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ABSTRACT

The physiological causes of intraspecific differences in fitness components such as growth rate are currently a source of debate. It has been suggested that differences in energy metabolism may drive variation in growth, but it remains unclear whether covariation between growth rates and energy metabolism is (i) a result of certain individuals acquiring and consequently allocating more resources to growth, and/or is (ii) determined by variation in the efficiency with which those resources are transformed into growth. Studies of individually-housed animals under standardized nutritional conditions can help shed light on this debate. Here we quantify individual variation in metabolic efficiency in terms of the amount of ATP generated per molecule of oxygen consumed by liver and muscle mitochondria, and examine its effects both on the rate of protein synthesis within these tissues and on the rate of whole-body growth of individually-fed juvenile brown trout (*Salmo trutta*) receiving either a high or low food ration. As expected, fish on the high ration on average gained more in body mass and protein content than those maintained on the low ration. Yet, growth performance varied more than 10-fold amongst individuals on the same ration, resulting in some fish on low rations growing faster than others on the high ration. This variation in growth for a given ration was related to individual differences in mitochondrial properties: a high whole-body growth performance was associated with high mitochondrial efficiency of ATP production in the liver. Our results show for the first time that among-individual variation in the efficiency with which substrates are converted into ATP can help explain marked variation in growth performance, independent of food intake. This study highlights the existence of inter-individual differences in mitochondrial efficiency and its potential importance in explaining intraspecific variation in whole animal performance.

INTRODUCTION

Individual animals may grow at widely differing rates despite living under the same conditions - a finding that has been documented across a broad range of taxa (reviewed in [1, 2]). This phenomenon is often interpreted in terms of variation in individual quality. For instance, individuals that grow faster typically reach maturity more quickly and can have higher fecundity than slower growing individuals, suggesting direct fitness consequences of growth rate [3, 4]. However, the physiological processes underlying this among-individual variation in growth rate are currently poorly understood.

Faster growth can obviously be achieved by increasing food intake. Individuals with high rate of food intake grow faster compared to individuals that have lower rate of resource intake, because high amounts of food intake can lead to increased rate of resource allocation to energetically costly processes, such as biomass production and, in turn, growth. However, variation in growth rate may persist even when food intake is standardised. For example, individual fish fed to satiation and consuming similar amount of food exhibited three-fold differences in growth performance [5]. Similarly, five-fold differences in the rate of growth have been shown amongst fish consuming an identical amount of food [6]. This suggests that variation in growth may be, at least partly, attributed to variation in the efficiency of resource utilization and its allocation to biomass production. Yet surprisingly little research has investigated the possible mechanisms that might underlie this variation in metabolic efficiency and thus growth performance [7].

Variation in the efficiency with which food is converted to energy is thought to play an important role in the association between food intake and animal growth [7-9]. Energy derived from nutrients becomes usable for cellular processes only following transformation into high-energy molecules of adenosine triphosphate (ATP). ATP is the principal energy source for most cellular functions, such as DNA, RNA and protein synthesis (and hence biomass production). The main sites of energy conversion are the mitochondria, which provide over 90% of a cell's ATP [10]. Mitochondrial ATP is produced via oxidative phosphorylation, a process through which energy substrates are oxidized to generate a proton gradient that drives the phosphorylation of ADP to ATP. Although ATP production depends on the rate of substrate oxidation, the number of ATP molecules produced for each molecule of oxygen and energy substrate (i.e. pyruvate, glutamate, acetyl-CoA, etc) consumed by the mitochondria can vary [11]. A proportion of the energy that is generated from substrate oxidation is dissipated through proton leakage across the inner mitochondrial membrane and this leakage might decrease the energy available to produce ATP [12]. The amount of energy dissipated in the mitochondrial proton leak varies amongst individuals [13, 14] and this variation is known to correlate

with animal performance [15, 16]. This raises the possibility that variation in growth among individuals could involve differences in the efficiency through which mitochondria produce ATP.

Mitochondrial efficiency can be quantified through measurement of the ATP/O ratio; that is the ratio in the amount of ATP generated per unit of oxygen consumed [17]. Thus, the higher this ratio, the more efficiently an animal converts its metabolic substrates into ATP, with the ATP then available for energy-demanding cellular processes such as protein synthesis and biomass production [18]. A number of studies have found positive links between mean growth rate and mean mitochondrial efficiency when comparing among treatment groups, populations or selection lines [9, 19-23], but until now there has been no assessment of whether mitochondrial efficiency could explain variation in growth rate amongst individual animals maintained with the same food intake.

In this study, we tested, for the first time, whether individual variation in growth performance – measured both as the rate of whole-body gain in mass and as the rate of protein synthesis - was related to among-individual variation in mitochondrial efficiency. To test this hypothesis, we assessed the relationships between ATP/O ratio, fractional rate of protein synthesis and growth performance (growth rate, growth efficiency and protein gain) among individually housed brown trout (*Salmo trutta*) of the same age and maintained under standardized conditions. In order to standardize their food intake, fish were fed on individual limited rations to ensure that differences in growth performance could be attributed to mitochondrial efficiency differences. We chose juvenile brown trout as our study organism because larger body size in brown trout is a major determinant of fitness, with fast growth resulting in increased survival [24] and larger body size being linked to higher fecundity [25]. We analysed mitochondrial properties and protein synthesis in the liver and the white muscle, since the physiological properties of these tissues are known to influence growth performance [16, 26]. We predicted positive inter-individual correlations among mitochondrial efficiency, protein synthesis and growth performance.

MATERIALS AND METHODS

Experimental animals

Brown trout fry were moved from the hatchery (Howietoun, UK) to the University of Glasgow in June 2015. The fish were then kept in a communal tank and maintained under a 12 h light: 12 h dark photoperiod at 12˚C and fed daily in excess with trout pellet food (EWOS, West Lothian, UK). In September 2016, fish (n = 60) were transferred to individual compartments within a stream tank

system that allowed individual daily feeding while maintaining fish under the same water quality conditions. Each individual compartment contained a small shelter (a section of opaque plastic pipe).

The fish were first acclimated for two weeks in their individual compartments, during which they were hand-fed daily to excess on the same trout pellets. Fish were then fasted for 22h and briefly anesthetized (50 ml l^{-1} benzocaine in water) for measurement of body mass (± 0.001 g) to allow calculation of caloric intake and thereby food rations (as number of pellets). For the next 5-10 weeks (see below) the fish were fed once daily on an intermediate ration of pellets (presumed sufficient for growth but less than a maximal rate of intake) using an equation from Elliott [27]; this allowed calculation of individual-specific rations in calories as a function of the fish's body mass (W) in grams and water temperature (T) of 12˚C as follows:

$$\text{Intermediate ration} = 24.062 \times W^{0.737} \times \exp(0.105 \times T)$$

Fish were fed their ration in the early morning; all fish consumed their entire daily ration within 2 h. Body mass was measured every two weeks, and food rations were recalculated to adjust for gains in mass. Fish were fasted for 22h before each body mass measurement, and on return to their compartment were fed 2 h later than usual to allow time to recover from the anaesthetic and to ensure they ate the ration. All fish consumed their entire daily ration and gained mass during this acclimation period.

