



Possibility for Improving Carcass Composition and Meat Quality Traits by Selective Breeding

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ABSTRACT

An advantage of aquaculture farming compared with fisheries is that it is possible to genetically improve economically important traits through selective breeding. This is possible because many traits have underlying heritable genetic components and individuals carrying those desirable traits can be selected as the parents of the next generation. A difficulty however, is how to measure the quality traits on the potential breeders. Traditionally, measuring the traits on relatives like full- and half-sibs have been applied. However, with new technologies such as near-infrared reflectance spectroscopy, X-ray tomography (CT) and Fotofish, it is now possible to measure fat% and fillet color with high precision. Furthermore, new technological advances have opened new doors to potentially estimate fat% and fillet color on live animals. Improving fat% by selective breeding is possible, as the heritability of the trait is relatively high ($h^2 = 0.25$) and a genetic gain of 4 % per generation has been reported for rainbow trout. On the other hand, the heritability for flesh color shows high variation, but it is particularly high when measured using CT ($h^2 = 0.47$). Finally, fillet yield has a rather low heritability ($h^2 = 0.16$) and reported genetic gain per generation is close to zero.

Key Words: Aquaculture, Genetic gain, Heritability, Meat quality, Selective breeding

INTRODUCTION

Quality traits and carcass composition in fish and shellfish are important characters for both consumers and farmers. In general, from marketing perspective there product can be a complicated process, as different markets may have different quality preferences. For farmers, the size and variation as well as dressing%, fillet yield, shape and color decide the price. Important factors in the market are processors and for salmon smoking operations to improve the product quality. For consumers, the size of the fillet, fat%, texture and color are important quality traits. For Furthermore, in some fish species such as carp and silver barbnnumber of intramuscular bones usually have a better market acceptance. This trait seems to be highly variable within species. For instance, it has been reported that the number of intramuscular bones in different ploidies of crucian carp (*Carussiusauratus*) can vary from 77 to 86[1]. In Blunt snote bream (*Megalobramaamblycephala*) the number of intermuscular bones is estimated to vary from 108 to 129 [2]. For consumers these small bones can be a concern, as they are usually difficult to remove, making them unpopular.

However, one of the main problems of including quality traits in breeding goals is that these traits can not only vary extensively between species, but their preferences can also greatly differ across markets. From a breeding point of view, it is therefore often difficult to decide which traits should be included in the breeding goal and how to rank those traits according to their economic values. With this in mind, the purpose of this short review paper is to discuss possibilities on how to improve quality traits in fish and shellfish through selective breeding. One of the main difficulties of improving carcass and quality traits is how to record the traits on the live animal with high repeatability. However, there are some new promising technologies on the horizon, considering that currently we are mainly relying on recording the traits on the relatives (full- and half-sibs) of potential breeders. Subject scoring has been widely used, which in general has low repeatability and chemical analysis are laborious and expensive. For the purpose of this review, I will not discuss hybridization and monosex culture.

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Methods to measure quality traits

In recent years, much work has taken place to investigate different technologies to measure quality traits both on live animals as well as on carcasses. For instance, using ultrasound imaging, Bosworth et al. [3] explained 48-56% and 31-38% of the variation in meat yield traits in female and male catfish, respectively. Sang et al. [4] studied methods to measure quality traits of river catfish by taking measurement of the live fish. The correlation between the predicted and the observed values for fillet weight, fillet yield and fillet fat were 0.93 (5 measurements), 0.86 (4 measurements) and 0.85 (4 measurements). Texture is another example of important quality trait in fresh as well as in processed products. Mørkøre [5] used mechanical pressure to measure texture. It was found that sensory hardness is correlated with a Warner-Blatzler blade of 12.5 mm in diameter in raw salmon ($r = 0.70$). Gjerde and Martens [7] studied near-infrared reflectance spectroscopy (NIR) to measure water, fat % and protein % in the fillet of rainbow trout. They found very high correlations between chemical analysis and NIR measurements for water, fat % and protein %, ranging from $r = 0.97-0.99$. Folkestad et al. [6] applied near infrared (VIS/NIR) spectroscopy to estimate fat % in live Atlantic salmon and reported a correlation of 0.94 with chemical estimates. NIR is also an efficient tool for estimating fat % in the gutted and fillet weight. Further, VIS showed to be efficient in estimation of pigments in the fillet. Wold et al. [8] showed that Raman spectroscopy was a suitable method for non-destructive estimation of pigments ($r = 0.95$) and fat % ($r = 0.97$) in the ground salmon meat.

