1	to ICES Journal of Marine Systems 'Food for Thought'
2	Pelagic food-webs in a changing Arctic: A trait-based perspective suggests a mode of resilience
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### 24 Abstract

25 Arctic marine ecosystems support fisheries of significant and increasing economic and nutritional 26 value. Commercial stocks are sustained by pelagic food webs with relatively few keystone taxa 27 mediating energy transfer to higher trophic levels, and it remains largely unknown how these taxa will 28 be affected by changing climate and the influx of boreal taxa. Calanus species store large quantities of 29 lipids, making these zooplankton a critical link in marine food-webs. The Arctic Calanus species are 30 usually larger and, importantly, have been suggested to contain disproportionately larger lipid stores 31 than their boreal congeners. Continued climate warming and subsequent changes in primary 32 production regimes have been predicted to lead to a shift from the larger, lipid-rich Arctic species, C. glacialis and C. hyperboreus, toward the smaller, boreal C. finmarchicus in the European Arctic, with 33 34 negative consequences for top predators. Our data show that lipid content is closely related to body 35 size for all three species, i.e. is not a species-specific trait, and that there is considerable overlap in 36 size between C. finmarchicus and C. glacialis. A trait-based life-history model was used to examine an idealized scenario where, in a changed Arctic with a longer period of primary production, C. glacialis-37 38 and C. hyperboreus-like copepods are indeed replaced by C. finmarchicus-like individuals, whether 39 through competition, plasticity, hybridization, or evolution. However, the model finds that transfer of 40 energy from primary producers to higher predators may actually be more efficient in this future 41 scenario, because of the changes in generation length and population turnover rate that accompany 42 the body-size shifts. These findings suggest that Arctic marine food webs may be more resilient to 43 climate-related shifts in the *Calanus* complex than previously assumed.

#### 44 Introduction

45 Large-scale re-organization of Arctic marine communities and significant functional changes in the 46 ecosystem are expected as a result of accelerated climatic warming and sea-ice withdrawal (Wassmann et al., 2011; Sunday et al., 2012; Fossheim et al., 2015; Kortsch et al., 2015). Empirical 47 48 studies have already detected some structural and functional changes (Wassmann et al., 2011; 49 Fossheim et al., 2015; Wiedmann et al., 2014), but predicting specific compositional changes and the 50 ecosystem consequences of such changes is challenging. These consequences are not just of academic 51 interest as seasonal migrations of tens of millions of seabirds, valuable commercial fisheries (Atlantic 52 cod, Pacific pollock), and recovery of large baleen whales (blue, fin, bowhead, humpback) all depend 53 on the temporally and spatially concentrated productivity of the Arctic and its marginal seas. A key 54 link between primary producers and commercial stocks are large copepods of the genus Calanus, 55 which usually dominate zooplankton biomass in temperate and polar seas. Calanus spp. can be 56 thought of as part of the "wasp waist" in the food web (a concept usually applied to forage fish (Hunt 57 and McKinnell, 2006)), in the sense that they sit at a trophic nexus at which the organism- and 58 population-level biology of just a few species has ecosystem-level consequences.

59 Large-scale biogeochemical models have predicted widespread changes in response to Arctic warming 60 and sea-ice loss, particularly at and near the base of the food web. Such changes include a longer 61 season of pelagic primary productivity, a moderate increase in total primary production (Slagstad et 62 al., 2011; Slagstad et al., 2015), an increase in Atlantic zooplankton species (Calanus finmarchicus) and 63 strong reduction in Arctic zooplankton (Calanus glacialis) in the Barents Sea, and spreading of C. 64 glacialis along the Eurasian shelves (Slagstad et al., 2011; Feng et al., 2016). C. finmarchicus has 65 expanded northward in the western Atlantic over the last 30 years (Chust et al., 2014), and is 66 increasing in abundance at the expense of C. glacialis in the Barents Sea (Dalpadado et al., 2012). The 67 fate of the third Calanus species in the region, C. hyperboreus, has so far not been considered (Slagstad 68 et al., 2015; Feng et al., 2016; Feng et al., 2017). Although C. hyperboreus occurs on the shelf, it is

69 primarily an oceanic species (Conover, 1988; Hirche, 1991; Kosobokova and Hirche, 2009) with 70 markedly different life history strategies, grows considerable larger than *C. glacialis* and *C.* 71 *finmarchicus* (Falk-Petersen *et al.*, 2009), and, therefore, is likely subject to different environmental 72 forcing than the smaller, short-lived *Calanus* species.

