

Genetic effects on carcass-quality traits in hybrid striped bass (*Morone chrysops* ♀ × *Morone saxatilis* ♂)

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Abstract

A 10 × 10 factorial mating design was used to examine the genetic effects on various carcass-quality traits in hybrid striped bass (*Morone chrysops* ♀ × *Morone saxatilis* ♂). A total of 448 offspring were raised in a 'common-garden' environment and carcass-quality traits were assessed at 389 days post fertilization; parentage of each fish was inferred from genotypes at 5–10 nuclear-encoded microsatellites. There was a significant effect of dam and sire on body weight and fillet weight and a significant effect of dam on viscera weight and condition factor. When carcass-quality traits were standardized to body weight, there was a significant effect of dam, sire and dam × sire interaction on viscera percentage (proportion of viscera weight to body weight). Phenotypic correlations between body weight and non-standardized carcass-quality traits were high ($r_p = 0.80–0.92$), whereas phenotypic correlations between body weight and standardized carcass-quality traits were low ($r_p = 0.13–0.19$). Genetic correlations between body weight and fillet weight (dams and sires), and body weight and viscera weight (dams only) were significant and positive, while the genetic correlations between body weight and viscera percentage (dams and sires) were significant and negative. Significant general combining ability values for favourable carcass-quality traits in the same breeder (dam or sire) occurred only in one or two of 20 (dams and sires) used in this study, suggesting that simultaneous improvement in multiple traits in hybrid striped bass may require evaluation of large numbers of candidate breeders. The effect of sex on body weight and all non-standardized carcass-quality traits was significant and appeared to be due to faster

growth in females. These results indicate that selection for faster growth of hybrid striped bass would lead to a correlated increase in fillet weight and viscera weight but not necessarily to an increase in the proportion of fillet and waste product generated. The significant dam, sire and dam × sire interaction effects on viscera percentage and the negative genetic correlations between body weight and viscera percentage indicate that selection for reduced proportion of viscera relative to body weight might be feasible.

Keywords: genetics, carcass-quality traits, hybrid striped bass

Introduction

Hybrid striped bass (*Morone chrysops* Rafinesque ♀ × *Morone saxatilis* Walbaum ♂) is one of the fastest-growing segments of the U.S. aquaculture industry (Carlberg, Van Olst & Massingill 2000; Kohler, Sheehan, Myers, Rudacille, Allyn & Suresh 2001). Although similar in appearance to the parental species, the hybrid possesses traits such as aggressive feeding behaviour and tolerance to a wide range of environmental conditions that make it highly suitable for aquaculture (Bishop 1968; Myers & Kohler 2000). Increased production of hybrid striped bass, however, is limited at present because of suboptimal production efficiency stemming from uncontrolled variation in the performance of fish derived from undomesticated broodstock (Woods 2001).

In a previous study, Wang, Ross, Saillant, Gatlin III & Gold (2006) reported moderate to high estimates of

family-mean heritability for growth rate in hybrid striped bass, suggesting that genetic improvement in the growth of hybrid striped bass would be successful. However, selection of candidate breeders based on their estimated genetic value for growth rate could result in a correlated response in other traits that might be unfavourable for either consumers or fish farmers (Neira, Lhorente, Araneda, Díaz, Bustos & Alert 2004; Perry, Tarte, Croisetière, Belhumeur & Bernatchez 2004). Knowledge of genetic effects and of correlations among traits other than growth rate is critical when developing a selective breeding programme in order to prevent offsets in genetic gain from selection on single characters by economic losses in correlated traits (Falconer & Mackay 1996), given that many carcass-quality traits directly or indirectly affect the yield of the final product and/or consumer acceptance (Kause, Ritola, Paananen, Mantysaari & Eskelinen 2002; Neira *et al.* 2004).

Hybrid striped bass are sold in the U.S. market as whole fish and as processed products (fillet and gutted fish). Therefore, maximizing body weight and fillet yield and minimizing relative viscera weight are potentially important goals for hybrid striped bass aquaculture. The level of fat deposition in fish tissue is another trait of potential interest as it may influence market acceptance (Quinton, McMillan & Glebe 2005). The objective of this study was to assess (i) genetic effects on body weight, fillet weight, visceral fat weight and viscera weight, (ii) phenotypic and genetic correlations between these carcass-quality traits and growth rate (measured as body weight) and (iii) the general combining ability (GCA) of each dam and sire for each trait and specific combining ability (SCA) for each dam \times sire combination.

