

ABSTRACTS

SESSION 4: SELECTIVE BREEDING AND QUANTITATIVE GENETICS

GENETIC PARAMETERS OF CAVIAR PRODUCTION IN DNA-PEDIGREED OCTOPLOID SIBERIAN STURGEON (*ACIPENSER BAERII*)

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Abstract

Concomitantly with the collapse of wild sturgeon stocks from 1950 onwards, farming captive fish has been developing since the beginning of 1980s. Still, several factors remain detrimental to the development of breeding programs such as the long generation interval (> 7 years) and lethal trait measurement (caviar production). Moreover, very few publications reported genetic parameters in sturgeon species. The aim of our study was to estimate heritability of female reproductive traits and their genetic correlations to design breeding program in the octoploid Siberian sturgeon. 77 families were produced using 21 dams and 11 sires. Families were mixed after hatching and reared until the first female maturation. 494 females exhibiting a minimum oocyte size for caviar production were slaughtered for trait recording: body weight (BW), gonads weight (GW), total egg weight (TEW), egg size (ES), egg color (EC) and egg firmness (EF). Caviar yields were calculated related to body weight and gonads weight (BCY, GCY). The fish were DNA-pedigreed with microsatellite markers. Genetic parameters were estimated using VCE software with an animal mixed linear model allowing a multi-trait analysis. Heritabilities of BW, GW, TEW and ES were 0.40 ± 0.08 , 0.24 ± 0.07 , 0.31 ± 0.08 and 0.36 ± 0.07 , respectively. Heritabilities of BCY and GCY were 0.52 ± 0.07 and 0.45 ± 0.09 and those of EC and EF were 0.42 ± 0.08 and 0.13 ± 0.06 . Caviar yields were slightly negatively correlated with BW (-0.28 ± 0.09 and -0.37 ± 0.08) but strongly correlated with TEW (0.63 ± 0.09 and 0.76 ± 0.05). ES was negatively correlated with all traits except BW and EF. This work reports the first estimates of genetic parameters in Siberian sturgeon. Heritabilities are favorable to genetic improvement. Some limited negative genetic correlations may require attention to balance breeding index to prevent impairing some traits while trying to gain on others. Further investigations should confirm these results obtained with limited number of parents even if they are already used to adapt selection strategy on reproductive traits in fishes.

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Keywords:

Sturgeon, caviar, polyploid, genetic parameters, breeding program

* PH, AM, DG and BP designed the experiment. AB, OB, AM and PB organised and performed the data collection. AB, PH, FE and HC estimated genetic parameters. All authors contributed to the interpretation of the results.

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HERITABILITY OF GROWTH, AND IMMUNE TRAITS OF BIGHEAD CATFISH, *CLARIAS MACROCEPHALUS* GÜNTHER, 1864

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Abstract

The bighead catfish, *Clarias macrocephalus* Günther, 1864 (CMA) is an important freshwater fish in Southeast Asia in the sense that it receives high preference among consumers. Owing to its slow growth rate and disease susceptibility, the culture of this species has been replaced by the interspecific hybrid (CMA × the introduced *Clarias gariepinus*). However, the demand for the pure species was still high to be used as female brooder and also for the premium markets. The ultimate goal of this project is to genetically improve CMA for growth rate and disease resistance. In this study, a domesticated population of CMA was used to generate 74 full-sib families (31 half-sib families) following the factorial mating design. The fry were separately reared in hapas before being tagged by families using elastomer tags at the age of 120 days following by communal rearing in two replicates of polyethylene ponds. The data were collected at 310 days old when they reached a market size. The heritabilities estimated from 736 records were low for total length ($h^2_{TL} = 0.13 \pm 0.04$) and body weight ($h^2_{BW} = 0.09 \pm 0.03$). The immune traits (haematocrit-H, bactericidal activity-BA, lysozyme activity-LA, and alternative complement activity-ACH50) had low to moderate heritability ($h^2_H = 0.09 \pm 0.03$; $h^2_{BA} = 0.05 \pm 0.02$; $h^2_{LA} = 0.16 \pm 0.04$; $h^2_{ACH50} = 0.32 \pm 0.06$). The heritability of survival rate after disease (*Aeromonas hydrophila*) challenge was moderate ($h^2_{SUR} = 0.27 \pm 0.15$). Genetic correlation was high only between BW-TL, and BA-LA. Based on this information, the selection was performed by selecting 20% top families based on TL among the families with survival rates after disease challenge greater than overall mean (39%).

