

THE EFFECT OF RAINBOW TROUT GROWTH HORMONE GENE ON THE MORPHOLOGY, DRESSING PERCENTAGE AND CONDITION FACTOR IN THE COMMON CARP, CYPRINUS CARPIO (L)

N. Chatakondi¹, A.C. Ramboux¹, A. Nichols¹, M.Hayat^{1,4}, P.L.Duncan^{1,5}, T.T. Chen², D.A. Powers³ and R.A. Dunham¹

¹Department of Fisheries & Allied Aquacultures, Auburn University, Auburn, AL 36849. ²Center for Marine Biotechnology, The University of Maryland, Baltimore, MD 21218. ³Hopkins Marine Station, Stanford University, Pacific Grove CA 93593. ⁴Ministry of Food Agriculture and Cooperatives, Islamabad, Pakistan. ⁵USDA Fish Disease and Parasite Research laboratory, Auburn AL 36849 (^{4,5}Current address)

SUMMARY

The effect of rainbow trout growth hormone gene on morphology, dressing percentage and condition factor in the common carp, Cyprinus carpio, was studied in the four families. Length and weight were correlated for both genotypes. Transgenic families that grew faster than controls also had larger ($P < 0.05$) morphometric ratios than controls. Head and body measurements were 4.5 - 8.5 % larger. Caudal changes were more dramatic, an increase of 15-18%. A negative correlation was observed between dressing percentage and morphometric ratios. The condition factor and dressing percentage for transgenic and control carp in all the families were not different ($P > 0.05$).

INTRODUCTION

Dunham (1990) and Powers (1991) have provided a thorough review of the gene transfer work conducted in fish. Phenotypic changes are expected to occur as a consequence of integration or expression of the foreign gene construct in transgenic fish. Estimation of phenotypic variability and changes in important correlated genetic parameters is necessary for assessment of environmental impacts of transgenic fish and to assure undesirable correlated responses for commercially important traits do not occur. No quantified information is available on changes in traits genetically or phenotypically correlated to the trait targeted by the inserted transgene for fish, particularly changes in morphology and dressing percentage. The objective of the present study was to determine the effect of rainbow trout growth hormone cDNA (rtGHcDNA) on the morphology, dressing percentage and condition factor of the common carp, Cyprinus carpio.

MATERIALS AND METHODS

P₁ transgenic common carp were produced by microinjection of rtGH cDNA linked to the long terminal repeat of Rous Sarcoma virus into the fertilized eggs of carp (Zhang et al., 1990). All transgenic carp that have been evaluated produce rainbow trout growth hormone (Chen et al., 1993). Four P₁ transgenic males were crossed with four transgenic females and the F₁ spawn were reared separately, one family per experimental group. The families were designated 1, 7, 8 and 18. These carp were reared for 16 months in USDA approved confinement ponds at Auburn University. Morphometric measurements were recorded to the nearest 0.1 mm with a dial calipers following the procedure described by Dunham et al (1983). The morphometric measurements

included were total length, head length, head depth, head width, body length, body width and body depth, caudal peduncle width and depth. The morphometric measurements were transformed to ratios by dividing by total length to standardize for body size (Dunham et al., 1985). Dressing percentage, weight of the fish after beheading, eviscerating and removal of fins, was obtained. Length and weight data were used to determine condition factor (CF), $(\text{weight}/\text{length}^3) \times 100$ (Piper et al., 1986). Means of morphometric measurements, dressing percentage and condition factor were calculated for transgenic and control fish and compared with student's t test using families 1,7,8 and 18 in which observed growth of transgenic and control individuals were different as replicates. Correlations between morphometric ratios and either weight, length, dressing percentage or condition factor were computed. Correlation coefficients were transformed to inverse hyperbolic tangents (Zar, 1984) to test the difference ($p < 0.01$) between correlation coefficients of the transgenic and control carp.

RESULTS

The observed differences in body weight were 22, 14, 3 and 37 %, respectively, for families 1,7,8 and 18 (table 1). Transgenic families that grew faster than controls also had larger ($P < 0.05$) morphometric ratios than controls. Head and body measurements were 4.5 - 8.5 % larger and caudal changes were more dramatic, an increase of 15 - 18 %. A significant phenotypic correlation ($p < 0.01$) existed between the weight and length of carp of transgenic and control carp in all the families (data not shown). However, the correlation between length or weight and head measurements were negatively correlated in all the families of carp, suggesting that the head does not grow proportionately to its length or weight. The correlation coefficients between length and weight were different ($p < 0.01$) for transgenic and control carp in families 7 and 18. Also in family 18, the head length of the transgenic fish grew more slowly than that of the controls. In family 7, head width grew more slowly for controls than the transgenic full-siblings ($P < 0.05$). Most of the morphometric ratios were negatively correlated with dressing percentage (data not shown). This negative correlation indicates that a fusiform body will give a better dressing yield than a truncate fish. The range in body characteristics for transgenic and control common carp are provided in table 2. Condition factor and dressing percentage were not significant between transgenic and control carp in all the four families tested. Most correlations between dressing percentage and morphology or size were not different for transgenic and control carp.

