion in the literature search, the different kinds of data (e.g., composition or concentration based), detection limits, and the environmental variables in each of the published studies.

1. Dataset inclusion

Using ISI Web of Science searches including the terms 'fatty acids', 'phytoplankton' and each of the phytoplankton group names, we sought out papers that cultured algae in diverse and yet controlled conditions. We also identified additional potential datasets using a combination of prior knowledge of the literature and through tracing the citations of other key studies in the field. We purposely included studies that we expected would produce 'outlier' fatty acid (FA) profiles based on experimental manipulation of conditions expected to affect FA composition. The justification for this varied approach is that phytoplankton FA profiles are reported throughout a diverse literature with very different original study goals.

Relevant studies are from a wide range of disciplines, from research on prospecting for potential sources for energy and natural products, to studies in aquaculture, experimental food webs in aquatic ecology, and general phycological surveys. This made it difficult to make the meta-analysis paper search simple and purely objective and repeatable. Our use of prior knowledge in searching for papers does potentially introduce bias; however, given the unprecedented sample sizes used in this analysis (1145 FA profiles) and the focus particularly on including papers that would manipulated environmental variables, we argue that our conclusions are robust to this sampling bias. We included data from 58 studies out of the 399 studies initially deemed promising using our search criteria (see S1 Table). Below we provide a detailed account of the reasoning behind dataset inclusion, with citations of one or two studies providing

representative examples of these criteria. Exclusion from this meta-analysis does not imply flaws in the original papers, just that they did not meet our particular criteria.

We did not include FA profiles of mixed phytoplankton taxa [e.g., 1], studies that cultured phytoplankton in outdoor holding tanks or culture tanks larger than an arbitrary volume of 100 L volume [e.g., 2] in an attempt to partially standardize potentially important but unknown conditions from such circumstances that make such studies harder to compare with the majority of the studies. For studies with a combination of profiles from different or unknown categories, we used the subset of FA profiles that met the criteria or where key conditions were known or reported by the authors [e.g., 3,4]. We included FA profiles from cultures that were described by the authors as not 'axenic', because this ideal standard is almost never met in culture experiments.

Researchers do not always report the same FA for various reasons. To include data from as many studies as possible, we initially recalculated each published FA profile to comprise of 11 consistent individual FA or categories. The 8 individual ω-3 and ω-6 EFA are: 18:2ω6 (LIN), 18:3ω6 (GLA), 18:3ω3 (ALA), 18:4ω3 (SDA), 18:5ω3, 20:4ω6 (ARA), 20:5ω3 (EPA), and 22:6ω3 (DHA). In addition, we compiled 3 summary fatty acid categories for each profile, including; sum of saturated fatty acids (SAFA), sum of monounsaturated fatty acids (MUFA), and sum of non-EFA PUFA, or 'other PUFA'. The other PUFA variable was calculated by subtracting the total of the 8 individual EFA from the total remaining PUFA in the original datasets. This ensured that the analytical dataset did not have double sampled variables. The other PUFA variable mostly captures the sum of C_{16} PUFA and other relatively rare $>C_{18}$ PUFA.

We did not include FA data from studies that reported a large proportion (e.g., mean across samples >5%) of 'other' or 'unknown' FA [5,6] because we could not assign these other

FA to matching variables in our database. In addition, we included data only from studies that reported data from total FA (e.g., not split by lipid classes), to maintain consistency among the analytical units. We did not include data from studies that reported only the number of carbons and double bonds, without reporting the position of the position of the final double bond from the methyl group [e.g., 7,8] because we could not verify that FA reported this way corresponded to those in our database. Studies that combined key PUFA variables as one were also excluded [e.g., 9] for the same reason.

We did not include studies that did not report information for a majority of the explanatory variables we used in the analysis [10] or studies that did not report the FA data used for their analysis as tables or supplementary material [e.g., 11]. If authors reported multiple extractions from the same algal strain [12,13] or if it was not clear from the methods that experimental conditions varied between these replicates [14], we entered the mean of these values for each distinct strain. We did not remove what we perceived to be potential 'outlier' data from the master file except for in the case of Viso and Marty [13]; concentration data reported in this paper were ca. one order of magnitude lower from other published concentration data for related phytoplankton taxa. In this case, the Viso and Marty [13] proportional data were still used but the concentration data were removed prior to analyses. Finally, in the few cases where our explanatory data is different than what is reported in original papers, or if it was not reported in the original paper, the discrepancy is because these data were provided by the original authors via email correspondence.