<u>Diet treatment and growth measurements</u>

Following this period of acclimation to an intermediate diet, fish were switched to the final diet treatment for 14 days. This duration was chosen because it limited the extent of mitochondrial turn-over that would occur over the growth period but was sufficient to detect differences in the rate of growth between individuals [28]. Since only two individuals per day could be analysed for their mitochondrial function at the end of the experiment, the start of the diet treatment was staggered over a 5-week period (so that the preceding acclimation period varied between 5 to 10 weeks). Two fish per day (which would subsequently be processed together 14 days later) were thus randomly allocated to the treatments: one fish had its ration increased to 150% of the intermediate ration (high ration, n = 30) and the other had its ration decreased to 50% of the intermediate ration (low ration, n = 30). The low ration was estimated to provide sufficient energy to cover maintenance requirements and relatively slow growth [27], while the high ration approximated the maximal rate of food intake of juvenile brown trout [27]. Body mass ranged from 3.61 to 15.48 g across individuals at the start of the experiment but did not differ between fish subsequently assigned to the two food

treatments (High ration: 8.15 ± 0.49 g, Low ration: 8.18 ± 0.48 g, T test: t = -0.041, df = 58, P = 0.967). Body mass was re-measured (as above) at day 7 of the diet treatment, and rations were recalculated to adjust for growth. All but one fish consumed their entire daily ration within 2 h during the experimental period; this fish was removed from all analyses so giving a final sample size of 59 fish (High food: n = 29; Low food: n = 30).

Growth rate and growth efficiency were simultaneously estimated over a 7-day period starting at day 7 of the experimental treatment (termed the initial fish mass in the following equation) and ending at day 14 (final fish mass). Specific growth rate (% day^{-1}) was defined as:

$$\text{Specific growth rate} = \frac{\ln(\text{final body mass}) - \ln(\text{initial body mass})}{\text{days elapsed}} \text{X } 100$$

Daily food intake was calculated from the daily food ration, and was expressed in terms of pellet mass. Growth efficiency (mg gain in body mass mg^{-1} food eaten) was measured for each fish as:

$$\text{Growth efficiency} = \frac{\text{gain in body mass day}^{-1}}{\text{mass of pellets eaten day}^{-1}}$$

At the end of the food treatment period, fractional rates of protein synthesis and mitochondrial properties were measured in the fish following protocols described below.

<u>Estimate of gain in whole-body protein</u>

The relationship between whole-body protein content and body mass of fish reared under Intermediate, Low and High rations was used to estimate the protein content of each fish at the start and at the end of the diet treatment and thereby estimate the gain in protein content over the treatment period. Specifically, we first determined the relationship between the body mass of a fish and its whole-body protein content (Figure S1), using a separate group of brown trout of the same age and size (See electronic supplementary material – ESM - for full details in section "Whole-body protein content").

The initial whole-body protein content of each experimental fish was therefore estimated from its body mass at the start of the food treatment, using the calibration regression for fish on the intermediate ration. The final whole body protein content of each experimental fish was likewise estimated from its body mass at the end of the food treatment, using the appropriate equation for its diet treatment. Specific protein gain rate (% day^{-1}) was then defined as:

$$\text{Specific protein gain} = \frac{\ln(\text{final whole-body protein content}) - \ln(\text{initial whole-body protein content})}{\text{days elapsed}} * 100$$

Measurement of the fractional rate of protein synthesis

The percentage of the protein mass synthesized per day – the fractional rate of protein synthesis - was measured using the flooding dose assay [29], modified for using stable isotope tracer, the ring-D5-phenylalanine (D_5-Phe) [30]. In short, the ratios of the amount of D_5-Phe relative to the amount of total phenylalanine (D_5-Phe plus its natural version) in both the protein pool and the free pool of amino acids allow calculation of the fractional rate of protein synthesis. The assay was first validated for brown trout of this age and size by conducting a preliminary time-course experiment (see ESM). From this validation experiment, we determined that a D_5-Phe incubation period of approximately 60 min was an appropriate incorporation duration.

For the main experiment, the fish were fasted for 21h before being injected into the peritoneum with the D_5-Phe solution. Each fish was then immediately placed in an individual tank containing 2 L of aerated water for a period of approximately 1h (mean ± SE: 1h05min ± 0h00min) without food and in darkness. The fish were then culled and their livers were immediately dissected, weighed and rinsed with distilled water. A subsample of liver was weighed and kept in ice-cold respirometry buffer (0.1 mM EGTA, 15 µM EDTA, 1mM $MgCl_2$, 20mM Taurine, 10mM KH_2PO_4, 20mM HEPES, 110 mM D-sucrose, 60 mM lactobionic acid, 1g L^{-1} bovine serum albumin essentially fatty acid-free, pH 7.2 with KOH) for subsequent measurement of mitochondrial properties (see below). A second aliquot of liver for measurement of protein synthesis was weighed and immediately flash-frozen in liquid nitrogen and stored at -70°C until further analysis. Likewise, two samples of white muscle were taken dorsally to the lateral line (to avoid contamination with red fibres) and just behind the dorsal fin. One aliquot was collected from one side of the fish and kept in respirometry buffer while the other aliquot was collected from the other side and immediately flash-frozen. After extraction and quantification of the the phenylalanine isotopes in both the free amino acid pool and in the protein pool (Details in ESM), the fractional rate of protein synthesis (Ks in % day^{-1}) was calculated as:

$$\mathrm{Ks} = \frac{24}{t} * \frac{(\mathrm{D5Phe\ /\ Total\ Phe})\ \mathrm{in\ protein\ amino\ acid}}{(\mathrm{D5Phe\ /\ Total\ Phe})\mathrm{in\ free\ amino\ acid}} * 100$$

where t is the actual duration of D_5-Phe exposure in hours.

Measurement of mitochondrial properties

Since only two samples could be run simultaneously to measure mitochondrial properties, liver samples of the two individuals in a processing batch were first homogenized as in [15, 16] and

assessed for mitochondrial function, while the subsample of white muscle was preserved in respirometry buffer on ice for the subsequent run.

Oxygen and magnesium green fluorescence signals were detected simultaneously using two respirometry chambers equipped with fluorescent sensors and recorded using DatLab software (Oroboros Instruments, Innsbruck Austria). Tissue homogenate from each fish was added to one of the two measurement chambers immediately following preparation. Mitochondrial efficiency was measured as in Salin, Villasevil [31]. Briefly, we used a protocol for estimating the ATP/O ratio that simultaneously measures both oxygen consumption and ATP production on the same sample. Cytochrome c oxidase (COX) respiration was then measured to allow standardization of the mitochondrial density of the tissues [32]. The rate of oxygen consumption simultaneously to ATP production was assessed by adding saturating ADP to the chamber containing complex I and II substrates. COX activity was measured after addition of ascorbate and N,N,N',N'-Tetramethyl-p-phenylenediamine dihydrochloride. The muscle trial was identical to the liver trial but adenylate kinase inhibitor was added to the measurement chamber with the subsample of muscle that was kept on ice (see ESM for full details of the protocol).

Rates of mass-specific oxygen consumption and ATP production at each step of the protocol were averaged over 30 to 60 seconds of stabilisation. Fluxes of O_2 and ATP were expressed in pmoles s^{-1} mg^{-1} wet weight of tissue. The ATP/O ratio was calculated as the ratio of corrected ATP production to double the rate of O_2 consumption at the time that the ATP was being produced.

