1	Improving feed efficiency in fish by selective breeding: a review
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ABSTRACT

Improving feed efficiency (FE) is key to reducing production costs in aquaculture and to achieving sustainability for the aquaculture industry. Feed costs account for 30 to 70 % of total production costs in aquaculture much work has been done on nutritional and husbandry approaches to improve FE but only a limited amount of research has been devoted to using genetics, despite its potential. This paper reviews past work to improve FE in fish by selective breeding and assess future directions. Direct selection on FE traits requires methods to measure individual feed consumption and estimate FE efficiently and accurately. This is particularly difficult to do in fish because of the environment in which they live. Many of the published studies on FE were found to be inaccurate because of methodological problems. The relatively low heritability estimates of FE traits in fish published to date are probably partly as a result of inaccurate measurements of feed intake. Improving ways to measure the individual feed intake with high accuracy will be critical to the successful application of genetics to improving FE. Indirect selection criteria that could be used to improve FE (including growth after starvation/refeeding, body composition, neuropeptides or hormone levels) are discussed. Promising approaches to measuring feed intake accurately that may enable these studies to be undertaken are identified. More work using these will be needed prior to assessing the practicality of the introduction of direct or indirect traits for FE in fish genetic improvement programs.

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Keywords: feed efficiency, genetics, selection, feed conversion ratio, feed intake, fish

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1. Introduction

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With an increasing world population predicted to attain 9.6 billion in 2050, the sustainable 51 increase of food supply, and more specifically animal protein production, is a key challenge. 52 53 Animals not only need to become more productive but, more importantly, they also need to become more efficient. Farmed fish species offer an opportunity in that regard. Compared to 54 farmed terrestrial species, farmed fish are more efficient in converting feed to biomass (Table 55 1) using feed amount as the reference. Feed compositions differ significantly amongst 56 different animals; in terms of protein rates, fish diets contain around 35% protein compared to 57 58 around 18-20 % in pigs or chickens. Total fish harvested has grown 2.87 % per year since 1950, essentially through increased 59 farmed fish production (1.93 % per year; Earth Policy Institute 2013). In 2014, global 60 aquaculture production (excluding algae and plants) was estimated at 74 million tons, roughly 61 similar to the global production of beef cattle. At the same time, farmed fish species consume 62 around six times less feed than beef cattle to produce the same volume of body mass (Table 63 64 1). Despite the higher efficiency compared to livestock species, the cost of feed - ranging from 30 to 70% of the total production costs - is the primary expenditure of intensive fish 65 farming systems (Doupé and Limbery 2004; Kolstad et al. 2004). Improving feed efficiency 66 67 (FE) is therefore key to reducing production costs. In salmon for example, a 2 - 5 % improvement in FE would save 42.9 - 107 million USD feed costs per year, respectively 68 (following Table 1 and with a feed price of 1.35 USD.kg⁻¹). 69 Improving FE would also have a positive effect on the environmental impact of fish farming. 70 71 Whatever the species, a FE improvement will result in a reduction of emissions (Pym 1990; Pinares-Patino et al. 2003; Zhang and Aggrey 2003; Hill and Azain 2009; de Verdal et al. 72 2011a, Besson et al. 2016). For example, Bouvarel et al. (2006) showed that a 4.8% 73

improvement of FE in broiler chicken reduced nitrogen and phosphorus excretions by 9 and 74 75 14%, respectively. In aquaculture production, several life cycle assessment (LCA) studies (Aubin et al. 2009; Samuel-Fitwi et al. 2012; Mungkung et al. 2013) have investigated the 76 77 major environmental impacts of improving FE. These studies showed that improving FE will have less negative impact on eutrophication, acidification, climate change and energy demand 78 per ton of fish produced, mainly as a results of reduced nitrogen excretion of fish (Aubin et al. 79 80 2009; Besson et al. 2016). In terrestrial species, selective breeding has played an important role in improving feed 81 efficiency (Table 2). Since 1960 feed efficiency has increased by ~20 to 30% (broilers, laying 82 hens and pigs respectively). Most of this gain is due to selection, next to improved 83 management practices and feed formulation. Several studies have estimated genetic 84 parameters for FE traits in livestock (reviewed by Hoque and Suzuki 2009; Grima 2010; 85 86 Willems et al. 2013) and found moderate to high heritabilities, ranging from 0.12 to 0.67. However, direct selection for feed efficiency remains difficult, as it requires the precise 87 recording of individual feed intake. In terrestrial livestock, it is widely recognized that much 88 of the historical gain on FE has been obtained indirectly through selection for growth rate 89 (Emmerson, 1997). 90 91 In fish, measuring FE implies measuring feed intake, which is highly complex since fish are generally reared in water and in large groups. In such conditions, it is impossible to measure 92 individual feed consumption and collect uneaten food. Furthermore, according to the species, 93 social interactions between fish may modify FE (see section 3), which could lead to large 94 95 differences between measurements performed on isolated fish and measurements obtained in group rearing conditions. As a consequence, most past efforts aimed at improving FE in 96 97 aquaculture have focused on feed formulation (Reigh and Ellis 1992; Nematipour and Gatlin III 1993; Elangovan and Shim 2000; Gaylor and Gatlin III 2001; Lin et al. 2008; Tacchi et al. 98

2011; Guroy *et al.* 2013; Yao *et al.* 2014) and/or husbandry (Alanärä 1996; Bendiksen *et al.* 2003; Imsland *et al.* 2005; Li *et al.* 2008; Magnussen *et al.* 2008; Yilmaz and Arabaci 2010; Arbelaez-Rojas *et al.* 2011; Zhao *et al.* 2013). These studies have shown strong effects of nutrition, diet and husbandry on FE. In contrast, little work has been done on genetics. Any genetic selection approach would need, of course, to pay specific attention to the feeds used and the age/size of the fish as key aspects of the environment / selection subject that could influence the genetic outcome.

The objective of the present paper is therefore to review the possibilities to improve FE in fish by selective breeding. In the first part, we will explore the concept of FE and how it can be measured. In the second part, we review the different ways to measure feed intake in fish, while in the third part, we focus on the possibilities to directly select for feed intake or FE. Finally, in the last part, we outline various possibilities to use indirect selection criteria to improve FE, based on growth and bio-energetics models.

2. What is feed efficiency and what are the parameters used to measure it?

Improving feed efficiency means reducing feed consumption per kg of fish produced, or increasing fish production from the same amount of feed. It is important to note that FE will vary from one species to another, with rearing environment (i.e. temperature, salinity, pH and feed composition, Árnasson *et al.* 2009) and the developmental stage of the fish (Henryon et al. 2002; Árnasson *et al.* 2009). One major aspect determining FE is the level of feed intake (FI): FE tends to improve up to an optimum when FI increases, and then decreases until maximum FI is reached (Jobling, 1994). If for some reason FI is less than optimal, increasing FI will increase FE. Conversely, if FI is higher than the optimum, increasing FI will decrease FE.

