

ABSTRACTS

SESSION 8: GENETICS OF NUTRITION

GENETIC IMPROVEMENT OF FEED CONVERSION RATIO IN SEA BASS USING NOVEL PHENOTYPES AND GENOMIC DATA

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Abstract

Feed conversion ratio (FCR) is difficult to improve by selective breeding because individual feed intake is impossible to measure in groups of fish. Therefore, we tested if two different indirect traits (easier to measure) could explain FCR of fish in groups. The first trait was weight loss during fasting. Theoretically, fish with lower weight lost during fasting have better FCR due to lower maintenance needs. The second trait was individual FCR measured in aquarium under restricted feeding. Under restricted feeding, the fastest growing animals are the most efficient. Finally, we tested if the FCR of groups of fish would depend on one or the other indirect trait. First, 764 sea bass were phenotyped for their individual FCR and daily growth coefficient (DGC_aquarium) in aquariums by counting uneaten pellets daily and measuring body weight gain over 4 weeks. Second, the 764 fish were phenotyped for their weight loss during fasting calculated as the average (negative) DGC over 2 feed deprivation periods (DGC_fasting). The 764 fish were then arranged in 16 tanks for 6 weeks to measure FCR per tank by counting uneaten pellets daily and measuring body weight gain. Finally, 466 of these fish as well as their parents and their grand-parents were genotyped for 1,110 SNP markers to estimate genomic heritability and genomic estimated breeding value (GEBV) for the different traits using single-step GBLUP. Individual FCR, DGC_aquarium and DGC_fasting were all heritable ($h^2 = 0.40, 0.73$ and 0.17 respectively). Additionally, individual FCR and DGC_aquarium were strongly genetically correlated ($r = -0.98$), which was a direct consequence of the restricted feeding condition. However, the genetic correlations between individual FCR or DGC_aquarium and DGC_fasting were not significant ($r = -0.21 \pm 0.19$ and $r = 0.05 \pm 0.12$ respectively). Finally, the FCR per tank was significantly linked to the average phenotypic individual FCR of the fish composing the tank and to the average GEBV for DGC_fasting of the fish composing the tank. This means that both indirect traits, individual FCR and DGC_fasting, can be improved via selective breeding and that their improvement should generate correlated response in FCR of fish in groups.

Keywords: feed efficiency, individual phenotypes, genomic, sea bass

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CYSTEAMINE PATHWAY: A MAJOR TAURINE SYNTHESIZING PATHWAY IN COMMON CARP *CYPRINUS CARPIO*

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There are three identified taurine synthesizing pathways namely cysteine-sulfonic acid, cysteamine and cysteic-acid pathways. In cysteamine pathway the product of co-enzyme A turnover will form cysteamine and the cysteamine dioxygenase (ADO) will then convert cysteamine into hypotaurine. To verify the taurine synthetic ability of common carp, cysteine and cysteamine (CHS) was injected to juvenile common carp at dose of 0, 0.25, 0.5 and 1mM and samples were collected at 0,2,4,8,12 and 24hrs. Injection of L-cysteine showed interaction and significantly affects levels of plasma taurine. High amount of L-cysteine significantly affected the plasma methionine level. Both L-cysteine and CHS did not show interacting effect on hepatic total amino acid but significant increased in taurine after 24 hrs was observed in 0.25 mM injected samples. The interacting effect of injecting L-cysteine significantly affects cysteine dioxygenase 1 (CDO1), cysteine sulfonic acid decarboxylase (CSD) and ADO but not cysteine dioxygenase 2 (CDO2). CHS showed significant interacting effect on the gene expression of CDO1, CDO2 and ADO but not CSD. The effect of dietary sulfur amino acid related compounds on content of sulfur amino acid related compound in hepatopancreas, gene expression of taurine synthesizing enzymes, somatostatin and growth hormone, growth and morphology was investigated. Common carp were fed either of eight diets supplemented with different level of 1.0 and 1.5% CHS, 1.5 and 3.0% cysteine, 1.0 and 1.5% methionine, and 0.5 and 1.0% taurine for 30 days. All sulfur amino acids increased taurine deposition in the carcass (18.5-86.9 g/kg), and highest taurine content was observed in fish fed 1.5% CHS. The CDO1/2 tend to be down-regulated by supplementing cysteine and 0.5% taurine. Addition of cysteine, methionine and CHS down-regulate CSD. ADO was down-regulated by methionine, cysteine and 0.5%taurine. The somatostatin 14 (SST14) was up-regulated by CHS. While insulin-like growth factor (IGF-1) was up-regulated by 1%taurine and cysteine. The present study suggests that CHS pathway is major taurine synthesizing pathway in common carp.