73 Any prediction regarding the ecological consequences of a replacement of Arctic Calanus by C. 74 finmarchicus inevitably hinges on current understanding of Calanus physiology and life-history. 75 Empirical data (Pasternak et al., 2013; Alcaraz et al., 2014) suggest an upper thermal tolerance of 76 approximately 6° C for C. glacialis. Additionally, Arctic species have been suggested to possess 77 inherently higher species-specific lipid-storage than their boreal congeners: 60-70 mass % in Arctic 78 Calanus species versus up to 30-50% in C. finmarchicus (Scott et al., 2000). Despite the limited data 79 supporting these estimates, this understanding underlies the current paradigm on how warming will 80 affect Arctic food-webs. The paradigm posits that a shift in species dominance from C. glacialis to the 81 smaller, boreal C. finmarchicus will lead to a reduction in lipid production at the population level, and 82 a loss in nutritional value for iconic predators of Calanus, including fish, seabirds, and baleen whales 83 (Dalpadado et al., 2012; Kwasniewski et al., 2012; Fossheim et al., 2015). Thus, replacing one species 84 with the other, with all else remaining equal, has been predicted to have major consequences for the 85 entire Atlantic Arctic food web.

It can be misleading, however, to treat species as fixed types, with no plasticity or variation, in 86 87 investigations of how ecosystems are likely to respond to unprecedented conditions. In fact, this kind 88 of fixed-species approach can prevent important questions from being asked in the first place. It is 89 increasingly clear that C. glacialis and C. finmarchicus have diverse and plastic strategies for 90 reproduction, foraging, and dormancy that are in part responses to environmental variation (Falk-91 Petersen et al., 2009; Daase et al., 2013; Melle et al., 2014). In addition, morphology-based 92 identification of these two species has been shown to be unreliable in some areas (Lindeque et al., 93 2006; Gabrielsen et al., 2012; Choquet et al., 2018), and reports of hybridization between the two

94 species (Parent et al., 2012) complicate the picture further still. In this study, we use a combination of 95 molecular tools for species identification and a recent, well-validated life-history model (Banas et al., 96 2016a) to show that a trait-based, as opposed to species-based, approach allows us to formulate and 97 test hypotheses that cut across the organismal, population, and community scales. We find that intra-98 and interspecific variation in key organismal traits (body size, lipid content) may be more congruent 99 across species than thought, allowing a huge conceptual simplification. The model, by placing 100 individual life history and population dynamics in a common mathematical frame, lets us scale up to 101 the expected tradeoff between these organismal traits and population productivity. In this framework, 102 we can begin to reason systematically about whether the sum of these changes is a net gain or loss for particular classes of predator. 103

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# 105 A UNIFIED VIEW OF BODY SIZE AND ENERGY CONTENT

106 To evaluate overlap in size between C. finmarchicus and C. glacialis, and whether lipid content is 107 species or size dependent, we sampled Calanus in three fjords in Svalbard (78-81 °N, 10-24 °E, 108 including Arctic and Atlantic hydrographic domains) using a Hydrobios Multi Plankton Sampler or a 109 WP2 net (mesh size 200 μm, mouth opening 0.25 m<sup>2</sup>). Samples were taken between mid-September 110 and early October in 2012 (Billefjorden 180-0 m, Rijpfjorden 265-0 m) and 2014 (Kongsfjorden 320-0 111 m, Rijpfjorden 265-0 m). This is the start of the overwintering period of Calanus spp. when lipid 112 content is commonly at its highest, thus the variability in lipid content and size reflects natural 113 variability in the population, but not seasonal variability. We measured the prosome length of more 114 than 1500 individual copepods (copepodite IV and V, and adult females) and each specimen was 115 preserved in absolute ethanol and identified to species using molecular techniques as described in 116 Gabrielsen et al. (2012). Prior to being preserved, approximately 650 individual copepods (copepodite 117 stages IV, V and VI) were photographed while still alive using a Leica MZ 95 stereomicroscope with a 118 Motec camera. The pictures were used to measure prosome length, prosome area and area of the

119 lipid sac. Total lipid content was calculated based on lipid sac area following Vogedes et al. (2010). To 120 compare the lipid- size relationship in the C. finmarchicus and C. glacialis complex with that of the 121 third Calanus congener in the study area, C. hyperboreus, we included measurements of prosome length and lipid sac area of 430 C. hyperboreus (CIII-CV and adult females) from Svalbard waters 122 123 sampled between August and October (2010, 2012, 2014, max. sampled depth 2000 m). C. 124 hyperboreus were not genetically identified as they are substantially larger than the other two Calanus 125 species and can be distinguished morphologically by a spine at the last thoracic segment, which is 126 present from stage CIV.