Materials and methods

Experimental fish

A full, factorial-mating design, where 10 white bass females were crossed *inter se* with 10 striped bass males, was used to produce full-sib, half-sib and unrelated progeny. Matings were carried out during the spring of 2003 at Keo Fish Farms in Lonoke, Arkansas. White bass females were obtained by personnel at Keo Fish Farms via angling in the Arkansas and Mississippi river drainages. The striped bass males had been maintained at Keo Fish Farms for several years. The exact origin of each individual male was unknown. Both females and males were induced to spawn by injection of human chorionic gonadotropin

according to established procedures (Hodson & Hayes 1989). Eggs from each white bass female were artificially fertilized with milt from each of 10 striped bass males, thereby generating 100 full-sib families. Fingerlings were incubated separately and then mixed for grow-out as described in Wang *et al.* (2006). At 152 days post fertilization, 600 fish (group A) were marked individually with Passive Integrative Transponder (PIT) tags and allocated at random into six 1200 L tanks (100 fish per tank) connected as a recirculating system. Another group of 400 fish (group B) were too small to be PIT tagged at 152 days post fertilization. They were further grown until 201 days post-fertilization, when they were PIT tagged and allocated at random into another four tanks connected to the same recirculating system. The experimental conditions during grow-out of the fish are detailed in Wang *et al.* (2006).

Sampling and measurement

A total of 474 fish were selected randomly from nine of the 10 tanks (29–84 fish tank⁻¹) at 389 days post fertilization and killed by immersion in a lethal dose (110 mg L⁻¹) of tricaine methane sulphonate (MS-222). Each fish was weighed to the nearest gram (g) and the total length was measured to the nearest millimetre. Fillets were obtained manually by cutting along the rib cage and processing to the tail; fillets (both sides together) were weighed to the nearest gram. Fish were eviscerated and viscera from each fish were weighed, and visceral fat and gonads were then separated from other viscera and weighed individually. The phenotypic sex of each fish was recorded by visual examination of the gonads; testes were identified based on their triangular section and high density, while ovaries were recognized based on their tubuliform section, pink colour and occurrence of an ovarian cavity. All fish were immature sexually.

Parental assignment

A small clip from the dorsal fin of each fish was removed at sampling (389 days post fertilization) and stored in 70% ethanol for subsequent parentage assignment. Tissue samples (fin clips) from all 10 dams and 10 sires used in the study had been obtained previously. The parentage of offspring was determined using genotypes at 10 nuclear-encoded genetic markers (microsatellites) optimized and/or developed for this study (Ross, Wang, O'Malley, Gatlin III & Gold

2004). Procedures regarding DNA isolation, microsatellite assays and parentage assignment are detailed in Wang *et al.* (2006).

Traits and statistical analysis

The carcass-quality traits evaluated were body weight, fillet weight, visceral fat weight and viscera weight. Gonads from each fish contributed negligibly to body weight and viscera weight (and hence were not evaluated further). Each trait evaluated was standardized (normalized) to body weight by multiplying the weight of each trait for each fish $\times 100$ and dividing by the body weight recorded for that fish. Standardized traits generated were fillet percentage, visceral fat percentage and viscera percentage. Fulton's condition factor (K) was also recorded for each fish; K was estimated (after Ricker 1975) as body weight $\times 10^5$ (body length)³.

All carcass-quality traits were assessed according to Model 1 (below)

$$Y_{ijklmn} = \mu + \text{dam}_i + \text{sire}_j + (\text{dam} \times \text{sire})_{ij} + G_k + T(G)_{kl} + \text{Sex}_m + \varepsilon_{ijklmn}$$

where Y_{ijklmn} is an individual observation, μ is the overall mean, dam_i represents the random effect of the i th dam, sire_j represents the random effect of the j th sire, $(\text{dam} \times \text{sire})_{ij}$ represents the random interaction between the i th dam and j th sire, G_k represents the fixed effect of the k th group, $T(G)_{kl}$ represents the fixed effect of the l th tank nested within the k th group, sex_m represents the fixed effect of sex and ε_{ijklmn} is the random residual. The significance of random and fixed effects was determined by analysis of variance (ANOVA); the sum of squares for the effects tested were estimated using Type IV estimable functions in SAS (SAS Institute Inc., Cary, NC, USA).

