Poster 3001

Title: Expression of four muscle protein genes in the Günther's walking catfish *Clarias macrocephalus*

Presenting Author: Supawadee Poompuang, Department of Aquaculture, Faculty of Fisheries, Kasetsart University, Bangkok 10900 Thailand

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Abstract:
Skeletal muscle proteins represent more than half of the fish body mass. Expression of muscle genes affects development and growth of the animal. Because growth is an important trait in fish farming, it is useful to identify genes associated with muscle growth. In this study, we identified the complete cDNA sequences of muscle genes and analyzed their expression profiles from larval to adult stages of walking catfish. The complete cDNA sequences of parvalbumin (*PV*) (670 bp), troponin C (*TnC*) (1,065 bp), troponin I (*TnI*) (843 bp), and myosin light chain III (*MLC*III) (953 bp) were obtained from the skeletal muscle cDNA library. The *PV* cDNA encoded a protein of 109 amino acids. The deduced amino acid sequences of *TnC*, *TnI*, and *MLC*III were 160, 176, and 150 residues, respectively. The transcript levels of each muscle gene were determined by semi-quantitative RT-PCR. Significant variations of gene transcripts were observed during larval development, with the *TnC* mRNA showed its highest levels. Expression of *PV*, *TnC*, *MLC*III, and *TnI* were highest in skeletal muscle of juvenile and adult fish with lower expression in skin and gills. The levels of *PV*, *TnC*, and *MLC*III transcripts were similar in muscle of juvenile fish while higher expression of *PV* was observed in adult fish.

Poster 3002

Title: Characterization of seven microsatellites in the Black Sea stellate sturgeon (*Acipenser stellatus*)

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Abstract:
Sturgeon populations from Romania have declined because of anthropogenic influences. In this context, the necessity to develop conservation programs for these species requires knowledge of their genetic diversity.
The aim of this study was to optimize a protocol for microsatellites multiplexing in order to estimate genetic variability in *Acipenser stellatus.* Genomic DNA extracted from fin clips was amplified in two PCR reactions using seven primer pairs labelled with four different fluorescent dyes to detect seven different microsatellites (LS-19, LS-34, LS-54, LS-57, LS-68, Aox23 and Aox45). The amplicons analyzed with an ABI-Prism-310 Genetic Analyzer were examined with specialized software.
The number of allele peaks depends on the level of ploidy of the studied species and on whether the fish is heterozygote or homozygote. The size of the alleles at every locus varied between 95-200 bp. A high level of polymorphism was observed for the population studied. Seven to thirteen alleles where detected with a mean of eight alleles per locus.
The co-amplification of the microsatellites is a very good method allowing the evaluation of intraspecific genetic diversity, used for the first time in Romania. It will allow us to characterize the genetic variations in Black Sea sturgeon populations.

Poster 3003

Title: Genetic characterization of the hybrid between two commercially important Brazilian catfishes

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Abstract:
The Pimelodidea catfish species *Pseudoplatystoma corruscans* (surubim or pintado) and *P. fasciatum* (cachara) are large, migratory fishes that represent an important fishery resource in their respective areas of occurrence in Brazil. The hybrid form of the two species is of great importance to the local aquaculture industry. In this study, it was investigated whether the two species could be distinguished genetically by sequencing the mitochondrial 16S rRNA of pure strains and hybrids. Samples of *P. corrucans* were collected in the São Francisco River over a period of 3 years. These were compared with captive *P. fasciatum* and with hybrids of the two species. Five 16S rRNA

haplotypes of *P. corruscans* were recovered. A fourth haplotype was found in *P. fasciatum* and in hybrids only, indicating that the two species can be genetically distinguished and that the hybrids sequenced in this study are descendants of the females of *P. fasciatum*. (This work was supported by FAPEMIG-CBB 243/04)

Poster 3004

Title: Culturing diversity? Contrasting genetic diversity between wild and cultured populations of Pacific lion-paw scallop

Presenting Author: Jessica L. Petersen, University of California Davis, Dept of Animal Science, Davis CA 95616, USA

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Abstract:
Because cultured lion-paw scallops achieve sexual maturity before harvest, introgression with adjacent wild populations is possible. Eleven microsatellite loci were used to evaluate if cultured populations in the Lagoon Guerrero Negro, Mexico, encompass the genetic variation present in the wild by examining the genetic diversity of: 1) wild lion-paw scallops around the Baja California Peninsula, Mexico, 2) three artificially spawned cohorts of scallops grown for aquaculture, and 3) a sample of wild spat collected by producers for the purpose of future artificial spawns. Genetic data coupled with observed shell abnormalities in one aquaculture cohort infer high levels of inbreeding. Pairwise F_{ST} values show all three aquaculture cohorts are significantly different than the wild aggregations, even from the supposed source populations. In contrast, the wild spat collected for future spawns was not different than the wild source population, suggesting that spawning methodology and/or unrecognized selection pressures in aquaculture produce populations that do not capture the diversity found in the wild. These results warn that unless aquaculture propagation methods are amended to conserve natural diversity, introgression of aquaculture populations into the wild could alter the natural genetic make-up of the species at the possible demise of fitness and potential for adaptation.