127 We found considerable overlap in prosome length of C. glacialis and C. finmarchicus identified to 128 species using molecular tools (Figure 1), indicating that size-based classification is inaccurate for the 129 larger developmental stages included in this study (copepodite IV, V, and females) (Figure 1). The 130 relationship between size and lipid content was statistically indistinguishable for the two species 131 (Table 1, Figure 2). The relationship for copepodite stages CIII and CIV of C. hyperboreus, a range of body sizes that better matches C. finmarchicus and C. glacialis CIII-AF (Table 1, Figure 2), was also 132 133 indistinguishable from that of the two smaller species. The relationship for all size classes of C. 134 hyperboreus (Figure 2) displayed a significantly lower exponent coefficient (a in the equation in Table 135 1). This difference, however, appears to be an effect of scale—the range of body size considered in 136 relation to intraspecific variability in lipid content—rather than a true species difference. Our results, 137 therefore, suggest that there is little inherent, species-specific difference in lipid-storage capacity 138 between the Arctic C. glacialis and the boreal C. finmarchicus (Figure 1), or indeed the younger stages 139 of C. hyperboreus. The amount of lipid that can be stored, therefore, is dependent largely on body size 140 (and developmental stage as it relates to size). This is in contrast to previous studies that have reported 141 or assumed a higher species-specific lipid content in Arctic C. glacialis compared with C. finmarchicus 142 (Scott et al., 2000; Falk-Petersen et al., 2009). This misconception has probably been caused by a 143 general underrepresentation of C. glacialis in the community based on morphological identification 144 (Choquet et al., 2018).

145 The high number of *C. glacialis* individuals not growing as large as previously assumed suggests there 146 is considerable plasticity in morphology across its geographic range (Gillooly, 2000; Leinaas et al., 147 2016; Choquet et al., 2018). A reduction in body size has been suggested to be a universal response 148 to warming (Gillooly, 2000; Daufresne et al., 2009; Gardner et al., 2011). Since body size is viewed as 149 a 'master trait,' it can have an overarching influence on a large number of physiological processes and 150 ecological functions (Stamieszkin et al., 2015). C. glacialis is known to exhibit large spatial variability in its phenology and energy allocation to reproduction (Daase et al., 2013). Such a high variation in 151 152 body size is consistent with the findings of misidentified individuals when only morphological 153 taxonomy is used (Parent et al., 2011; Gabrielsen et al., 2012; Choquet et al., 2018) (Figure 3). It may 154 also result from hybridization between C. finmarchicus and C. glacialis (Parent et al., 2012), although 155 no evidence of hybridization has been found in a large scale survey including our study area (Choquet 156 et al., 2017). In fact, populations of C. glacialis overlapping in size with C. finmarchicus have been 157 found all along the coast of Norway (Niehoff and Hirche, 2005; Choquet et al., 2017). Similarly, at the 158 southern end of its range, C. finmarchicus has been found to overlap in size almost completely with C. 159 helgolandicus as a function of temperature (Wilson et al., 2015). While there is little overlap in size 160 with older copepodites and adults of C. hyperboreus, there is an overlap in size with the younger 161 copepodite stages CIII and CIV of that species. Being lipid-rich overwintering stages, they are in a 162 similar life history stage as older stages of the smaller *Calanus* species, and likely provide similar energy 163 subsidies for predators. These findings suggest that environmental plasticity, changes in geographic 164 range, and potentially hybridization all contribute to a continuum in size, and therefore lipid content, 165 with analogous consequences at the ecosystem level. This suggests the potential utility of a trait-166 based, instead of species-based, approach when investigating ecological functions of assemblages.

## 167 SCALING UP FROM INDIVIDUAL TRAITS TO POPULATION PRODUCTIVITY

As shown by the review of growth and development studies by Banas and Campbell (2016), body size in copepods can be thought of as a direct consequence of the combination of individual development time and the mean rate of energy gain during that time, i.e., life-history strategy and foraging strategy.