Keywords: taurine, CHS, cysteamine dioxygenase, cysteamine pathway

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ADAPTATION OF RAINBOW TROUT GENOTYPES TO SIMULTANEOUS CHANGES IN MULTIPLE PLANT-BASED DIET INGREDIENTS

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Abstract

Feed composition is one of the fastest changing environmental factors for farmed fish. Production of industrial aquafeeds is a dynamic process in which raw materials and their concentrates are varied from one feed batch to another, depending on the availability, nutritional quality and price of the ingredients. There is not a single fixed diet formula but rather many different combinations of several ingredients that can be used to produce a feed with more or less the same proximate composition. We tested the genetic adaptation of rainbow trout to such a dynamic process in which several plant-based raw materials are simultaneously changed. We reared 1400 rainbow trout from a pedigreed population on 7 different diets to analyse fish performance along three changing diet ingredient mixes: fish meal (FM), a soya protein-wheat gluten concentrate (S-MIX) and a pea protein-wheat gluten concentrate (P-MIX). This mixture diet design analysed with random regression animal model allowed the identification of diet mix combinations that support good fish performance, identified as the area on the response surface at which fish performance is at least 95% of the maximum observed performance. As expected, FM was the most optimal diet supporting high growth for all progenies of sires, but the progenies differed in the extent of the area with at least 95% of the maximum growth. The genotypes growing the fastest on FM generally had small 95% optimal response area, i.e., they were specialists and suffered the most when FM was replaced with S-MIX and P-MIX. The genotypes growing the slowest on FM had much larger 95% area (more generalist genotype). This was due to the among-family variation in the sensitivity to plant protein concentrate mixes, and the fast-growing genotypes having unique physiological needs for maintaining their high genetic potential. Nevertheless, the analysis showed that with the availability of genetic variation and the limited amount of adverse genotype-by-diet interactions, breeding programmes can make fish more adapted to the novel plant-based feeds. There is further need to genetically improve feed utilisation on new feeds, and simultaneously, to tailor-make feeds specifically for the genetically superior fish with their unique nutritional needs.

Keywords: FCR; Genetic correlation; Genotype-by-diet interaction, Heritability.