Computer assisted X-ray tomography (CT) was first used to measure body and carcass composition in live pigs [9]. In rainbow trout, Gjerde [10] estimated correlation between the observed and predicted CT values of 0.88 for water %, 0.89 for fat % and 0.68 for protein %. In a dataset of 174 Atlantic salmon, Rye [11] obtained a correlation of 0.92 between the observed and predicted values for fat and water content. For protein, no significant prediction was recorded. Quillet et al. [12] used Distell Fish Fatmeter in selection for muscle lipid content in rainbow trout. Fillet color is another example of important quality trait particularly in salmonid species. In 2003, researchers (Erland Austreng and Kjell Arne Rørvik) at AKVAFORSK (now Nofima) took the initiative to develop an instrument named Fotofish, which was revised later. In addition to color, Fotofish can also be used to measure the % pigment in the fat. Rørvik et al. [13] report correlations between Fotofish predictions and the following quality traits: pigment (mg/kg), $r = 0.94$ for salmon and $r = 0.97$ for rainbow trout, fat %, $r = 0.95$ for salmon and 0.85 for trout, and color score $r = 0.95$ for both species. At present, there are several efficient methods for obtaining estimations of the most important quality traits with high precision on both live fish as well as on the carcasses. These are potentially important tools and approaches for further improvements of

economically important traits in aquatic species.

Heritability and genetic variation in quality traits

A literature survey for heritability estimates of quality traits and their averages have been presented in Tables 1 and 2, respectively. For most traits, the heritability estimates seem to vary considerably. Such variations might be due to low repeatability of measurements, variations among populations, species and differences in environmental conditions that the animals were exposed to. On average, the reported heritability estimates for protein % is close to zero ($h^2 = 0.03$), the heritability for carcass and quality score are rather low ($h^2 = 0.10 - 0.15$) and this is further followed by $h^2 = 0.16$ for dressing % and fillet texture. For fillet yield there are at least 10 different h^2 estimates, with the average across all estimates to be approximately 0.16. The fat % and carotenoids both seem to have a moderate heritability ($h^2 = 0.25$). On the other hand, the heritability for flesh color, measured by tomography, is very high ($h^2 = 0.47$). In general, we can see that most economic traits of interest show genetic variation [14, 15]. For many of these traits extensive work is now underway to better understand their underlying molecular architecture. For example Wan et al. [16] showed that abundant microRNA were functionally involved in regulating the development and differentiation of intermuscular bones and connective tissues in the blunt snout bream. Bai et al. [17] investigated quality traits in triangle pearl mussel. The authors found four QTL explaining 26%-28% of the trait variation, which will provide valuable information for marker-assisted selection of the freshwater pearl mussel. Kuang et al. [18] investigated the genetic variation in fat % in common carp. A genome-wide significant QTL was detected, explaining 36.2% of the phenotypic variance. Further, they identified three QTL with significant effects explaining 14.3%-19.5% of fat content in the common carp. These findings suggest that the observed phenotypic variations of many quality traits might mainly be explained by a few major genes and QTL.

Phenotypic and genetic correlations between quality traits

While the phenotypic correlations (r_p) between body weight and fat % are positive, varying from 0.05%-0.72%, the genetic correlations (r_G) have been reported to range from -0.21 to 0.80 (Table 3). On the other hand, both phenotypic and estimated genetic correlations between body weight and flesh color are low with one exception ($r_G = -0.21$). The genetic correlations between fat % and flesh color are also all low and negative while the phenotypic correlations vary from low negative to high positive. Both phenotypic and genetic correlations between dressing % and quality traits are low with a couple of exceptions ($r_G = -0.03$ with body weight and $r_p = -0.22$ with flesh color). Quality traits are in general meas-

ured on carcasses of animals, all with the same age but usually of varying sizes. Using a different approach, Kristiansson [24] estimated correlations between quality traits and body weight on animals of the same age (sa) and similar weights (sw). Both phenotypic and genetic correlations between body weight (sa) and fat % were high and significant. On the other hand, the genetic and phenotypic correlations between weight (sw) and fat % was low. Haffray et al. [33] estimated high negative genetic correlations between body weight and body tissue development as head yield or the head and vertebral column yield (-0.48 to -0.57).

Genetic gain

Table 3 shows estimates of genetic gain for some important traits. For fat % in rainbow trout a genetic gain of 4% per generation has been reported [12]. This means that it is possible to improve this important quality trait in farmed fish only over a few generations. For fillet yield, the pattern is different. For Nile tilapia, the genetic gain is close to zero as it was estimated for the meat yield in mussel.