171 In highly seasonal environments, these strategies are strongly constrained by external conditions (prey 172 availability, temperature, predation risk), such that relatively few combinations of ontogenetic 173 development rate, dormancy strategy, foraging strategy, and reproductive strategy lead to viable 174 annual energy budgets when the period of prey availability is short (Banas et al., 2016a; Sainmont et 175 al., 2014). As a result, generation length (and thus population turnover rate), body size, and lipid 176 content are not independent, uncorrelated traits once all possible combinations are passed through 177 the environmental filter. These emergent associations among traits form testable model predictions 178 (Banas et al., 2016a), and provide a basis for predicting how linked traits may change in the future. 179 One simple model experiment along these lines-examining only one mode of environmental 180 variation out of many that deserve consideration—is described below.

181 The copepod life-history model Coltrane (Copepod Life-history Traits and Adaptation to New 182 Environments) version 1.0 is described in detail by Banas et al. (2016a). Matlab source code is available 183 at http://github.com/neilbanas/coltrane. Coltrane is an individual-based model that represents the 184 time-evolution of one cohort of a clonal population, all bearing the same traits and spawned on the 185 same date, with four state variables: relative developmental stage D (0 at spawning, 1 at adulthood), 186 survivorship N (the fraction of initially spawned individuals that remain after some amount of 187 cumulative predation mortality); structural biomass per individual S, and individual reserve or storage-188 lipid biomass R (Fig. 4a). Families of cases of the cohort model are then combined to produce 189 population- and community-level results, as shown in schematic form in (Banas et al., 2016a) for a 190 complete model description. A population in Coltrane (Fig. 4b) is considered to have identical traits, 191 and to have a seasonal pattern of spawning dates that maximises fitness (lifetime egg production per 192 initial egg) while also solving internal life-history mismatch (Varpe et al., 2007). Mathematically, this 193 optimization involves running the cohort model (Fig. 4a) for a complete spectrum of spawning dates 194 and also a spectrum of imposed delays between maturation and the start of spawning (Fig. 4b; Banas 195 et al. 2016a). A community—or rather a metacommunity, an estimate of "all possible ways to be a 196 copepod" in a given environment—is generated in the present version of the model by varying a single

197 life-history trait, the prey-saturated development rate  $u_0$ . This rate was varied from 0.005 – 0.01 d<sup>-1</sup>, 198 corresponding to a total egg-to-adult development time of 100–200 d at 0°C under prey-saturated 199 conditions (Banas and Campbell, 2016).

200 An environmental scenario in Coltrane is defined by annual cycles of three variables: total 201 concentration of phytoplankton/microzooplankton prey, surface temperature, and deep 202 temperature. The model does not explicitly predict absolute abundance or biomass, but rather 203 compares the fitness value of competing strategies and predicts trait correlations. For example, 204 Coltrane is able to predict the relationship among body size, generation length, and income/capital 205 breeding strategy across the three coexisting Calanus spp. in Disko Bay, West Greenland (Banas et al., 206 2016a). In each scenario, a spectrum of copepod types was generated by varying  $u_0$  and calculating an 207 optimal population-level solution for each case. Adult size (Figure 5b), generation length (Figure 5c), 208 and the division of egg production into capital and income fractions (Figure 5d) were calculated as in 209 Banas et al. (2016a: see the Disko Bay experiment in that study). Additional metrics were calculated 210 by integrating the mortality (survivorship) term over time to produce total energetic yield to predators

211  $Y = \int m(S+R)N dt$ 

212 and the lipid fraction of that yield

213  $Y^{-1}\int mRN dt$ .

214

In this study, the model was run for a pair of idealised scenarios, which differed only in the duration of prey availability, in order to evaluate the common assumption that a longer ice-free period of spring-autumn pelagic phytoplankton production will lead to shrinking individual sizes and potential species shifts, and how such a shift toward smaller, faster-reproducing individuals would affect total secondary production by *Calanus*. The first of the two scenarios assumes phytoplankton prey occur in a Gaussian seasonal window equivalent to 3.5 months of saturating prey per year, as opposed to a