Variance components and their standard errors were estimated based on Model 1 and using the REML algorithm implemented in VCE-5 (Kovac & Groeneveld 2002). Broad-sense heritability based on family means (h_f^2) was estimated as the proportion of the variance of dam half-sibs or sire half-sibs relative to the phenotypic variance of family means for a particular trait. Estimates of h_f^2 values followed equations given in Wang *et al.* (2006). Approximate standard errors for estimates of h_f^2 used the 'delta' method described in Hohls (1996). REML estimates of variance and covariance components used to compute h_f^2 and their standard errors were obtained from PROC MIXED in SAS. The magnitude of the effect of sex on body weight and the carcass-quality traits was estimated

as the difference between the Best linear unbiased estimator (BLUE) of the mean trait value for male offspring and the BLUE of the mean trait value for female offspring; BLUE values were generated in PEST 4.2.3 (Groeneveld & Kovac 1990) and were based on Model 1.

Phenotypic and genetic correlations (and their standard errors) between body weight and each of the carcass-quality traits were estimated using two-trait REML analysis in VCE-5 (Kovac & Groeneveld 2002). Genetic correlations were based on dams and sires, respectively, and employed Model 1. The dam \times sire interaction effect was not included in two-trait analysis when the variance component associated with this interaction effect did not differ significantly from zero in single-trait analysis.

Best linear unbiased predictors (BLUP) of individual dams, sires and crosses, and their respective standard errors, were generated in PEST 4.2.3 (Groeneveld & Kovac 1990) and used as estimates for each trait of GCA of each dam and sire and SCA of each dam \times sire combination. Single-trait analyses were performed to generate BLUPs for each non-standardized and standardized carcass-quality trait, using Model 1.

Results

Data were recorded for a total of 474 tagged fish. Of these, 448 were assigned to a single parental pair, based on multilocus genotypes; the remaining 26 fish were assigned to a single dam but could not be assigned to a single sire. A total of 91 of the possible 100 full-sib families were represented with at least one offspring, and all 20 dams and sires contributed to the sample. Contributions ranged from 1.9% (dam 8) to 17.1% (dam 9) for dams, and 5.1% (sire 1) to 19.8% (sire 10) for sires. Contribution of individual dams and sires to groups and tanks was relatively even. Sex ratio among the progeny was balanced (236 females, 238 males). Mean and standard deviation (SD) of body weight and the various carcass-quality traits measured at 389 days post fertilization are given in Table 1 for all offspring and for females and males separately. The mean body weight (SD) in grams over all fish was 275.3 (75.0); mean body weight (SD) for females and males were 279.5 (75.8) and 272.5 (69.9) respectively. The mean length (SD) in millimetre over all fish was 269.4 (21.8); mean length (SD) for females and males were 269.1 (21.8) and 269.8 (19.0) respectively.

Results of tests of significance of genetic effects on the non-standardized carcass-quality traits for each

Table 1 Mean (SD) of body weight, total length and carcass-quality traits of hybrid striped bass measured at 389 days post fertilization

Carcass-quality trait	Total (n = 474)	Females (n = 236)	Males (n = 238)
Body weight (g)	275.3 (75.0)	279.5 (75.8)	272.5 (69.9)
Total length (mm)	269.4 (21.8)	269.1 (21.8)	269.8 (19.0)
Fillet weight (g)	98.6 (31.4)	100.3 (33.2)	96.8 (29.5)
Visceral fat weight (g)	23.6 (5.3)	141.2 (5.8)	13.2 (4.9)
Viscera weight (g)	29.3 (9.4)	30.8 (9.1)	28.0 (8.3)
Fillet percentage	35.6 (4.6)	35.7 (4.2)	35.5 (4.9)
Visceral fat percentage	4.9 (1.2)	5.00 (1.2)	4.8 (1.2)
Viscera percentage	10.6 (1.4)	10.9 (1.3)	10.2 (1.3)
Condition factor	1.4 (0.8)	1.4 (0.1)	1.4 (0.1)