A second major point is the relation of FE to fish size, with smaller fish generally having a better FE than larger fish (Andersen and Riis-Vestergaard, 2003). FE is related to metabolic rate which is function of fish size. To correct for size differences, weights are scaled to metabolic weights (kg^{0.8}, Clarke and Johnstone, 1999; Jobling, 2002). While improving FE is the general objective, we need to define ways to measure it. The most used measure of FE is the ratio of FI to body weight gain (BWG), and is named feed conversion ratio (FCR). However, its inverse (feed efficiency ratio, FER = BWG.FI⁻¹) measures the same trait. Improving feed efficiency thus means reducing FCR or increasing FER. In these two measurements of FE, the part of FI allocated for body maintenance is not distinguished from the part of FI dedicated to growth (Willems *et al.* 2013). Another way to measure FE is thus to estimate the residual feed intake (RFI).

The equation for calculating RFI in a phenotypic approach is given as:

$$FI = \beta_0 + \beta_1 * MBW + \beta_2 * BWG + RFI$$

with FI being the feed intake, β_0 the regression intercept, β_1 the partial regression coefficient of animal's FI on metabolic body weight, MBW the average metabolic body weight during the experiment, β_2 the partial regression coefficient of animal's FI on body weight gain, BWG the body weight gain, and RFI the residual error of the model. This model allocates the feed intake according to expected maintenance and growth requirements, the remaining part being defined as the residual feed intake.

RFI is phenotypically independent from growth rate (Koch *et al.* 1963; Kennedy *et al.* 1993; Doupé and Limbery 2004; Crew Jr. 2005), which is not the case for FCR or FER ratios (Arthur *et al.* 2001; Martins *et al.* 2011). Used for the first time by Koch *et al.* (1963) on beef cattle, RFI is defined as the difference between feed consumed by an animal and its predicted consumption estimated by a regression model taking into account the feed requirements for

maintenance and growth as independent variables (Kennedy *et al.* 1993; Doupé and Limbery 2003; Martins *et al.* 2011). Individuals with positive RFI consume more than the average whereas animals with negative RFI consume less, suggesting the latter are more efficient. RFI has been widely investigated in terrestrial animals (i.e. pigs, cattle, hens, chicken), and genetic parameter estimates are generally moderate to high with heritabilities ranging from 0.10 to 0.47 (Johnson *et al.* 1999; Arthur *et al.* 2001; Gilbert *et al.* 2007; de Verdal *et al.* 2011b; Do *et al.* 2013; Wolc *et al.* 2013).

The main issue about RFI estimation is the difficulty of modeling it in the correct parameters. A lot of different models could be implemented depending on whether nutritional composition of the feed, coefficient of digestive utilization of metabolizable energy, protein, lipid or starch, or body composition of the fish is considered. Equations developed on livestock species, where selection schemes had already been developed using RFI, show that even more traits could be included (Luiting and Urff 1991; Arthur *et al.* 2001; Robinson and Oddy 2001; Hoque and Suzuki 2009; Willems *et al.* 2013). As an example, in laying hens, the RFI model takes into account the egg weight to correct RFI by the energy used to produce eggs (Luiting and Urff 1991). The same approach is used in dairy cattle for milk production (Kennedy *et al.* 1993; Connor *et al.* 2013). In this context, the model used is as follows:

$$y = \beta_0 + \beta_1 * MBW + \beta_2 * BWG + \beta_3 * PW + RFI$$

with β_3 being the partial regression coefficient of animal's FI on production weight and PW the production weight (egg or milk production for example). This type of model could be interesting to use in fish, for example to correct for visceral and/or intramuscular lipid content.

An important question in terms of selective breeding for feed efficiency is the choice of the trait(s) to include in the index. As FCR and FER are ratios, they are genetically correlated

with the two terms of the ratio, BWG and FI, and so genetic change of FCR or FER cannot be simply related to underlying genetic variation for growth, feed consumption, or both (Turner 1959; Sutherland 1965). As a consequence, selecting directly on FCR or FER will lead to poor selection response (Gunsett 1984; Lin 1980) and does not enable an accurate prediction of genetic gain (Gunsett 1987). However, linear indexes combining body weight gain and FI can be designed which have optimal properties in terms of accuracy and achieved genetic gain (Turner 1959; Lin 1980; Gunsett 1984, 1987; Lin and Aggrey 2013). Alternatively, residual feed intake can also be used as the selection criterion, especially in multiple trait selection combining RFI and growth (Kennedy et al. 1993). When used in single trait models, RFI should be based on genotypic and not phenotypic regression of feed intake on production, to avoid a component linked to the genetic variation for one or more elements of production (Kennedy et al. 1993). In any case, in order to develop a selective breeding program to improve feed efficiency characteristics, it is important to have individual data of the trait under selection. Whatever the trait used to calculate FE, the crucial issue is to measure both growth and FI. Whilst

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3. How to measure FI for selective breeding in fish?

The simplest way to measure FI in fish is to rear fish in a group and to calculate the FE of the group. Using separately reared full sib families, it is possible to estimate the genetic variability of the trait (Henryon *et al.* 2002) and then do between-family selection.

growth and growth rate are easily measurable, measuring FI of individual fish is much more

A frequently proposed way to measure FI is the use of automatic or self-feeders on family groups, with recovery of the feed waste to calculate the feed consumption of the aquarium or the tank (Helland et al. 1996; Aknes et al. 1997; Lemieux et al. 1999; Thodesen et al. 2001; Mambrini et al. 2004a; Li et al. 2005a; Albrektsen et al. 2006; Aknes et al. 2006). The main advantage of this technique is that it enables the estimation of the family FI, and the genetic variation between families (Kolstad *et al.* 2004). However, this technique is also widely criticized. First, it leaves unexplored the intra-familial variations for the trait considered, resulting in overestimated heritabilities (Doupé and Limbery 2004, Kause et al 2006a). Consequently, this type of selection will be less efficient than selection that also acts on the within-family component. A way of by-passing the problem is the use of self-feeders with registration of the triggering individual and the quantity of feed delivered. However, in practice only some of the fish will activate the self-feeder while the other fish eat the feed they find in the tank, so this method would be a measurement of the feeding motivation/behavior rather than a real measurement of individual FI (Brännäs and Alanärä 1993; Millot and Bégout 2009). Moreover, the feeding system itself could be responsible for bias in FE estimation. Individual fish that are fed using self-feeders or with automatic feeders do not grow with the same rate. Mambrini et al. (2004a) showed that brown trout (Salmo trutta) fed with self-feeders grew faster and showed an improved FE compared to trout fed in excess with automatic feeders. Very careful manual feeding to avoid loss of feed is also difficult to manage. There is a large effect of the "feeder" and, consequently, a low repeatability of the measurement (de Verdal, pers. comm.). An alternative method in fish to measure FI of "genetic individuals" reared in groups could be the use of clonal lines, as shown by Grima et al. (2008) for rainbow trout. In fish, isogenic clonal lines are obtained by pair mating unrelated homozygous gynogenetic or androgenetic