CONCLUSION

Fish and shellfish both from fisheries and aquaculture are healthy food for people, considering their protein and fat contents and important micronutrients such as omega 3 fatty acids. In aquaculture, it is possible to change feed composition and in addition, it is possible to change and improve product quality and carcass composition through selective breeding. For some traits, at least, the possibilities for genetic improvement is highly promising, with perhaps one of the best examples being the fillet fat % which shows moderate heritability ($h^2 = 0.25$) and a genetic gain of 4 % per generation in rainbow trout. Of course, while in some species it might be of interest to increase fat %, in some other species it might be more desirable to reduce it. By using new technological, it is possible to measure various traits like flesh color and carotenoids on the live animal opens numerous possibilities and opportunities for genetic improvements of these economically important traits, particularly in salmonids. For protein % the heritability is close to zero ($h^2 = 0.03$) indicating low genetic variation and no response to selection. For fillet yield the heritability is rather low ($h^2 = 0.16$) and the two estimates of genetic gain in tilapia and one in mussel are close to zero. Gjerde et al. [42] discussed the low genetic gain in tilapia, and concluded: “*The close to unity genetic correlation between round body weight and fillet weight indicates that genetic improvement of one of the traits without achieving a proportional genetic change in other is difficult or even impossible. This implies that improvement of fillet yield through direct selection is difficult to achieve*”.

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Table 1: Heritability and standard deviation for carcass composition and quality traits.

Species	Mean	SD	Heritability	References
Atlantic salmon:				
Dressing %	90	4	0.03 (0.02)	[19]
Dressing %	93.9	1	0.20 (0.07)	[20]
Dressing %			0.17 (0.02)	[21]
Fat %	15.6	16	0.30 (0.09)	[20]
Fat %	15.9	1.96	0.13 (0.07)	[22]
Fat %	22	17	0.46 (0.21)	Rye (pers. Com.)
Fat %			0.21 (0.03)	[21]
Fat %	13.5	4.26	0.28 (0.05)	[23]
Fat % SA (same age)			0.25 (0.08)	[24]
Fat% SW (same weight)			0.17 (0.04)	[24]
Flesh colour SA			0.10 (0.04)	[24]
Flesh colour SW			0.10 (0.04)	[24]
Flesh colour score	3.6	16	0.01 (0.03)	[19]
Flesh colour score	3.3	18	0.09 (0.05)	[20]
Flesh colour score	26.2	0.79	0.13 (0.07)	[22]
Flesh colour, tomografi	7.7	18	0.47 (0.13)	[25]
Pigment			0.28 (0.02)	[21]
Astaxanthin	6.6	0.7	0.09 (0.06)	[22]
Canthaxantin	6.5	0.9	0.11 (0.06)	[22]
Carcass quality score	3.8	19	0.16 (0.05)	[19]
Fillet yield	69.0	0.08	0.03 (0.03)	[23]
Texture	9.7	4	0.26	[26]
Texture	11.2	2.1	0.16	[27]
Rainbow trout:				
Dressing %	87.3	2	0.36	[28]
Dressing %	83.3	6	0.01 (0.05)	[19]
Dressing %	86.1	17	0.45 (0.07)	[29]
Fat %	15.9		0.16 (0.06)	[29]
Fat %	14.8	17	0.47	[28]
Fat %	14.7	23	0.17(0.09)	[30]
Fat %	9.7	10	0.47 (0.34)	[31]
Muscle lipid %	5.8	27	0.39 (0.12)	[32]
Muscle protein %	13.3	15.7	0.19 (0.10)	[32]
Protein %	20.0	7.0	0.03	[28]
Protein %	20.1		0.02 (0.04)	[29]

Flesh colour score	3.4	23	0.06 (0.08)	[19]
Flesh colour score	4.3	15	0.27	[28]
Carcass quality score	3.6	20	0.14 (0.06)	[19]
Fillet yield	63.2	2.0	0.33 (0.06)	[29]
Fillet yield	68.8	2.0	0.3 (0.05)	[33]
Coho salmon:				
Colour			0.11 (0.02)	[34]
Carotenoid, 1980 stock			0.50 (0.16)	[35]
Carotenoid, 1981 stock			0.30 (0.14)	[35]
Lipid %, 1980 stock			0.18 (0.13)	[35]
Lipid %, 1981 stock			0.19 (0.23)	[35]
Fillet yield			0.11 (0.05)	[36]
Arctic char:				
Fat %	20	12	0.06 (0.08)	[37]
Colour	1	46	0.28 (0.17)	[37]
Gilthead sea bream:				
Dressing %	88.3	0.35	0.07 (0.06)	[38]
Dressing %	93.0	1.4	0.31 (0.07)	[39]
Fat %	7.4	1.7	0.05 (0.03)	[39]
Fillet %	36.4	0.33	0.11 (0.05)	[38]
Visceral fat %	6.26	0.08	0.20 (0.06)	[38]
Common carp:				
Processed body %	67.2	2.2	0.28 (0.06)	[40]
Fat %			0.14 (0.15)	[41]
Fillet with skin	41.1	2.2	0.38 (0.09)	[40]
Fillet without skin	32.1	2.0	0.21 (0.07)	[40]
Nile tilapia:				
Fillet yield			0.06 (0.04)	[42]
Fillet yield			0.12 (=0.06)	[43]
Fillet yield			0.25 (0.07)	[44]
Channel catfish:				
Dressing %, female	69	2	0.00 (0.20)	[45]
Dressing %, male	68	2	0.00 (0.27)	[45]
Fat %, female	42	9	0.08 (0.25)	[45]
Fat %, male	43	7	0.00 (0.23)	[45]
Fat %	43	7	0.61 (0.78)	[46]
Striped catfish:				
Fillet yield with skin	47.6	9.0	0.03 (0.04)	[4]
Fillet yield without skin	35.6	7.0	0.05 (0.04)	[4]
Intestinal fat index	2.6	1.2	0.04 (0.06)	[4]
Fillet colour	1.4	0.5	0.04 (0.06)	[4]
Seabass:				
Dressing%	86.1	2.5	0.48 (0.06)	[47]
Fillet yield	55.4	3.6	0.28 (0.04)	[47]
Fat%	6.5	2.8	0.47 (0.05)	[47]
Fillet %	33.7	2.4	0.25 (0.10)	[48]
Visceral fat%	6.9	2.0	0.68 (0.19)	[48]