DISCUSSION

In an earlier study, Zhu (1990) reported an increase in muscle thickness and body width for transgenic common carp, and an alteration in the shape of the transgenic loach both containing human GH gene. This observation was not quantified and very few individuals were observed. In the current study, transgenic and control carp were different in morphology, confirming Zhu's (1990) contention that transgenic fish expressing growth hormone have altered body shapes. Apparently, different body areas do not respond in a proportionate manner to the elevated GH levels. Relative to total length, transgenic carp had larger heads, wider and deeper bodies. However, these changes did not affect dressing percentage and condition factor.

REFERENCES

- CHEN, T. T., K. KIGHT, C.M.LIN, D.A. POWERS, M.HAYAT, N.CHATAKONDI, A.C.RAMBOUX, P.L.DUNCAN AND DUNHAM, R.A. (1993) Molecular Marine Biology and Biotechnology, 2:88-95
- DUNHAM, R.A., M.BENCHAKAN, R.O.SMITHERMAN and CHAPPELL, J.A. (1983) Journal of the World Mariculture Society, 14:668-675
- DUNHAM, R.A., C.JOYCE, K.BONDARI and MALVESTUTO, S.P. (1985) Progressive Fish Culturist, 47:169-175
- DUNHAM, R.A. (1990) AgBiotech New and Information, 2: 401-406
- PIPER, R.G., I.B.McELWAIN, L.E.ORME, J.P.McCRAREN, L.G.FOWLER and LEONARD J.R. (1986) Fish Hatchery Management., 517p.
- POWERS, D. A. (1991) Advances in Genetics, 29 : 119-228
- ZAR, J.H. (1984) Biostatistical Analysis, 718p.
- ZHANG, P., M.HAYAT, C.JOYCE, L.I.GONZALEZ-VILLASENOR, C.M.LIN, R.A.DUNHAM, T.T.CHEN and POWERS, D.A. (1990) Molecular reproduction and development, 25:3- 13
- ZHU, Z. (1990) In Transgenic fish ed. C.L.Hew., 92-119

Table 1. Means for morphological characteristics of transgenic (+), containing rtGH cDNA and control (-) common carp

mean ± standard deviation								
Group	N	Weight (g)	Total length	Head* width	Head* length	Head* depth	Body* width	Body* depth
1(-)	13	457	280	.194	.199	.141	.294	.126
		±349	±78	±.043	±.053	±.033	±.081	±.032
1(+)	7	562	315	.215	.214	.149	.325	.134
		±283	± 64	±.028	±.028	±.057	±.037	±.066
7(-)	39	325	262	.206	.199	.143	.299	.125
		±193	± 56	±.033	±.040	±.029	±.057	±.031
7(+)	23	371	285	.196	.205	.155	.312	.131
		±174	± 49	±.041	±.036	±.026	±.047	±.036
8(-)	86	319	259	.221	.211	.152	.321	.133
		±187	± 49	±.040	±.037	±.030	±.063	±.029
8(+)	23	328	256	.206	.209	.151	.311	.135
		±238	± 70	±.056	±.056	±.044	±.097	±.041
18(-)	12	155	207	.191	.226	.149	.285	.139
		± 68	± 47	±.025	±.037	±.022	±.041	±.024
18(+)	12	211	233	.212	.227	.153	.314	.146
		±140	± 47	±.043	±.030	±.029	±.060	±.033

Group	N	Caudal* peduncle depth	Caudal* peduncle width	Condition factor	Dressing percentage
1(-)	7	.047 ±.014	.102 ±.036	1.826 ±.391	55.9 ± 3.4
1(+)	13	.062 ±.012	.121 ±.032	1.721 ±.339	58.7 ±4.3
7(-)	39	.056 ±.011	.111 ±.028	1.627 ±.590	63.3 ±12.2
7(+)	23	.060 ±.013	.121 ±.027	1.583 ±1.040	61.0 ±10.4
8(-)	86	.061 ±.016	.120 ±.033	1.646 ±0.694	60.8 ± 9.0
8(+)	23	.060 ±.018	.117 ±.040	2.537 ±0.543	60.2 ±9.56
18(-)	12	.054 ±.013	.108 ±.025	1.475 ±.019	59.6 ±0.6
18(+)	12	.065 ±.017	.125 ±.030	1.478 ±.014	58.89 ±0.9

^{a,b}means of transgenic families larger than controls ($P < 0.05$, t-test). Only families 1, 7 and 18 considered.

*each measurement divided by total length.

All ratios, dressing percentage and condition factor were corrected by regression to a standard length for each family.

Table 2. Range of body characteristics for transgenic (+) containing the rtGH cDNA and control (-) common carp.

Group	Weight (g)	Total length (mm)	Conditon factor	Dressing percentage
1(-)	127-999	195-398	1.50-2.61	51.1-61.8
1(+)	204-998	221-434	1.34-2.64	52.8-65.1
7(-)	72-852	146-390	1.12-2.59	36.4-84.8
7(+)	170-851	205-410	0.67-3.96	43.5-81.6
8(-)	52-928	156-375	0.86-2.71	39.8-82.4
8(+)	57-980	149-439	1.75-3.55	42.7-79.9
18(-)	50-311	111-283	1.43-1.49	59.1-68.0
18(+)	88-522	179-325	1.45-1.50	58.1-59.1