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parents (Komen and Thorgaard 2007, Quillet et al. 2007). In such lines, all individuals are strictly genetically identical but heterozygous and exhibit performance in the range of those of conventional trout. Isogenic lines are an exceptional tool that allows the measurement of the genetic variability of traits showing a high environmental variability, as is the case for FE traits. However, clonal lines can only be used for experimental purposes and consequently, results are not representative of production conditions, nor can they be used in the implementation of a breeding program. Another way to estimate individual FI is by rearing animals separately in aquaria. This type of rearing requires large number of aquaria and confounds the environmental effect of aquarium with the phenotype of the individual evaluated. More importantly, as stated before, it does not take into account the social interactions and feeding ranks between fish, which may have a significant impact on FI and FE. In sunfish, Hayward et al. (2000) showed that group rearing reduces both growth rate and FI probably due to competitive social interactions, which has a negative impact on FE. McComish (1971) estimated a reduction of more than 50 % for FI and around 30 % for growth when bluegill are reared in group rather than in isolation, in aquaria with an ad libitum feeding regime. In rainbow trout, Silverstein (2006) demonstrated a moderate phenotypic correlation ($r_p = 0.66$) between FE estimated in fish held individually or in a social group, the latter showing greater RFI than isolated fish, in agreement with studies from Hayward et al. (2000) and McComish (1971). Therefore, according to fish species and their degree of social interactions, the FI measured in isolation will differ from measurements taken in groups. This implies that it is necessary to consider behavioral aspects and the impacts it can have on performance traits. Since rearing isolated fish can have an impact on the estimation of FI, it would be more accurate if FI could be measured on individuals that are kept in groups. Several methods and techniques have been developed to measure individual FI on fish held in groups (Jobling et al.

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2001). The simplest method is to analyse the stomach content of each fish obtained by 243 dissection (Bromley 1994; Cortés 1997; Rindorf and Lewy 2004). However this method is 244 limited to the evaluation of a single meal; it is not suited to follow the feed consumption over 245 time. 246 Another method, much used in the past, is the use of chemical markers integrated in the feed 247 (Walsh et al. 1987; Morris et al. 1990; Johnston et al. 1994; Unprasert et al. 1999). 248 249 Essentially used to study the digestive process and the gastro-intestinal transit time, it requires 250 measuring the quantity of a marker in the feces, which is only possible if feces can be collected individually, or when done directly in the gastro-intestinal tract, which involves 251 252 sacrificing the fish before analyses or at least handling and anaesthetizing it. A third method is X-radiography of eaten meals, using X-ray dense markers (generally radio-253 opaque ballotini glass beads) included in pellets (Talbot and Higgins 1983; McCarthy et al. 254 255 1993; Silverstein et al. 2001; Jobling et al. 2001; Boujard et al. 2006; Kause et al. 2006a; Quinton et al. 2007a, b; Grima et al. 2008). Just after feeding this labeled feed, fish are 256 257 anaesthetized and the number of radio-opaque beads in the gastro-intestinal tract is counted on an individual radiography of each fish, allowing the estimate of FI of each fish. This 258 technique is highly accurate for one meal but has the disadvantage that it allows only 259 260 measuring the FI of one meal at each time, since recovery can take days or weeks before a new measurement can be performed. Furthermore, it seems that some fish can distinguish 261 feed with and without radio-opaque beads, which can modify their feeding behavior and their 262 ingestion (Chatain, pers. comm.). This method is therefore not suited for measuring FI for a 263 long period or for species that show high day-to-day variability in FI as this causes a low 264 repeatability of the measurements (r=0.09 to 0.32, Kause et al. 2006a, Grima et al. 2008). 265 Kause et al. (2006a) estimated that at least three FI measurements were needed to ensure a 266 good estimation of the average FI, while 4 to 6 measurements were better. 267

The last method consists in direct observation or video recording of individual daily feed intake (Adams *et al.* 1995; Tuene and Nordvedt 1995; Smith *et al.* 1995; Hughes and Kelly 1996; Damsgard and Ugedal 1997; Ang and Petrell 1997; Baras *et al.* 2012; de Verdal *et al.* 2016). Feed consumption can be measured for each fish by counting the number of eaten pellets during a given time span. Video registration of feed consumption for a specific period (potentially a few consecutive days) is possible without disturbing the fish, but much time is required to observe the fish or to analyze the video recordings. Duration of the observation is variable according to the fish species ranging from some minutes to several hours. Whatever the duration, it should be done at the same time every day, since the feeding response and behavior may change over the day (Toguyeni *et al.* 1996). Furthermore, the need for external tagging and individual tracking of each individual limits the group size to 10-20 fish. Such sizes are not representative of farm rearing conditions.

It can be concluded that all methods described above have their shortcomings and that there is still a need for more accurate and tractable methods to help us measure individual variation in FI and FE. However, in the absence of any better techniques, the methods above have been used to estimate genetic parameters of FI and FE in different species. The results of these experiments will be reviewed in the next section.

4. What is the variability of FE and can we select for FE directly?

As noted before, there are two levels at which genetic variation in FE can be estimated. The first one is to rear fish in full sib families, to measure the family mean FI and estimate the existence of genetic variability between these families (Thodesen *et al.* 2001; Henryon *et al.* 2002; Kolstad *et al.* 2004). The second one is to measure individually each fish and estimate

the heritability of the trait considered (Silverstein et al. 2001; Kause et al. 2006a, b; Quinton et al. 2007a, b; Grima et al. 2008). The heritability is a genetic criteria estimating the amount of variation in a phenotypic trait in a population explained by the genetic variation among individuals in this specific population. It can be expressed as a ratio of genetic variance over phenotypic variance (broad sense heritability) or more commonly additive genetic variance over phenotypic variance (narrow sense heritability). Using family as the measurement unit, it can be concluded that while FE traits do show some genetic variation (Thodesen et al. 2001; Kolstad et al. 2004), they present a low coefficient of variation; ranging from 4.0 to 13.9 % (Henryon et al. 2002). Many studies have used the Xray method to estimate individual FI and heritabilities of FI or FE (FER or FCR). Whatever the species and the experimental procedure, estimation of heritability of FE is always low (ranging from 0 to 0.07) while those of FI are low to moderate ranging from 0.07 to 0.23 (Kause et al. 2006b in rainbow trout Oncorhynchus mykiss; Quinton et al. 2007a, b in European whitefish *Coregonus lavaretus*). The only exception is the study of Silverstein *et al.* (2001) who estimated heritabilities of FI of channel catfish *Ictalurus punctatus* to be 0.37±0.15. The most likely reasons to explain this high value compared to other studies are i) that the authors performed their experiment with only one meal (without any repetition) and with only 290 fish, which implies a limited accuracy of the FI measurement, and ii) the fullsib genetic design confounds the environmental common effects with the additive genetic variance, which tends to increase heritability estimates. In fish, the only study using RFI to estimate genetic variability of FE was performed on rainbow trout clonal lines using the X-ray methodology (Grima et al. 2008). These authors showed substantial genetic variability among individual genotypes ($h^2 = 0.23$). According to Quinton et al. (2007a), the generally observed low heritability could be explained by the fact that fish are poikilotherms. Energy intake (by the feed) is used for