Poster 3005

Title: **Immunological and genetic characterization of a rainbow trout selection strain *via* expression profiling**

Presenting Author: Rebl, Alexander, Forschungsinstitut für die Biologie landwirtschaftlicher Nutztiere, (Research Institute for the Biology of Farm Animals), Molecular Biology Research Unit, Wilhelm-Stahl-Allee 2, 18196 Dummerstorf, Germany

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Abstract:
The Gram-negative bacterium *Aeromonas salmonicida* causing furunculosis, a systemic disease in salmonid fish, is responsible for considerable losses to the aquaculture industry. Selection of Steelhead rainbow trouts has been started in 1975 at the fishery institute in Born in order to breed fish with an elevated fitness in brackish water. Current investigations prove that the strain BORN exhibits a higher resistance towards *A. salmonicida* than the non-selected STEELHEAD trouts. We aim to examine the physiological mechanisms underlying this improved resistance. In the present pilot study, we compared gene expression profiles in liver tissue of healthy rainbow trout from the strains STEELHEAD and BORN *via* microarray technology.
Among the 151 genes that were identified as being significantly differentially expressed we chose two genes to validate expression in a variety of tissues by real-time RT-PCR. $Alfa_1$-antitrypsin gene is significantly up-regulated in kidney and liver of BORN trouts. This proteinase inhibitor is an acute-phase protein contributing to early immune response in mammals. However, dehydrodolichyl diphosphate synthase, a key enzyme of dolichol biosynthesis, was significantly down-regulated in muscle, kidney, spleen, gills, liver, and heart of BORN trouts. Further microarray experiments are planned to identify different molecular features in both strains after *A. salmonicida* infection.

Poster 3006

Title: Molecular investigation of resistance to amoebic gill disease (AGD) in Atlantic salmon.

James W. Wynne, Mathew T. Cook, Maree G. O'Sullivan, Glenn Stone, Barbara F. Nowak, Richard S. Taylor, David R. Lovell, Nicholas G. Elliott

Presenting Author: James Wynne, CSIRO National Food Futures Flagship, Aquafin Cooperative Research Centre, CSIRO Marine and Atmospheric Research Hobart, Tasmania, Australia

Abstract:
Amoebic gill disease is a parasite mediated proliferative gill disease capable of affecting a range

of teleost hosts. While a moderate heritability for AGD resistance in Atlantic salmon has been reported previously, the mechanisms by which individuals resist the proliferative effects remain poorly understood. To gain more knowledge of this commercially important trait, we compared the gill transcriptome of Atlantic salmon putatively resistant and putatively susceptible to AGD using the 17k TRAITS/SGP Atlantic salmon cDNA microarray. We identified a large number of transcripts that were differentially expressed between the AGD resistant and susceptible animals, many of which were involved in the immune and cell cycle responses. Individuals resistant to AGD displayed significantly higher expression of genes involved in adaptive immunity and negative regulation of the cell cycle. In contrast, AGD susceptible individuals showed higher expression of acute phase proteins and positive regulators of the cell cycle. Expression of a sub sample of transcripts was further examined with real-time quantitative RT-PCR (qPCR) in the AGD resistant and susceptible animals, as well as non-infected naïve fish. The identification of these responses has provided new insight into the molecular mechanisms controlling AGD resistance.