Table 2 Probability of significance of genetic and non-genetic effects for body weight and non-standardized carcass-quality traits

Effect	Body weight	Fillet weight	Visceral fat weight	Viscera weight
Dam	0.0007	0.0011	0.0901	0.0181
Sire	0.0201	0.0239	0.2194	0.0906
Dam × sire	0.9839	0.9655	0.6144	0.8054
Sex	0.0401	0.0094	0.0121	<0.0001
Group	0.4057	0.8114	0.3029	0.4618
Tank (group)	<0.0001	<0.0001	<0.0001	<0.0001

trait are shown in Table 2. There was a significant effect of dam and sire on body weight and fillet weight, and a significant effect of dam on viscera weight. The estimate of the dam component of variance was considerably larger than that of the sire component of variance in body weight (9.83% vs. 4.56%), fillet weight (11.35% vs. 3.68%), visceral fat weight (2.07% vs. 0.22%) and viscera weight (4.76% vs. 2.02%). The effect of dam × sire interaction was not significant for any non-standardized trait. Estimates of h^2 for body weight and fillet weight were 0.72 ± 0.12 and 0.76 ± 0.11 , respectively, for dams, and 0.60 ± 0.16 and 0.54 ± 0.17 , respectively, for sires; the estimate of h^2 for dams on viscera weight was 0.56 ± 0.21 .

The effect of sex was significant on body weight and all non-standardized carcass-quality traits (Table 2) and appeared to be due to faster growth (leading to larger body size) in females, as females had a 4.36% higher body weight, 5.93% higher fillet weight, 8.89% higher visceral fat weight and 18.51% higher viscera weight than did males. The effect of group was not significant on any non-standardized

Table 3 Probability of significance of genetic and non-genetic effects for condition factor (K) and standardized carcass-quality traits

Effect	Fillet	Visceral fat percentage	Viscera percentage	Condition factor (K)
Dam	0.3722	0.1563	0.0093	0.0033
Sire	0.7349	0.2890	<0.0001	0.3604
Dam × sire	0.7371	0.8976	<0.0001	0.7088
Sex	0.2354	0.0754	<0.0001	0.8783
Group	0.0011	0.3131	<0.0001	<0.0001
Tank (group)	<0.0001	0.0043	<0.0001	<0.0001

carcass-quality trait, while the effect of tank was significant on all the traits (Table 2).

The results of tests of significance of genetic effects on the standardized carcass-quality traits, including condition factor, are shown in Table 3. There was a significant effect of dam, sire and dam × sire interaction on viscera percentage and a significant effect of dam on condition factor. Dam, sire and dam × sire interaction effects on all other traits were non-significant. The effect of sex on viscera percentage was significant, as was the effect of group on all traits, except for visceral fat percentage. The tank effect on all standardized carcass-quality traits was significant (Table 3).

Phenotypic correlations between body weight and non-standardized carcass-quality traits were relatively high and differed significantly from zero: fillet weight ($r_p = 0.92$), visceral fat weight ($r_p = 0.80$) and viscera weight ($r_p = 0.92$). Phenotypic correlations between body weight and standardized carcass-quality traits also differed significantly from zero but were relatively low: fillet percentage ($r_p = 0.15$), visceral fat percentage ($r_p = 0.19$) and viscera percentage ($r_p = 0.19$). The phenotypic correlation between body weight and condition factor ($r_p = 0.62$) differed significantly from zero.