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growth, maintenance or physical activities. The relative share of maintenance requirement is much lower in fish. For example white grouper (*Epinephelus aeneus*), European sea bass (Dicentrarchus labrax) and gilthead seabream (Sparus aurata) use 34.05, 45.38 and 47.89 kJ of digested energy (DE) kg^{-0.80} day⁻¹ respectively which is less than terrestrial animals (e.g. 459.8 kJ of DE kg^{-0.75} day⁻¹ in pigs; Martins et al. 2011). There is a possibility that maintenance requirement variability, being relatively lower in fish than in terrestrial animals, results in a lower variability of FE, as hypothesized by Gjedrem (1983). Another reason that could explain these low heritability estimates is that measurements were performed during the exponential growth phase where most of the feed is used for growth (Quinton et al. 2007a). Finally, the low repeatability of the X-ray method itself (range from 0.09 to 0.32) sets an upper bound for heritability estimates which are consequently also low (Falconer and Mackay, 1996). It is important to keep in mind that all estimations of FE traits in fish were done at specific ages, and it is consequently not possible to generalize these results for the global rearing period. Regarding the age effect, it is known that FE decreases with the age of the fish. Studying rainbow trout families and using family measurements of FI, Henryon et al. (2002) estimated a higher FER (1.09) during the final period of measurement (i.e. days 186 to 215) compared to the first phase of measurement (1.68, i.e. days 52 to 76). From these studies, it can be concluded that direct measurement of FE is difficult and results in low estimates of heritability, often with high standard errors. The main reason seems to be the low repeatability of the methods used to measure FI. Furthermore, none of methods reviewed here, are suitable for large scale phenotyping as required for selective breeding. Consequently, finding traits highly correlated with FI and FE that could be used as indirect

criteria for selection could be a better option for selective breeding for FE in fish.

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5. Which indirect criteria could be used to estimate and improve FE?

Different categories of traits have been proposed to account for variations in FE, the major two categories being traits derived from growth models and traits derived from bio-energetic models.

5.1. Growth model traits

5.1.1. Growth models

- The most widely selected trait in aquaculture is growth rate. Growth can be defined in different ways (Dumas *et al.* 2010; Jobling 2003):
- 351 1) body weight gain (BWG), which is the difference in two body weight measurements 352 taken at time t and t+ Δt : $BWG = BW_2 - BW_1$,
 - 2) the specific growth rate (SGR), which is BWG expressed at a logarithmic scale to reduce the heterogeneity of variance between two body weight measurements, taken at different ages, and divided by the time between the two measurements t and $t+\Delta t$:

$$SGR = (lnBW_2 - lnBW_1)/\Delta t * 100$$

3) the daily growth coefficient (DGC), which uses the cubic relation between BW and length to make growth rate linear over time:

$$DGC = 100 * ((BW_2^{(1/3)} - BW_1^{(1/3)})/\Delta t$$

4) the thermal growth coefficient (TGC), which is the same as DGC but now corrected for the water temperature of the rearing environment during the measurement period:

$$TGC = (BW_2^{(1/3)} - BW_1^{(1/3)})/(T * \Delta t) * 100$$

5.1.2 Correlations of growth with FE

In livestock species, it is generally admitted that FE is correlated with growth rate, but in fish, this is still debatable. Estimations of phenotypic and genetic correlations between growth traits and FE traits are summarized in Table 3. At the phenotypic level and using X-ray method, Thodesen et al. (1999, 2001) and Kolstad et al. (2004) reported positive correlations, ranging from 0.60 to 0.90, between growth rate (expressed as TGC and BWG, respectively) and FE (expressed as FER) in Atlantic salmon Salmo salar. Using video analyses to record feed intake, de Verdal et al. (2016) found high phenotypic correlation between growth rate (expressed as BWG) and FCR (of 0.62±0.06) in Nile tilapia Oreochromis niloticus, which was in the same range as that estimated in Atlantic salmon. The results from tilapia agree with those of Thodesen et al. (1999) who compared wild Atlantic salmon with a selected strain and concluded that an improvement of growth rate of around 10 % could result in a 4.6 % improvement in FER by one generation of selection. The authors explained this high potential impact of selection for growth on FER by the fact that it could be associated with a reduction of the energy costs per unit of gain, and consequently, an increase of metabolizable energy available for gain rather than for maintenance requirements. However this explanation is questionable since the energy needed for maintenance requirement in fish is low. Ogata et al. (2002) compared Japanese flounder selected on growth rate for two generations with wild individuals and concluded that the selected line had higher growth rate and FI, as well as a better FE after correction for a phenotypic effect of body size. In both studies (Thodesen et al. 1999; Ogata et al. 2002) selected fish were compared with wild-caught fish. Therefore, the selected and wild groups differed not only for selection for growth, but also for domestication state, which could bias the results as wild fish are expected to show poor growth and high FCR in captivity (Millot et al. 2010, 2011). The difference for FE or FI

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between selected and wild fish could therefore be due to domestication, selection, or a 389 390 combination of both. In another study on amago salmon (Oncorhynchus masou), fish selected for improved growth 391 on a low fishmeal diet were compared to controls, both on a fishmeal and on a low fishmeal 392 diet (Yamamoto et al., 2015). The selected fish had a better FER than the controls, especially 393 394 on the low fishmeal diet (0.98 vs. 0.84). This seems to be due to a strong increase in feed intake in the selected fish fed the low fishmeal diet (2.01 vs 1.71 % BW.d⁻¹) whereas control 395 and selected fish had the same feed intake when fed the fishmeal diet. In such a case, it is 396 likely that the increase in FE is linked to the fact that control fish have a suboptimal feed 397 398 intake level when fed a low fishmeal diet, thus increasing the relative cost of maintenance. This also highlights that the type of feed used may have a high impact on the components of 399 400 the genetic response (growth and feed intake). 401 The general conclusion of a number of studies comparing FI and FE on brown trout selected for growth with fish from a control line (Sanchez et al. 2001; Mambrini et al. 2004a, b; 402 403 Mambrini et al. 2006; Boujard et al. 2006), is that the improvement of growth is only explained by the increase of feed consumption in selected fish, and that FE is not affected. 404 This lack of response in FE could be explained when we assume that faster growing fish will 405 406 most likely be those that feed more, and these are not necessarily the ones that are also more efficient. This effect is likely to be more pronounced in situations where fish are fed ad 407 libitum with automated feeders. As discussed earlier, fish fed with automated feeders can 408 have lower FE than fish fed with self-feeders. This theory is supported by phenotypic 409 410 observations on responses to six generations of selection on growth and FCR in Nile tilapia. In this selection experiment, growth rate, expressed as DGC increased from 2.29 to 4.46 while 411 412 FCR remained constant at 1.3-1.4 across generations (Komen, personal comm.). In this experiment, fish were fed with automated feeders, and feeding rate was adjusted each 413

generation to accommodate the higher growth rate as a result of selection. Consequently, 414 415 using ad libitum feed ration, selected fish would be fish that are faster growing and feed less, but also fish that are faster growing because they feed more. 416 Estimates of the *genetic* correlation between FE and growth are scarce in fish. Kause *et al.* 417 (2006b) and Quinton et al. (2007a) found correlations between FI and body weight, ranging 418 419 from 0.72 to 0.90 and from 0.93 to 0.97 in full/half sib families of rainbow trout and European whitefish, respectively. Quinton et al. (2007a) concluded from this high genetic relationship 420 that an indirect selection for FE combining selection for high growth and low FI would be at 421 least twice as efficient as selection for growth only. 422 Henryon et al. (2002) also estimated the genetic correlations between FE (expressed as FER) 423 and growth (expressed as body weight at a given age) in full-sib families of rainbow trout. 424 425 The genetic correlations estimated for seven successive periods of growth between 52 and 215 days of age, and for the cumulative periods, were found ranging from 0.63 to 0.99, with an 426 average of 0.87 for the cumulative rearing period. The moderate to high genetic correlations 427 between FER and BW indicate that these two traits share some genetic control. However, it is 428 important to note that in this study, fish were fed with a restricted amount of feed. Due to this 429 430 restricted feeding regime, FER and growth were congruent (fish who grew faster are those showing higher FER), there was less variation for voluntary feed intake, and consequently 431 estimates of the genetic correlation between FER and growth traits are high (Henryon et al. 432 2002). 433 434 The results discussed in this section could be summarized as follows: positive correlations between growth and FE were observed when selected fish were compared with wild fish. 435 436 These correlations are likely biased by domestication effects on behavior which makes fish 437 less stressed and better adapted to the farming environment. Phenotypic trends in growth and

FE within selection lines indicate that selection for higher growth rate alone could favor fish which have higher FI but these are not necessarily more efficient – and this may depend on the starting level of FI before selection, and to the type of feed used.

