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1	Simulating nutrient release from parental carcasses increases the growth,
2	biomass and genetic diversity of juvenile Atlantic salmon
3	
4	Darryl McLennan ^{1,2*} , Sonya K. Auer ^{1,3*} , Graeme J. Anderson ¹ , Thomas C. Reid ¹ , Ronald
5	D. Bassar ³ , David C. Stewart ⁶ , Eef Cauwelier ⁶ , James Sampayo ⁶ , Simon McKelvey ⁴ †,
6	Keith H. Nislow ⁵ , John D. Armstrong ⁶ , and Neil B. Metcalfe ¹
7 8	¹ Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow Glasgow, G12 8QQ UK.
9 10	² Department of Fish Ecology and Evolution, EAWAG, Seestrasse 79, 6047, Kastanienbaum, Switzerland.
11	³ Department of Biology, Williams College, Williamstown, MA 01267 USA
12	⁴ Cromarty Firth Fishery Trust, Inverness, IV2 3HF UK.
13	⁵ USDA Forest Service Northern Research Station, Amherst, MA 01003 USA.
14	⁶ Marine Scotland – Science, Freshwater Fisheries Laboratory, Pitlochry, PH16 5LB UK.
15	
16	†Deceased 2 December 2018
17	
18	* These authors contributed equally to this work
19	Corresponding author: darrylmclennan@outlook.com
20	

ABSTRACT

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1. The net transport of nutrients by migratory fish from oceans to inland spawning areas has 22 23 decreased due to population declines and migration barriers. Restoration of nutrients to 24 increasingly oligotrophic upland streams (that were historically salmon spawning areas) have shown short-term benefits for juvenile salmon, but the longer-term consequences are little known. 25 26 2. Here we simulated the deposition of a small number of adult Atlantic salmon Salmo salar 27 carcasses at the end of the spawning period in five Scottish upland streams ('high parental nutrient' 28 treatment), while leaving five reference streams without carcasses ('low parental nutrient' 29 treatment). All streams received exactly the same number of salmon eggs (n = 3,000) drawn in 30 equal number from the same 30 wild-origin families, thereby controlling for initial egg density and 31 genetic composition. We then monitored the resulting juvenile salmon and their macroinvertebrate prey, repeating the carcass addition treatment in the next spawning season. 32 3. Macroinvertebrate biomass and abundance were five times higher in the high parental nutrient 33 34 streams, even one year after the carcass addition, and led to faster growth of juvenile salmon over 35 the next 2 years (but with no change in population density). This faster growth led to more fish 36 exceeding the size threshold that would trigger emigration to sea at 2 rather than 3 years of age. There was also higher genetic diversity among surviving salmon in high parental nutrient streams; 37 genotyping showed that these effects were not due to immigration but to differential survival. 38 4. Synthesis and applications: This field experiment shows that adding nutrients that simulate the 39 presence of small numbers of adult salmon carcasses can have long-term effects on the growth rate 40 of juvenile salmon, likely increasing the number that will migrate to sea early and also increasing 41 their genetic diversity. However, the feasibility of adding nutrients to spawning streams as a 42

43	management tool to	boost salmon p	opulations wi	ll depend on	n whether the l	benefits at this stage a	are
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44 maintained over the entire life cycle.

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KEYWORDS: marine derived nutrients, oligotrophic, phosphorus, smolt

47 1 | INTRODUCTION

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Anadromous species are born and reproduce in fresh water but achieve most of their growth in the ocean. This life cycle has consequences for freshwater ecosystems since migratory fishes can act as vectors for marine nutrients (Naiman et al. 2002), subsidized mostly via the production of gametes, waste products and the decomposition of adult carcasses arising from post-spawning mortality (Willson & Halupka 1995). While emigrating juveniles also transport nutrients in the opposite direction, the relative scale of the nutrient flows is such that the majority of anadromous populations generate a net import of marine-derived nutrients to freshwater communities (Naiman et al. 2002; Walters, Barnes & Post 2009; Flecker et al. 2010; Childress, Allan & McIntyre 2014). The effect - generally in the form of increased productivity and/or biomass - is detectable in freshwater food webs, especially when ecosystems are otherwise oligotrophic (Claeson et al. 2006; Nislow et al. 2010; Guyette et al. 2014). Recent declines in adult populations may result in the export of nutrients from fresh waters (by emigrating juveniles) being greater than the import by the breeding adults (Moore & Schindler 2004; Scheuerell et al. 2005; Moore et al. 2011). This consequent steady decline in nutrient inputs ('oligotrophication') may significantly alter the architecture of the food webs that exist within these freshwater ecosystems (Doughty et al. 2016; Gerwing & Plate 2019). This process is exacerbated by a rise in the number of artificial barriers to riverine migration, such as weirs or dams constructed for the purpose of hydropower generation or water storage. These have undoubtedly contributed to observed declines in anadromous fish populations (Limburg & Waldman 2009; Lenders et al. 2016), which in turn have reduced the level of nutrient subsidies in ecosystems upriver of the barriers (Williams et al. 2009).

Restoring nutrient levels to some presumed previous level is one mitigation measure, but this needs to be carefully managed and evidence-based to avoid causing eutrophication (Stockner, Rydin & Hyenstrand 2000). Nutrients can be administered to freshwater ecosystems via the addition of fertilisers (Griswold, Taki & Stockner 2003; Ward, McCubbing & Slaney 2003), fish carcasses (Bilby et al. 1998; Williams et al. 2009), or fish carcass 'analogues' (Kohler et al. 2012; Guyette, Loftin & Zydlewski 2013), the latter usually being in the form of dried pellets made from marine fish (Pearsons, Roley & Johnson 2007). The addition of carcasses or their analogues has been found to be more effective than adding liquid fertilisers (Kiernan, Harvey & Johnson 2010; Wipfli et al. 2010), probably because the nutrient pulse lasts longer and also allows organisms to feed directly on the added biomass in addition to creating bottom-up effects (Bilby et al. 1998; Wipfli, Hudson & Caouette 1998). Carcass analogues have similar effects on freshwater productivity to real carcasses (Wipfli, Hudson & Caouette 2004), but have the advantages that they are lighter (being dried) and are more easily stored and transported (Pearsons, Roley & Johnson 2007). To date, most studies on the impact of nutrient restoration in freshwater streams find that the addition of carcasses or carcass analogues increases invertebrate abundance and biomass (Wipfli, Hudson & Caouette 1998; Claeson et al. 2006; Nislow et al. 2010) and generally benefits fish growth and body condition (Wipfli et al. 2003; Williams et al. 2009; Guyette, Loftin & Zydlewski 2013). However, effects on fish density and biomass are unclear, in part due to the limitations of field studies in controlling for the immigration of non-experimental fish into restored areas, as shown by Bilby et al. (1998). There is also little knowledge of the longer-term consequences of nutrient manipulations, since most studies have only lasted for a few months after supplementation (e.g. Wipfli et al. 2003; Williams et al. 2009). It is therefore unclear whether observed increases in growth rate are sustained in the long term and/or influence subsequent life histories. For