<u>Statistical analysis:</u>

We first used correlation analysis to test whether physiological parameters (mitochondrial efficiency [ATP/O ratio], mitochondrial density [COX activity] and fractional rate of protein synthesis [Ks]) were correlated between the liver and white muscle within the same fish. We then used linear mixed models to determine the links between mitochondrial efficiency of the liver and/or muscle and the fractional rate of protein synthesis for different rates of food intake. The models included Ks of liver or muscle as the dependent variable, ATP/O ratio of liver and muscle as continuous predictors, and the food intake (high or low) as a fixed factor, and two-way interactions between food intake and covariates. To control for effects of mitochondrial density on the fractional rate of protein synthesis, the models included COX activity of the liver and muscle as a covariate and in two-way interactions with food intake, with Ks as the dependent variable. Processing batch was included as a random effect to control for the order in which fish were processed. Preliminary analyses showed that the fractional rate of protein synthesis was not affected by the duration of D_5-Phe exposure or the mass

of sample used for the extraction of the phenylalanine isotopes, so exposure duration and mass of sample were not included as covariates in the final models. We finally tested whether the degree of mitochondrial efficiency and the fractional rate of protein synthesis of the liver and/or the muscle explained individual variation in growth performance using a linear mixed model approach. The models included the growth performance (Specific growth rate, Growth efficiency and Specific protein gain) as dependent variables, and ATP/O ratio and Ks of liver and muscle as continuous predictors, the food intake as a fixed factor, with processing batch as a random factor. To control for effects of mitochondrial density on growth performance, COX activity of the liver or muscle were included as a covariate in the models with specific growth rate, growth efficiency and specific protein gain as the dependent variable. These models also included two-way interactions between covariates and food regime. To control for effects of initial body size on growth performance, initial body mass was included as a covariate in the models with specific growth rate or growth efficiency as the dependent variable, while the initial estimate for whole-body protein content was included as a covariate in the model for specific protein gain. All models were simplified by removing non-significant terms in a backward deletion procedure, starting with two-way interactions; significance was tested when terms were dropped from the model. All statistical analyses were performed in IBM SPSS Statistics 21 (Chicago, IL). Data are presented as means ± standard error, and the significance level was set to $P<0.05$.

RESULTS

The mitochondrial efficiency (ATP/O ratio) showed significant inter-individual variation, varying at least twofold for each tissue across individuals having the same food intake (table S1). The fractional rate of protein synthesis Ks differed up to two- or five-fold in liver and muscle, respectively, among individuals with the same food intake (table S1). There was no correlation between the physiological traits (ATP/O ratio and Ks) of the liver and muscle from the same fish (table S2).

The fractional rate of muscle protein synthesis Ks in a fish depended on the ATP/O ratio of its liver mitochondria, although this effect depended on food intake (liver ATP/O by food intake interaction, table 1). While muscle Ks was positively related to the ATP/O ratio in the liver mitochondria of fish with the high food ration ($t = 2.80$; df = 36; $P = 0.008$), there was no such relationship in fish receiving a low food ration ($t = -0.92$; df = 36; $P = 0.362$; figure 1). Amongst-individual variation in the fractional rate of protein synthesis Ks in the liver was not explained by the mitochondrial efficiency in either liver or muscle (LMM, $P > 0.05$).

Not surprisingly, food intake had a positive effect on specific growth rates, with fish on average having a specific growth rate threefold higher at the high compared to the low ration (table S1). However, individuals from the same food treatment varied considerably in their specific growth rate, with the fastest growing fish in the low ration exceeding the growth of some fish on the high ration (figure 2a; low food intake: -6.00 to 110.57 mg day^{-1}; high food intake: 68.86 to 394.43 mg day^{-1}). This individual variation in growth rate was partially explained by differences in liver mitochondrial efficiency, although the effect depended on food intake (liver ATP/O by food treatment interaction; table 2). The specific growth rate of fish receiving high rations was strongly and positively linked to the ATP/O ratio in their liver mitochondria (t = 4.46, df = 41, P < 0.001, figure 2a), whereas the trend was not significant when food intake was low (t = 0.33, df = 41, P = 0.745). Regardless of the food intake, the specific growth rate of a fish was strongly but negatively linked to the Ks in its muscle after controlling for liver ATP/O (table 2). Specific growth rates under either ration were unrelated to the ATP/O ratio in muscle mitochondria, or to the Ks in the liver (table 2).

Growth efficiency varied among individuals from -0.13 to 2.23 gain in body mass per mass of food eaten but did not differ between low and high food fish (table S1). Regardless of their food intake, individuals that had the higher ATP/O ratio in the liver had the highest growth efficiency (table 2, figure 2b).

The rate of protein gain of the trout also differed considerably amongst individuals, ranging from -1.98 to 17.74 mg day^{-1} for fish eating the low ration and from -0.21 to 60.79 mg day^{-1} for fish on the high ration. Individuals that had a higher ATP/O ratio in their liver mitochondria, and a lower Ks in their muscle had a faster specific gain in protein mass (table 2). The specific rate of protein gain was not related to ATP/O ratio in the muscle mitochondria nor to Ks in the liver (table 2).

DISCUSSION

While the general trend was for growth performance to increase when food intake was higher, individuals exhibited markedly differing growth performance even when having identical food intake. This variation in growth was related to mitochondrial function: individuals that were more efficient at producing ATP within their liver mitochondria grew faster, more efficiently and accumulated more protein than those individuals with less efficient mitochondria. Individuals that had a higher liver mitochondrial efficiency under high food levels had a faster rate of protein synthesis in their muscle. However, these differences in protein synthesis had an effect on growth performance in the completely opposition direction to our initial prediction that “protein synthesis promotes growth”. In

summary, our study shows for the first time that under conditions of a fixed food intake, the mitochondrial efficiency of an individual animal can determine whether it grows fast or slow.

Individual variation in growth performance is likely to be a complex, integrative characteristic influenced by several physiological and behavioural traits. Because individual differences in growth rate covary with behaviours that increase feeding rates [33], only studies of animals with controlled food intakes can shed light on the physiological drivers of growth differences. Food intake in our experiment was standardized, revealing that growth of fish under the same ration could vary more than 3-fold amongst individuals. Consequently, some fish on the low ration treatment were actually faster growing than others on the high ration treatment that were consuming three times as much food. While it has previously been shown that increased mitochondrial efficiency promotes fitness-related traits (physical performance [34], growth performance [9, 21-23, 35], reproductive output [36] and ageing [9, 14, 36, 37]), here we demonstrate that this relationship can even occur when animals are experiencing similar rates of food intake. As well as varying amongst individuals, mitochondrial efficiency is a flexible trait that can change in response to environmental conditions [38, 39] and stage of life [34, 40]. A higher mitochondrial efficiency may also have a cost, since mitochondria are a major producer of reactive oxygen species (ROS) and mitochondrial efficiency can be positively related to ROS production [17, 37]. When the generation of ROS in an organism exceeds the capacity of its antioxidant defence and repair mechanisms to combat its effects, there can be an accumulation of oxidative damage [41]. ROS have been proposed as an important factor underlying cellular and whole-organism senescence [41] and therefore, a potential cost linked to fast growth [42, 43]. Despite this cost, in some contexts natural selection may favour phenotypes with relatively high mitochondrial efficiency (since this can lead to faster growth, increased body size at maturity, minimized mortality risk and higher number of eggs), whereas in other contexts a lower mitochondrial efficiency and decreased ROS production might be beneficial (e.g. under conditions of *ad libitum* food availability) [7, 17, 37, 44]. This hypothesis is in accordance with several recent studies suggesting that variation in mitochondrial function is a key target of natural selection [45, 46]. Our findings that fish with high liver mitochondrial efficiency had a high rate of protein synthesis in their muscles and faster growth match our predictions that a higher efficacy at converting food into ATP can lead to an increased allocation to energetically-costly processes such as protein synthesis and growth. Contrary to expectations, the rate of protein synthesis in white muscle was negatively correlated with growth performance; individuals that grew the best displayed lower rates of muscle protein synthesis for a given liver mitochondrial efficiency. An explanation for this discrepancy might lie in the fact that rates of protein synthesis are tissue-specific [47] and the correlation of protein synthesis rates across different tissues in the same individual can be poor (as