There is the risk of a bias if comparisons are done on small and big fish in the same analyses given the relationship between FE and fish size. However, in nutrition experiments, this bias is usually dealt with by calculating FE on the basis of metabolic FI and growth rate (i.e FI in gr/kg^{0.8} and growth rate in gr/kg^{0.8}). In genetic experiments, fish are compared usually at the same age rather than same weight/size. Indeed, the aim is to estimate the phenotype of a large number of fish and it is impossible in practice to measure the feed intake of each fish individually at the same size even if the experiment is started with fish of similar size. However, from a genetic perspective such experiments should detect those fish that are more efficient. The relationship between efficiency and fish size does mean that FE needs to be measured over a series of size/age classes over the production lifetime of the fish (and on a defined feed) to obtain a practical measure for selection for a given production system.

5.1.3 Growth after starvation and refeeding periods

In order to bypass the issues associated with the measure of FI, some authors have investigated the potential of indirect but tractable criteria linked to growth under specific conditions to predict FE. Grima *et al.* (2008; 2010a) proposed that body weight loss and gain during respectively feed deprivation (FD) and re-feeding (RF) periods could serve as possible proxies of FE (defined as RFI in their work). Figure 1 outlines the general principle of measuring FD and RF. The loss of weight during FD is assumed to be correlated to the maintenance requirement of the fish (Lupatsch *et al.* 2003; Grima *et al.* 2008). The RF period is also known as a compensatory growth period, where an unusually rapid growth follows a period of starvation (Xie *et al.* 2001, Ali *et al.* 2003). Russel and Woottom (1992) defined this

period as "the ability of a dietary restricted animal to achieve its normal body weight and form by a growth spurt on re-alimentation". Compensatory growth has been reported in a large range of fish species (Russell and Wootton 1992; Jobling et al. 1994; Nicieza and Metcalfe 1997; Mélard et al. 1997; Boujard et al. 2000; Wang et al. 2000; Gaylor and Gatlin III 2000; Chatakondi and Yant 2001; Barreto et al. 2003). There is large variability in the protocols used to measure the weight loss during FD, with measurements performed on groups or on isolated fish, with different durations of FD period, with repetitive FD periods or not, and with different sizes and ages of fish at the beginning of the experiment (Li et al. 2005b; reviewed in Ali et al. 2003). Using a specific procedure with three weeks of FD followed by three weeks of RF, repeated twice in rainbow trout, Grima et al. (2008) found no significant correlation between RFI and weight loss during FD or growth capacity during RF considered separately. However, combining both traits increased the proportion of variance in RFI explained, and the best criterion to estimate RFI was the combination of all the measurements over the two periods of survey, which explained 60% of RFI variation. More recently, Grima et al. (2010b) observed that European seabass sorted for low weight loss during FD and high compensatory growth during RF exhibited an improvement of RFI when compared to groups sorted for opposite characteristics, but that most of the difference came from the weight loss during FD. However, Daulé et al. (2014) did not find any significant response on FE (FCR or RFI) after one generation of divergent selection of seabass for weight loss during FD only. Several authors showed significant positive correlations between the increase of growth after a FD period and the improvement of FE (Russell and Wootton 1992; Barreto et al. 2008). This was considered to be due to a reduction of the basal metabolic rate of the fish during the FD period which continued for a small period of time after the end of the FD period (Russel and Wootton 1992). However, this hypothesis is questionable since it is known that the

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energy needed for maintenance is low in fish (Gjedrem 1983; Martins *et al.* 2011). Using fish selected for high or low weight loss during starvation, Dupont-Prinet *et al.* (2010) showed no significant difference in standard metabolic rate during fasting. Other authors proposed that compensatory growth is only explained by a hyperphagia without any modification of FE (Hayward *et al.* 2000; Wang *et al.* 2000; Xie *et al.* 2001; Nikki *et al.* 2004).

5.2. Bio-energetic models

An alternative approach to the use of growth models is to look into the bio-energetics of growth to identify traits that could be used for selection on FE (Jobling 1993; Karjalainen et al. 1997; Cho and Bureau 1998). Growth models do not take into account the available and digestible energy and nutrients in the feed, nor the energy and proteins retained by the fish. Both digestibility of nutrients and energy flux can have a large impact on growth and FE of animals.

It is possible to model FI in energetic terms, as described in Figure 2 and in the following equation (Strand 2005):

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$$FI = (E_F + E_N + E_M) + (M_S + M_R + M_A + M_F) + (G_S + G_R)$$

where FI is feed intake; E_F the faeces excretion; E_N the urinary loss and gill excretion; E_M the mucus epidermal cells loss; M_S the basal metabolism; M_R the voluntary activity; M_A the thermal regulation; M_F the heat energy; G_S the somatic growth and G_R the gamete production (Figure 2).

Such a model takes into account all the energetic components from FI to excretion, growth and heat production. The interest here is to be able to estimate the optimal feed consumption and the energy losses with particular attention to different parameters as growth prediction,

estimation of the digestible energy needed, determination of digestible energy in the feed and growth (Cho and Bureau 1998; Kaushik 1998). Using these models could help finding new measurable traits explaining individual FE differences. It could be potentially important to estimate the physical activity of the fish or the thermal regulation which are easier to measure than individual faeces excretion, urinary loss or gill excretion.

Lipid and protein are energetically the most important components of body composition. The ratio between lipid and protein deposition could have an impact on FE (Azevedo *et al.* 1998). In this section, we will discuss lipid deposition and protein turnover rates in the context of the bio-energetic model, and show how they could be used in prediction for FE.

5.2.1. Lipid deposition

It is well established from terrestrial species like poultry or pigs that FE is linked to body fat deposition, with leaner individuals exhibiting increased FE. While protein content is mostly determined by fish size, lipid deposition is highly variable, depending on physiological age and feed composition (Shearer, 1994). Older fish tend to deposit more fat, resulting in lower FE. Because of the lower energy content of proteins (17kJ/g) compared to lipids (37kJ/g), the increased protein deposition and lower fat deposition in leaner animals contributes to the reduction of metabolic cost of tissue. Faure *et al.* (2013) for instance showed that pigs selected for low RFI have lower lipid content than pigs from the divergent high RFI line whatever the body compartment in which the fat was deposited (thinner back fat, less internal fat and lower intra-muscular fat).