Poster 3007

Title: GENETIC VARIATION OF FERAL AND CULTURED POPULATIONS OF ASIAN SEA BASS (*Lates calcarifer*) IN MALAYSIA INFERRED BY MICROSATELLITES

Presenting Author: Ahmad Sofiman Othman, School of Biological Sciences, Universiti Sains Malaysia, 11800, Penang, Malaysia

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Abstract:
Ten microsatellite loci were used to investigate genetic variability and differentiation of three feral and six cultured populations of Asian sea bass (*Lates calcarifer*) in Malaysia. Level of allelic richness ranged from 2.0 -11.3 while expected heterozygosities (H_e) ranged from 0.234 to 0.875. Genetic variation in terms of expected heterozygosity (H_e) and allele richness was slightly lower in three (Sungai Pendas, Punang and Sematan) of five hatchery samples than in samples of the feral populations. The Sematan cultured population exhibited a mode shift in its allele frequency distribution which suggests a recent bottleneck has occurred. Pairwise estimates of genetic differentiation between feral populations were low (F_{ST} = 0.0310-0.0899) but moderately high among cultured populations (F_{ST} = 0.0252-0.1637). STRUCTURE analysis suggests that the most likely number of clusters (K) for nine the populations in this study was equal to six. Based on results of pairwise F_{ST} values and Individual Assignment Tests, both Pulau Sayak (feral) and Semerak were suggested to have received either introductions of populations representing all the six clusters or represent the ancestral population of the species, thus contributing to the observed admixture in the populations.

Poster 3008

Title: **Molecular characterization of Alpine and Northern European populations of Arctic charr Salvelinus alpinus (Linnaeus, 1758) by means of nuclear and mitochondrial markers**

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Abstract:

The Arctic charr, *Salvelinus alpinus*, is an Holarctic Salmonid species adapted to cold-water habitats and whose populations, either anadromous or landlocked, are characterized by an extremely variable morphology. The presence of S. alpinus in Southern Europe is deemed as a relict of the Pleistocenic glaciations which strongly influenced both the distribution and the genetic variability of the species due to repeated isolation and bottleneck events. Previous genetic studies revealed a very low mitochondrial diversity in contrast with the high genetic variability, both within and among populations, highlighted by microsatellites. In this study, 537 specimens from 35 Alpine and 5 Scandinavian populations were characterized by AFLP polymorphisms and mtDNA control region sequences.

The results of AFLP analyses were evaluated by Factorial Correspondence Analysis (individual level) and by Multi-Dimensional Scaling (population level), while hidden genetic structures were investigated by a Bayesian clustering approach. The control region data were aligned with GenBank sequences to build a Median-joining network. Multivariate statistical analyses showed that individuals and populations

mostly clustered according to the geographic origin. Furthermore, some populations displayed low levels of genetic polymorphism which is probably due either to past demographic fluctuations or to a strong impact of anthropic activities in the recent decades.

Poster 3009

Title: MOLECULAR MARKER-ASSISTED COHORT SELECTION OF YELLOW PERCH

Presenting Author: Han-Ping Wang, Ohio Aquaculture Research and Development Integration Program (OARDIP), Ohio State University, 1864 Shyville Road, Piketon, Ohio 45661 USA

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Abstract:
Approximately 800 broodfish from eight stocks representing major populations were obtained from eight states. Those fish serve as a base population for a genetic improvement program. Genetic variance analysis suggested that all strains had genetic value to the program. Two improved lines were created in 2006 from selected broodfish of 2004 year-class, and three improved lines in 2007 from selected broodfish of 2005 year-class by performing cross- breeding of the base population. For each generation, approximately 500 fish were selected and genotyped from the base population and base generation using microsatellite to construct a pedigree. Among the 500 fish, 100 pairs of the least related, with highest breeding value were selected and divided into five cohorts based on their pedigree. The selection lines were created by pair-mating 20 pairs within each cohort to found the next generation of improved lines. On-station and on-farm tests showed that the two improved lines of 2006 grew 54.0% and 28.0% faster than unimproved fish, respectively, and the improved lines of 2007 grew 25% - 42%% faster than controls. Parentage analysis techniques using six molecular makers in yellow perch have been developed. Two mapping families have been established and reared to maturation for QTL mapping.

Poster 3010

Title: **Genetic structure from the anchovy of the Bay of Biscay using microsatellites and SNP discovery in the European anchovy**

Presenting Author: Iratxe Zarraonaindia Martínez, Genetics, Physical Anthropology and Animal Physiology Department. Faculty of Science and Technology. University of the Basque Country.

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Abstract:
Our interest is focused on unravelling the genetic structure of anchovy populations in the Bay of Biscay using DNA molecular markers, microsatellites and single nucleotide polymorphisms (SNPs). Our aim is to provide useful data for an effective conservation programme in this species, recently suffering a severe biomass reduction.
In all, 10 microsatellite markers were analysed in 96 samples from each of two ICES divisions of the Bay of Biscay, and 96 samples from the Gulf of Cadiz and the Gulf of Lyon. Genetic structuring was detected in the Bay of Biscay's anchovies, suggesting that they do not behave as a panmitic population.
On the other hand, SNPs are rapidly emerging as the preferred genetic markers for molecular genetic analysis, but there is a lack of information about SNPs in the anchovy genome. That is why we carried out a SNP discovery development using two approaches: comparative sequencing of random DNA fragments and the exon primed intron-crossing (EPIC) method, which have proven to be successful in SNP identification.