shown by this study), and so the range of tissues that have been measured in our study might not be representative of the overall rate of protein synthesis in the entire animal since this would be defined as the sum of the individual tissue-specific rates of protein synthesis [48]. However, positive relationships between protein synthesis in white muscle and body growth have been reported in other species [26, 47]. An alternative explanation is based on the fact that body proteins are continually being broken down as well as synthesised, and so protein synthesis will only result in growth if the rate of synthesis exceeds the rate of degradation; it has previously been shown that growth variation among individual fish is more explained by variation in rates of protein degradation than rates of protein synthesis [26]. While measurements of protein degradation rates were beyond the scope of the present study, it may only be possible to explain observed patterns of protein growth if all aspects of protein metabolism (synthesis and degradation) are considered [49].

In conclusion, our study has demonstrated a clear positive relationship between the efficiency with which liver mitochondria convert energy substrates into ATP and whole animal growth performance. Future research should focus on quantifying the presumed costs of highly efficient mitochondria. Information on the causes and consequences of variation in mitochondrial efficiency would allow prediction of the consequences for whole animal performance of variation in mitochondrial function, so linking cellular processes to organismal fitness.

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Author contributions. KS, SGL, IMcC, CC and NBM conceived the ideas and designed methodology. KS, EMV, GJA, SGL and CAM collected the data. KS, EMV, IMcC, SGL and CAM analysed the data. KS led the writing of the manuscript; SGL, IMcC, CS and NBM revised the manuscript and added comments. All authors gave final approval for publication.

Competing interests. The authors declare they have no competing interests.

Data accessibility. The dataset supporting this article are available from the Dryad Digital Repository: DOI: https://datadryad.org/review?doi=doi:10.5061/dryad.5c5372c

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Table 1. Results from linear mixed model analysis of the fractional rate of protein synthesis (Ks) in the muscle of a brown trout as a function of its food intake and the properties (ATP/O ratio and cytochrome *c* oxidase [COX] activity) of mitochondria in its muscle and liver. Processing batch was included as a random effect to control for the order in which fish were processed. Non-significant terms were excluded from the final analysis. Bold denotes significant results.

Dependant variable	Source of variation	Parameter estimate ± SE	*F*	d.f.	*P*
Muscle Ks*	Intercept	-0.00 ± 0.41			
	Food Intake#	**0.88 ± 0.42**	**4.38**	**1, 39.71**	**0.043**
	Liver COX activity	0.00 ± 0.01	0.04	1, 46.95	0.837
	Muscle COX activity	**0.03 ± 0.01**	**5.25**	**1, 36.56**	**0.028**
	Liver ATP/O ratio	0.66 ± 0.23	1.30	1, 30.99	0.262
	Muscle ATP/O ratio	-0.03 ± 0.03	1.17	1, 26.98	0289
	Food Intake# x Liver ATP/O ratio	**-0.92 ± 0.39**	**5.58**	**1, 40.41**	**0.023**

#Food intake: Two-level fixed factor (Low and High food intake).

*Full model: Muscle Ks = Food intake + Liver COX activity + Muscle COX activity + Liver ATP/O ratio + Muscle ATP/O ratio + Food intake x Liver ATP/O ratio + Food intake x Liver COX activity + Food intake x Muscle COX activity + Food intake x Muscle ATP/O ratio .

Table 2. Results from linear mixed model analyses of indices of growth performance in individual brown trout as a function of their initial mass, their liver and muscle mitochondrial density (cytochrome *c* oxidase [COX] activity), food intake, liver and muscle mitochondrial efficiency (ATP/O ratio) and fractional rates of protein synthesis (Ks). Processing batch was included as a random effect to control for the order in which fish were processed. Non-significant terms were excluded from the final analysis. Bold denotes significant results.

Dependant variable	Source of variation	Parameter estimate ± SE	*F*	d.f.	*P*
Specific Growth Rate*	Intercept	-0.38 ± 0.59			
	Initial Body Mass	**0.05 ± 0.02**	**9.69**	**1, 41**	**0.003**
	Liver COX activity	-0.01 ± 0.01	0.71	1, 41	0.403
	Muscle COX activity	**0.06 ± 0.02**	**8.27**	**1, 41**	**0.006**
	Food Intake#	0.55 ± 0.59	0.87	1, 41	0.355
	Liver ATP/O ratio	1.61 ± 0.36	11.7	1, 41	0.001
	Muscle ATP/O ratio	-0.02 ± 0.04	0.18	1, 41	0.671
	Liver Ks	-0.01 ± 0.02	0.30	1, 41	0.586
	Muscle Ks	**-0.54 ± 0.20**	**7.58**	**1, 41**	**0.009**
	Food Intake# x Liver ATP/O ratio	**-1.49** ± 0.54	**7.56**	1, 41	**0.009**
Growth Efficiency¤	Intercept	0.13 ± 0.41			
	Initial Body Mass	**0.06 ± 0.02**	**10.8**	**1, 48**	**0.002**
	Liver ATP/O ratio	**0.72 ±0.33**	**4.87**	**1, 48**	**0.032**
Specific Protein Gain¥	Intercept	-3.03 ± 0.74			
	Initial Protein Mass	0.00 ± 0.00	81.3	1, 31.25	< 0.001
	Liver COX activity	0.02 ± 0.01	2.80	1, 39.94	0.102
	Muscle COX activity	0.09 ± 0.03	0.11	1, 33.93	0.299
	Food Intake#	2.15 ± 0.85	6.34	1, 33.81	0.017
	Liver ATP/O ratio	**1.04 ± 0.29**	**13.0**	**1, 30.84**	**< 0.001**
	Muscle ATP/O ratio	0.02 ± 0.05	0.16	1, 18.86	0.690
	Liver Ks	0.01 ± 0.02	0.28	1, 35.40	0.601
	Muscle Ks	**-0.51 ± 0.24**	**4.44**	**1, 37.94**	**0.042**
	Food Intake# x Initial Protein Mass	**-0.00 ± 0.00**	**29.4**	**1, 19.30**	**< 0.001**
	Food Intake# x Muscle COX activity	**-0.13 ± 0.05**	**6.84**	**1, 32.27**	**0.013**

#Food intake: Two-level fixed factor (Low and High food intake).

*Full model: Specific Growth Rate = Liver COX activity + Muscle COX activity + Initial Body Mass + Food intake + Liver ATP/O ratio + Muscle ATP/O ratio + Liver Ks + Muscle Ks + Food intake x Liver COX activity + Food intake x Muscle COX activity + Food intake x Initial Body Mass + Food intake x Liver ATP/O ratio + Food intake x Muscle ATP/O ratio + Food intake x Liver Ks + Food intake x Muscle Ks.