Similar relationships between body fat and FE have been recorded in fish. A divergent selection for muscle fat content has been carried out in rainbow trout (Quillet *et al.* 2005). A survey after four generations of selection showed that fish from the lean-muscle selected line

had lower body and muscle lipid contents, and that FCR was improved by about 6-9% compared to the fat-muscle selected line irrespective of the carbohydrate content of the diet (Kamalam et al. 2012). The difference in FE among lines was confirmed and enhanced after seven generations of selection (Quillet, pers. comm.). Similarly, in coho salmon Oncorhynchus kisutch, 16 generations of selection for growth resulted in both higher FE and body leanness than in the unselected parental stock (Neely et al. 2008). In European whitefish Coregonus larvaretus, Quinton et al. (2007b) found no significant phenotypic and genetic correlations between whole-body lipid content and daily FCR. Nevertheless, they calculated that combining selection for reduced lipid content with selection for high BWG, could accelerate indirect FCR improvement compared with selection for BWG only. Similar results were found in rainbow trout (Kause et al. 2016). In contrast with those studies, Grima et al. (2010b) concluded in sea bass that the most efficient individuals should be the ones having the highest muscle fat content. However, in this experiment, the whole body fat content was not measured, and the correlation was observed on fish that had experienced two fastingrefeeding periods a few months before, which may have influenced the results. Altogether, these results indicate that relationships between body lipids and FE in fish deserve further investigations. Traits related to lipid deposition are usually highly heritable (Quillet et al. 2005, 2007; Tobin et al. 2006; Kause et al. 2009). Moreover, it is now possible to estimate lipid content in different body compartments with non-invasive methods. Muscle fat content can be efficiently estimated using apparatus like the Distell Fish Fatmeter®. Internal ultrasound and 2D external imagery allow in vivo prediction of carcass yields (Haffray et al. 2014) which in turn is highly correlated to perivisceral fat, another important site of lipid deposition. Taken together these results suggest that it should be possible to use lipid deposition as indirect selection criterion to enhance FE. However, care should be given to selection against muscle fat content as this may interfere with meat quality. The most

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interesting target to select against is perivisceral fat as this is generally perceived as an economic loss.

5.2.2. Protein turn-over rates and nitrogen retention

Another criterion potentially interesting to focus on to improve FE could be the nitrogen retention (excretion to intake ratio). In chicken, this trait was previously described with a heritability of 0.29 and with a genetic correlation with FCR equal to 0.95 (de Verdal *et al.* 2011a). In pig strains, Saintilan *et al.* (2013) estimated genetic correlations ranging from 0.97 to 0.98 and from 0.38 to 0.83 between nitrogen retention and FCR and RFI, respectively, indicating that the nitrogen retention could be a good criterion in view to improve FE. However, despite its relatively easy measurement in terrestrial animals, this trait is highly complex to measure in fish since the ability to estimate the nitrogen retention of each individual reared in groups is difficult, reducing the practicality of this trait as a selection criterion in fish species. In European sea bass (*Dicentrarchus labrax*), McKenzie *et al.* (2014) found that the differences between fasting tolerant and sensitive phenotypes was more probably explained by differences in the use of dietary lipids and proteins, fasting tolerant fish using less proteins as metabolic fuel than fasting sensitive fish.

5.2.3. Oxygen consumption

The rate of oxygen consumed increases after feeding in fish. The first study using oxygen consumption to estimate FE was done by Kinghorn (1983) on young rainbow trout.

According to this author, a high FI associated with high genetic growth capacity will lead to improved FE by increasing the availability of metabolizable energy for body weight gain

relative to maintenance requirement costs. By measuring the metabolized energy, more specifically the oxygen consumption, and the energy required for growth, Kinghorn (1983) showed that oxygen consumed was highly negatively correlated with gross feed efficiency ratio. Furthermore, variation in oxygen consumption was highly heritable (0.51±0.12) with moderate coefficient of variation (CV=18.3 %, Kinghorn 1983). It is interesting to note that the family mean heritability of gross FER was very low (0.03±0.10), which is in the same range as reported from direct estimations of FER by X-ray techniques (ranging from 0 to 0.07, see section 2.2). Furthermore, feed consumption showed a moderate to high family mean heritability (0.41±0.13), but this trait was moderately correlated with FER (Kinghorn 1983). These results should be interpreted with care since calculations were based on a number of assumptions (oxygen consumption as an indirect measure of FI, a constant maintenance requirement, and heritability was estimated from family means-Thodesen *et al.* 1999).

5.3. Other traits

5.3.1. Neuropeptides and hormones

It is well known that many neuropeptides and hormones are involved in the FI and digestive processes, as illustrated in Figure 3. Feeding activities are regulated by a multitude of hormones and neuropeptides produced by the brain and other peripheral organs as the liver, the gut or the stomach. Complete reviews of the role of these neuropeptides and hormones in fish were written by de Pedro and Björnsson (2001) and Volkoff *et al.* (2010). There is no doubt that the regulation of FI in fish involves orexigenic and anorexigenic signals at the brain level (Lin *et al.* 2000; Bernier and Peter 2001; Volkoff *et al.* 2010). Feed deprivation generally causes an up-regulation of the expression of orexigenic factors and a down-regulation of the expression of anorexigenic factors (Volkoff *et al.* 2010).

Consequently, it would be interesting to study the potential regulation processes of these hormones and neuropeptides on FI and FE, and estimate the relationship between FE traits and the level of these hormones and neuropeptides. For example, it was previously shown that the level of plasmatic growth hormone (GH) in Nile tilapia tends to be negatively correlated with the increase in food ration (Toguyeni *et al.* 1996). Furthermore, regulatory hormone levels are heritable in humans (h² ranging from 0.34 to 0.67 for ghrelin, amylin, insulin and leptin; Fisher *et al.* 2007).

5.3.2. Gastro-intestinal tract morphology and functioning

The upper limit of FE is related with the digestive tract capacity to assimilate nutrients from feed (Lemieux *et al.* 1999). Consequently, FE is dependent on the digestive tract morphology and functioning. According to Volkoff *et al.* (2010), variations in fish feeding habits are linked with different morphologies and physiologies. These authors illustrated this by the development of teeth and stomach, generally poorly developed in omnivorous or herbivorous fish species but well-developed in carnivorous fish species (e.g. salmon, seabass). In Nile tilapia, Charo–Karisa *et al.* (2007) showed that selection for growth on a herbivorous diet for three generations in low input earthen ponds resulted in an increase of gut length index (GLI: gut length/ standard length) from 3.1 to 4.2. Heritability of GLI was low, 0.09, but the genetic correlation with body weight was 0.22. In chickens, genetic relationships were found between FE and the development of the gastro-intestinal tract in terms of weight, length and weight to length ratio (de Verdal *et al.* 2010, 2011b). In those two studies, chickens had been selected on the ability to digest a low quality diet. It was previously shown in chicken that difference in FE linked to increases in digestibility were apparent only when using the low quality diet, while they were not significant using a highly digestible diet (Mignon-Grasteau *et al.*, 2010).