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example, the timing of emigration to sea in many anadromous fish species is size-dependent; therefore, it is possible that the age structure of migrant fish could be altered by nutritional subsidies from their parents (Nelson & Reynolds 2015). Finally, to our knowledge no previous studies have considered how the addition of marine-derived nutrients may affect the longer term genetic diversity of freshwater fish populations, which is becoming increasingly recognised as an important aspect of conservation management (Garcia de Leaniz *et al.* 2007; Kahilainen, Puurtinen & Kotiaho 2014).

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Here we examine the effects of marine-derived nutrients on juvenile Atlantic salmon and their invertebrate prey. While Pacific salmon are semelparous and experience mass mortality after spawning, post-spawning mortality rates in Atlantic salmon are lower and vary on both a temporal and spatial scale (Fleming 1998; Jonsson & Jonsson 2003). Nevertheless, even relatively small influxes of marine nutrients have the potential to alter the highly oligotrophic upland streams in which these salmon typically breed (Jonsson & Jonsson 2003; Nislow, Armstrong & McKelvey 2004), and there is evidence that this species used to spawn at much higher densities than is currently the case (Lenders et al, 2016). Using a study system that allows us to exclude the potential effects of immigrant fish on calculations of fish biomass and density, we recently demonstrated experimentally that marine-derived nutrients from salmon carcass analogues can have a positive effect on juvenile Atlantic salmon genetic diversity, growth, and biomass over the first 3 months of life (Auer et al. 2018). Here we extend our work in this same study system to consider whether these effects persist across the freshwater stage. We also evaluate if such simulations of nutrient release may influence the age (and hence size) at which juveniles undertake the spring seaward migration, with potential implications for the subsequent marine phase of the Atlantic salmon's life history.

2 | METHODS

2.1 | Study sites and general experimental protocol

We selected 10 small headwater streams that were surrounded primarily by open moorland and drained into the Rivers Blackwater, Bran, and Meig of the River Conon catchment in northern Scotland (Fig. 1, Table S1; Auer *et al.* 2018). Hydropower dams along each of the rivers prevent the passage of most returning adult salmon (Gowans *et al.* 2003; Williams 2007). Atlantic salmon (stocked as eggs or juveniles) and resident brown trout (*Salmo trutta*) are the dominant fish species in the system. Five of the study streams were randomly assigned to the 'high parental nutrient' treatment (addition of analogue carcasses), while the other five study streams were assigned to the 'low parental nutrient' treatment (without carcasses). We then planted out eggs from genotyped salmon families in each of the streams and subsequently monitored prey availability and fish growth, biomass, density and genetic diversity of this focal cohort over the next 2 years (Fig S1). We also monitored these same fish variables in a second cohort of eggs planted out the second year to evaluate repeatability of parental nutrient effects during the first summer of growth (see Supplementary Information (SI) for details).

2.2 | Experimental families and planting out eggs and carcass analogues

Over a three-day period in December 2015, fifty-four full sibling families were created using *in vitro* fertilization of fish caught in a fish trap at a dam on the River Blackwater (Fig. 1). Parental fish were those previously stocked in headwater streams above the dam that were returning from the sea to spawn. Of the 54 families, we selected a subset of 30 families that were chosen at random with respect to paternal age but controlled for maternal life history; only families from females that had spent a single winter at sea, confirmed by scalimetry, were selected since that was the

dominant life history of captured adults. A small section of adipose fin was clipped from each parent and preserved in 100% ethanol for later DNA analysis (see SI). Fertilized eggs were then reared overwinter in family-specific trays under identical water and temperature conditions at a nearby hatchery.

In late February to early March 2016, when eggs had reached the eyed stage of embryonic development, 100 eggs from each of the 30 families were collected from the hatchery, mixed together, and then planted out in a 300m² experimental reach (75-100m in length depending on stream wet width; Table S1) in each of the study streams (Table S1). Eggs were buried beneath the gravel in two Vibert boxes at the lower and upper limit of each experimental reach (n = 100 eggs per box) and the rest of the eggs were planted out in 8 artificial nests (n = 350 eggs per nest; McLennan *et al.* 2016) at equidistant points between the upper and lower Vibert boxes. In total, each experimental 300 m² reach received 3,000 eggs, equating to a density of 10 eggs m⁻² that falls within the range of observed spawning densities for Atlantic salmon (Fleming 1996). The Vibert boxes were found to be empty of eggs when recovered in late May/early June 2016, indicating successful hatching in all streams. Similar methods were used to create the second cohort of eggs that were planted out in each of the study streams the following year (see SI).

At the time of egg planting and again the following winter (Table S1), analogue carcasses, composed of dried hatchery salmon pellets (Coral 2000+40PAX B12, made of 60% marine-derived fish-based nutrients, Skretting, Invergordon UK) and similar to salmon carcasses in their nutritional content and decay rate (Pearsons, Roley & Johnson 2007), were distributed in high parental nutrient streams. Each experimental reach in the high parental nutrient streams received 5 mesh bags of pellets, each weighing 3kg, and equivalent to 25 adult salmon carcasses, an amount similar to or less than that used in other nutrient supplementation experiments in Atlantic salmon

streams (Williams *et al.* 2009; Guyette, Loftin & Zydlewski 2013; Guyette *et al.* 2014). The bags were evenly spaced along the length of each experimental reach and anchored to the substrate of the stream by stones to prevent removal by scavengers. HOBO temperature data loggers (Onset Computer Corporation, Bourne MA, USA) were also placed in each stream at the time of egg deposition and programmed to record data every 4h (Fig S2).