2. FA concentrations and composition

69 Defining a common metric for expressing FA concentration is challenging due to the
70 diverse ways that researchers present data. The lack of a common standard is due to the varied
71 goals of researchers [discussed in 15,16]. Our data compilation effort included on both
72 compositional FA data and several of the most common concentration metrics [FA μg mg^{-1} C,
73 FA % dry weight (DW), and pg FA $cell^{-1}$]. Of the concentration metrics, we focused our
74 statistical analysis on the FA % of DW (hereafter referred to as FA % DW) dataset because this
75 was the only weight-based category with ample within-group taxonomic replication for statistical
76 evaluation of the effect of all variables.

77 Composition data (% FA of total lipids, hereafter referred to as % FA) was either taken
78 directly from the original paper or calculated from the raw concentration data if that is how the
79 researcher originally presented it. Concentration data was either taken directly from the original
80 paper or calculated by multiplying the given raw proportion data for each FA by the total FA
81 data provided by the authors (FA μg mg^{-1} C, FA % DW, and pg FA $cell^{-1}$) for each sample.
82 Because original FA % DW and pg $cell^{-1}$ data may be reported by the authors as from either the
83 total lipid or total FA (or both), we used only the most commonly reported approach for each of
84 these metrics, which was pg FA $cell^{-1}$ and FA % DW of total lipid content. Concentration data
85 was not included if this distinction was unclear from the original methods, or if the data were
86 presented in alternative formats [e.g., % organic weight (OW), nmol FA $cell^{-1}$, μg x 10^6 $cell^{-1}$,
87 μm^{-3}, mg L^{-1} day^{-1}].

88 Researchers may report concentration data as μg FA mg $carbon^{-1}$, particulate organic
89 carbon, or 'dry biomass'. We initially compiled the raw data for each of these types of data (see
90 the S1 Dataset), but performed analyses on only the composition data (% FA), FA % DW of total
91 lipid, and the FA μg mg^{-1} C datasets. Our approach provided a relatively simple and consistent

way of maximizing the number of profiles that were reported in a common way. These decisions were made prior to analyses.

3. Detection limits

Detection limits varies among papers, but most studies will report FA compositional data for all FA that comprise >0.05% of the total FA. Below this limit it is common for authors to indicate that samples have 'trace' amounts of particular FA because non-quantified peaks appear on chromatograms. When authors report 'trace' we entered a non-zero value in the raw file defined as the number just below the value defined by the authors for trace in their data. For example, Dunstan et al. [17] report that 'trace' is <0.05%; in these cases we entered as 0.04% in our file. When original study authors did not report trace values, we assumed that FA in these samples was below detection limits and cannot be differentiated from zero.

If original authors did not report certain very commonly identified PUFA that are in virtually all FA standards (e.g., ALA, ARA, DHA), we assumed that this omission was because these FA were not present above detection limits, and we therefore treat these as zeros in the database. The reasoning for this is that many algal strains do not have these FA that are common in the majority of studies, and dropping these profiles from later analyses because of 'missing data' would unfairly penalize these strains or studies that only worked with these strains. There is one PUFA we included in our FA list, which is not commonly in standards and is usually only identified in studies working with dinoflaggelates (18:5ω3). We entered 'nr' (not reported) in the master database for this FA when it was not reported. However, following the same logic used above 'nr' entries for this FA were assumed to indicate the absence of this FA above detection limits in the sample, and these values were therefore treated as zeros in our analyses.

115

116 *4. Variables*

117 The growth condition explanatory variables reported in nearly all studies were entered as
118 described by the original papers. In some cases, certain explanatory variables (light, culture
119 technique) was obtained from methods sections of other papers by the same author or other
120 papers that the primary paper cited for general methodological details [e.g., 18] or by direct
121 email communication with the authors. The following variables (in numbered sub-headings
122 below) were the variables included in distance based linear model [DISTLM; 19] analysis (See
123 the Analysis section below and in the main text). The raw dataset also has other meta-data
124 consistently reported by the original authors, including additional treatment explanations, growth
125 media used, and culture container used. These various other categories were not reported
126 consistently enough to be formally included in the analyses (see the S1 Dataset).

127

128 *4.1. Group (high order taxonomic group; categorical)*

129 For each taxon FA profile entered into the database (e.g., each unique row) the original
130 genus and species names reported by the authors was cross-referenced with AlgaeBase [20] to
131 ensure correct and consistent spelling and align current taxonomic affiliations for the taxonomic
132 designations of Phylum, Class, and Order, Genus and Species. The operative (i.e., analytical)
133 group unit was later defined by collapsing and splitting some of these categories; for example we
134 categorized multiple Classes commonly known as ‘diatoms’ as one distinct group rather than
135 lumping these classes with Eustigmatophyceae or Chrysophyceae, which are all also presently
136 aligned with Ochrophyta [20].