Keywords: immunity, disease resistance, growth, factorial design

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GENOTYPE BY ENVIRONMENT INTERACTIONS IN SHRIMP PRODUCTION: PRESENT SCENARIO, CONSTRAINTS, POTENTIAL AND IMPLICATION IN GENETIC IMPROVEMENT PROGRAMS.

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Abstract

The global shrimp aquaculture has increased from 1 million MT in 1995 to almost 5 Million MT in 2018. To meet the increasing demand for seafood, production has to be significantly increased. Sustainable and high production of shrimp needs the development of genetically-improved and efficient seed stock. To date, a number of breeding programs have been implemented in several countries. Despite the development of these breeding programs, potential genetic gain of shrimp has not as yet been realized with several factors identified that inhibit response to selection. Mounting evidence suggest that genotype by environment interactions (GXE), in which phenotypic expression of traits are different in different environments by genetically similar organisms, can effectively suppress the selection response in shrimp breeding programs. It is essential to understand the magnitude and pattern of GXE, e.g., genetic correlation of traits in various environments, to manage this problem. Presence of substantial GXE might compel shrimp breeders to develop environment-specific strains. Moreover, in the era of big data and genomic selection, GXE brings the prospect of genetic improvement across environments by developing novel selection strategies. With an aim to investigate the magnitude of this issue, we conducted a systematic review of literature on GXE in shrimp aquaculture. This review of 15 articles revealed that most of the GXE studies have been conducted with Pacific White Shrimp (*Litopenaeus vannamei*) and the traits most frequently studied are growth and survival. This suggests that GXE studies of shrimp are lacking for many economically important species and traits. A measure of non-unity genetic correlation between traits measured in different environments revealed a medium re-ranking average genetic correlation of 0.56 (ranged from -.82 to .99) of traits studied in shrimp, indicating that genetic improvement of shrimp in one environment may not be fully realised in other environments. Future studies should explore the framework of accounting and utilization of GXE in optimizing the structure of shrimp breeding program including genomic predictions across different environments.

Key words: Shrimp, aquaculture, breeding, genotype-by-environment interaction.

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ESTIMATION OF GENETIC PARAMETERS OF GROWTH, MORPHOLOGIC, IMMUNE AND BEHAVIORAL TRAITS IN A MIXED-FAMILY COHORT OF THE EUROPEAN ABALONE *HALIOTIS TUBERCULATA*.

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Abstract

Abalone aquaculture production has greatly increased in recent decades in response to a declining supply from fisheries. Selective breeding has been proposed to improve growth, the main trait constraining the increase of abalone aquaculture production. Among abalone species, *Haliotis tuberculata* is in an early stage of domestication and no estimates of heritability or genetic correlations were yet available for growth-related traits. In this context, weight, length, color, morphology, immunity and behavior traits were recorded on 945 offspring from a cohort generated by the full factorial mating of 24 sires and 16 dams reared under standard aquaculture conditions. SNPs were used to assign parentage in this cohort (Harney et al., *Aquaculture* 491 (2018): 105-113). BLUP was used to estimate additive genetic components and genetic correlations. Shell length showed moderate to high heritability estimates, ranging from 0.13 at 14 months old to 0.49 at 42 months old. Variation of foot color and bled meat yield were also proven to be significantly heritable, unlike circadian behavior rhythm and immune traits. Novel phenotyping methods such as ultrasound to estimate meat yield were developed and evaluated as potential tools for selection. A strong positive genetic correlation was observed between live weight and gonad yields, suggesting a trade-off between reproductive effort and meat yield. Sex ratio variation was measured between paternal half-sib families. Females were heavier at 32 months old but not at 42 months old, suggesting earlier reproductive allocation in males. As a result, a low but significant heritability of sex ratio (0.25 ± 0.11) was observed and moderate positive genetic correlations were estimated between sex ratio of families and weight when 32 and 42 months old. These observations raise the questions about sex determinism in *H. tuberculata* and the potential interest of selecting for high female-to-male ratios. Overall, our results provide essential information to initiate selective breeding to improve growth-related traits in the European abalone. More precise heritability estimates would however be needed to better predict the expected genetic gains.