2.3 | Macroinvertebrate prey abundance and biomass

Macroinvertebrates were sampled in each experimental reach during late May to early June 2016 and then again in late February to early March 2017, when the fish were in their first and about to enter their second year of life (age 0+ and 1+ respectively). The sampling in March 2017 took place immediately prior to the addition of the second set of carcass analogues. Invertebrates were collected using the electrobugging technique (Taylor, McIntosh & Peckarsky 2001), described in detail in the SI. Specimens were then later identified to the family level and their length and biomass was calculated. Only those macroinvertebrates equal to or smaller than 1 mm and 2.5 mm in width were included in estimates of prey abundance and biomass (for age 0+ and 1+ fish respectively), since these are the maximum prey sizes that gape-limited juvenile salmon can consume at their respective body sizes (Wankowski 1979). These smaller macroinvertebrates were primarily from the Orders Ephemeroptera, Plecoptera, Trichoptera, Coleoptera, and Diptera, all of which are known to be in the diet of juvenile salmon in the Conon and other Scottish river catchments (Table S2; Mills 1964; Maitland 1965).

2.4 | Recapture of juvenile salmon

Surviving juveniles were captured by triple-pass electro-fishing in July 2016 (when fish were age 0+, approximately 3 months old), in July 2017 (when fish were aged 1+, approximately 15 months

old, Table S1), and finally in March 2018 (when the fish were 22 months old, which we refer to as age 2; Table S1). A total of 1272 fish were captured at age 0+ within the experimental reaches of the streams, 458 at age 1+ (plus 292 caught within 50m of the experimental reaches) and 306 at age 2, this time within 100m of the experimental reaches. Captured fish were anaesthetized, weighed (± 1.0 mg), measured for body length (± 0.01 mm) and a small fin clip taken for later parental assignment (see SI). By conducting triple-pass electro-fishing (see SI), we were able to estimate the densities of age 0+ and age 1+ focal fish based on the removal method and analysed (using maximum-likelihood) by Microfish software (Van Deventer & Platts 1989; Dochtermann & Peacock 2013).

2.5 | Statistical analyses

Effects of parental nutrient levels on juvenile salmon and their macroinvertebrate prey were tested using a series of linear mixed models. All models included treatment (low versus high parental nutrients) and salmon age (age 0 and age 1+ for invertebrate analyses and age 0+ and 1+ for fish analyses) as categorical fixed effects and stream as a random effect in cases where the dependent variable was measured more than once. Residuals were not normally distributed for most dependent variables, so we used a hierarchical bootstrapping approach to generate mean effects and p-values (Adèr & Adèr 2008). For analyses of macroinvertebrate abundance and biomass and fish fork length, body mass, density and biomass, the bootstrap procedure first sampled with replacement among values within each stream and age, then streams and age within each treatment. Models were rerun 20,000 times. Significance values were then calculated as a two-tailed *P*-value from the bootstrapped distribution of the treatment effect. Results from models that included or excluded fish of unknown parentage were qualitatively the same since there were few fish with unknown parentage, so only results from models that excluded fish of unknown parentage are

reported. The same analyses, albeit without age as a fixed effect, were run for body size, density and biomass of the second fish cohort.

Effects of parental nutrient levels on family-level diversity were examined using a bootstrap procedure that sampled, with replacement, values for the numbers of families represented in the captures from each of the streams per treatment and fish age. The model was rerun 20,000 times, and p-values were calculated as above. The number of fish captured per stream was included as a covariate in the analysis of family diversity, but was not statistically significant (p > 0.05; presumably because similar numbers were collected in each stream) so was dropped from the model. We ran two models, one that included and one that excluded fish captured outside the experimental reach section (see above).

Finally, differences in fork length between treatments (low versus high parental nutrients) at age 2 were tested using a linear mixed model that included stream and family ID as random effects. The residuals from this model were normally distributed; therefore, the bootstrapping approach was not considered necessary.

3 | RESULTS

- Both macroinvertebrate abundance (treatment p < 0.001; season p = 0.18; season x treatment p = 0.336) and biomass (treatment p < 0.001; season p < 0.001; season x treatment p = 0.462) were higher in streams with high compared to low parental nutrient levels. These differences were consistent across both the spring and the following winter, when juvenile salmon were age 0 and 1+, respectively (Fig. 2).
- Differences in prey availability among stream types were associated with distinct differences in juvenile salmon body size at both age 0+ and age 1+. Specifically, fork length increased with age

as expected (Fig. 3; p < 0.001), but juvenile salmon in high nutrient streams were also consistently larger than their siblings in low nutrient streams (treatment: p = 0.001; age x treatment: p = 0.609). Likewise, body mass increased with age (Fig. 3; p < 0.001), but juvenile salmon in high nutrient streams were consistently larger than their siblings in low nutrient streams (treatment: p < 0.001; age x treatment: p = 0.681). Fish density declined with age (Fig. 4; p < 0.001) but was not affected by nutrient level (treatment: p = 0.966; age x treatment: p =0.495). Fish biomass had declined at age 1+ (Fig. 4; p=0.012) but was consistently greater in high compared to low nutrient streams (treatment: p = 0.034; age x treatment: p = 0.364). Results for body size, density, and biomass were qualitatively the same for the second cohort of fish at age 0+ (Fig. S3). Both length (p < 0.001) and biomass (p = 0.012), but not density (p = 0.200) were higher in streams with high compared to low parental nutrient levels. Significant treatment differences in fork length were also observed when focal fish were age 2 (Fig. 5, p = 0.008). Importantly, 89.6% of the captured individuals in high nutrient streams had reached the minimum fork length of 100mm required for smolt transformation in this river catchment (Malcolm, Millar & Millidine 2015), and so had a high likelihood of migrating to sea as an age 2 smolt. In contrast, only 38.3% of the fish in the low nutrient streams had fork lengths above this threshold size (Fig 5). Finally, parental nutrient levels also influenced the genetic diversity of surviving fish (Fig. 6). Specifically, there was a trend for surviving fish to be drawn from a higher mean number of families in streams with high compared to low parental nutrient levels (p = 0.111) at both age 0+ and age 1+ (age: p < 0.001, age x treatment: p = 0.559) when the analysis excluded age 1+ fish captured outside the bounds of the experimental reach. These differences in family-level diversity

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among stream types were statistically significant when these extra-limital fish were included (treatment: p = 0.016; age: p = 0.127; age x treatment: p = 0.559).