137 We therefore categorized the raw data into the following 9 groups: Diatoms
138 (Fragilariophyceae, Bacillariophyceae, Coscinodiscophyceae); Dinoflagellates; Chlorophytes;
139 Cyanobacteria; Ochrophyta (i.e., non-diatom Classes: Chrysophyceae, Raphidophyceae,
140 Eustigmatophyceae, Xanthophyceae); Cryptophytes; Euglenoids (Euglenozoa); Rhodophyta; and
141 Haptophyta. Due to limited sample sizes in the Ochrophyta, Euglenoids, Rhodophyta, our
142 analyses did not include these groups (see Analysis section below).
143
144 *4.2. Light (intensity; continuous)*
145 This variable is reported in the literature as W m^{-2}, μ Mol m^{-2} s^{-1}, or μE m^{-2} s^{-1}, or in
146 simply "cool fluorescent light", or Lux. We assumed the following conversions to express all
147 values as μ Mol m^{-2} s^{-1} [21]:
148 1 μ Mol m^{-2} s^{-1} = 1 μ E m^{-2} s^{-1}
149 1 μ Mol m^{-2} s^{-1} = 0.218 W m^{-2}
150 1 μ Mol m^{-2} s^{-1} = 74 Lux (for cool white fluorescent bulb)
151 1 μ Mol m^{-2} s^{-1} = 33 Lux (for plant growth fluorescent bulb)
152 If bulb type was not reported, we used the mean of the conversion factor for the two
153 fluorescent bulb types. If a range of light values was reported [e.g., 12], we used the mean of
154 these values. If conditions were not reported, data were obtained from personal communication
155 with the authors [e.g., 22].
156
157 *4.3. Light2 (hours light; continuous)*
158 Entered as the number of hours within the 24 hour day that the authors reported having
159 the lights on in the growth chambers.

160

161 *4.4 Temp (temperature; continuous)*

162 This is the temperature (°C) that is reported for each algal experiment or treatment (if
163 temperature was a treatment). If a range of values was reported we used the mean of the range.

164

165 *4.5. Salinity [salinity in parts per thousand (ppt), equivalent to gL^{-1}; continuous]*

166 For experiments with salt-water taxa, the salinity is entered as reported by the authors,
167 when they report it. If the original authors were clearly culturing algae in saltwater but did not
168 report the salinity we assigned an arbitrary value of 32 ppt to these samples. All profiles for
169 freshwater experiments were assigned a value of 0.

170

171 *4.6. Nutrient status (binary proxy for diverse conditions; categorical)*

172 Previous research has shown that FA profiles in microalgae are sensitive to nutrient
173 levels [16]. Diverse experiments have manipulated many potentially limiting nutrients (N, P, Fe),
174 and the degree of nutrient limitation among experiments varies greatly depending on the author's
175 original question. For example, nutrient limitation may be investigated as a binary, low-high
176 value [15] or along a gradient of minor to severe limitation [16]. In addition, experiments have
177 also shown that growth phase affects phytoplankton FA [17,23,24].

178 Here, we categorized these diverse experimental manipulations across all studies into a
179 binary, categorical 'nutrient' indicator factor as either 'limited' or 'replete'. All FA profiles from
180 studies were categorized as 'limited' when the authors either 1) limited concentration of a key
181 nutrient, or 2) manipulated experimental conditions which resulted in the cultures experiencing
182 nutrient limitation, or if extractions were performed when cultures were in a 'stationary' growth

phase [23,e.g., 25]. There is often less information about algal culture conditions in studies where the original objective of algal cultures was to grow biomass for feeding to heterotrophs. In these cases, which did not report algal culture growth phase or nutrient status, we assumed that the cultures were cultured in a nutrient replete status for the sake of producing biomass for the experiments [e.g., 26,27].

5. Analysis

We used a distance-based linear model (DISTLM) to quantify the relative contribution of categorical algal group affiliation and multiple culture condition variables, on multivariate algal FA composition [19]. The analysis was run on two distinct FA datasets [% FA of total lipids (% FA), FA % of dry weight (FA % DW)]; there were 6 taxonomic groups considered in these analyses. We could not perform meaningful or directly comparable DISTLM analyses using the FA μg mg^{-1} C data due to differences in the number of groups represented and due to the low number of taxa profiles within each group (S2 Table).

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