Keywords: Heritability, Genetic correlations, Selective breeding, Abalone, Aquaculture.

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A CLOSER LOOK AT TURBOT GENOME REVEALS A GENETIC COMPONENT OF PARASITE RESISTANCE: NEW TOOLS FOR SELECTION

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Abstract

Developing genomic tools for cultured species is fundamental for improving production traits. Genetic breeding programmes are underway for turbot (*Scophthalmus maximus*) since 1992, and in addition to growth rate, there is an increasing interest for achieving more robust broodstock resistant to diseases. In this study, a genotyping by sequencing approach (2bRAD-seq) was used to identify and genotype 18,125 SNPs in a sample of 1,439 turbot from 36 families coming from a disease transmission experiment specifically designed for disentangling the different components of host response to infection by *Philasterides dicentrarchi*. This parasite is responsible of scuticociliatosis, a disease that results in severe economic losses for the aquaculture industry. SNP data from full-sib families was used to construct a high-density genetic map that allowed anchoring most of the turbot genome scaffolds into an improved assembly (96.5% coverage), reflecting the 22 chromosomes of its karyotype. Physical and genetic maps were compared to assess the recombination rate pattern across the genome and between individuals and sexes. Males displayed shorter maps, mainly due to a lower recombination around centromeres. The presence of genomic reorganizations (i.e. inversions) at specific chromosomes was suggested when comparing individual maps. The results from the disease transmission experiment indicated that susceptibility explains a larger proportion of genetic variation in resilience than tolerance. Heritability for susceptibility was moderate, and within the range found for similar traits in aquaculture species. Genome-wide association analyses allowed the identification of a candidate QTL region for resilience to scuticociliatosis that explained 33% of the total genetic variance, and had an effect of about five days of increased survival. Twelve loci located in this region belonged to the same linkage block and were put forward for validation in a new set of challenged families for future application in MAS programs. Finally, a genome-wide comparison between turbot, Japanese flounder and tongue sole enabled to integrate the genomes of the three species facilitating the transfer of information for improving selection in other important flatfish. In summary, this study entails an important advance in turbot genomics and shows the potential applicability of genomic tools for breeding programmes in this species.

Keywords: Turbot, scuticociliatosis, high-density genetic map, GWAS, SNP validation

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GENOTYPING AND GENOMIC SELECTION IN ATLANTIC SALMON (*SALMON SALAR*) USING GENOTYPING-IN-THOUSANDS BY SEQUENCING (GT-SEQ) AND GENOTYPING-BY-SEQUENCING (GBS)

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Abstract

Genotyping-by-Sequencing (GBS) is a high-throughput and cost-effective method to both identify and screen genetic variation in plants and animals. The method provides sequence information for a proportion of the genome with the single-nucleotide polymorphism (SNP) genotypes supported by varying depth of sequence reads. Where particular SNPs underpin complex traits of economic value, a higher read depth is required to ensure high confidence in genotype calls at the SNP(s) of interest. Genotyping-in-Thousands by Sequencing (GT-Seq) uses sequencing technology to genotype many individuals at specific loci. The multiplexed PCR products of targeted SNPs for thousands of individuals can be run in a single Illumina HiSeq lane or, alternatively, the products for hundreds of individuals can be spiked into an existing GBS lane. Atlantic Salmon (*Salmon salar*) will be used as an example of how GT-Seq products targeting SNPs for IPN resistance, sex determination and age at maturity have been incorporated into our low-depth GBS workflow for genomic selection in the same species.

Keywords: GBS, GT-Seq, Salmon salar

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ESTIMATION OF THE GENETIC PARAMETERS OF FEED EFFICIENCY IN JUVENILE NILE TILAPIA *Oreochromis niloticus* USING VIDEO ANALYSES

