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ISSN 0792 - 156X

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PUBLISHER:  
Israeli Journal of Aquaculture - BAMIGDEH -  
Kibbutz Ein Hamifratz, Mobile Post 25210,  
ISRAEL  
Phone: + 972 52 3965809  
<http://siamb.org.il>

## **PREDICTION OF CARCASS QUALITY TRAITS OF COMMON CARP BY X-RAY COMPUTERIZED TOMOGRAPHY**

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(Received 9.11.02, Accepted 18.11.02)

Key words: carcass quality, common carp, computerized tomography, fat content, prediction

### **Abstract**

X-ray computerized tomography (CT) and chemical analysis were used to determine the fat and protein contents in the fillet of table-sized mirror carps. Serial CT scans were taken along the body from the operculum to the beginning of the caudal fin. After scanning, the anesthetized fish were immediately processed; slaughter value and fillet yield were determined before taking samples for chemical analysis. Independent variables of prediction equations were produced from the CT density values, which ranged from -90 to 160 on the Hounsfield scale. Based on the data derived from the CT scanning, areas (cm<sup>2</sup>) of muscle and fat tissue were identified. Fat deposition was highest in the dorsal fin region. The muscle area varied according to the body shape and seems to be inadequate for predicting the slaughter value of common carp. The fat and protein contents of the fillet, when predicted from scanning only the dorsal region, were as accurate as when predicted from scanning the whole body and were  $R^2 = 0.88$  and  $0.86$ , respectively.

### **Introduction**

Although common carp is the oldest domesticated fish species, carcass traits are not taken into account in breeding programs. One of the reasons is that, worldwide, an insignificant part of the produced carps are industrially processed. On the other hand, measurement of important carcass traits such as slaughter value and fillet yield is labor consuming and

difficult to standardize. Some indices, such as the profile index which describes the body shape of live fish (Ankorion et al., 1992) and the condition factor, have been accepted for a long time. Others are new in carp breeding, such as measuring belly thickness and cross-sectional areas at given points to quantify carcass quality (Sahu et al., 2000). Slaughter

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value (degutted carcass), fillet weight and fillet crude fat are measured in the final phase of performance testing of Hungarian common carp races (Carp Performance Testing Code 2, 1999). However, determination of the total body fat content could be important as carp can deposit substantial amounts of lipids as visceral fat.

Csengeri et al. (2000) found that the slaughter value of Hungarian carps varied between 53.6% and 60.4% and domesticated varieties had a higher (44.3%) fillet yield than wild ones (39.7%). Wide variance of the raw fat content in common carp fillets was reported by Lengyel et al. (2001) in both natural waters ( $3.1\pm 3.3\%$ ) and fish ponds ( $10.0\pm 4.5\%$ ) in Hungary. Schrenkenbach et al. (2001), determining the total body composition of German common carp from lakes and ponds, also found wide variance of fat ( $8.5\pm 4.4\%$ ). Fillets of Hungarian common carp races have significant differences in fat content (Hancz et al., 2002) but variance within a genotype has not been investigated until now. Substantial genetic variance in carcass value traits, including fat content, was found in Atlantic salmon (Rye and Gjerde, 1996). So, selective breeding may also produce higher valued common carp varieties.

Body composition of the common carp varies according to keeping conditions and is influenced mostly by feeding (Fauconneau et al., 1995). The effects of feeds on body composition were proved to be highly significant in various experiments. Feeding of high carbohydrate cereals is a general practice in the semi-intensive technology of pond culture and may result in a high level of body fat when protein rich natural feed sources are limited (Eröss, 1982; Oberle et al., 1997).

Prediction of body composition by *in vivo* methods has many advantages compared to traditional chemical analysis. Besides being able to use the examined fish for genetic improvement, *in vivo* methods can be used to study changes in body composition over time. Computer tomography (CT) was used by Gjerde (1987) in a study on rainbow trout selection. He found a high correlation between the observed and predicted values of

water (0.88), protein (0.68) and fat (0.89) content. Rye (1991) used CT to predict carcass composition of Atlantic salmon. The objective of the present study was to predict the slaughter value, fillet yield, and crude fat and protein contents of the common carp by CT scanning of live, anesthetized fish.