Table 2: Average of heritability for carcass composition and quality traits given in Table 1.

Trait	Number of estimates	Estimates of h ²	Variation in h ² estimates
Dressing %	11	0.19	0.00 – 0.48
Fat %	18	0.27	0.00 – 0.61
Protein %	3	0.08	0.02 – 0.19
Fillet yield	14	0.18	0.03 – 0.38
Texture	2	0.16	0.06 – 0.26
Carcass quality score	2	0.15	0.14 – 0.16
Carotenoids	4	0.25	0.09 – 0.50
Flesh color score	7	0.11	0.01 – 0.27
Flesh color, tomography	1	0.47	0.47
Lipid %	2	0.19	0.18-0.19

h² = heritability**Table 3: Phenotypic correlations below the diagonal and genetic above the diagonal**

Trait	Body weight	Fat %	Flesh colour	Dressing %	References
		0.42 (0.17)	0.31 (0.20)	0.61 (0.17)	[20] ²
		-0.19	0.21	0.07	[28] ³
		0.40 (0.35)			[30] ⁴
		0.65 (0.33)			[37] ⁵
		0.22	0.58		[35] ⁶
			-0.21 (0.33)		[25] ⁷
Body weight		0.38 (0.18)	0.00 (0.18)		[29] ⁸
		0.21			[45] ⁹
		0.08 (0.16)		0.02 (0.18)	[39] ¹⁰
		0.31	0.49		[22] ¹¹
		0.73 (0.17)		-0.03 (0.21)	[36] ¹³
		0.80 (0.06)			[23] ¹⁴
		0.63 (0.13)sa	-0.36(0.24)sa		[24] ¹⁵
		-0.21(0.23)sw	0.25(0.32)sw		[24] ¹⁵
			-0.18(0.09)	0.20 (0.06)	[21] ¹²
	0.63 ²		-0.34(0.25)sa ¹⁵		
	0.21 ³		-0.26(0.26)sw ¹⁵		
	0.45 (0.05) ⁴			0.78(0.07) ¹⁴	
	0.36 (0.05) ⁵				
Fat %	0.30 ⁶				
	0.30 ⁷				
	0.24 ⁹				
	0.05 ¹¹				
	0.05(0.02) ¹⁴				
	0.62-0.72sa ¹⁵				
	0.07-0.36sw ¹⁵				

	0.12 ²	0.03 ²		-0.39(0.32) ²
	0.07 ³	-0.23 ³		-0.45 ³
Flesh colour	0.64 ⁶	-0.05 (0.05) ⁵		
	0.19 (0.02) ⁷	0.33 ⁷		
		0.06 ¹¹		
		0.82 ¹²		
	0.26 ²	0.09 ²	0.05 ²	
	0.29 ³	0.13 ³	0.13 ⁸	
	-0.07 ¹⁰	0.07 ⁸	-0.22 ³	
Dressing %	0.06(0.03) ¹³	0.13 ¹⁰	0.51 ¹²	
		0.24 ⁹	0.15 (0.03) ¹³	
		0.11 ¹²		
		0.48 (0.03) ¹⁴		

sa (same age), sw (same weight)

Table 4: Genetic gain in quality traits.

Species and traits	Mean	SD	No of generations	Genetic gain (%)	References
Rainbow trout:					
Fat %	3.3	0.83	2	4.0	[12]
Fillet yield %	64.8	6.2	-	1.20	[49]
Tilapia:					
Fillet yield %	46.8	2.6	6	0.20	[50]
Fillet yield %	41.8	6.2	3	0.10	[42]
Mussel:					
Meat yield %			1	1.7	[51]