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In aquaculture, feeds represent 30 to 70% of the total production costs. Improving feed efficiency is therefore key to achieve economic sustainability of fish farming. Improved feed efficiency also has strong positive environmental impacts, by reducing pressure on feed fisheries as well as nutrient load to the environment. From a social perspective, improved feed efficiency should also reduce the competition for raw materials between human food and animal feed. Improving feed conversion ratio (FCR) is thus crucial to develop a more sustainable aquaculture. To date, the contribution of genetic improvement to this goal has been hampered by the lack of efficient phenotyping methods and accurate genetic parameters of FCR in fish. We used video assessment of feed intake on individual fish reared in groups to estimate the genetic parameters of growth traits, feed intake, FCR and residual feed intake on 1,000 fish from 40 pedigreed families of the GIFT strain of Nile tilapia, *Oreochromis niloticus*. Juvenile fish (22.4 g) were evaluated during 13 consecutive meals over 7 days. We demonstrate genetic control for feed intake and FCR in tilapia, with heritability estimates of 0.45 ± 0.09 and 0.32 ± 0.11 , respectively. Due to low genetic correlations between thermal growth coefficient (TGC) and FCR ($r_A = -0.29 \pm 0.28$), selection for TGC would only marginally improve FCR (2.6% by generation) while direct selection for FCR would improve FCR 16 % per generation. Interestingly, weight loss at fasting has a high genetic correlation with FCR (0.80 ± 0.25) and a moderate heritability (0.23 ± 0.12). This trait could be an easy to measure and efficient criterion to improve FCR by selective breeding in juvenile tilapia, but more work is needed to reach a final conclusion given that the observed phenotypic correlation is null between these two traits. We showed that FCR of juveniles could be efficiently improved by direct or indirect selection in Nile tilapia, but that selection on growth alone would only be marginally efficient. Additional work is required to measure FCR and correlated traits on older/larger fish for which the consumption of feed is maximal in the production cycle.

Keywords: Feed conversion ratio, growth, tilapia, heritability, correlations

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IMPACT ON GENOMIC PREDICTION OF MIXING BETWEEN PARALLEL YEARS GROUPS IN ATLANTIC SALMON BREEDING PROGRAMS

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Abstract

Because of the reproductive biology of Atlantic salmon, farmed populations typically follow a breeding program characterised by discrete generations with interval of four years. This results in the formation of four independent parallel lines within a breeding program. Genomic selection (GS) allows simultaneously using the information from parallel lines and, thereby, increasing the size of the reference population. However, despite all lines having a common selection objective, their relative isolation could have resulted in genetic differentiation, reducing the genetic relatedness between them. This could affect selection accuracy, as the candidates would be only distantly related to a large part of the reference population. GS might need to be implemented within each parallel line, leading to smaller reference populations and, eventually, a lower selection accuracy. Bringing in candidates from one line to another ('mixing') to connect the lines could improve GS accuracy. The aim of this study was to investigate the impact of various mixing strategies on the accuracy of prediction from genomic evaluation across lines. The effect of mixing between lines was tested by simulation. A salmon population was simulated assuming four parallel lines (500 fish/line) derived from a common ancestral population (lines were genetically related but drift started to differentiate them). One line reproduced each year in a rotational manner, so each line produced offspring every four years. In a given year, the next generation for a given line was created by randomly selecting four year old candidate parents from that line plus a proportion of three year old candidate parents from a parallel line. Each selected candidate has two randomly assigned mates to produce two full sib families of equal size. Ten discrete generations were created by line. Genetic distance between individuals (within and across lines) was calculated at each generation to study the impact of the mixing rate on genetic differentiation between lines. The accuracy of the breeding values from genomic evaluation achieved within and across population was compared. The relationship between the accuracy and degree of genetic distance between lines was quantified to determine the optimum mixing strategy to improve genetic prediction in farmed salmon.

Keywords: Atlantic salmon, mixing rate, simulation, genomic selection, accuracy

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SELECTIVE BREEDING OF A FAST-GROWING VARIETY AND GENETIC DISSECTION OF ECONOMICALLY IMPORTANT PRODUCTION TRAITS IN THE PACIFIC OYSTER *CRASSOSTREA GIGAS*