### Materials and Methods

The investigation was carried out in the Diagnostic and Radiation Therapy Institute and Fish Laboratory of the Faculty of Animal Science, University of Kaposvár, Hungary. Eighteen common carp (*Cyprinus carpio* L.) were scanned; all of them belonged to the mirror carp type. The fish were collected in the autumn harvest (November) and can be considered a random sample of Hungarian table-sized common carp. The live weight of the sexually matured fish was  $1837\pm 441$  g. Both sexes were represented at an equal rate (nine males and nine females). CT scans (images) were taken under anesthesia using Norcaicum (Matuk, 1987). Three fish at a time were placed in a specially designed holder. The examinations started by taking an overall topogram in which the anatomical points of the scans or body intervals could be marked (Fig. 1).

Twenty to 30 scans were taken from the end of the operculum to the beginning of the caudal fin, depending on the size of the fish. Altogether, seven body intervals were produced by combining 3-4 neighboring images. The CT scans were adjusted to scan 10 mm "slices" of the fish. The picture-forming pixels make it possible to determine density in the slice, measured in Hounsfield units (HU), which enabled us to estimate the volume of the muscle and fat tissue in the body from the serial scans. Pixel density data were collected from the fillet on the right side of the body. Extremely high or low density values corresponded to bone or air and were excluded. Only those that corresponded to fat and muscle were retained, i.e., those within the range of -90 to 160 HU (a range of 250 HU). Every ten consecutive HU values were combined, resulting in 25 HU variables. Details of CT scanning and

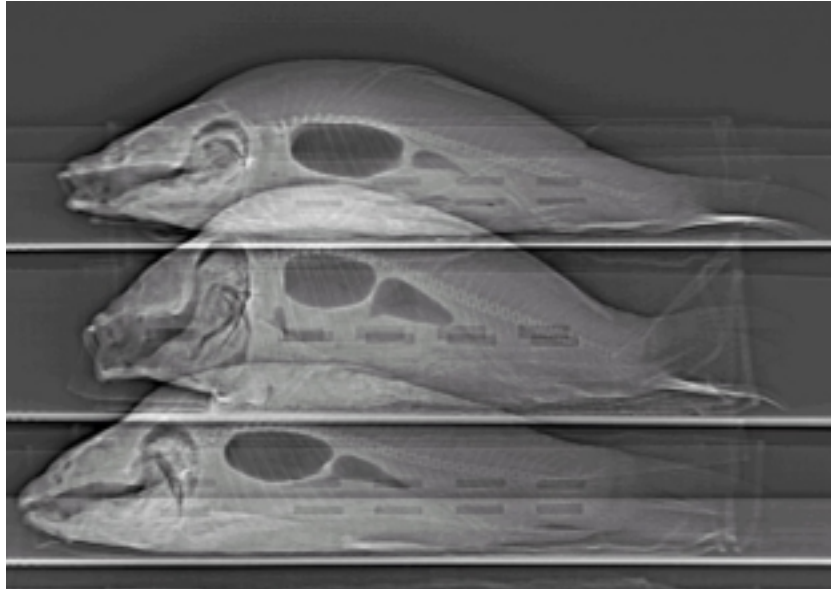


Fig. 1. Topograms of common carp.

data processing can be found in Romvári et al. (1998). Based on the data derived from the CT scanning areas ( $\text{cm}^2$ ), the muscle and fat tissue were determined.

Immediately after scanning, the anesthetized fish were processed. The fish were dissected and slaughter value was determined according to the codex of performance testing of Hungarian common carp races. For chemical analysis, the right-hand fillets were homogenized and aliquot samples were used. Dry matter was determined by drying the fillets at  $105^\circ\text{C}$  to a constant weight. Crude fat and crude protein were measured according to the Hungarian standard (MSz 6830).

Differences in carcass traits due to sex were evaluated by *t*-probe. Principal component analysis was applied to decrease the multi-collinearity of the neighboring HU variables (factor analysis; SPSS, 1996). The principal components were calculated from the HU variables of the body intervals. Prediction equations were produced by linear regression, using a stepwise method.