4 | DISCUSSION

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4.1 | Sustained effects on prey availability and salmon growth rate

Previous studies have shown that the addition of marine-derived nutrients via carcasses or carcass analogues increases invertebrate abundance and biomass (Wipfli, Hudson & Caouette 1998; Claeson et al. 2006; Nislow et al. 2010). Marine-derived nutrients from salmon carcasses may become incorporated at multiple trophic levels within a stream (Nislow et al. 2010; Samways, Soto & Cunjak 2018). Therefore, a short-term increase in invertebrate abundance and biomass is perhaps unsurprising, given that many invertebrates feed directly on the carcass analogues and/or benefit from bottom-up effects of a nutrient pulse (Nislow et al. 2010). We show here that these effects can be both persistent and substantial: a year after the carcass addition (just prior to the second deposit of analogue carcasses) both the abundance and biomass of macroinvertebrate prey types for juvenile salmon were around 5 times higher than in streams receiving no carcasses. Since salmon carcasses are naturally deposited at yearly intervals, our results indicate that these natural annual nutrient pulses may sustain macroinvertebrate prey numbers at higher levels throughout the year. Scottish upland streams are often naturally nutrient poor (Elliott et al. 1998; Nislow, Armstrong & McKelvey 2004) and this has been further exacerbated by anthropogenic influence (Williams et al. 2009). Therefore, it is perhaps not surprising that even a relatively modest addition of simulated carcasses could significantly boost the productivity of the food webs that exist within these otherwise nutrient limited habitats.

This sustained increase in prey availability may explain why we also found that the salmon in these nutrient-supplemented streams were significantly larger at the end of the experiment, when they were two years old. While there is evidence of correlations between prey availability and the growth rate of age 0+ salmon in the field (Kennedy, Nislow & Folt 2008), less is known about the older freshwater life stages, when other sources of growth limitation (e.g. enhanced risk averse behaviour; see Nislow, Armstrong and Grant (2011)) may act to decouple individual growth from the availability of prey. Here we have shown a similar growth response to a nutrient pulse and associated enhanced prey availability among the different freshwater age classes of salmon. Previous studies that report a positive effect of parental nutrients on fish biomass have been limited in determining the underlying mechanisms of such an effect (e.g. Williams et al. 2009). In the present study, all matings occurred at the same time and all streams received the same genetic mix of eggs, so the only explanation for the larger juvenile size-at-age in high nutrient streams is a faster growth rate. Likewise, the greater biomass of juvenile salmon in the high parental nutrient streams was driven by differences in growth rate since we found no effect on their density. Other studies have found a positive effect on fish density from adding carcasses (e.g. Williams et al. 2009), but this could be caused by increased immigration (Bilby et al. (1998), which might imply no overall increase in population size. Our study reduced the noise in estimating the effects of nutrients on juvenile salmon by seeding all streams with the same number and genetic diversity of salmon eggs, and then genotyping the surviving offspring, so allowing us to show that levels of immigration were trivial. The upper density limit (i.e. carrying capacity) of juvenile salmon populations is linked to size of feeding territory that the fish defend (Grant & Kramer 1990). However, stream salmonids (including Atlantic salmon) make only minor adjustments to territory

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size in response to changes in food supply (Grant, Weir & Steingrímsson 2017), which could explain the lack of difference in density between streams despite the difference in food abundance.

4.2 | Sustained effects on genetic diversity

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We have demonstrated previously that higher parental nutrient levels lead to the survival of a higher number of salmon families through to 3 months of age (Auer et al. 2018). Here we show that this higher genetic diversity persists until at least 15 months of age: of the original families present in a stream at the egg stage (which was the same for all streams), more families had surviving representatives in the high compared to low parental nutrient streams. This indicates stronger selection against particular families when nutrient levels are low (Auer et al. 2018). For this experiment, eggs were artificially planted in mixed family nests. While this may have possibly altered early life competition dynamics between the focal families, juveniles from different nests would have invariably become mixed (and so run into competition with each other), since average dispersal distances are likely to be much greater than average distances between the nests. The importance of including genetic diversity in conservation management plans is becoming increasingly recognised (Garcia de Leaniz et al. 2007; Kahilainen, Puurtinen & Kotiaho 2014). Though clearly a complex issue, genetic diversity is generally linked to the adaptive potential of a population (Kahilainen, Puurtinen & Kotiaho 2014), which is of particular current importance given increasingly unstable environmental conditions and associated new selection pressures (Hoffmann & Sgrò 2011). An additional reason for considering genetic diversity in conservation management plans is that low genetic diversity can be linked to inbreeding depression and population extinction (O'Grady et al. 2006). We still know very little about how Atlantic salmon populations are impacted by genetic loss, in part due to our limited knowledge of historic genetic diversity levels (Wang, Hard & Utter 2002). It has been suggested that salmon populations are

already under inbreeding risk by evolutionary design, since they exhibit a high degree of natal homing, which in turn restricts the genetic make-up of spawning aggregates (Allendorf & Waples 1996). There is evidence that Atlantic salmon have evolved inbreeding avoidance mechanisms and, in part, choose mates based on MHC dissimilarity (Landry *et al.* 2001). However, while mechanisms such as these can help to increase the genetic diversity of offspring, they rely on there being sufficient existing variation in MHC alleles, which may not be the case if low nutrient levels create selection pressures that reduce the genetic variation in already small populations. Restoring nutrient levels can thus have the benefit of improving genetic diversity and so increasing population resilience, even if it does not boost the size of the juvenile population size.