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Abstract

The Pacific oyster, *Crassostrea gigas*, is one of the most important aquaculture species in China and around the world. Toward breeding for elite oyster varieties with high yield and quality in China, we initiated a selective breeding program in 2006, through massive selection of three natural populations of Pacific oyster originated from Rushan (China), Miyagi (Japan) and Pusan (Korea). Successive selection for over ten generations has resulted in an elite Pacific oyster variety "Haida No. 1", which possesses superior production traits including fast-growth, high soft-tissue yield and uniformed shell shape. Along the great progress made on genetic improvement, genetic diversity and structure of breeding populations are yet to be assessed, and genomics/genetic basis of the production traits remains to be investigated, for directing the design of future breeding strategy. In this work, we evaluated the breeding progress based on multiple generations of breeding populations, which was estimated to be 15-27% increase in growth, with the average response of selection to be 0.6-0.7. Investigation of the genotype by environment interaction (GXE) effect on growth and survival suggested that GXE had significant effects on survival rather than growth. Assessment of the genetic diversity indicated that the breeding populations still retains relatively high levels of genetic diversity. Signatures of selection across the genome were identified, providing insights into genomic regions underlying economically important traits. Various production traits, including growth, shell morphometrics and pigmentation, soft-tissue yield, and glycogen content, were also genetically mapped through genetic linkage and association analysis. Together, putatively functional genes that could play critical roles in growth and glycogen content were identified, which include genes involved in the insulin pathway (*oIRP*, *IRR* and *Ras* genes) and the metabolic biological process (β -glucosidase gene). Association and haplotype analyses of genetic variations within these genes revealed the most advantageous haplotypes for growth and glycogen content for each of the genes, respectively. These results would provide valuable genetic information to direct future breeding practice and accelerate whole-genome based breeding program in the Pacific oyster as well as other oyster species.

Keywords: Pacific oyster, Selective breeding, Fast-growth, Genetic analysis, Molecular mechanism

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DELIVERY OF GENOMIC SOLUTIONS TO THE NEW ZEALAND AQUACULTURE INDUSTRY

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Abstract

High-throughput molecular genotyping methods coupled with efficient tissue sampling through to the bioinformatic and statistical analyses have enabled development and implementation of genomic tools for aquaculture species. Genotyping by sequencing (GBS), a simultaneous genotyping and SNP discovery platform, has emerged as an alternative technology to array based genotyping for genetic diversity and genetic mapping studies as well as for industry implementation of genomic selection in aquaculture. AgResearch has developed a generic algorithm that produces unbiased genomic relationship matrices (GRM) based on allele read depths from GBS data. This overcomes issues associated with missing genotypes and genotype calling accuracy at low coverage when SNP density and samples numbers per lane are maximised. The GRM produced can be interrogated to estimate: strain composition, pedigree, traceability, inbreeding and co-ancestry as well as be included directly in existing mixed models to estimate breeding values. An overview of the use of GBS in six species in the New Zealand Aquaculture industry is presented.

Keywords: GBS, genetic diversity, genomic selection

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GENOME EDITING TO INTRODUCE NEW TRAITS IN AQUACULTURE BREEDING POPULATIONS

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Abstract

Genome editing (GE) is a new technology with the potential to make a big impact on breeding programs. New traits can be introduced, for instance from known QTL in other species, or desired alleles can be increased in frequency faster than with selection alone. A large number of QTL for disease resistance and other traits, have been reported in aquaculture species. In this study we investigated the impact of GE to bring a new trait, a disease resistance allele, into a population. Currently reported success rates for GE are in the range of 1% to 10%. A breeding program was simulated that applies genomic selection for growth rate with 120 male, and 240 female parents per generation, producing 40 offspring per female as selection candidates. GE was applied to all 40 offspring of the best 6 families (240 fertilized eggs edited), best 30 families (1200 eggs), or all families (9600 eggs) based on parents estimated breeding values. Selection for the introduced allele was added in some scenarios and comparisons were made in generation 20. With GE success of 1%, the desired allele frequency reached 1%, 5% or 16% respectively with 6, 30 or all families edited. With 10% success, allele frequency reached 10%, 34% or 89% respectively. With moderate selection for the desired allele, fixation (>99% frequency) was reached after 13, 10 or 8 generations with 1% success and after 9, 7 or 6 generations with 10% success. The response for growth rate was not affected by applying GE only. When adding selection for the desired allele, the cumulative response for growth rate in generation 20 was behind by 0.61, 0.52 or 0.49 generations and inbreeding level increased by 0.1%, 0.4%, or <0.1% when editing 6, 30 or all families per generation with 1% success. With low GE success, selection is needed to effectively introduce a new trait. Application of reproductive techniques such as gynogenesis may improve the speed of introduction but have not been considered here. Without selection for the introduced disease resistance allele, many GE procedures are needed and desired allele frequencies will remain low for many generations.

Keywords: genome editing, breeding program design, selection, fixation, inbreeding

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