



Can genetic improvement in aquaculture reduce impact on fisheries? Case of European sea bass ([i]Dicentrarchus labrax[/i]) with total substitution of marine products in the diet

Richard Le Boucher, Marc Vandeputte, Mathilde Dupont-Nivet, Edwige Quillet, David Mazurais, Jean Robin, Alain Vergnet, Françoise Médale, Sadasivam Kaushik, B. Chatain

► To cite this version:

Richard Le Boucher, Marc Vandeputte, Mathilde Dupont-Nivet, Edwige Quillet, David Mazurais, et al.. Can genetic improvement in aquaculture reduce impact on fisheries? Case of European sea bass ([i]Dicentrarchus labrax[/i]) with total substitution of marine products in the diet. ICES Annual Science Conference, Sep 2010, Nantes, France. pp.1-6 - communication J:04. hal-01193728

HAL Id: hal-01193728

<https://hal.science/hal-01193728>

Submitted on 3 Jun 2020

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Can genetic improvement in aquaculture reduce the impact on fisheries ? The case of European sea bass (*Dicentrarchus labrax*) fed on a totally plant-ingredient based diet

Le Boucher R., Vandeputte M., Dupont-Nivet M., Quillet E., Mazurais D., Robin J., Vergnet A., Médale F., Kaushik S., Chatain B.

In recent years, the increase of aquaculture production has led to changes in feed composition with an increasing substitution of fish meal (FM) and fish oil (FO) with terrestrial plant products. During the same period, selective breeding procedures have been developed with a recent focus on genetic variability for the ability to grow on plant-ingredients based diets.

Genetic parameters were estimated in a context of extremely contrasted diets in European sea bass. 784 individually tagged fish from 328 families were reared in a common garden design and DNA sampled for parentage assignment using microsatellites. At 192 g, they were distributed into 4 tanks, two fed on a diet (diet M) based on FM and FO, and two fed on a FM and FO-free diet (diet PB). Body weight, length, and lipid content of the fillet were recorded at 850 days post-fertilisation. Traits were analyzed with a restricted maximum likelihood (ASREML) methodology.

Analyses of data show that : (i) there was no difference for weight, length, and fillet lipid content among diets ($P=0.06$), (ii) family ranking for these 3 traits was not consistent among diets (genetic correlations between 0.51 and 0.87), (iii) heritability estimates (PB: 0.37 ± 0.18 ; M: 0.47 ± 0.24). Our results clearly point out that exploitation of such a variability could (i) modify the genetic gain in current selection programs and (ii) be used to select fish adapted to novel FM and FO free feeds.

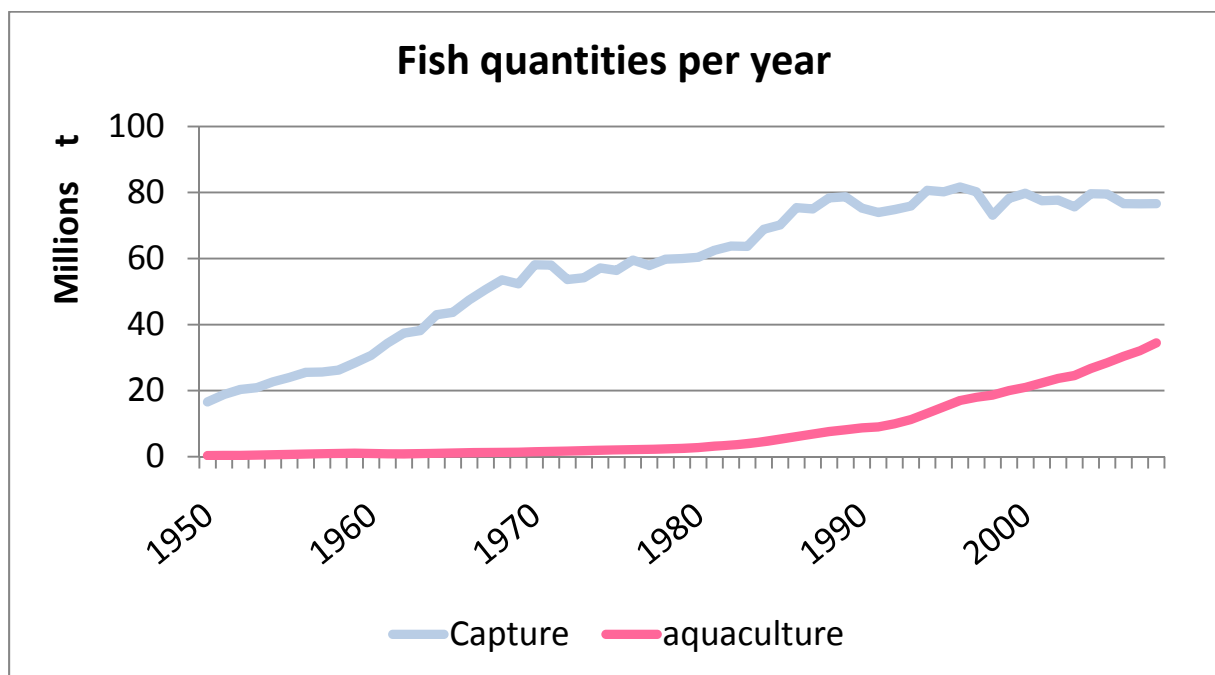
Keywords: Genetic improvement, *Dicentrarchus labrax*, genotype-diet interaction, plant-ingredient based diet