¤Full model: Growth Efficiency = Liver COX activity + Muscle COX activity + Initial Body Mass + Food intake + Liver ATP/O ratio + Muscle ATP/O ratio + Liver Ks + Muscle Ks + Food intake x Liver COX activity + Food intake x Muscle COX activity + Food intake x Initial Body Mass + Food intake x Liver ATP/O ratio + Food intake x Muscle ATP/O ratio + Food intake x Liver Ks + Food intake x Muscle Ks.

¥Full model: Specific Protein Gain = Liver COX activity + Muscle COX activity + Initial Protein Mass + Food intake + Liver ATP/O ratio + Muscle ATP/O ratio + Liver Ks + Muscle Ks + Food intake x Liver COX activity + Food intake x Muscle COX activity + Food intake x Initial Protein Mass + Food intake x Liver ATP/O ratio + Food intake x Muscle ATP/O ratio + Food intake x Liver Ks + Food intake x Muscle Ks.

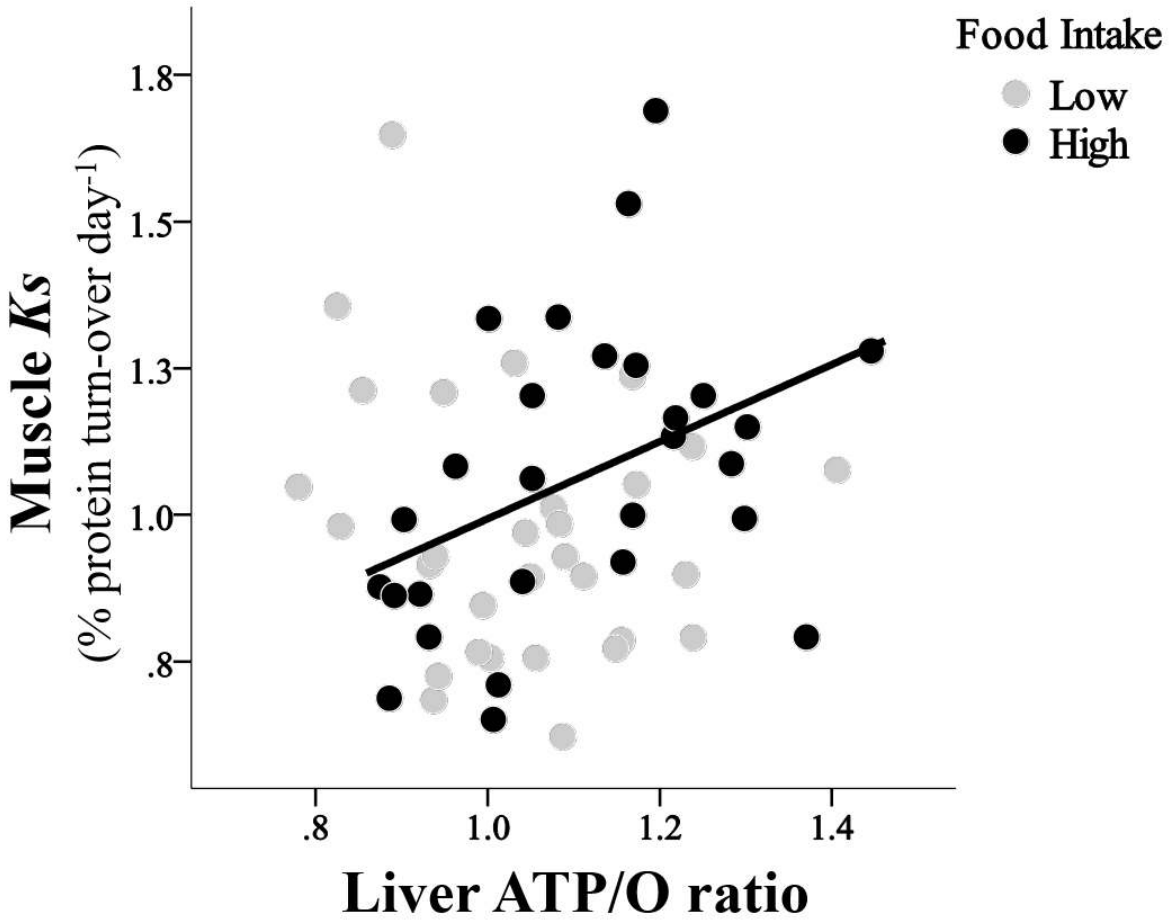
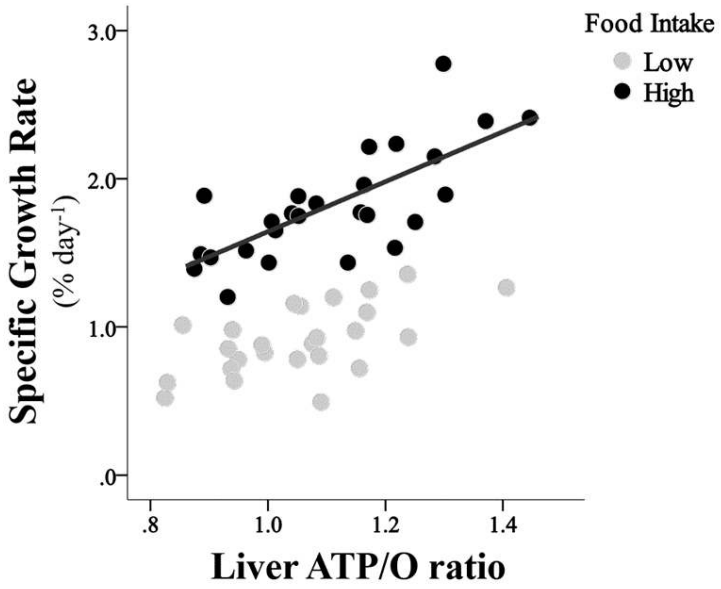


Figure 1. Relationship between the fractional rate of protein synthesis (K*s*) in the muscle and mitochondrial efficiency (ATP/O ratio) in the liver of juvenile brown trout at low vs high food intake. Continuous lines show significant effect. N = 28-30 fish per food level. See Table 1 for statistical analyses.

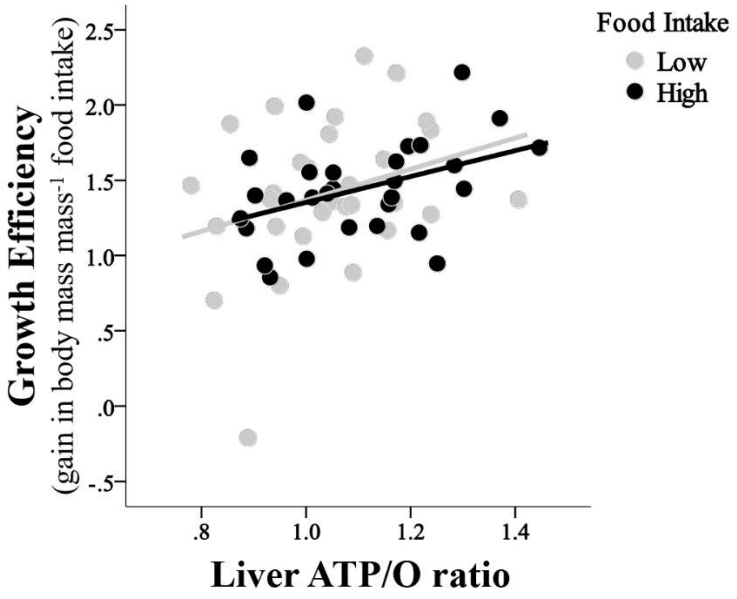
Figure 2. Relationships between indices of growth performance and mitochondrial efficiency in juvenile brown trout at low *vs* high food levels. **(a)** Specific Growth Rate in relation to liver mitochondrial efficiency (ATP/O ratio), and **(b)** Growth Efficiency in relation to liver ATP/O ratio. Continuous lines show significant effects. N = 29-30 fish per food level. See Table 2 for statistical analyses.