4.3 | Possible effects on later life stages

The age at which juvenile Atlantic salmon transform into the smolt stage of the life cycle and migrate to sea is variable, but since the seaward migration only takes place in the spring this generates discrete year classes of smolts. Across the geographic range of the species, migrants range in age from 1-8 years, with most rivers containing 1-4 year classes (Metcalfe & Thorpe 1990); those in the River Conon catchment are generally either 2 or 3 years old (McLennan et al. 2017). The probability of an individual smolting is governed by whether it is on course to exceed a threshold body size by the time of the smolt migration; presumably because survival rates of the smolts are strongly dependent on body size at the time of the migration (Jokikokko *et al.* 2006; Armstrong *et al.* 2018). Those individuals that are projected to fall short of the threshold will exhibit suppressed growth over winter and will delay smolting for at least a further year (Metcalfe 1998; Dodson *et al.* 2013). These differences in growth strategy make it is possible (with up to 90% accuracy) to differentiate those fish that will/will not migrate, several months prior to the migration (Pearlstein, Letcher & Obedzinski 2007). Therefore, although the last sampling was

conducted in March, prior to smolts developing the characteristic silver body coloration, we can presume that the larger individuals would have smolted. Given the size distribution of migrating smolts in this river system (Malcolm, Millar & Millidine 2015), it is reasonable to assume that the majority of fish larger than 100mm when captured in March would have smolted that spring. Therefore, it is likely that the nutrient manipulation greatly boosted the proportion of fish that would have become 2- rather than 3-year-old smolts, since almost 90% of individuals in the high nutrient streams were > 100mm in March, compared to less than 40% in the low nutrient streams. If the simplifying assumption is made that all fish ≥ 100 mm in March smolted at age 2, and that 80% of the remaining fish smolted at age 3 (the remainder having died or were males that failed to smolt after becoming sexually mature), then the addition of nutrients reduced the mean age of smolts from 2.56 to 2.09. In an analysis covering the geographic range of the Atlantic salmon, Metcalfe and Thorpe (1990) showed that the mean age of smolts in a river was closely related to growth conditions (measured in 'degree-hours' during which foraging could occur, being the annual sum of monthly mean temperatures above a baseline of 5.5°C (the threshold for growth) multiplied by daylight hours each month). Using the same approach as used in Metcalfe and Thorpe (1990), we calculate that at the latitude of the Conon river system the nutrient addition was the equivalent of an average increase in annual mean water temperature of 1.3°C. How this acceleration of the freshwater phase of the life cycle might influence overall population dynamics is not clear, since there are a number of potential interacting factors. Individuals that migrate to sea after only two years in fresh water have an increased likelihood of surviving the freshwater phase of their life cycle, since age-3 smolts are subjected to freshwater mortality for an additional year. All else being equal, an increased smolt yield due to a greater proportion of age-2 smolts could cause a substantial decrease in generation time, with an associated increase in the

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population growth rate. However, age-2 smolts are also typically smaller than those migrating a year later from the same river (Jonsson, Jonsson & Hansen 1998), and so may experience higher mortality during migration (Jokikokko et al. 2006; Armstrong et al. 2018), which could then counteract the positive effect of increased smolt production on population size. Aspects of growth, size and age during the freshwater stage of the Atlantic salmon life cycle are often correlated with subsequent marine growth dynamics and the numbers of years spent at sea (Hutchings & Jones 1998). These interactions are complex; however, if there were a negative relationship between smolt age and the duration of the marine phase (i.e. younger smolts spending an extra year or more at sea), the overall generation time would not be reduced and there would be no effect on population growth rate. This considered, an increased proportion of age-2 smolts could still result in a net population gain via reduced inter-cohort competition within the stream (Einum et al. 2011). Older fish are likely to be competitively superior to those of younger age classes but have differing microhabitat requirements, so the impact of a reduction in the size of older cohorts is not straightforward (Nislow, Armstrong & Grant 2011). However, it is possible that reduced competition from older cohorts could increase the carrying capacity of younger cohorts (Nordwall, Näslund & Degerman 2001), which might also increase the number of smolts being produced. Though clearly complex, the results of our study suggest that restoring nutrients to the spawning grounds of Atlantic salmon could have significant implications for both population dynamics and fisheries management. Further work is needed to evaluate whether the gains from both increasing genetic diversity and reducing the time spent by fish in fresh water are actually sufficient to offset the higher mortality that individuals may then experience as a result of potentially being smaller at the time of migration. However, the groundwork is now partially laid for encouraging a greater

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- 383 consideration of how the nutrient decline of fresh waters may affect the species that live within
- these ecosystems, and how such effects may be better managed and mitigated.

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AUTHOR CONTRIBUTIONS

D.M, S.K.A., S.M., K.H.N., J.D.A. and N.B.M. conceived the ideas and designed the methodology; D.M., S.K.A., G.J.A., T.C.R., S.M., K.H.N., R.D.B., D.C.S, E.C, J.S and N.B.M collected the data; D.M., S.K.A. and R.D.B. analysed the data; D.M., S.K.A. and N.B.M. led the writing of the manuscript. All authors contributed critically to the drafts and gave final approval for publication.

DATA ACCESSIBILITY

Should this paper be accepted for publication, data sets corresponding to the statistical models would be deposited in a Dryad repository.

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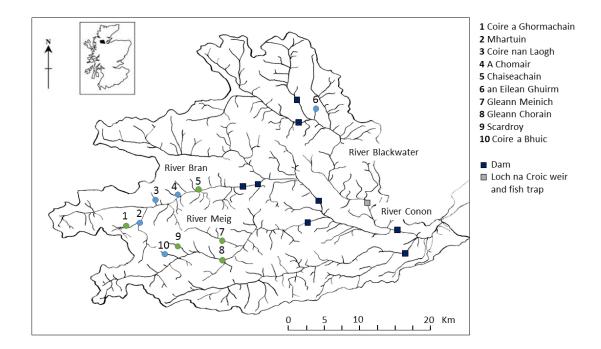


Figure 2. Mean (± 1 SE) macroinvertebrate prey abundance and biomass when fish were age 0 (May-June 2016) and age 1+ (March 2017) in streams with low (blue, n = 5) and high (green, n = 5) parental nutrient levels. Only invertebrates equal to or less than 1mm in width during Spring 2016 and equal to or less than 2.5 mm in width in Winter 2017 were included since they represent the maximum prey size for age 0 and wintering age 1+ juveniles, respectively. Estimates are given as the mean catch per unit effort for 1-minute samples taken at three locations at each of 50, 25, and 0 m above the downstream limit of each experimental reach. Data for May-June 2016 are from Auer et al. 2018.