Contact author: R. Le Boucher, Ifremer, Chemin de Maguelone, F-34250 Palavas-les-Flots, France *E-mail* : richard.le.boucher@ifremer.fr

Not to be cited without prior reference to the author

Can genetic improvement in aquaculture reduce the impact on fisheries ? The case of European sea bass (*Dicentrarchus labrax*) fed on a totally plant-ingredient based diet

When we look at the FAO data, we can see that fish capture quantities (in blue) has now reached a limit when fish aquaculture production (red curve) is still strongly increasing. But as a consequence, marine products (fish meal and fish oil) usually composing the feeds, became expensive and limited. That's why partial replacements of fish meal and fish oil by plant-based products have been deeply experienced. And nowadays, in seabass, it is 80 % of the fish meal and 82% of the fish oil which have been replaced by plant products with no impact on health and growth.

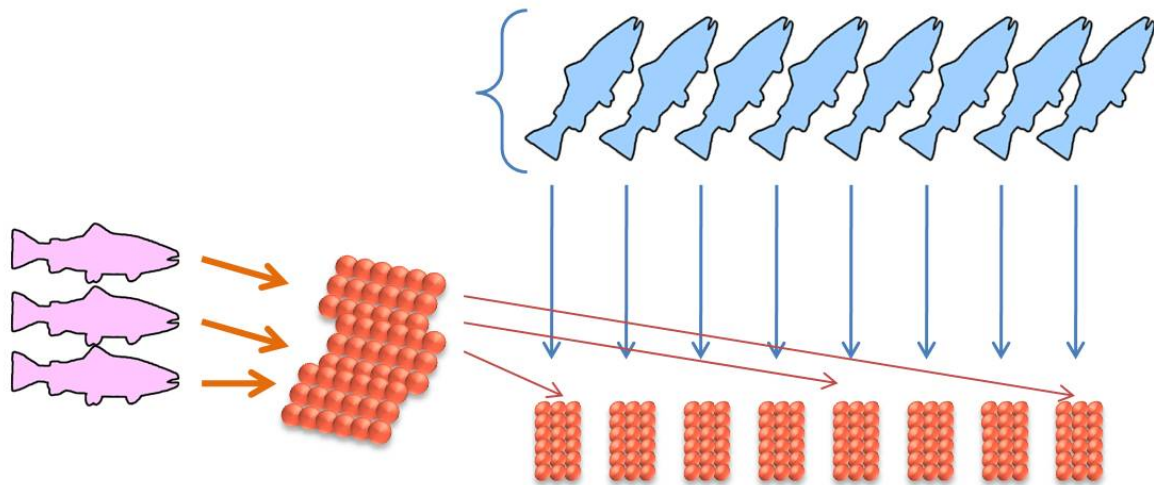


FAO, 2008

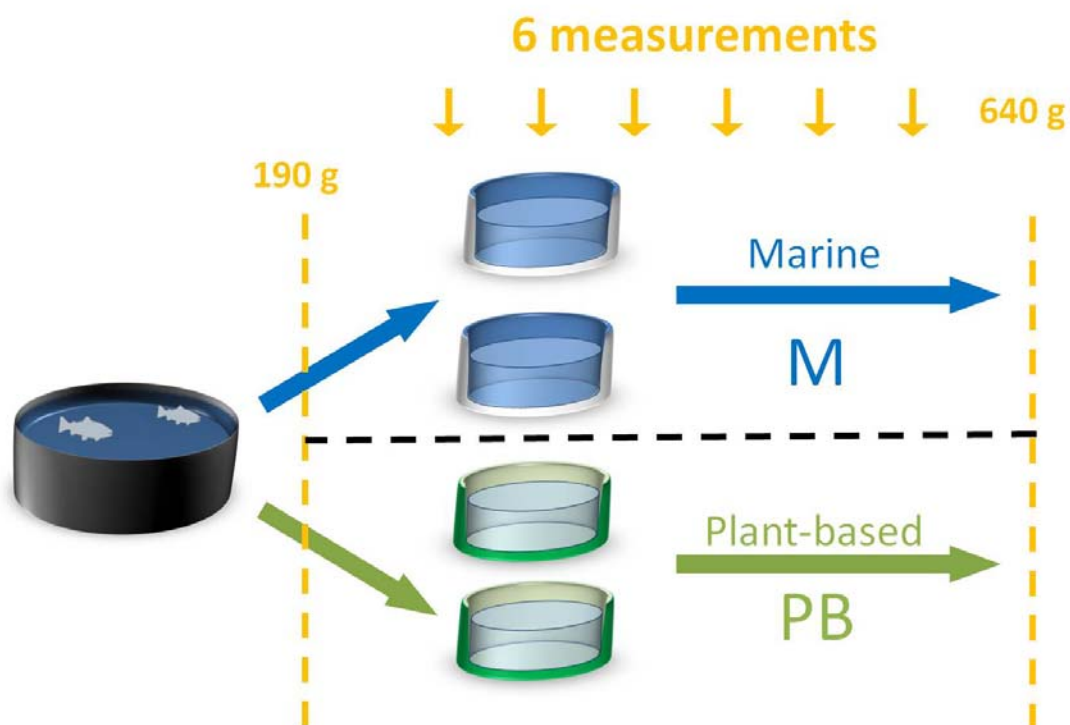
In the same time, genetic selection and breeding programs became usual in fish farming. Starting in the 1980's, we can now consider that 80 % of the European sea bass come from a genetically improved population.

In this context, two main questions raised for the management of genetic improvement of the commercial strains. The first one is how will breeding programs be impacted by the evolution of these feeds? And the second one is: Is it possible to adapt breeding programmes to lead to fish more adapted to new diets ?

To answer those questions, a preliminary trial has been conducted in Ifremer facilities. Animal material was obtained from a full factorial cross between 41 sires and 8 dams, all issued from one mediterranean strain, in order to obtain 328 full sib families. Those fish were reared all together in a recirculated system until they reached 190 g



After that, about 550 fish were split up into four tanks. Two of them were then fed with an experimental marine diet that we called M diet and the other part was fed with the plant-based diet that we called PB diet, until they approximately reached 640 g. And all along this trial, we measured six times some interesting parameters which are:

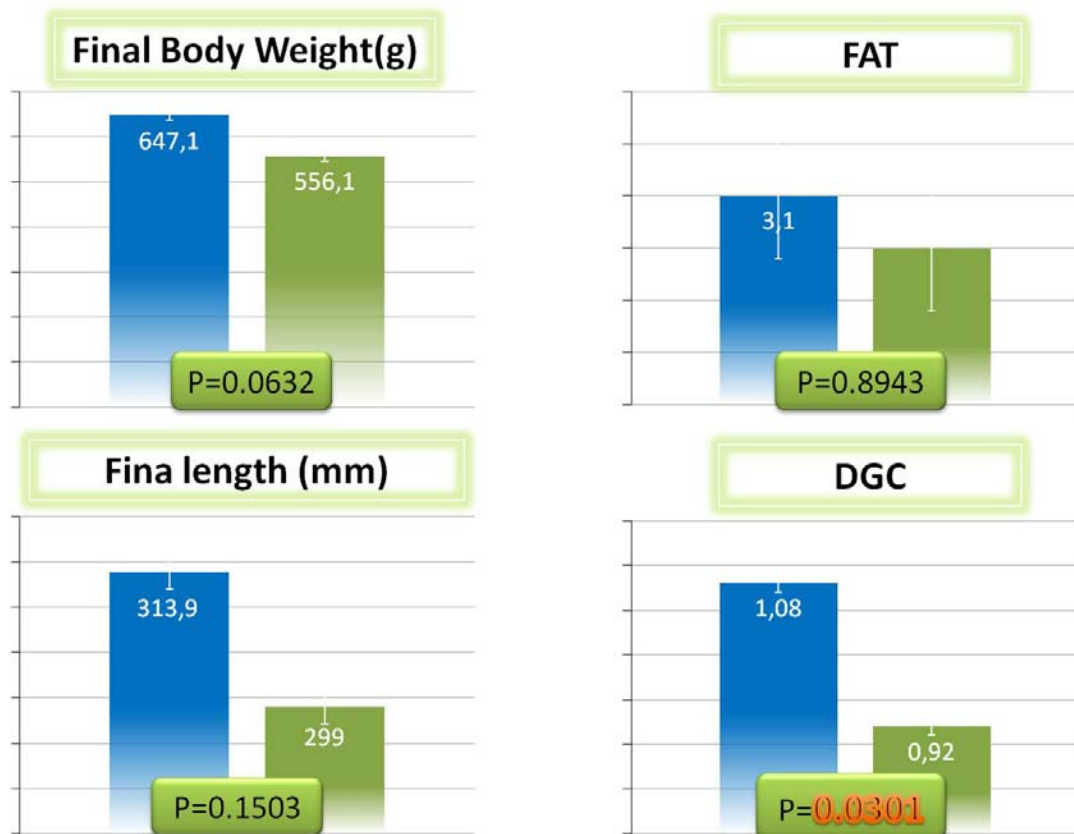


The body weight, the length and the fillet lipid content using a fish fatmeter. These traits were followed because fish have been previously tagged with passive integrative transponder. At the same time, we also sampled a fin clip for DNA extraction. This DNA was used to rebuild parentage of each fish using a set of microsatellites.

There is a difference between them for the final weight, but this difference is not significant after 9 months.

We can do the same conclusions for final length and the lipid content of the fillet divided by the logarithm of weight. Same conclusions also for condition coefficient which informs us on the fish shape.

However, growth rate mean calculated between the end and the beginning of the trial is significantly higher in M fish.



To analyze these data, I first used a SAS MIXED procedure and estimation of genetic parameters was done with ASREML.

Statistical analyses

SAS (SAS Institute Inc., Cary, NC)

MIXED Model associated with ANOVA:

$$Y_{ijklmn} = \mu + \text{Diet}_i + \text{Sex}_j + \text{tank}(\text{diet})_{k(i)} + \text{sire}_l + \text{dam}_m + \text{sire} * \text{diet}_{il} + \text{dam} * \text{diet}_{im} + e_{ijk(l)mn}$$

Diet_i Fixed Diet effect

Sex_j Fixed Sex effect

tank(diet)_{k(i)} random tank effect nested in Diet effect

sire_l random sire effect

dam_m random dam effect

Sire*Diet_{il} interaction between sire l and diet i

Dam*Diet_{im} interaction between dam n and diet i

e_{ijk(l)mn} random residual error

ASREML (Gilmour, Gogel & Cullis 2002), :



Animal Model:

$$Y_{ijklmn} = \text{Diet}_{ij} + \text{Sex}_{ik} + \text{Tank}_{il} + a_{im} + d_{in} + e_{ijklmn}$$

Diet_i Fixed Diet effect on trait i

Sex_j Fixed Sex effect on trait i

Tank_l fixed tank effect on trait i

a_{im} random genetic effect of trait i on animal m

d_{in} random dam effect on trait i

e_{ijklmn} random residual error on trait i

Heritabilities are around 0.3-0.4 for body weight and length, which can be considered as moderate to high and indicate that these traits can be efficiently selected even when fish are fed on plant-based diet.

Genetic correlations are around 0.5. And we know that the more important they are, the lower are the interactions. So, here, we can consider that genotype by diet interactions exist for these traits and that rerankings of the families occur between diets.

	Genetic correlation	Héritability (\pm SE)	Héritability (\pm SE)
<i>Weight</i>	0.51 \pm 0.34	0.47 \pm 0.24	0.37 \pm 0.18
<i>Length</i>	0.58 \pm 0.36	0.37 \pm 0.22	0.36 \pm 0.19
<i>FAT*</i>	0.83 \pm 0.17	0.94 \pm 0.28	0.56 \pm 0.22
<i>DGC</i>	0.6 \pm 0.6	0.12 \pm 0.15	0.36 \pm 0.18

However, we also see how limited is the experimental design as standard errors are high for all the estimates. Unfortunately, they don't allow to definitely conclude on the existence of such interactions. It comes mainly from the small sizes of the half sib families. Present results can only indicate a tendency.

Reranking of the families between diets seem to exist but more analyses are conducted to conclude.