221 window equivalent to 4.5 months in the second scenario (Fig. 5a). These can be taken as idealisations 222 of present-day and reduced-ice conditions in a West Svalbard fjord or a similar Arctic environment 223 (mathematically, these cases correspond to the "global" experiment of Banas et al. (2016a) with  $\partial t' =$ 224 40, 50 d). In reality, the length of the productive season need not correlate closely with the overall 225 amount of food, or its nutritional quality, or its timing relative to the annual light cycle: all details that 226 deserve consideration in a more complex, spatially-resolved model study. Seasonal cycles were 227 assumed to repeat exactly, such that the model results here describe optimal strategies in two 228 contrasting but stable environments. For simplicity, both surface and deep temperature were held 229 constant at 0°C in both scenarios, although Banas et al. (2016a) explored the effect of temperature 230 variation in relation to prey variation in the same model. Specific mortality *m* is assumed to follow the 231 same allometry as specific ingestion (Banas et al., 2016a): this simplifying assumption has a theoretical 232 and coarse empirical basis (Hirst and Kiørboe, 2002), but may well be inappropriate in a high-latitude 233 context where gradients in light availability and thus visual predation may be particularly strong (Varpe 234 et al., 2015).

235 Across these simple model scenarios at 0°C, lengthening of the primary-productivity season does, 236 indeed, shift the optimal strategy of modelled mid-size Calanus analogs toward smaller adult size 237 (Figure 5b), from a 2-year to a 1-year life-cycle (solid symbols, Figure 5c), and from a combination of 238 capital and income breeding to almost pure income breeding (Figure 5d). In the short-season scenario, 239 a 1-year life cycle is unviable for these mid-size cases because of internal life-history mismatch (Varpe 240 et al., 2007): the initial generation is able to survive to maturity without starving only if it is spawned long before the bloom maximum, but is unable to spawn the next generation at the same time of year, 241 242 such that no stable cycle is possible. A 2-year life cycle in the short-season scenario solves this internal 243 mismatch problem, although productivity (LEP) under this strategy is very low (Figure 5e, blue solid 244 symbols). Under the longer growing season, the mismatch problem observed for a 1-year generation 245 time is solved, such that either a 1- or 2-year life cycle is possible, and survivorship and lifetime egg 246 production are much higher for the 1-year cycle (Figure 5e, red solid symbols).

247 Thus, the assumptions and review of laboratory data behind Coltrane (Banas and Campbell, 2016; 248 Banas et al., 2016a) support the idea that whether by plasticity, hybridization, evolution, or 249 competitive replacement—the model is agnostic regarding the mechanism—we might indeed expect 250 a shift in the changing Atlantic Arctic in which mid-sized, long-generation-length *Calanus* are replaced 251 by smaller, shorter-generation-length organisms. Replacing a two-year reproductive cycle with a one-252 year cycle increases survivorship and turnover, such that this shift is accompanied by more than a two-253 fold increase in lifetime egg production per adult (Figure 5e). More surprising, it is also accompanied 254 by a more than two-fold increase in specific energetic yield to predators (Figure 5f). The fraction of 255 the yield to predators that consists of storage lipid decreases from ~30% to ~20% (Figure 5g; note that 256 the lipid fraction of yield, summed across all life stages, is not directly comparable to measurements 257 of the lipid content of late stage individuals). However, the increase in total energetic yield outweighs 258 the decrease in lipid fraction, so that the total yield of lipid to predators (per initial copepod egg) 259 actually increases slightly in the longer-productive-season scenario.

260 Translating these trait-based results into species-specific predictions is ambiguous, particularly given 261 the idealized nature of the model experiment. Body size depends on growth and development rates 262 via a high exponent, such that 10% uncertainty in each of those rates translates into fourfold 263 uncertainty in adult size (Banas and Campbell, 2016). Accordingly, body-size/generation-length 264 combinations are likely to be skewed relative to the real *Calanus* populations (a more realistic 265 application would address this through systematic parameter tuning). One could interpret the mid-266 sized cases that change generation length between scenarios as larger C. glacialis analogs, shifting 267 toward a C. finmarchicus-like life history under a longer productive season, or else as small C. 268 hyperboreus analogs, replaced by C. glacialis and C. finmarchicus in a more boreal environment. 269 Predicting these specific futures is a complex oceanographic and spatial-ecology problem, well beyond 270 an idealized model (or for that matter any first-principles biological argument). It is likely that currently 271 observed shifts in size distributions are consequences of internal population-level plasticity, and it is 272 not clear whether any required genetic shifts (as climatic shifts surpass the range of phenotypic flexibility) could occur fast enough to reach these modeled optima. What we *can* conclude from this model experiment is that ecological shifts along the body size–lipid content curve in high-latitude *Calanus* (Figure 2) are likely to be accompanied by shifts in generation time and population turnover rate that have strong, compensating effects on energy transfer to predators.