Genetic correlations between body weight and various carcass-quality traits were estimated for those traits where a significant 'genetic' (dam, sire, or dam × sire interaction) effect was indicated by ANOVA (Tables 2 & 3). The genetic correlations between body weight and fillet weight were $r_g = 0.99 \pm 0.01$ (dams) and $r_g = 0.99 \pm 0.01$ (sires), while the genetic correlation between body weight and viscera weight (dams only) was $r_g = 0.99 \pm 0.01$. The genetic correlations between body weight and viscera percentage were $r_g = -0.95 \pm 0.25$ (dams) and -0.70 ± 0.25 (sires), while the genetic correlation between

Table 4 Estimates and standard errors (SE) of general combining ability (GCA) for body weight, fillet weight, visceral fat percentage and viscera percentage for each of 10 dams and 10 sires

Trait	Body weight (g)		Fillet weight (g)		Viscera fat percentage		Viscera percentage	
	Mean	SE	Mean	SE	Mean	SE	Mean	SE
Dam 1	-24.18	11.38	-9.56	4.82	0.18	0.16	0.48	0.94
Dam 2	5.16	9.86	3.06	4.12	0.04	0.14	0.04	0.91
Dam 3	-3.51	9.58	0.74	4.00	-0.06	0.14	-0.27	0.90
Dam 4	-2.59	9.22	-0.02	3.84	0.20	0.13	0.28	0.89
Dam 5	-23.78	9.91	-9.76	4.14	0.07	0.14	0.54	0.91
Dam 6	34.74	11.65	16.74	4.16	0.04	0.16	0.04	0.95
Dam 7	-1.23	10.38	-0.54	4.36	-0.01	0.15	0.11	0.92
Dam 8	-1.93	14.21	-6.16	6.10	-0.09	0.18	-0.17	0.98
Dam 9	12.31	9.03	4.52	3.76	-0.06	0.13	-0.07	0.88
Dam 10	4.99	9.94	0.98	4.16	-0.30	0.14	-0.97	0.91
Sire 1	-9.91	9.34	-0.92	3.64	0.03	0.19	0.74	1.67
Sire 2	6.93	7.66	1.96	3.02	0.13	0.16	1.82	1.47
Sire 3	-6.14	8.13	-3.26	3.20	-0.10	0.17	0.27	0.15
Sire 4	5.83	8.72	1.10	3.42	0.20	0.18	0.49	1.60
Sire 5	-12.29	8.56	-3.68	3.36	0.27	0.17	0.09	0.16
Sire 6	-14.96	6.48	-5.78	3.38	0.22	0.17	0.49	0.16
Sire 7	-0.84	9.08	-1.92	3.56	-0.08	0.18	-0.75	1.63
Sire 8	8.81	7.70	3.72	3.04	-0.08	0.16	0.44	1.49
Sire 9	2.65	8.57	1.38	3.36	-0.16	0.17	-0.14	1.58
Sire 10	19.93	6.95	7.40	2.74	-0.45	0.14	-3.42	1.40

GCA values in bold differ significantly from zero ($P < 0.05$).

body weight and condition factor (dams only) was 0.51 ± 0.25 .

Estimates (and standard errors) of GCA for each of the 10 dams and 10 sires for body weight, fillet weight, visceral fat percentage and viscera percentage are presented in Table 4. Positive and significant (means greater than two standard errors) GCA values for body weight and fillet weight were found for dam 6 and sire 10, whereas negative (and significant) values were found for dams 1 and 5. A significant and negative GCA value for body weight, but not fillet weight, was found for sire 6. Significant, negative GCA values were found for visceral fat percentage (dam 10 and sire 10) and viscera percentage (sire 10), while a significant, positive value was found for viscera percentage (sire 6). Of interest is that sire 10 had significant, positive GCA values for body weight but significant, negative GCA values for visceral fat percentage and viscera percentage. Estimates of GCA values (for both dams and sires) for the remaining carcass-quality traits (non-standardized and standardized) and condition factor did not differ significantly from zero (data not shown). With one exception, estimates of SCA for each possible dam × sire combination (91

pairwise combinations total) for all carcass-quality traits (standardized and non-standardized) also did not differ significantly from zero (data not shown). The exception was for viscera percentage in the cross of dam 1 × sire 4 where the estimated SCA value was 6.