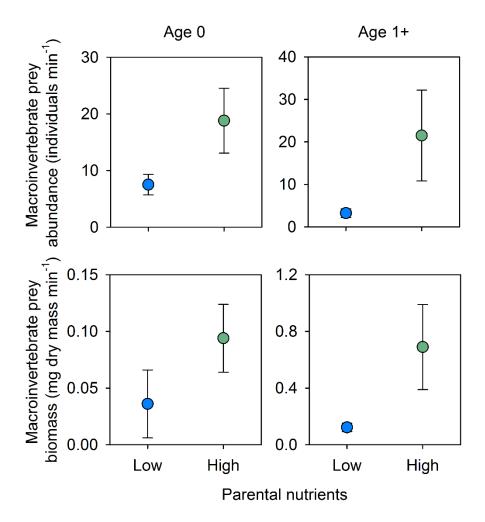


Figure 3. Mean (± 1 SE) fork length and body mass of juvenile Atlantic salmon ($Salmo\ salar$) in streams with low (blue, n = 5) and high (green, n = 5) parental nutrient levels recaptured at age 0+ (July 2016) and age 1+ (July 2017). Data for age 0+ fish are from Auer et al. 2018.

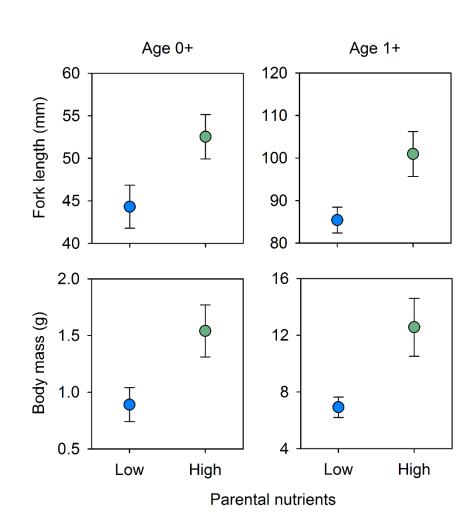


Figure 4. Mean (± 1 SE) density and biomass of juvenile Atlantic salmon (*Salmo salar*) captured at age 0+ (July 2016) and again at age 1+ (July 2017) in streams with either low (blue, n = 5) and high (green, n = 5) parental nutrient levels. Fish density for each age class was estimated from depletion curves of the number of fish captured during triple-pass electrofishing. Fish biomass was calculated as the product of the average fish body mass and the estimated density for each stream. Data for age 0+ fish are from Auer et al. 2018.

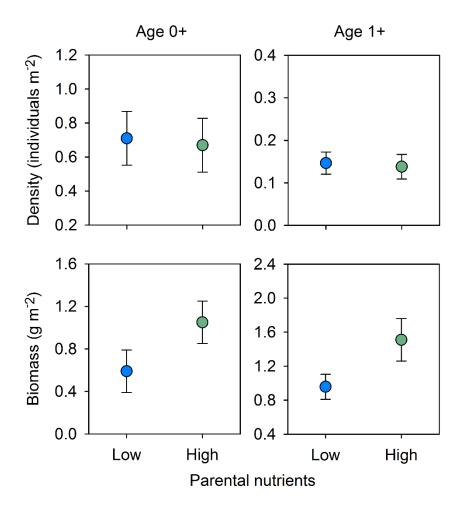


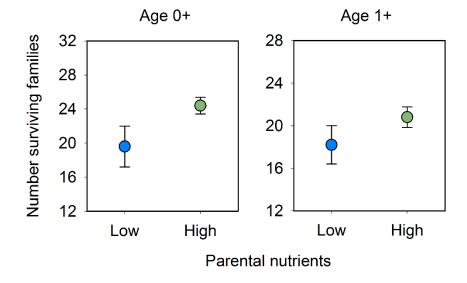
Figure 5. Distribution of fork length in streams with low (blue, n = 5) and high (green, n = 5) parental nutrient levels. Blue represents low parental nutrients, green represents high parental nutrients and purple represents overlaid data. The red dotted line corresponds to the minimum smolting size for this river system.

Parental nutrients High Low

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Age 2 fork length (mm)

Figure 6. Genetic diversity of Atlantic salmon (*Salmo salar*) from streams with low (blue, n = 5) and high (green, n = 5) parental nutrient levels. Plotted are raw estimates for the mean ($\pm 1SE$) number of surviving families among fish captured at age 0+ (July 2016) and age 1+ (July 2017). Data include fish captured in the experimental reach as well as extra-limital areas 50m up and downstream of the experimental reach. Data for age 0+ fish are from Auer et al. 2018.



637	Supplementary Information corresponding to:
638	Simulating nutrient release from parental carcasses increases the growth,
639	biomass and genetic diversity of juvenile Atlantic salmon
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641	Darryl McLennan ^{1,2*} , Sonya K. Auer ^{1,3*} , Graeme J. Anderson ¹ , Thomas C. Reid ¹ , Ronald
642	D. Bassar ³ , David C. Stewart ⁶ , Eef Cauwelier ⁶ , James Sampayo ⁶ , Simon McKelvey ⁴ ,
643	Keith H. Nislow ⁵ , John D. Armstrong ⁶ , and Neil B. Metcalfe ¹
644 645	¹ Institute of Biodiversity, Animal Health and Comparative Medicine, University of Glasgow, Glasgow, G12 8QQ UK.
646 647	² Department of Fish Ecology and Evolution, EAWAG, Seestrasse 79, 6047, Kastanienbaum, Switzerland.
648	³ Department of Biology, Williams College, Williamstown, MA 01267 USA
649	⁴ Cromarty Firth Fishery Trust, Inverness, IV2 3HF UK.
650	⁵ USDA Forest Service Northern Research Station, Amherst, MA 01003 USA.
651	⁶ Marine Scotland – Science, Freshwater Fisheries Laboratory, Pitlochry, PH16 5LB UK.
652	
653	* These authors contributed equally to this work
654	Corresponding author: darrylmclennan@outlook.com
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SUPPLEMENTARY METHODS