Feed efficiency is also dependent on the availability of digestive enzymes and on their capacity to degrade and transport nutrients from the digestive tract to the blood (Lemieux et al. 1999). For example, pepsin is the main enzyme in the stomach and is active in protein digestion, and alkaline phosphatase is involved in the transport and absorption of lipid and carbohydrates. However, it is complex to identify if the enzyme activities are based on gastrointestinal digesta (from the feed) or on gastro-intestinal tissues (from the gut). Several studies on proteolytic enzymes in fish have provided the evidence that trypsin and chymotrypsin are key enzymes for feed utilization and growth through their involvement in the processes of protein digestion (Lemieux et al. 1999; Belanger et al. 2002; Rungruangsak-Torrissen et al. 2006; Chan et al. 2008). In two salmonid species (Atlantic salmon and rainbow trout), a strong linear correlation was found between trypsin activity and protein digestibility (Krogdahl et al. 1994; Rungruangsak-Torrissen et al. 2006). Trypsin and chymotrypsin are the major protease enzymes secreted by the pancreas in the anterior part of the intestine (Dabrowski 1983). Trypsin activity is also correlated with FER, while chymotrypsin was not, according to Lemieux et al. (1999) in a study on Atlantic cod Gadus morhua. This link can be as strong as the relation with growth rate [trypsin activity expressed in U. g of fish⁻¹ exhibited a significant relationship with growth rate, FI and FER ($r^2 = 0.58$, 0.38 and 0.19, respectively), which supports the hypothesis of trypsin activity in feed utilization. In the same way, the protease activity ratio of trypsin to chymotrypsin (T/C ratio) was shown to be linked with growth rate (Rungruangsak-Torrissen et al. 2006) and FER (Sunde et al. 2001) in Atlantic salmon. Considering the correlation between FER and pyloric caecal T/C ratio, it would be interesting to use this last trait as an indicator of FE (Rungruangsak-Torrissen, 2007; Sunde et al. (2004).

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While these traits might be useful to estimate FE, a lot of work is still needed from a genetic point of view. Most correlations described are phenotypic and estimates of genetic correlations are in almost all cases lacking. It is necessary to have an accurate idea of the correlations between each of these traits before including them in a selection process. Since some of these traits show common pathways, there is a possibility that selecting on one trait could result in negative correlations with other traits in the same pathway. It should be also noted that the measurement of almost all these indirect metabolic traits is lethal, which reduces their potential efficiency and increases the cost of selective breeding, as in this case recording of additional slaughtered sibs would be necessary to implement a breeding program. Finally, genomic tools could be useful as was previously highlighted that some genomic regions were linked with FE characteristics in livestock species (Chen et al. 2011; Wolc et al. 2013; Tran et al. 2014; Al-Husseini et al. 2014). However, nothing has been reported to date on fish to our knowledge. The rapid development of new sequencing technologies in aquaculture (Robledo et al. 2017) will allow improving quicker FE traits when these will be well measured or estimated.

Conclusion

Improving FE in fish by the selective breeding will have high positive economic and environmental impacts. Many methods have been suggested and tested to improve FE using genetics, but results in terms of response to selection are often inconclusive as FE-related traits show little genetic variation. Furthermore, many results are questionable due to flawed experimental protocols, especially for measuring individual feed intake. There is an urgent need for sound experimental procedures that are economically and practically feasible at production scales. The primary issue appears to be improving methods to measure individual FI with high accuracy. Increasing the repeatability of the measurements over time and

environments, and the assessment of FE over the whole rearing period, are two other critical elements that require a lot more attention.

Nevertheless, while FE improvement by selective breeding in fish will not be easy, it is likely to be feasible. One way forward would be to combine different traits showing a correlation with FE and implement a multitrait selection using BLUP (Best Linear Unbiased Prediction). The development of genomic tools for FE, as was recently done for livestock animals where some genomic regions were found linked with FE could also be investigated in fish. Since it is difficult to measure FI, the identification of molecular markers linked to QTLs (quantitative trait loci) or metabolism pathways associated with genes controlling FI or FE, would be valuable. In the event of a trait under highly polygenic control, the development of genomic selection may allow significant increases in the precision of estimated breeding values, as well as easier selection if the association of genomic markers and phenotype can be done in controlled reference populations, while selection itself would rely solely on the multilocus genotype of selection candidates (Meuwissen *et al.* 2016).

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1231 Appendix

- 1232 List of abbreviations used in the present review
- 1233 FE Feed Efficiency
- 1234 FI Feed Intake
- 1235 FCR Feed Conversion Ratio
- 1236 FER Feed Efficiency Ratio
- 1237 RFI Residual Feed Intake
- 1238 BWG Body Weight Gain
- 1239 SGR Specific Growth Rate
- 1240 BW Body Weight
- 1241 DE Digested Energy
- 1242 DGC Daily Growth Coefficient
- 1243 TGC Thermal Growth Coefficient
- 1244 L Initial specific growth rate
- 1245 K Maturation rate
- 1246 Ti Age of inflexion
- 1247 FD Feed deprivation
- 1248 RF Refeeding
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1251 Tables

Table 1 – Feed efficiency and feed consumption of the main livestock and fish species at the world scale

Species	FCR ¹	World production (in 2011; 10 ⁶ tons)	Feed consumption (estimated, 10 ⁶ tons)
Beef cattle	$8 - 12.7^2$	63 ⁶	504 - 800
Sheep and lamb	$5 - 16.9^3$	13 ⁶	65 - 220
Pig	$5-6.5^2$	110^{6}	550 - 715
Broiler chicken	$2-2.5^2$	95^{6}	190 - 237.5
Fish species	1-2.68	62^{6}	62 - 166.2
- Carps and other cyprinids (10 major species) ⁵	1.40-2.68 ⁷	22.95^4	32.1 – 61.5
- Nile tilapia (Oreochromis niloticus)	1-1.328	2.814	2.81 - 3.71
- Atlantic salmon (Salmo salar)	$0.65 - 0.92^9$	1.73 ³	1.12 - 1.59
- Rainbow trout (Oncorhynchus mykiss)	1.01-1.29 ¹⁰	0.77^4	0.78 - 0.99

- ¹FCR (Feed Conversion Ratio) = Feed intake * Body weight gain⁻¹
- ²Cassidy *et al.* 2013

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- ³United States Department of Agriculture (USDA) 2013
- 1257 ⁴ FAO yearbook. 2012
- ⁵Cyprinus carpio, Ctenopharyngodon idellus, Carassius carassius, Megalobrama
- amblycephala, Mylopharyngodon piceus, Catla catla, Labeo rohita, Cirrhinus mrigala,
- 1260 Hypophthalmichthys molitrix, Hypophthalmichthys nobilis
- ⁶Earth Policy Institute 2013
- ⁷Másílko *et al.* 2014; Abidi *et al.* 2014
- ⁸Crovatto Veras *et al.* 2013; Koumi *et al.* 2011; Wang *et al.* 2009
- ⁹Mundheim *et al.* 2004; Kolstad *et al.* 2004; Sunde *et al.* 2004; Quinton *et al.* 2007a
- ¹⁰Farhangi and Carter 2007; Grima 2010; Henryon et al. 2002; Sanchez et al. 2001

Table 2 – Improvement in productivity and efficiency due to selective breeding

		Performance			
Species	Trait	1960	2005	Δ (%)	
Pigs ^{1, 2}	Growth g/d	629	925	47	
Pigs /	FCR	3.24	2.65	18	
Broilers ³	Growth g/d	10	40	400	
Dioners	FCR	2.85	1.98	30	
Laying hens ⁴	# eggs per year	230	315	30	
Laying nens	FCR (g/ g egg)	3.13	2.28	27	
Nile tilapia ⁵	Growth g/d	0.61	4.75	780	
mie mapia	FCR	1.58	1.45	8	

1267 ¹Rauw *et al.* 1998

²Saintilan et al. 2013 (estimates for 2005 from average of data collected between 2000 and

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1270 ³Zuidhof *et al.* 2014

⁴Leenstra et al 2016

⁵Omasaki and Komen (unpublished data from a domesticated and unselected Kenyan strain and from the GIFT strain, generation 5 of growth selection, commercial results from 2005).