(a)



Plotted are partial residuals of specific growth rate for fish at high food ration evaluated at mean initial body mass = 9.59 g.

(b)



Plotted are partial residuals of growth efficiency evaluated at mean initial body mass = 9.02 mg.

Electronic Supplementary Material

TITLE: Differences in mitochondrial efficiency explain individual variation in growth performance

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RUNNING TITLE: ATP/O ratio explains growth performance

KEYWORDS: ATP/O ratio, brown trout, energy metabolism, intraspecific, mitochondrial plasticity, protein synthesis.

Whole-body protein content

Three supplementary groups of nine fish were used to determine the initial and final protein content of the experimental fish for the calculation of whole-body protein growth rates. These supplementary groups were of the same origin, age and size distribution, and were maintained simultaneously and in exactly the same manner, as the experimental fish described in the main manuscript. The fish in each of the 3 groups were maintained on the intermediate ration for 5 to 10 weeks. One group was then culled and frozen to determine the relationship between whole-body protein content and wet weight in fish on this intermediate ration (body mass range 2.95-20.31 g). This relationship was used to estimate the initial protein content of the experimental animals. The two other groups were switched to the low or high ration for 14 days and then culled and frozen to determine the relationship between whole-body protein content and wet weight in fish on low and high rations (3.28-15.04 g and 4.91-20.84 g respectively). Variation in fish body mass within each food treatment covered the range of masses for the experimental fish (those used for the analyses of

the physiological assays). These relationships between whole-body protein content and wet weight in fish were used to estimate the final protein content of the experimental animals.

All fish were fasted for 22h prior to culling, and were then weighed and and kept at -70°C for subsequent extraction and quantification of the whole-body protein content [1]. Thawed fish were cut into pieces in lysis buffer (1g tissue per 10 mL of 1x RIPA) supplemented with SDS (2%) and urea (2M). The contents were incubated for an hour at 60°C and shaken every twenty minutes. After this incubation, the tissue lysates were homogenized with an electric homogenizer (Kinematica Polytron PT 1200) until no visible piece of tissue remained. The homogenates were incubated another hour at 60°C, followed by centrifugation at 15,000 g for 10min at 4°C. The supernatants were collected and stored at -70°C until protein content was determined. The protein concentration of the lysates was determined with the Pierce bicinchoninic acid Protein Assay Kit following the manufacturer's specifications (Sigma Aldrich, Dorset, UK). The protein concentration was determined based on the standard curve using bovine serum albumin supplemented with SDS (2%) and urea (2M). Reagent was added to the lysates and incubated at 60°C for 15 minutes. The protein assays of samples and standards were run in duplicate. The absorbance was read at 562 nm. This allowed us to create a calibration regression relating fish body mass to fish whole body protein content in each food treatment (figure S1). Separate regression analyses were performed on data obtained from each food ration to predict the whole-body protein content as a function of body mass:

- Intermediate ration: Whole-body protein content = $0.1026W + 0.0657$
- High ration: Whole-body protein content = $0.1228W – 0.1206$
- Low ration: Whole-body protein content = $0.1226W – 0.0623$

where W is the wet weight of the fish.

For each ration group the protein content determined by protein extraction was highly correlated with the body mass of the fish ($0.92 \leq r^2 \leq 0.97$, figure S1). The estimated protein content as predicted by the body mass measurement thus appeared to be a robust technique to evaluate the whole protein content of the experimental fish whose organs were needed for other assays (fractional rate of protein synthesis and mitochondrial properties).

Validation of the fractional rate of protein turn-over assay.

Use of the flooding dose technique developed by Garlick, McNurlan [2] is based on meeting the following criteria: 1) that the rate of protein synthesis is not affected by high intracellular concentrations of the amino acid tracer (here phenylalanine or phe); 2) that the flooding dose

injection results in a rapid elevation of tracer in the body free amino acid pools that remains elevated and stable, or shows a slow linear decline over time, and 3) that the incorporation of the amino tracer into body protein is linear over time. With regards to criteria 1, previous work has indicated that although high doses injections of some amino acids (e.g. valine and leucine) may affect protein synthesis rates, phenylalanine is not thought to do so [3]. With regards to criteria 2 and 3, although previous work has validated an intraperitoneal flooding dose injection of D_5-Phe to measure rates of protein synthesis [4-6], we conducted a time course validation experiment for the conditions (e.g. temperature, animal model, animal size and stage of life) in this study.

Twenty fish received an intraperitoneal injection of 150 mM phenylalanine containing 50% deuterated phenylalanine (ring-D_5-phenylalanine, Cambridge Isotope Laboratories) dissolved in an aqueous solution of 154 mM NaCl at a dosage of 10 µL per gram of body mass. Fish were immediately returned to their individual tanks and, following an incubation period of 30, 60, 120 or 240 min (n = 5 fish per time point), the fish were culled, and their tissues sampled and stored at -80°C until further analysis. After extraction of the phenylalanine isotopes in liver and muscle tissues, the levels of D_5-Phe and the natural version of phenylalanine in both the free amino acid pool and in the protein pool were determined by gas chromatography coupled with mass spectrometry (GC model 7890B and MS model 5977B, Agilent Technologies Inc.) as described in [4, 7]. Peak detection and integration was performed using MassHunter software (Version B07.01 SP2, Agilent).

The D_5-Phe enrichment in the free pool of phenylalanine in both tissues was elevated and stable for 240 min (figure S2). In the liver, the slope of the free pool in relation to time did not significantly deviate from zero. However, in the white muscle it decreased at a rate of -0.037 % min^{-1} (regression analysis p = 0.001). Although statistically significant, this represents a decrease of 2.2% over the one hour incorporation period and is considered negligible. The phenylalanine enrichment of the protein pool increased linearly with incorporation time (regression analyses - Liver: $r^2 = 0.937$, $P < 0.001$; Muscle: $r^2 = 0.755$, $P < 0.001$; figure S2). From these results, we elected to use an incorporation period of 60 minutes as it allowed sufficient time for the tracer to incorporate into the protein pool while limiting the decrease in level of D_5-Phe in the free pool of amino acids in muscle.

Measurement of mitochondrial properties

The liver was shredded using micro-dissecting scissors to obtain a homogenous solution with a particle size less than 0.5 mm (tested by pipetting through 1 ml tip) in 1 mL of respirometry buffer as in [8, 9]. The shredded homogenate was then diluted further in respirometry buffer to obtain the

desired final concentration (mean ± SE: 5.00 ± 0.26 mg liver mL^{-1}). The liver homogenization was carried out on ice, and the procedure was completed within 30 min of the fish being culled.

Oxygen and magnesium green fluorescence signals were detected simultaneously using two respirometry chambers equipped with fluorescent sensors and recorded using DatLab software (Oroboros Instruments, Innsbruck Austria). The oxygen electrodes were calibrated at two points: air-saturated respirometry buffer (daily) and zero oxygen after sodium dithionite addition (fortnightly). Stepwise additions of $MgCl_2$ at each run were performed for calibration of the fluorescent signal into Mg^{2+}. The two binding affinity (K_d) values of ATP and ADP for Mg^{2+} were determined in absence of tissue in [10] ; the values were $K_{d\text{-ATP}}$ = 0.1545 mM and $K_{d\text{-ADP}}$ = 2.1333 mM.