277 Ecosystem consequences

278 As long as there are still large C. qlacialis and small C. finmarchicus found in the same region, energy 279 transfer from the mesozooplankton to predators can still be species dependent as well as size 280 dependent, with C. hyperboreus functioning as an especially lipid-rich treat. For many predators, 281 however, total nutrition available from the mesozooplankton community may be more dependent on 282 secondary production at the population level, than on mean individual lipid content. Crucially, results 283 of the life-history model suggest that changes in population-level energy content accompanying a shift 284 to smaller body size outweigh the effects of a body-size reduction on individual lipid content (Figure 285 4, 5). Predators that target individual copepods and predators that feed on copepods en masse may 286 thus experience opposite trends in their prey.

287 Parallel model experiments varying mean water temperature (Banas et al., 2016a) suggest that, at the 288 community level, the direct effects of near-surface warming on Calanus trait patterns are similar to 289 the effects of lengthening of the productive season, although at the population level, thermal 290 thresholds (Alcaraz et al., 2014) may be limiting. This is another factor that complicates the translation of model results into species terms. Warming of deeper water, or loss of early-spring ice-associated 291 292 blooms, may drive some *Calanus* populations past thresholds of overwintering survival. This appears 293 to be the case for the southeastern Bering Sea in warm, low-ice years (Hunt et al., 2011; Stabeno et 294 al., 2012; Eisner et al., 2014), as the measured summer abundance of C. glacialis/marshallae crashes 295 in temperature and ice conditions similar to those projected to be the new normal by the 2040s (Banas 296 et al., 2016b). Indeed, the same model that predicts the positive effects of extended pelagic

productivity in this study (Figure 4) finds *Calanus* to be non-viable in the southeastern Bering Sea
without an extended period of sea ice and ice algae (Banas *et al.*, 2016a).

299 Increasing air and sea temperatures and significant reductions in sea ice have already been observed 300 in the Arctic (Stroeve et al., 2014), and may impact food supply, growth rates, and relative distributions 301 of Calanus spp. Furthermore, sea-ice loss changes the light regime of the water column, potentially 302 altering seasonal and/or size-specific predation pressure on zooplankton in a future Arctic Ocean 303 (Varpe et al., 2015). In addition, advection of heat, food, and species from boreal areas northward 304 substantially alters plankton community structure in some regions (Orlova et al., 2015). Any 305 reconsideration of the paradigm of species replacement and its effect on ecosystem function, 306 therefore, must consider the spatial variability in the drivers of change. Likewise, all the environmental 307 drivers discussed here vary over a range of timescales as well, from interannual variability to true 308 multidecadal trends. On very long timescales, it can be a powerful simplification to elide the 309 differences among disparate mechanisms of adaptation—individual plasticity, competitive exclusion, 310 hybridisation, range shifts and species replacement, true natural selection—as a trait-based approach 311 allows one to do. However, these mechanisms have their own intrinsic timescales, and understanding 312 shorter-term change in *Calanus* may require that we distinguish between mechanisms more precisely 313 and apply trait- and optimality-based methods more selectively.

314 Our findings suggest that borealisation of marginal seas in the European Arctic may not be detrimental 315 in terms of either carbon- and lipid-based food-web contributions from Calanus, regardless of whether 316 warming results in a species shift to C. finmarchicus, or in smaller sizes of C. glacialis (Figure 5). Record 317 high stocks of age 3+ Atlantic cod in the Barents Sea in recent years suggest that there is no shortage 318 of food, despite more than a decade of warming, a weakening in trophic links with their traditional 319 prey (capelin) (Johannesen et al., 2015), and a dominance of C. finmarchicus in many areas. A size shift 320 in the zooplankton prey field may, however, impact predators that actively select larger individuals, 321 regardless of the sensory mechanisms involved in the search process (Martens et al., 2015). There are,

however, only two explicit examples of this phenomenon from Arctic systems, and the results of one (Dalpadado *et al.*, 2000) could be explained by other mechanisms leading to apparent selection. The little auk (*Alle alle*) searches visually for its prey and actively selects larger individuals (Karnovsky *et al.*, 2003; Kwasniewski *et al.*, 2012; Vogedes *et al.*, 2014), and this predator may be negatively affected by shifts to a system with smaller prey (Kidawa *et al.*, 2015). One recent study, however, suggests that chick growth and adult body-condition may not decline when they fed on small zooplankton instead of larger congeners (Amélineau *et al.*, 2016).