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Macroinvertebrate collection and analysis

Invertebrates were collected using the electrobugging technique (Taylor, McIntosh & Peckarsky 2001), in which an electrofisher (500W electrofishing backpack system from E-fish ltd, Grangeover-Sands, UK; 350 V, 60 Hz and a 10% duty cycle) was operated for 60 s with its anode held stationary and immediately upstream from a Surber sampler (250 µm filter; EFE and GB Nets, Totnes, UK) resting on the stream substrate. This procedure was carried out at three contiguous locations at each of three positions (0, 25, and 50 m up from the downstream limit of the experimental reach) in each of the 10 streams. Macroinvertebrates collected from the three contiguous locations were preserved together in 70% ethanol. They were later identified to the family level under a dissecting microscope, enumerated to determine their abundance, and measured to the nearest 0.5mm. Length measurements were then used to determine their biomass using published length-mass regressions for the relationship between dry mass and length for each taxonomic family (Table S2; Bird & Prairie 1985; Benke et al. 1999; Baumgärtner & Rothhaupt 2003; Mroczyński & Daliga 2016). The area upstream from the anode was not blocked off, so abundance and biomass were defined as catch per unit effort. Only those macroinvertebrates equal to or smaller than 1 mm and 2.5 mm in width were included in estimates of prey abundance and biomass for age 0+ and 1+ fish, respectively, since those prey sizes are the maximum that gapelimited juvenile salmon can consume at their respective body sizes (Wankowski 1979). These were primarily macroinvertebrate from the Orders Ephemeroptera, Plecoptera, Trichoptera, Coleoptera, and Diptera, all of which are known to be in the diet of juvenile salmon in the Conon and other Scottish river catchments (Table S2; Mills 1964; Maitland 1965).

Electrofishing protocols

A total of 907 age 0+ focal fish were captured via triple-pass electrofishing in two different sections (each at least 10m in length) of riffle habitat within the experimental reach of each stream. At the same time age 0+ fish outside these two sections, but within the boundaries of the experimental reach (n = 365), were also captured via single-pass electrofishing to increase the family-level sample sizes needed to estimate genetic diversity. In July 2017, focal age 1+ fish and non-target 0+ fish from the next cohort were captured using the same triple-pass electrofishing technique but now covering the entire experimental reach (n = 458 1+ focal fish). Again, age 1+ fish within 50m upstream and 50m downstream (n = 292) were also captured via single pass electrofishing to increase family-level samples sizes needed to estimate genetic diversity. The area that was electrofished increased from the first to the second year due to the decrease in density with age, also since territory size increases and microhabitat use shifts from shallower riffles to deeper pools as the fish grow larger (Armstrong *et al.* 2003), so requiring a larger sampling area to obtain adequate sample sizes of focal fish.

During each sampling period, captured fish were anaesthetized with clove oil (20 ppm), weighed (\pm 1.0 mg) and then measured for body length (\pm 0.01 mm). In the case of focal fish, a small section of anal (age 0+) or adipose (age 1+) fin was clipped and stored in ethanol for later parental assignment (see SI)). Densities of age 0+ and age 1+ fish were estimated using Microfish (Van Deventer & Platts 1989).

The final electrofishing when the focal fish were age 2 allowed assessment of the proportion of focal fish that had reached the minimum size (100mm for this river system (Malcolm, Millar & Millidine 2015)) at which fish would undergo smolt transformation and migrate to sea as two year olds. To maximise capture numbers, but at the expense of estimating density, we captured fish via single-pass electrofishing, both within and ~100m below the experimental reaches. Captured fish

were anaesthetized, weighed and measured as before, and a small fin clip was again taken for parental assignment. This survey was timed to be at least one month prior to the onset of the main smolt migration period in the River Conon catchment (McLennan *et al.* 2017; McLennan *et al.* 2018), but it is possible that smolting individuals may have already started moving down from our study streams into the main river (McCormick *et al.* 1998), so results need to be interpreted with caution. In total, 306 age-2 fish were captured across our 10 experimental streams, and genotyping (see SI) confirmed that 282 of these individuals came from our focal families.

Genotyping and parental assignment

Captured fish of age classes 0+ and 1+ were genotyped and assigned to a specific focal family by commercial suppliers (Landcatch Natural Selection Ltd, Stirling, Scotland). In brief, an E-Z 96 tissue DNA Tissue kit (Omega Bio-Tek, Georgia, USA) was used to extract DNA from the fin clips of parental fish and captured progeny. Fish were then genotyped using a panel of 110 informative SNP markers scattered across the genome using individual end point PCR assays (KASP TM technology, UK). Parentage assignment by exclusion was carried out blind to experimental treatments with the programme Vitassign 8.3 (Vandeputte, Mauger & Dupont-Nivet 2006) with some modifications to allow the analysis of more than 100 markers.

Captured fish of age class 2+ were genotyped and assigned to a specific focal family by Marine Scotland – Science, Pitlochry, Scotland. DNA was extracted from fin clips using a Chelex protocol (Walsh, Metzger & Higuchi 1991). Samples were screened at a panel of 96 polymorphic SNPs, using a SNPtype assay on a Fluidigm EP1 platform (Fluidigm, UK), according to manufacturer's protocols. Parentage assignment was carried out in Colony 2.0.5.0 (Jones & Wang 2010) assuming polygamy, using a 0.95 probability of the parent being included in the dataset and allowing for 0.001 marker error rate. Genotyping successfully assigned almost all fish to parents

(98% at 0+, 97% at 1+ and 92% at age 2, the decrease presumably a consequence of greater movements of fish from other stocked non-experimental streams).