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COMPARATIVE GENOMICS STUDY IN CHINESE PERCH AND GRASS CARP

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Abstract

As economically relevant traits, feeding behavior and food preference domestication determine production cost and profitability. Chinese perch (*Siniperca chuatsi*), as an intensively aggressive piscivore, has very unique food preference. In the wild, once the fry start feeding, it feed solely on live fry of other fish species. In rearing conditions, Chinese perch also accept only live prey fish, refusing dead prey fish or artificial diets. Among major species of Chinese perch, *S. scherzeri*, is much easier to accept dead prey fish compared to *S. chuatsi*, and the individual difference in accepting dead prey fish is further amplified in the hybrid F1 of *S. chuatsi* (♀) × *S. scherzeri* (♂). Multiple differentially expressed genes involved in retinal photosensitivity, circadian rhythm, appetite control, learning and memory pathways, as well as SNPs account for this dramatic difference. To further study on the specialized traits, the diploid *S. chuatsi* genome has been sequenced by PACBIO SMRT and assembled as the first “nearly finished” teleost genome assembly. Three other members of the family of Siniperidae (*S. kneri*, *S. scherzeri* and *C. whiteheadi*) have been re-sequenced. Comparative genomics study provides insights into the specialized biological characteristics of Chinese perch, including aggressive behavior, feeding on live prey fish only, degraded chemical sensation and low visual acuity, fast growth. Grass carp (*Ctenopharyngodon idella*) is an ecologically appealing model of vertebrate herbivore. Grass carp goes through a transition from carnivory to herbivory during its life cycle. However, little is currently known about genes determining the food habit transition, and how they could achieve higher growth rates on plant materials, which have a relatively poor nutritional quality. We showed that grass carp fed with duckweed (modeling fish after food habit transition) had significantly higher relative length of gut than fish before food habit transition or those fed with chironomid larvae (fish without transition). Using transcriptome sequencing, we identified 10,184 differentially expressed genes between grass carp before and after transition in brain, liver and gut. We suggest that the food habit transition from carnivory to herbivory in grass carp might be due to genes related to enhanced gut growth, increased appetite, resetting of circadian phase and enhanced digestion and metabolism. We also found extensive alternative splicing and novel transcript accompanying food habit transition. Elucidating the genes regulating these unique food preference, including the live prey in Chinese perch as carnivorous fish, and the food habit transition from carnivory to herbivory in grass carp as herbivorous fish, could lead to a better understanding of mechanisms controlling food habit, promoting the intake and utilization of feedstuff in fish, increasing the replacement of animal protein by plant protein in animal feed, and decreasing the cost of cultivation and the pollution of the environment.

Keywords: food intake regulation; Chinese perch; live prey fish; grass carp; food habit transition

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DIETARY CARBOHYDRATE PROMOTES HEPATIC *DE NOVO* LIPOGENESIS IN BARRAMUNDI (LATES CALCARIFER).

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Barramundi are a highly valued aquaculture species, and advanced formulated feeds underpin optimised growth performance. As obligate carnivores, they have a demonstrated preference for dietary protein over lipid or starch to fuel growth energy. As an alternative to fishmeal, dietary protein sources for carnivorous fish have been replaced with plant-based ingredients, but tend result in the deposition of substantial amounts of lipid. However, it is still unclear whether this overall increased adiposity can be directly attributed to dietary carbohydrates. In order to investigate how carnivorous fish regulate the nutritional cues for these ingredients, we examined the changes in metabolic regulation that occur after long-term feeding iso-energetic diets that contained an elevated proportion of digestible protein or starch energy. Fish fed a high proportion of dietary starch energy had a higher proportion of liver saturated fatty acids, elevated liver fatty acid synthesis and pentose phosphate pathway gene expression levels, but showed no change in plasma glucose levels, aminotransferase gene expression or growth signalling pathway activity. To further investigate how they metabolically affect lipid retention and synthesis, we determined lipogenic fluxes in barramundi using deuterated water ($^2\text{H}_2\text{O}$) as a metabolic tracer. Lipogenic fluxes for hepatic triglyceride (TAG) biosynthesis were estimated by measuring triglyceride TAG ^2H -enrichment by ^2H -NMR. The fractional synthetic rate for hepatic TAG (= *de novo* lipogenesis) was significantly higher in barramundi fed with the Starch diet compared with the Protein diet (0.62 ± 0.08 vs. 0.35 ± 0.10 % d^{-1} , respectively). Hepatic TAG-bound glycerol synthetic rates were much higher, but were not significantly different (Starch, 2.80 ± 0.31 vs. Protein, 3.40 ± 0.34 % d^{-1}), highlighting the role of glycerol as a metabolic intermediary. Curiously, fractional synthetic rates for hepatic free fatty acids were not statistically different. Water soluble hepatic metabolites were analysed by ^1H -NMR, and multivariate analysis of proton spectra showed partial separation due to dietary ingredients with variations in taurine and nicotinurate/niacinimide. Overall, dietary starch significantly reprogrammed hepatic metabolism, and promoted the storage of energy in the form of hepatic TAG through increased *de novo* lipogenesis. However, we speculate that free fatty acids and glycerol, as part of structural functioning, remain unaltered by dietary starch.

Keywords: Liver; metabolism; fish; nutrigenomics

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