While we only consider bottom-up effects in this study, predation pressure may also be important in driving *Calanus* life-history traits (Kaartvedt, 2000; Varpe *et al.*, 2007; Berge *et al.*, 2012). A continued northwards expansion of boreal fish, as well as increases in whale populations, may also select for Arctic *Calanus* species with shorter life-spans and smaller body sizes (Berge *et al.*, 2012), thus eliciting similar effects as shown in our models incorporating ocean warming and lengthening of the productive season. The effects of increased predation on zooplankton production and population size, however, are less clear.

### 336 Conclusion and recommendations

337 Since climate change affects ecosystems both directly and indirectly, many unknowns could 338 significantly affect the generality of our findings. Warmer temperatures, reduced ice cover, and the 339 spread of boreal species are already affecting timing, quantity, and composition of phytoplankton 340 production. Here we have focused on a likely species shift within the *Calanus* species complex. 341 Interactions of new taxa with both resident and other new species are difficult to predict (Williams 342 and Jackson, 2007), and not incorporated into our conceptual model. A replacement of Calanus spp. 343 with even smaller copepod species (i.e. Pseudocalanus spp., Oithona similis) having different 344 nutritional values and life history traits may prove to be much more detrimental in terms of available 345 carbon and lipid for predators and food web structure (Coyle *et al.*, 2011).

346 Our dataset is geographically and seasonally limited, and a large-scale survey of species and size 347 specific lipid content would be necessary to assess the robustness of our regional observations. The 348 use of a trait-based rather than a species based approach to assess ecosystem changes may be particularly useful where species identification is challenging, which has become increasingly evident 349 350 for Calanus (Choquet et al., 2018). Our results clearly demonstrate, however, that the basis for 351 previous concerns regarding species replacement within the Calanus complex may be unfounded, or at least not universal, and that food subsidies from Calanus may continue to support many top 352 353 predators in the European Arctic.

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- **Table 1:** Results of exponential fits to total individual lipid content LC (in mg) as a function of548prosome length PL (in mm), across *Calanus* spp. and life stages (see Figure 2). Each fit is specified by549an exponent *a* and log coefficient *b* such that LC =  $e^b PL^a$ . Confidence limits at the 95% level are also550given, and non-overlapping confidence intervals are considered statistically significant. All data are551from live animals collected Aug–Oct. Outliers with LC < 0.002 mg have been omitted (n=18, < 2% of</td>552samples).

Species, stage	Exponent <i>a</i>	Log coefficient b
C. finmarchicus, CIII–AF	4.9 ± 0.5	-6.6 ± 1.5
C. glacialis, CIII–AF	5.1 ± 0.3	-7.2 ± 1.0
C. hyperboreus, CIII–CIV	5.1 ± 0.2	-7.9 ± 1.1
C. hyperboreus, CIII–AF	$3.6 \pm 0.2$	-6.0 ± 1.2
all species, CIII–AF	$3.4 \pm 0.1$	-5.5 ± 1.3

#### 557 Figure legends

**Figure 1:** Prosome length frequency distribution of copepodite stages CIV (N=341) and CV (N=886) and adult females (AF, N=329) of *C. glacialis* (blue) and *C. finmarchicus* (red). Species determined based on genetics. Grey shaded area indicates size classes classified as *C. glacialis* (Daase and Eiane, 2007) (see also Figure 3).

**Figure 2**: Total lipid content in relation to prosome length across *Calanus* species and stages. Five regression lines match the exponential fits and 95% confidence intervals given in Table 1. Nonoverlapping confidence intervals indicate statistically significant differences. *C. finmarchicus* CIII–AF (red; n=373), *C. glacialis* CIII–AF (blue; n=290), *C. hyperboreus* CIII–AF (black, solid; n=430) and CIII– CIV only (gray, dashed; N=337), and all species (dotted).

Figure 3: Length range of prosome length of copepodite stage CV of *Calanus finmarchicus* (red) and *C. glacialis* (blue) based on size-frequency analysis (morphology) and genetic analysis (genetics). Broken
lines: no minimum/maximum size defined. References: 1. Tande *et al.* (1985); 2. Kwasniewski *et al.*(2003); 3. Arnkværn (2005); 4. Daase and Eiane (2007); 5. Weydmann and Kwasniewski (2008); 6.
Breur (2003); 7. Hirche *et al.* (1994); 8. Choquet et al. (2018) 9. Parent *et al.* (2011); 10. Gabrielsen *et al.* (2012); 11. This study (includes data from Gabrielsen *et al.* (2012)). Svalbard waters: Stations in open water, outside fjords.