Second fish cohort

Methods used to create families for the second cohort were the same as used for the focal cohort, with the exception that parents were not genotyped. Eggs were drawn from a random sample of eggs in the hatchery and planted out planted out in the same numbers and locations as described for focal fish. At age 0+, fish were captured via triple-pass fish (n = 1830) of the entire experimental reach (as described for age 1 fish). Analyses of growth, density, and biomass were the same as described for focal cohort.

SUPPLEMENTAL TABLES AND FIGURES

Table S1. Location, sampling times, and characteristics of ten study streams in the northern highlands of Scotland. Nutrients refers to whether streams had low or high parental nutrient levels; the latter each received carcass-analogs in an amount equivalent to 25 salmon carcasses.

			Egg/			Egg/		
	Location	Nutr-	Carcass	Invert	Fish	Carcass /	Fish	Fish 2018
Stream	(N Lat./W Long.)	ient	2016	2016	2016	Invert 2017	2017	
A Chomair	57.595, 5.002	Low	7 Mar	31 May	15 July	13 Mar	19 July	8 March
An Eilean Ghuirm	57.706, 4.696	Low	25 Feb	31 May	11 July	1 Mar	12 July	17 March
Chaiseachain	57.598, 4.949	High	25 Feb	8 June	12 July	3 Mar	17 July	9 March
Coire a Ghormachain	57.549, 5.129	High	3 Mar	4 June	12 July	3 Mar	22 July	13 March
Coire nan Laogh	57.581, 5.059	Low	3 Mar	4 June	16 July	3 Mar	16 July	14 March
Coire a Bhuic	57.513, 5.001	Low	26 Feb	2 June	13 July	1 Mar	14 July	22 March
Gleann Chorain	57.500, 4.916	High	26 Feb	7 June	21 July	1 Mar	21 July	16 March
Mhartuin	57.555, 5.096	Low	3 Mar	4 June	24 July	3 Mar	20 July	12 March
Scardroy	57.519, 4.992	High	26 Feb	2 June	22 July	1 Mar	18 July	22 March
Gleann Meinich	57.543, 4.935	High	26 Feb	10 June	14 July	28 Feb	13 July	25 March

Table S2. Published coefficients for length-mass equations (DM = aLb where DM = dry mass in mg and L = length in mm) for aquatic larvae from macroinvertebrate families in five different taxonomic orders.

5	Coefficients					
,		а	\boldsymbol{b}	Reference		
	Ephemeroptera					
3	Baetidae	0.00530	2.875	Benke et al. 1999		
)	Heptageniidae	0.01080	2.754	Benke et al. 1999		
	Plecoptera					
	Nemouridae	0.00560	2.762	Benke et al. 1999		
	Taeniopterygidae	0.00720	2.665	Benke et al. 1999		
	Leuctridae	0.00280	2.719	Benke et al. 1999		
	Chloroperlidae	0.00650	2.724	Benke et al. 1999		
	Trichoptera					
	Hydropsychidae	0.00460	2.926	Benke et al. 1999		
	Hydroptilidae	0.01220	2.570	Baumgartner and Rothhaupt 2003		
	Psychomyiidae	0.00390	2.873	Benke et al. 1999		
	Coleoptera					
	Elmidae larvae	0.00740	2.879	Benke et al. 1999		
	Hydrophilidae	0.01760	2.580	Mroczyński and Daliga 2016		
	Diptera			,		
	Chironomidae	0.00180	2.617	Benke et al. 1999		
	Simuliidae	0.00200	3.011	Benke et al. 1999		
	Empididae	0.00540	2.546	Benke et al. 1999		
3						

Figure S1. Outline of experimental timeline.

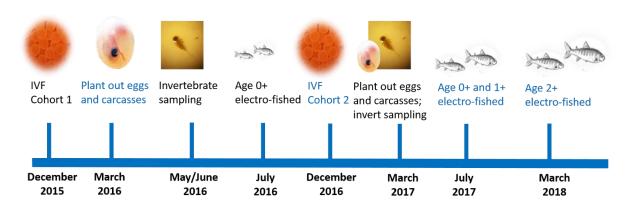


Figure S2. Temporal changes in mean ($\pm 1SE$) daily water temperature in 8 study streams with either low (n = 4, blue) or high (n = 4, green) nutrient levels in the northern highlands of Scotland. Temperatures were measured from the time eggs were planted out to their recapture as age 1+ parr.

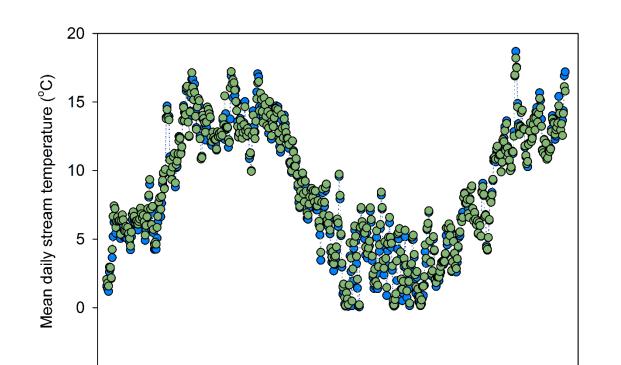
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Mar '16



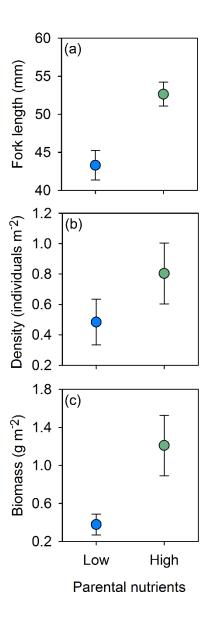
Nov '16

Mar '17

Jul '17

Jul '16

Figure S3. Mean (± 1 SE) (a) fork length as an index of growth, (b) density, and (c) biomass of a second cohort of juvenile Atlantic salmon (*Salmo salar*) in streams with either low (blue, n = 5) or high (green, n = 5) parental nutrient levels. Fish were captured in July 2017 at age 0+. Fish density was estimated from depletion curves of the number of fish captured during triple-pass electrofishing. Fish biomass was calculated as the product of the average fish body mass and the estimated density for each stream. Both length (p < 0.001) and biomass (p = 0.012), but not density (p = 0.200) were higher in streams with high compared to low parental nutrient levels.



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