Tissue homogenate from each fish was added to one of the two measurement chambers immediately following preparation; fish from a processing pair were measured in parallel. After addition of homogenate to the respiration chamber at 12˚C, pure oxygen gas was added to reach a concentration of 650 µM (Figure S3). Magnesium green (2.2 µM) was added to the respirometry chambers to allow us to detect changes in [Mg^{2+}] and so measure the rate of ATP production (Figure S3).

Mitochondrial properties were measured as in [10]. We used a protocol for estimating the ATP/O ratio that simultaneously measures both oxygen consumption and ATP production on the same sample. Oxygen consumption was recorded using the Oxygraph-2k high-resolution respirometer (Oroboros Instruments, Innsbruck, Austria). To measure ATP production we used the magnesium-sensitive fluorescent probe (Magnesium Green) to estimate changes in the concentration of free magnesium [11]. ATP production is calculated from the rate of change in [Mg^{2+}] and is based on the differential affinities of ATP and ADP for Mg^{2+} [12]. Oxygen and magnesium green fluorescence signals were detected simultaneously using two respirometry chambers equipped with fluorescent sensors and recorded using DatLab software (Oroboros Instruments, Innsbruck Austria).

A sequential substrate/inhibitor protocol as in [10] was run simultaneously for each fish. Figure S3 displays representative traces of oxygen flux and magnesium fluorescence in homogenized (a) liver and (b) muscle. The rate of oxygen consumption to support ATP production was assessed by adding a saturating concentration of ADP (2 mM, Mg^{2+} free) to the chamber containing complex I substrates (5 mM pyruvate and 0.5 mM malate) and complex II substrate (10 mM succinate). The raw rate of ATP production was also measured in this condition. The rate of ATP hydrolysis was then measured after inhibition of mitochondrial ATP synthesis (with 4 µM carboxyatractyloside). The rate of ATP hydrolysis was then added to the raw rate of ATP production to obtain the corrected rate of ATP production. Addition of complex I inhibitor (0.5 µM rotenone) and complex III inhibitor (2.5 µM

Antimycin A) allowed determination of residual oxygen consumption, which was then subtracted from all other oxygen consumption values. Finally, cytochrome c oxidase (COX) respiration, a measure of the mitochondrial density of the tissues [13], was measured by adding ascorbate (8 mM) and N,N,N',N'-Tetramethyl-p-phenylenediamine dihydrochloride (0.5 mM).

The muscle trial was identical to the liver trial but an inhibitor of adenylate kinase (25 µM P^1,P^5-di(adenosine-5') pentaphosphate) was added to the measurement chamber with the subsample of muscle that was kept on ice (Figure S3b). The final concentration for muscle homogenate was higher (mean ± SE: 18.53 ± 1.03 mg wet muscle mL^{-1}) since the oxidation and phosphorylation fluxes were smaller. The titration protocol of the muscle was completed within 4 h of the fish being culled. Each fish's liver and muscle were run in the same measurement chamber. Every second day, the measurement chamber associated to a treatment group was reversed to control for any inter-respirometry chamber difference in readings. No effect of the choice of measurement chamber on mitochondrial properties was detected.

Sample sizes for statistical analyses

The data from a muscle mitochondrial assay for one fish were excluded from the experiment because the addition of ADP led to a very small elevation in the respiration rate, indicating that either the mitochondrial preparation might have failed or this fish was not "healthy". This fish ate its entire ration during the growth trials but lost body mass. The pattern of results of the analyses of growth performance were the same whether or not this individual was included in the models, so models including data from this fish (excluding those for its muscle mitochondrial properties) are reported in the text. The data from the muscle ATP/O ratio assay for three fish were excluded because the fluxes of ATP production were too low to be detected. The data on the fractional rate of protein synthesis in the liver and in the muscle from three and one fish, respectively, were also removed or missing for the following reasons: extremely high values for the enrichment of phenylalanine in the free amino acid pool (in the muscle of one fish and liver of another) indicated that the tissues had likely been contaminated during sampling, one liver sample for the Ks assay was lost, and the D_5-Phe enrichment of the protein pool value in the liver of one fish was extremely high, indicating a potential error during the extraction steps. Thus, differences in the sample sizes between analyses reflect missing values (Table S1).

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Table S1. Statistics of indices of growth performance, mitochondrial properties (ATP/O ratio and cytochrome *c* oxidase [COX] activity), and fractional rate of protein synthesis (Ks) in brown trout fed different rations. Linear mixed models were used to determine the effect of food intake (high or low) on growth performance, mitochondrial properties of the liver and/or muscle and the fractional rate of protein synthesis. Processing batch was included as a random effect to control for the order in which fish were processed.

	Low Food Intake				**High Food Intake**				**Statistics**		
	N	Min.	Max.	Mean ± SE	N	Min.	Max.	Mean ± SE	*F*	d.f.	*P*
Growth Performance											
Specific Growth Rate (% day^{-1})	30	-0.06	1.02	0.63 ± 0.04	29	1.01	2.70	1.83 ± 0.08	237	1,29	< 0.001
Growth Efficiency (gain in body mass per mass food intake)	30	-0.13	2.23	1.39 ± 0.09	29	0.73	2.16	1.47 ± 0.07	29.0	1, 29	0.422
Specific Protein Gain (% day^{-1})	30	-0.47	1.28	0.79 ± 0.08	29	-0.20	2.94	1.79 ± 0.14	54.2	1, 29	< 0.001
Mitochondrial density											
Liver COX activity (pmol O_2 s^{-1} mg^{-1} wet weight of tissue)	30	23.55	37.95	31.13 ± 0.70	29	20.31	35.32	28.01 ± 0.68	19.6	1, 29	< 0.001
Muscle COX activity (pmol O_2 s^{-1} mg^{-1} wet weight of tissue)	29	10.83	19.68	14.03 ± 0.37	29	9.47	19.20	14.36 ± 0.41	0.43	1, 29	0.519
Mitochondrial Efficiency											
Liver ATP/O ratio	30	0.78	1.41	1.04 ± 0.03	29	0.87	1.45	1.10 ± 0.03	2.50	1, 57	0.119
Muscle ATP/O ratio	26	0.48	3.62	1.60 ± 0.16	29	0.05	3.53	1.36 ± 0.16	1.02	1,53	0.318
Fractional rate of Protein Synthesis											
Liver Ks (% day^{-1})	29	2.84	13.44	7.79 ± 0.37	27	3.27	11.00	6.98 ± 0.42	3.09	1, 28	0.090
Muscle Ks (% day^{-1})	30	0.62	1.65	0.97 ± 0.04	28	0.65	1.69	1.06 ± 0.05	4.03	1, 28	0.055

Table S2. Coefficients of the correlations between physiological traits of the liver and of the white muscle from the same fish. Measured traits were mitochondrial efficiency (ATP/O ratio), mitochondrial density (measured as cytochrome *c* oxidase (COX) activity) and fractional protein synthesis rate (Ks); n = 55 fish for ATP/O ratio, n = 58 fish for COX activity and n = 55 fish for Ks.