Discussion

The objectives of this study were to assess (i) the genetic effects on body weight, fillet weight, visceral fat weight and viscera weight, (ii) phenotypic and genetic correlations between these carcass-quality traits and growth rate (measured as body weight) and (iii) GCA of each dam and sire for each trait and SCA for each dam × sire combination. Significant genetic (dam and sire) effects, moderate to high estimates of family-mean heritability ($h_f^2 > 0.72$ for dams and $h_f^2 > 0.54$ for sires), absence of a dam × sire interaction effect and high phenotypic and genetic correlations between body weight and fillet weight were obtained. These results indicate that selection for superior dams and sires to increase both traits simultaneously would be effective, and moreover, that genetic effects on both traits are mostly additive. In addition, the high genetic correlations ($r_g = 0.99 \pm 0.01$ for both dams and sires) suggest that related genes affect both traits and that increasing fillet weight or mass likely would be best realized by selecting simply for increased body weight. We did not find a significant genetic effect for fillet percentage, suggesting that prospects of selection to increase fillet yield at an equal body weight would not be especially effective. Fillet percentage also was not correlated with body weight, indicating that selection for increased body weight would not lead to a modification of fillet percentage. Similar findings have been reported in other cultured fish, including various salmonids (Gjedrem 1997; Kause *et al.* 2002; Neira *et al.* 2004), Nile tilapia, *Oreochromis niloticus* Linnaeus (Rutten, Bovenhui & Komen 2005), channel catfish, *Ictalurus punctatus* Rafinesque and blue catfish, *Ictalurus furcatus* Valenciennes, (Argue, Liu & Dunham 2003). Neira *et al.* (2004), however, did find a positive genetic correlation between body weight and fillet percentage in coho salmon (*Oncorhynchus kisutch* Walbaum). Based on our findings, selection for faster body weight gain in hybrid striped bass should result in a correlated gain in fillet weight and hence should enhance hybrid striped bass products for both the whole/gutted fish and fillet markets.

No significant genetic effects were found for visceral fat weight and percentage. A significant effect of dam on viscera weight was detected as well as significant dam, sire and dam \times sire interaction effects on viscera percentage. Studies of visceral fat weight and percentage in other cultured fishes (Kause *et al.* 2002; Neira *et al.* 2004) have often indicated significant genetic effects on one or both traits, along with a positive genetic correlation with body weight, suggesting that the genetic factors affecting body weight may generate an undesirable correlated response in these traits. The absence of significant genetic effects on visceral fat weight and percentage in hybrid striped bass, however, indicates that these traits likely cannot be improved (lowered) by directional selection and that selection for increased body weight would not modify (increase/decrease) either visceral fat trait.

The finding in hybrid striped bass of significant dam, sire and dam \times sire interactions on viscera percentage suggests that selection for reduced proportion of viscera (waste products) relative to body weight may be feasible. The significance of additive (dam and sire) effects suggests that genetic improvement could be achieved by selecting breeders in both sexes based on their additive genetic values. The significant dam \times sire interaction suggests that reduced viscera percentage also may be achieved by selecting specific dam \times sire crosses. The negative genetic correlations (both dams and sires) observed between body weight and viscera percentage also suggest that selection for increased growth rate (body size) could lead to a reduction in viscera percentage. However, the phenotypic correlation between body weight and viscera percentage, although low ($r_p = 0.19$) was positive and differed significantly from zero. Although phenotypic and genetic correlations can differ in magnitude, it is unusual that they differ in sign (Lynch & Walsh 1998). In addition, estimates of genetic correlations are more prone to sampling errors than estimates of phenotypic correlations (Lynch & Walsh 1998). Because of the latter, we view the observed negative genetic correlations with caution.

A significant genetic effect of dam on condition factor (K) was detected and both phenotypic ($r_p = 0.62$) and genetic (dam only, $r_g = 0.51 \pm 0.25$) correlations with body weight differed significantly from zero. K is considered to be an approximate indicator of shape (Ricker 1975; Gjerde & Schaeffer 1989) and can contribute to market acceptance (Ankorion, Moav & Wohlfarth 1992; Kause *et al.* 2002), as longer,

less deep-bodied fish (K values < 1) are preferred in some markets, while shorter, more deep-bodied ones (K values > 1) are preferred in other markets (Barnham & Baxter 1998). The estimates of K in our experiments averaged ~ 1.4 , suggesting that an increase in body weight in hybrid striped bass conceivably could lead to a moderate increase in body depth. However, the observed positive phenotypic correlation between K and body size could reflect an allometric coefficient for K that is greater than unity. If so, fish could display an increase in K when they grow larger regardless of their growth rate. Further assessment of phenotypic and genetic variation in shape using indicators uncorrelated to body size may be warranted. Based on the above, it would appear that selection for increased body size and fillet weight in hybrid striped bass would not be seriously constrained by adverse gains in visceral fat (which may affect consumer acceptance), waste viscera or undesirable body shape.