Table 3 – Estimations of phenotypic and genetic correlations between growth traits and feed intake and FE traits¹.

	Species	Growth trait ²	Feed trait ³	Correlations	Results
Thodesen et al. (1999)	Atlantic salmon (Salmo salar)	TGC	FER	Phenotypic	r = 0.90
Thodesen et al. (2001)	Atlantic salmon (Salmo salar)	TGC	FER	Phenotypic	r = 0.79
Silverstein (2006)	Rainbow trout (Oncorhynchus mykiss)	TGC	RFI	Phenotypic	Fed at satiation ($r = -0.31$) 5%BW ration ($r = -0.57$)
Kolstad <i>et al.</i> (2004)	Atlantic salmon (Salmo salar)	BWG	FI FER	Phenotypic	Between FCE and BWG ($r = 0.6$) Between FCE and FI ($r = 0.45$) Between BWG and FI ($r = 0.98$)
Doupé and Limbery (2004)	Black bream (Acanthopagrus butcheri)	BWG	FI	Phenotypic	After 42 days (r = 0.78) After 56 days (r = 0.69)
V 4 -1 (200GL)	Rainbow trout (Oncorhynchus mykiss)	DWG BW	DFI	Phenotypic	Between DFI and BW: 0.48 to 0.54 Between DFI and DWG: 0.51 to 0.74
Kause et al. (2006b)				Genetic	Between DFI and BW: 0.72 to 0.90 Between DFI and DWG: 0.86 to 0.96
	European whitefish (Coregonus lavaretus)	DWG	DFI	Phenotypic	r = 0.86 to 0.88
Quinton <i>et al.</i> (2007a)				Genetic	r = 0.93 to 0.97
Henryon et al.(2002)	Rainbow trout (Oncorhynchus mykiss)	BW	FER ⁴	Genetic	0.63 to 0.99
de Verdal <i>et al</i> . (2016)	Nile tilapia (Oreochromis niloticus)	BWG	FI FCR RFI	Phenotypic	Between BWG and FI: 0.74 Between BWG and FCR: -0.62 Between BWG and RFI: -0.03

¹All the measurements were done with the X-ray methods or by measuring directly the feed intake of the family group.

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²TGC=Temperature Growth Coefficient; BW= Body Weight; BWG=Body Weight Gain; DWG=Daily Weight Gain (=BWG. number of experimental days⁻¹);

³FER=Feed Efficiency Ratio; RFI= Residual Feed Intake; FI=Feed Intake; DFI=Daily Feed Intake (=FI. number of experimental days⁻¹)

⁴FER estimated as the cumulative FER for all the grow out period

Figures

Figure 1- Variation of body weight after feed deprivation (FD) and re-feeding (RF) period, based on Jobling (1994), modified from Ali et al. (2003).

Figure 2– Energy flux in fish, criteria used in the bio-energetic models (from Strand 2005, modified from Bailey 2003)

Figure 3 – A model for FI regulation by hormones and neuropeptides in fish (modified from de Pedro and Björnsson 2001)

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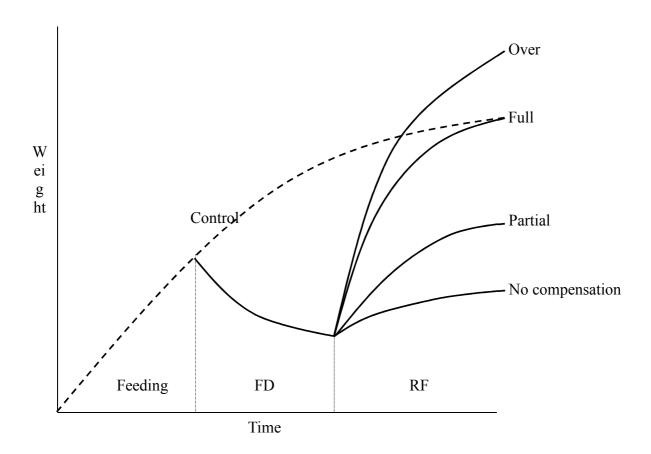


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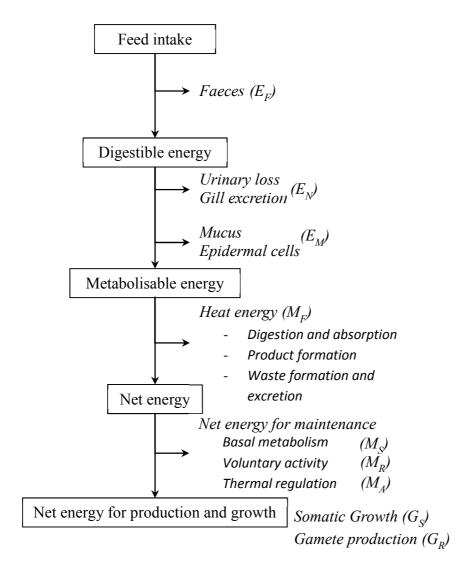


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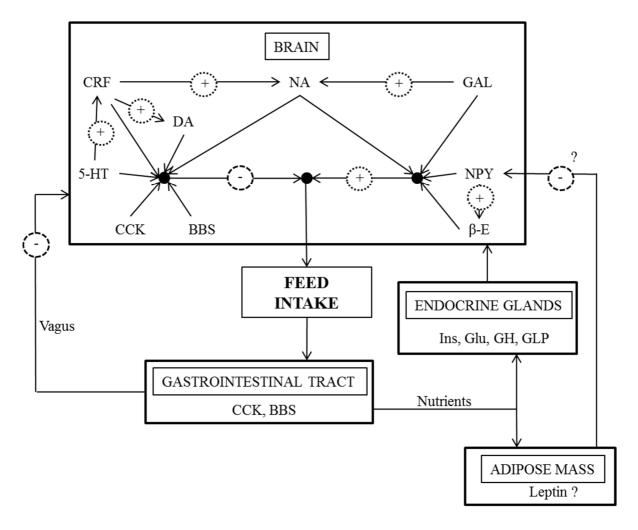


Figure 3 – A model for FI regulation by hormones and neuropeptides in fish (modified from de Pedro and Björnsson 2001) with CRF, corticotrophin-releasing factor; NA, noradrenaline; GAL, galanin; DA, dopamine; 5-HT, serotonin; CCK, cholecystokinin; BBS, bombesin; NPY, neuropeptide Y; β -E, β -endorphin; Ins, insulin; Glu, glucagon; GH, growth hormone; GLP, glucagon-like peptide; +, stimulatory input; -, inhibitory input.