	Pearson's *r*	***p***
ATP/O ratio	-0.093	0.499
COX activity	-0.005	0.972
Ks	0.090	0.514

Figure S1. The relationships between whole-body protein content as determined by protein extraction and measurement of whole-body wet mass, for juvenile brown trout maintained on different food rations (Low, Intermediate and High). N = 9 fish per food level.

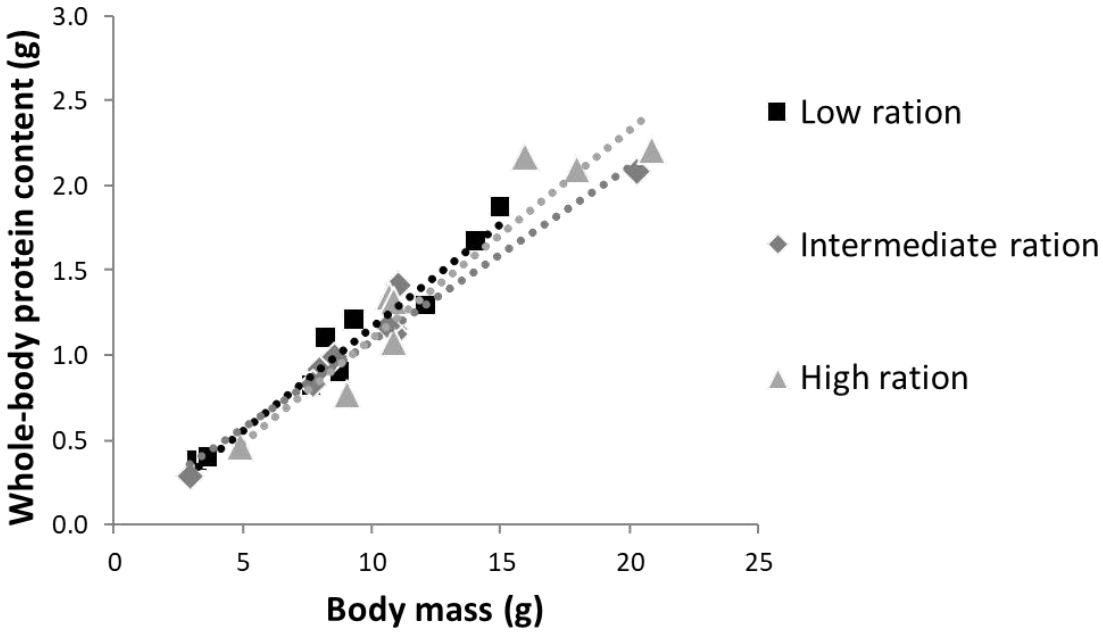

Figure S2. Specific enrichment of the free D_5-phenylalanine pool (squares) and protein D_5-phenylalanine pool (circles) of liver (a) and white muscle (b) in relation to time after injection of the tracer in brown trout (mean ± SE, n = 5).

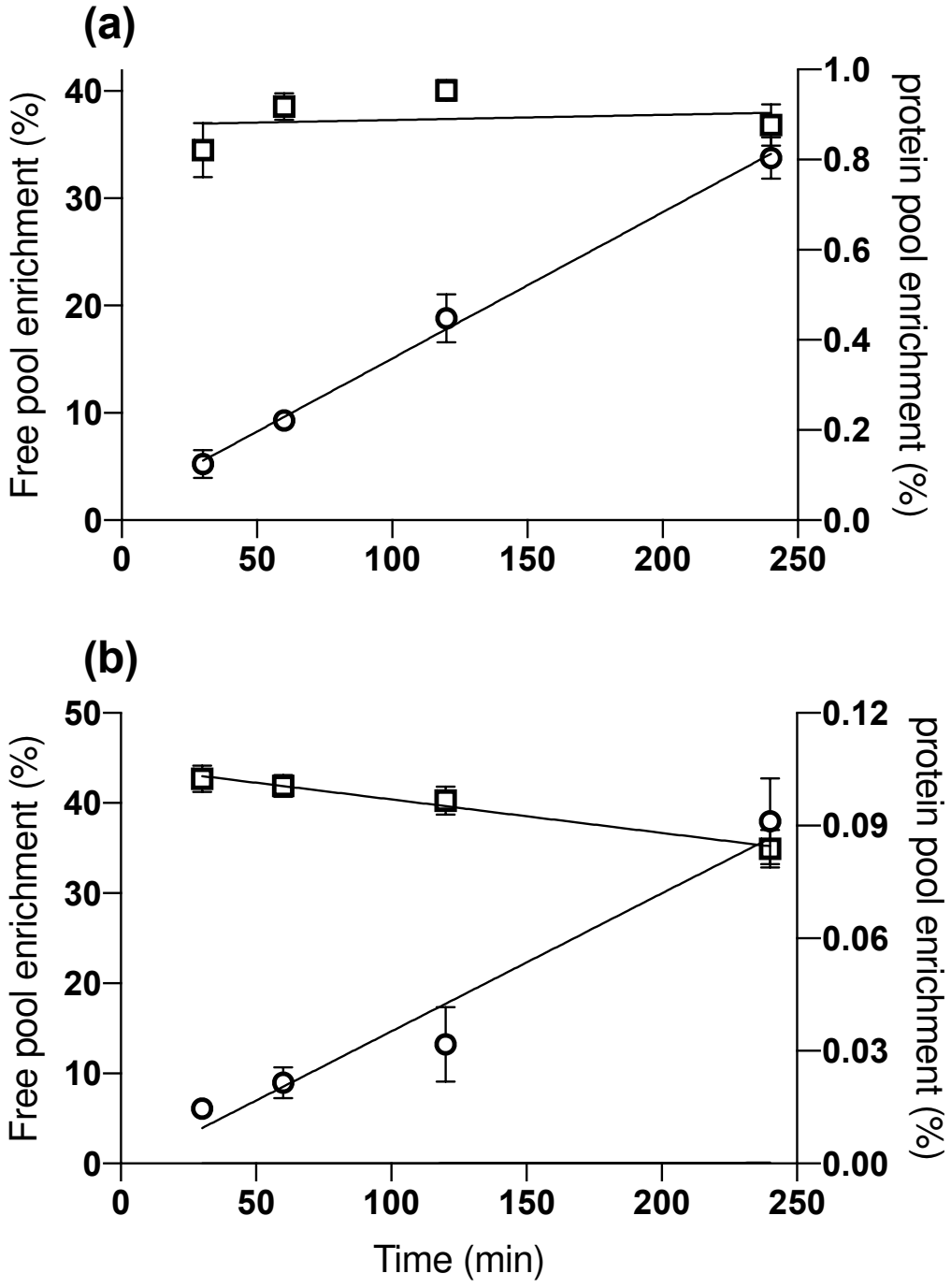

Figure S3. Output from a representative experiment, using homogenized brown (a) trout liver and (b) muscle, showing changes in magnesium green (MgG) fluorescence (black line) and oxygen concentration (blue line). See section "Measurement of mitochondrial properties" for details. An inhibitor of adenylate kinase, P^1,P^5-di(adenosine-5') pentaphosphate, was added to the measurement chamber with the homogenate of muscle. Arrows show sequential titrations of pyruvate malate (Pyr/Mal), succinate (Succ), MgG, EDTA, EGTA, $MgCl_2$, ADP, carboxyatractyloside (cATR), Antimycine and Rotenone (Ant/Rot) and ascorbate and N,N,N',N'-Tetramethyl-p-phenylenediamine dihydrochloride (Asc/TMPD).