### Results

The means, standard deviations and coefficients of variation of the live weight and carcass traits are summarized in Table 1. The slaughter value and fillet ratio varied little while the coefficients of variation of the chemical components of the fillet samples were very high. Differences between the two sexes were not significant. The areas ( $\text{cm}^2$ ) of muscle and fat tissue were determined by the number of pixels falling into the density intervals that are characteristic of muscle and fat. Fat deposition was highest in the region where the dorsal fin begins (Fig. 2).

The measured muscle tissue area followed the body shape and provided little information about slaughter value ( $R^2=0.55$ ) or fillet ratio ( $R^2=0.38$ ). The slaughter value and profile index have practically no connection ( $R^2=0.002$ ). Using the stepwise method where the dependent is the slaughter value, only the weight of the right-hand fillet remains in the regression model as a significant independent variable ( $R^2=0.60$ ).

In studies on rabbits (Romvári et al.,

Table 1. Means, standard deviations (S.D.) and coefficients of variation (CV) for different traits of common carp (n=18).

	Mean	S.D.	CV (%)
Body weight (g)	1837	441	24.0
Slaughter value (%)	58.3	2.41	4.1
Fillet (%)	42.6	1.89	4.4
Water (%)	70.5	6.63	9.4
Crude protein (%)	12.7	3.61	28.4
Crude fat (%)	15.3	6.31	41.2
Crude ash (%)	0.96	0.31	32.3

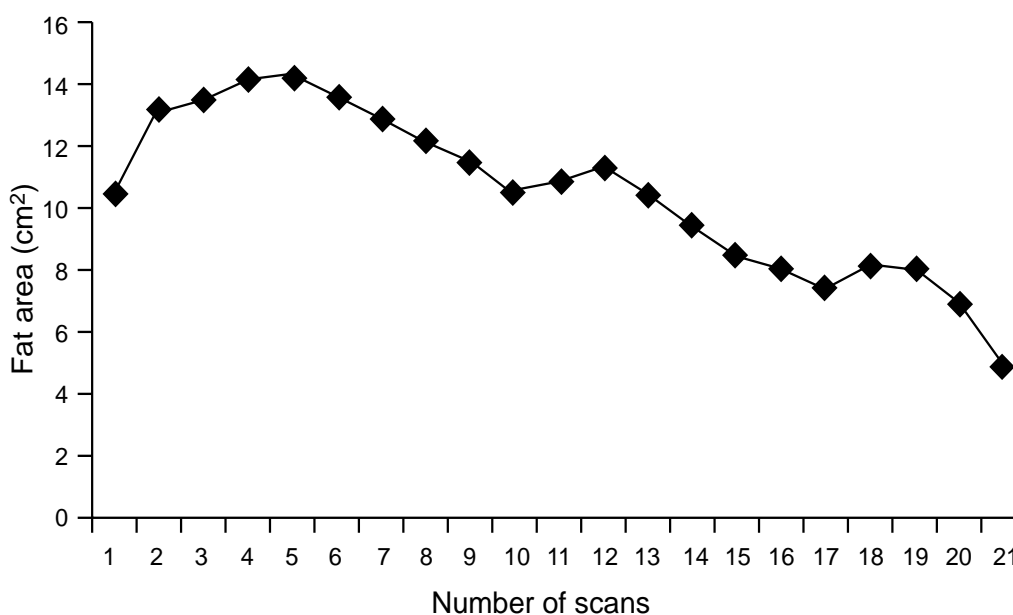


Fig. 2. Distribution of fat tissue along the body of common carp. Low numbers refer to areas near the dorsal fin, high numbers are near the operculum.

1998), the variables of the equation used to predict carcass components originated from HU values that ranged between -200 and 200 and corresponded to the fat and muscle tissues. The corresponding values in the present study varied from -90 to 160. The rela-

bility of predicting crude fat and/or crude protein may have been decreased by the strong linear connection between neighboring HU variables. With the applied principal component analysis, this effect was lessened by finding linear combinations of those variables

that explain most of the variability. Several principal components explained approximately 90% of the total variance of the original variables (HU1 – HU25), depending on the method applied. Predictions of raw fat and raw protein content were made using the HU values created on the basis of all the intervals and on the basis of only of the dorsal region, respectively. Results are given in Table 2.