Poster 3011

Title: Use of SNP-chips and selective DNA pooling for identifying disease resistance markers in Atlantic salmon

Presenting Author: Matthew Baranski. Nofima Marine. Postbox 5010. N-1432 Ås. NORWAY

Other authors (name only):
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Abstract:
Diseases such as infectious salmon anemia (ISA) continue to present a large problem for Atlantic salmon aquaculture in Norway. Current approaches to improve resistance by selective breeding involve challenge testing of a small number of individuals from a large number of families to obtain family rankings and breeding values. This strategy doesn't exploit within family variation, meaning there is great

potential for the application of marker assisted selection. Simulation studies have shown that combined linkage / linkage disequilibrium analysis has high power to detect QTL using this population structure with a high density SNP marker resource. This project aims to identify QTL for ISA resistance using challenge test samples stored in a biobank from the SalmoBreed breeding population, and a SNP chip containing up to 60,000 markers. In addition, the selective DNA pooling methodology, where DNA pools of extreme individuals are typed rather than individual samples, will be evaluated as a means of dramatically reducing genotyping requirements. Families showing high variation for ISA resistance have been identified and preparation of DNA from these animals is currently underway. Markers identified in LD with disease resistance QTL will provide a powerful tool for improved selection for disease resistance across the whole breeding population.

Poster 3012

Title: GENETIC CONSEQUENCES OF DIFFERENTIAL SURVIVAL RATES IN CULTURED SILVER-LIPPED PEARL OYSTERS, *Pinctada maxima*.

Presenting Author: Curtis E. Lind, Aquaculture Genetics Group, School of Marine & Tropical Biology, James Cook University, Townsville QLD, 4810

Other authors (name only):
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3. Dean R. Jerry

Abstract:
The pearling industry can benefit substantially from selective breeding programs; however, sustained genetic response to selection is highly dependent on the maintenance of genetic diversity within cultured populations. It has been recently shown that genetic diversity of Pinctada maxima is significantly reduced due to the culture process. What are still unknown are the underlying factors contributing to this loss. A possible strategy to overcome this and maintain genetic diversity is to equalise family sizes, which can be performed in the hatchery prior to communal rearing. However, this effort may be inconsequential if differential family survival through the larval rearing period ultimately results in highly variable family sizes. Through DNA pedigree analyses, this presentation scrutinises how genetic diversity is affected by differential survival of communally reared families, and whether equalising family sizes prior to communal rearing will influence effective genetic sizes. Results show that variance in family survival rates are present and can have detrimental effects on effective population sizes and genetic diversity. In one instance, complete dropout of families was observed. Consequently, the practice of equalising family sizes to maximise diversity may be ineffective and alternative approaches should therefore be investigated to avoid diversity loss and maximise response to selective breeding.

Poster 3013

Title: **The Atlantic Cod Genomics and Broodstock Development Project (CGP)**

Presenting Author: Rise M, Ocean Sciences Centre, Memorial University of Newfoundland, St. John's, Newfoundland and Labrador, Canada

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Abstract:
The objective of the CGP is to develop breeding programs and fundamental genomics tools which will be used to supply the developing Atlantic cod aquaculture industry in Canada with improved broodstock. Three major spawning seasons have been completed in Newfoundland and New Brunswick / New Hampshire. Evaluations of progeny include assessment of family performance related to growth, survival and overall health. In addition, investigations related to cod physiology and immunology are conducted. Considerable variations among families in growth, tolerance to elevated temperatures and stress have been observed. Heritability estimates for growth are high, suggesting that the breeding programs can select fish for improved performance. The CGP has dramatically improved availability of genomic resources for cod. Approximately 158,000 sequences have been submitted to GenBank. Genes of interest

have been selected and development of a 20,000 element oligonucleotide microarray is underway. Development of gene-linked markers and a high density genetic map is ongoing. Marker identification has yielded >4,500 "predicted informative" SNPs and >140 microsatellite markers. A substantial investment has been made by Genome Canada and other partners to fund the CGP (www.codgene.ca). Resources developed by the CGP will enable marker assisted selection, and provide valuable tools for researchers interested in Atlantic cod.