Our finding that the dam component of variance for body weight, fillet weight and viscera weight was at least twice that of the sire component may indicate the presence of maternal effects on growth rate (body size). However, because hybrid striped bass represent F_1 progeny of a cross between two species, determining the extent of maternal effects minimally would require a multigenerational experimental design (Lynch & Walsh 1998). In addition, estimating maternal effects in hybrid striped bass is problematic, given the expected genetic disequilibrium associated with interspecific hybrids (Gordon 1999). A second issue associated with the genetic disequilibrium expected in interspecific F_1 hybrids is that estimates of heritability are 'broad sense' because the genetic variances estimated cannot be related to the additive variance typically exploited in selection programmes implemented in randomly mating species (Gordon 1999). However, this does not necessarily render a selection programme for hybrid striped bass meaningless, as additive and non-additive effects can be exploited in a selective breeding programme where F_1 progeny are the production unit by estimating breeding values via progeny testing (Hallerman 1994).

The estimates of heritability (h^2_f) for both body weight and fillet weight generated in this study were relatively high, suggesting that a substantial fraction of the selection differential would be expected to be gained in offspring of selected parents. The estimates of heritability, however, were based on family means and should be viewed in the context of a selection programme based on half-sib family units where separate lines of the two species (white bass and striped

bass) are crossed to generate hybrids for production purposes. The current practice in the hybrid striped bass industry is to capture dams each spring and to propagate F_1 progeny by mating repeatedly with sires that have been maintained in captivity (Carlberg *et al.* 2000). The h_f^2 estimates for body weight and fillet weight obtained in this study suggest that both 'backward selection' (Gordon 1999) and 'reciprocal recurrent selection' (Falconer & Mackay 1996) could be used to improve both body weight and fillet weight in hybrid striped bass. Further economic evaluation of the two approaches in the context of hybrid striped bass production industry is needed.

Examination of the GCA values of the 10 dams and sires used in this study suggest that selection for multiple traits of potential interest could be achieved. Progeny from sire 10, for example, had a significantly lower visceral fat percentage, lower viscera percentage and higher body weight. Such breeders potentially could be bred repeatedly (backward selection) to produce progeny that would have desired phenotypes for multiple traits. However, significant GCA values for favourable carcass-quality traits in the same breeder (dam or sire) occurred only in one or two of 20 (dams and sires) used in this study, suggesting that simultaneous improvement of multiple traits in hybrid striped bass likely would require evaluation of large numbers of candidate breeders. Further study is needed to estimate (genetic) correlations between carcass-quality traits and the feasibility of selecting breeders with high GCAs for multiple traits.

There was a significant effect of sex on all non-standardized carcass-quality traits that appeared to be due to a scale effect stemming from more rapid growth in females. Similar sexual dimorphism favouring females or males has been documented in other cultured fish [females – Eurasian perch (*Perca fluviatilis* Linnaeus), Fontaine, Gardeur, Kestemont & Georges 1997; European sea bass (*Dicentrarchus labrax* Linnaeus), Saillant, Fostier, Menu, Haffray & Chatain 2001; dab (*Limanda limanda* Linnaeus), Lozan 1992; males – Nile tilapia, Toguyeni, Fauconneau, Fostier, Abucay, Mair & Baroiller 2002; channel catfish, Simco, Goudie, Klar, Parker & Davies 1989; coho salmon, Fleming & Gross 1994] and often occurs at sexual maturity when the investment in sexual maturation differs among sexes (Thorpe 1994). In our study, however, both female and male fish were immature with very little, if any, development of gonad tissue. Similar sexual dimorphism in early growth (i.e. at a sexually immature stage) has been observed in European sea bass (Saillant *et al.* 2001;

Saillant, Chatain, Menu, Fauvel, Vidal & Fostier 2003), and may suggest a relationship between growth and gonad physiology during the early stages of gonad differentiation.

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