Six principal components calculated from 161 original variables (Interval1, Interval2...Interval7 x HU1, HU2...HU25) described 90.3% of the original variance of the

whole body and four factors explained a slightly larger part of the variance when only the data of the dorsal fin region were used. Equations for predicting fillet raw fat and protein were constructed by the stepwise procedure. Basic data of the equations are presented in Tables 3 and 4.

Almost the same estimation precision was achieved by scanning only the dorsal fin region as by scanning all seven body regions. The close correlations between the predicted and measured fat and protein contents are seen in Figs. 3 and 4.

Table 2. Principal components explaining the variance (%) of the original Hounsfield unit (HU) variables.

Factor number	Variance explained (%)	
	All regions	Dorsal fin region
1	54.8	57.3
2	17.3	18.4
3	6.9	8.5
4	4.6	5.9
5	4.0	-
6	2.3	-
Total	89.9	90.1

Table 3. Basic data of the prediction equations for fat content.

All regions	$R^2 = 0.867$		Dorsal fin region	$R^2 = 0.881$	
	Variable	B		Sig.	Variable
FAC 1	8.570	0.000	FAC 1	8.402	0.000
FAC 4	-2.229	0.001	FAC 4	-3.022	0.003
FAC 6	3.178	0.025	-	-	-
Constant	50.789	0.000	Constant	50.789	0.000

Table 4. Basic data of the prediction equations for protein content.

<i>All regions</i>			<i>Dorsal fin region</i>		
<i>Variable</i>	<i>B</i>	<i>Sig.</i>	<i>Variable</i>	<i>B</i>	<i>Sig.</i>
FAC 1	-7.639	0.000	FAC 1	-7.449	0.000
-	-	-	FAC 4	2,937	0.003
Constant	43.767	0.000	Constant	43.767	0.000

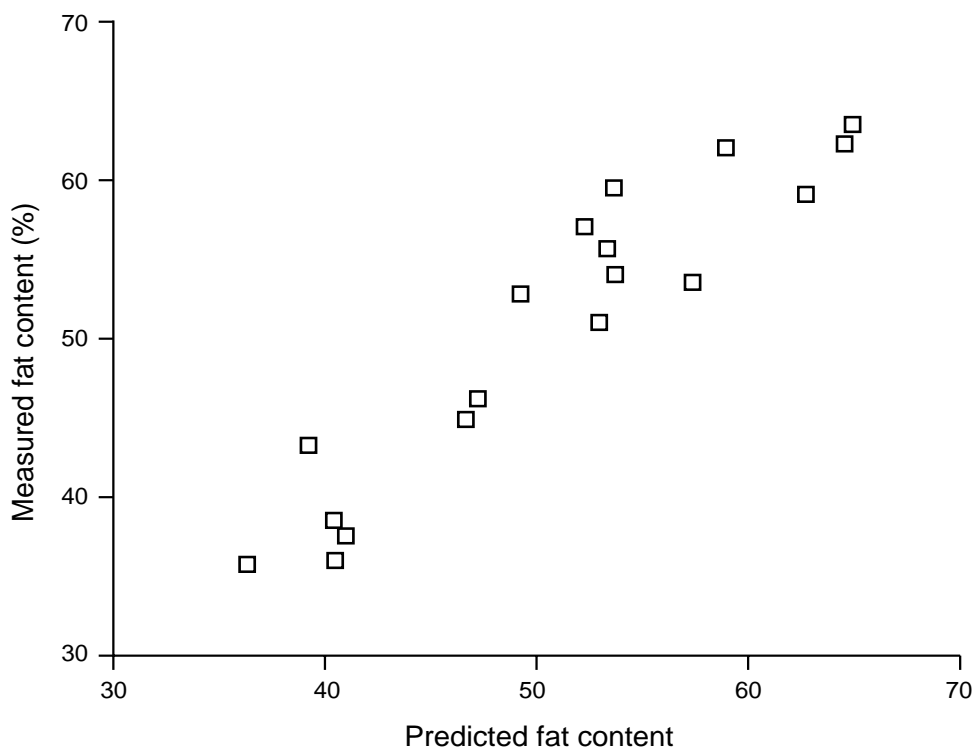


Fig. 3. Correlation of predicted and measured fat content in the fillet of common carp in the dorsal region ( $R^2 = 0.881$ ).