574 Figure 4: Schematic of the Coltrane copepod life-history model. (a) The time-evolution of one cohort 575 of individuals, with identical traits and spawned on the same date  $t_0$ , are tracked by state variables 576 representing development, structural and reserve biomass, and survivorship. Egg production by this 577 cohort is calculated from these state variables, as a function of an additional strategy decision  $t_{egg}$ , 578 which allows a delay between maturation and the start of spawning. (b) An annual routine 579 representing a population is generated from the cohort solutions by varying t<sub>0</sub> and t<sub>egg</sub> systematically 580 and identifying the seasonal pattern of spawning dates and the value of tegg that maximise fitness while 581 also solving internal life-history mismatch. (c) A metacommunity is generated by varying the relative-

development-rate parameter  $u_0$ , which controls development time directly and adult size indirectly, as previously shown for a metastudy of laboratory experiments (Banas and Campbell 2016). See Banas et al. (2016a) for a full description of the model.

585 Figure 5: Results of the life-history model across the Calanus size spectrum, under a pair of idealized 586 Arctic scenarios, which differ only in the duration of the availability of (a) phytoplankton prey. In all 587 panels, blue symbols represent the shorter-duration, present-day scenario, and red symbols the 588 longer-season, future scenario. (b) A size spectrum from C. finmarchicus analogs at the small end to C. 589 hyperboreus analogs at the large end is generated by varying the food-saturated development rate u<sub>0</sub>. 590 A single red or blue symbol represents a model population (Fig. 4b) and the set of blue symbols or red 591 symbols represents a model metacommunity (Fig. 4c). (c) At the small, fast-developing (C. 592 finmarchicus-like) end of the spectrum, the model predicts that a 1-year life cycle is optimal in both 593 environmental scenarios (open circles). At the large, slow-developing (C. hyperboreus-like) end, 2 594 years is optimal in both (dotted circles). Over a middle range, the optimal strategy changes from a 2year cycle in the shorter productive season to 1 year in the longer case (solid circles). Note that these 595 596 three cases, which are distinguished by symbol type in all panels, are not imposed but rather a 597 classification of the emergent results in (c). (d) The middle-range cases that change generation length 598 (solid symbols) also switch from a hybrid income/capital breeding strategy to an almost pure income-599 breeding strategy. These changes are accompanied by (e) more than doubling of lifetime egg 600 production per successful adult and (f) more than doubling of the specific energetic yield to predators. 601 (g) The fraction of the yield to predators that consists of storage lipid decreases, from  $\sim 30\%$  to  $\sim 20\%$ .

**Figure 6:** Conceptual understanding of the effects of borealization of the Arctic on length of productive season, body size, indvidual lipid content, life span and population turn over of Arctic (blue) and boreal (red) *Calanus* populations, and on total population lipid production. Where seasonal ice cover and low temperature prevail (central Arctic Ocean, towards the left of the continuum), large, lipid-rich and long-lived species may prevail, but population turn-over rates and total lipid production remain low.

- 607 A high degree of borealisation (right side) characterized by increased water temperatures, loss of sea
- 608 ice and prolonged productive season, short life cycles and high population turn over may lead to high
- 609 population lipid production despite a shift towards smaller individual size and lipid content.





Prosome length (mm) 2 5 1.5 2.5 3 3.5 4 4.5 Barents Sea W<sup>1</sup> Kongsfjorden<sup>2</sup> ..... Billefjorden<sup>3</sup> N Svalbard<sup>4</sup> ..... ..... Hornsund⁵ ..... ..... ..... Billefjorden<sup>6</sup> Greenland Sea<sup>7</sup> morphology genetics Lurefjord<sup>8</sup> Saltenfjord/Skjerstadfjord<sup>8</sup> Canadian Arctic/Atlantic<sup>9</sup> Billefjorden<sup>10</sup> Kongsfjorden<sup>10</sup> Rijpfjorden<sup>10</sup> Billefjorden<sup>11</sup> Kongsfjorden<sup>11</sup> Rijpfjorden<sup>11</sup> C. finmarchicus Svalbard waters11 -C. glacialis

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