

POTENTIAL FOR GENETIC IMPROVEMENT OF THE MAIN SLAUGHTER YIELDS IN COMMON CARP WITH *IN VIVO* MORPHOLOGICAL PREDICTORS

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Slaughter traits are of high importance especially for species sold as processed body parts, similarly as in common carp. However, recording of processing yields is impossible on live breeding candidates, and alternatives for genetic improvement are either sib selection based on slaughtered fish, or indirect selection on correlated traits recorded *in vivo*. However, morphological predictors that can be measured on live fish and that correlate with real slaughter yields hence remain a possible alternative. Thus, the aim of this study was to i) determine morphological predictors by external (phenotyping, 2D imaging) and internal measurements (ultrasound imagery) that can be combined by linear regression to predict slaughter yields (headless carcass and fillet yields), ii) estimate genetic parameters of slaughter yields and their predictors, iii) predict and compare the potential genetic gain based on mass selection, sib selection and indirect selection of slaughter yields.

The experimental stock was established by a partial factorial design of 20 dams and 40 sires, and 1553 progenies were assigned to their parents using 12 microsatellites and reared communally until market size under semi-intensive pond conditions. Fish were phenotyped for body weight (BW), standard length (SL), head length (HL), body height (BH), muscle fat (% Fat) and slaughter yields – headless carcass (hl-Carss) and fillet yields (Fill). External measures were performed using 2D imaging (Canon EOS 1000D) and twenty coordinates of morphological points were digitized using ImageJ with the Point Picker plugin. These coordinates were used to calculate lengths, heights and areas. Five internal measurements were collected through ultrasound imagery (Hospimedi LC1000, 7.5 MHz). Slaughter yields were calculated as log-log residuals instead of common percent-expressed slaughter yields, and their predictors were estimated using a multiple linear regression model, including BW, % Fat and external and internal morphometric variables using the reg.best function of the FactoMineR of R software. Genetic parameters were calculated using single trait (heritabilities) and multi trait (genetic correlations) animal model in DMU software. Genetic gains were calculated for theoretical mass selection (MS), full-sib selection (FSS) and indirect selection (IS) using 10% and 30% selection intensities.

Slaughter yields were highly heritable ($h^2 = 0.46$ for headless carcass yield, 0.50 for fillet yield) and strongly genetically correlated with each other ($r_g = 0.96$). The accuracy of the phenotypic prediction was high for headless carcass yield ($R^2 = 0.63$) and intermediate for fillet yield ($R^2 = 0.49$). Interestingly, heritability of predicted slaughter yields ($0.48 - 0.63$) was higher than that of the real yields to predict, and had high genetic correlations with the real yields ($r_g = 0.84 - 0.88$). In addition, both predicted yields were highly phenotypically and genetically correlated with each other (0.95 for both), suggesting that using predicted headless carcass yield in a breeding program would be a good way to also improve fillet yield. Besides, two individual predictors (P_1 and P_2) included in the prediction models and two simple internal measurements (E4 and E23) exhibited intermediate to high heritability estimates ($h^2 = 0.34 - 0.72$) and significant genetic correlations to the slaughter yields ($r_g = 0.39 - 0.83$). The expected genetic progress per generation on fillet yield using indirect selection criteria was even slightly higher than the expected gain obtained by traditional sib selection (IS = 0.40% , 0.61% ; FSS = 0.43% , 0.66% for 30% and 10% selection pressure, respectively). The overall results show that there is a solid potential for genetic improvement of slaughter yields by selecting for predictor traits recorded on live breeding candidates of common carp.

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