### Discussion

The use of Norcaicum to anesthetize the common carp was successful; all the fish survived the average 12-15 min needed for the simultaneous scanning of three fish. The slaughter value of the carps ( $58.3 \pm 2.41\%$ ) was in the

range given by Csengeri et al. (2000) but was lower than the  $63.2 \pm 2.5\%$  value for 13 mirror carp races tested during the past five years in Hungary (Hancz et al., 2002). This difference can be explained by the fact that the fish

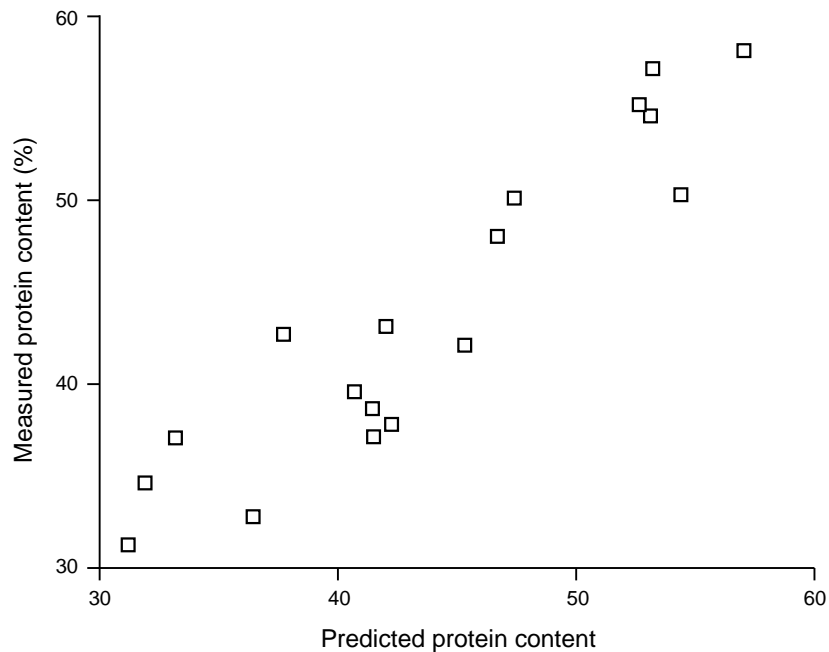


Fig. 4. Correlation of predicted and measured protein content in the fillet of common carp in the dorsal region ( $R^2 = 0.862$ ).

investigated here were of a commercial stock while the officially tested carps (Hancz et al., 2002) were from a higher level farm breeding stock. In any case, the slaughter value seems to be a trait difficult to predict by *in vivo* CT scanning, even determining the muscle area of the whole body was difficult. It could be calculated from the fillet weight but only with an accuracy of  $R^2 = 0.60$ . Presumably the small number of fish investigated caused the relatively low prediction accuracy obtained in this study.

Fillet yields were close to the values given by Csengeri et al. (2000) and Hancz et al. (2002) for Hungarian common carp. The dry matter, raw fat and raw protein values of the fillet were comparable to values in the relatively rich literature on this topic. Correlations between these components were in accordance with the results of Schrenkenbach et al. (2001).

The fat and protein contents of the fillets were predicted with high accuracy using the

applied methods. Our results are very close to those of Gjerde (1987) who received  $R = 0.89$  and  $R = 0.68$  between predicted and measured fat and protein contents, respectively, using similar methodology for salmon carcasses. The dispersion of fat deposits can also be detected by CT scanning. Fillet fat and protein contents predicted from CT data derived from scanning only the dorsal region resulted in the same accuracy as data derived from scanning the whole body, making the methodology cost effective.

Preliminary results of performance tests of Hungarian common carp races in the last five years suggest that mirror carp genotypes, especially, show high individual variance (coefficient variation = 9.4-10.6%) in fillet fat content (Hancz and Gorda, unpubl.). Therefore, the *in vivo* methodology described here can be very promising from the point of view of future selection programs. More investigation is needed to clarify the correlation of fillet and total body fat content.



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