Poster 3014

Title: Recent advances in the development of genomic resources in *Crassostrea gigas*: towards the sequencing of the Pacific oyster genome.

Presenting Author: Pierre Boudry, UMR M100 Physiologie et Ecophysiologie des Mollusques Marins, Ifremer - Technopole de Brest-Iroise, BP 70, 29280 Plouzane, France

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Abstract:
An international community, the Oyster Genome Consortium, uniting >70 biologists from 12 countries, presents the Pacific oyster *Crassostrea gigas* as a genome-sequencing candidate. In the USA and Europe, several EST sequencing projects have been successfully initiated by the Genoscope (Evry, France), the Joint Genome Institute (Walnut Creek, California) and the Max Plank Institute (Berlin, Germany), considerably increasing the number of ESTs. In Europe, the collaborative work developed within Marine Genomics Europe (www.marine-genomics-europe.org) and Aquafirst (aquafirst.vitamib.com) notably led to the development of (1) a cDNA microarray to study the functional genomics of survival during the reproductive period and (2) a dedicated EST database (www.sigenae.org/aquafirst). In the USA, inbred lines, F2 mapping families, SSR linkage maps, and transcriptomic analyses are aimed at understanding causes of growth heterosis. EST and BAC sequencing are currently being performed by the Joint Genome Institute. A BAC library made with DNA from a fourth generation inbred male was fingerprinted at the Genome Sciences Center (Vancouver, Canada) and the construction of BAC contigs-based physical map is well under way. It is now anticipated that the Institute of Oceanology (Chinese Academy of Sciences) and the Beijing Genomics Institute will sequence the oyster genome using the new generation sequencing technology.

Poster 3015

Genomic tools for breeding, fisheries and evolutionary biology of European Sea Bass

Filip AM Volckaert [1], Luca Bargelloni[2], Costas Batargias[3], Adelino Canario[4], Dimitris Chatziplis[5], Alexander Chistiakov[6], Richard Guyon[7], Chris S Haley [8], Bart Hellemans [1], Georgios Kotoulas [9], Heiner Kuhl[10], Jacques Lagnel [9], Angelo Libertini[11], Bruno Louro[4], Cécile Massault[8], Richard Reinhardt[10], Fabrice Senger[7], Erika Souche[1], Costas S Tsigenopoulos [9], Guo Yuanmei [8], Francis Galibert[7] (The Sea Bass Genomics Consortium)

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Abstract
European sea bass (*Dicentrarchus labrax* L.) sustains a regional fishery and is commonly farmed in the Mediterranean basin; it has been subjected to genetic improvement for a short time. The Sea Bass Genomics Consortium developed a suite of new molecular tools over the past eight years. Genetic markers amount to 221 (176 mapped) AFLPs, 323 (196 mapped) microsatellites, more than 20 allozymes and an increasing number of SNPs. 30,000 EST traces from 14 cDNA tissue libraries have been generated. They have been used to prepare an updated linkage map of 374 markers and a radiation hybrid map of more than 1000 markers. The radiation hybrid panel of 92 cell lines was constructed from spleen tissue. A previously constructed BAC library has been assembled to a physical map of BAC end sequences. All three maps have been linked. The consortium has compared the genomes of European sea bass and several model teleosts, first as a modest undertaking based on 186 microsatellite flanking regions, but more recently by high-throughput BAC end sequencing and comparative mapping. A high percentage (>80%) of evolutionary conserved regions were spotted with the genome of the three-spined stickleback. Conservation of synteny dropped with phylogenetic distance as analysed in spotted pufferfish, fugu, medaka and zebrafish. Combining synteny data of stickleback and medaka the comparative BAC map of *D. labrax* has improved to a physical BAC map. The European sea bass genome is also in the process of being sequenced by whole genome shotgun (to date ~1.1 Gb / ~2 fold coverage). Based on the physical BAC map, the homologeous group to stickleback chr 21 (~11.7 Mb) has been sequenced with high coverage through a combination of Sanger sequencing and pyrosequencing; fragments are being assembled. Based on a growth and stress experiments under commercial conditions, QTLs for growth have been detected and several BACs related to the QTLs have been sequenced. Additional BACs for immunological traits have been sequenced and the sequence assembled. Our findings contribute to a better understanding of fish evolution, provide excellent prospects for evaluating variation in the genome and enhanced selection in sea bass aquaculture, provide tools for tracing of fisheries products and open new perspectives towards understanding the application and effects of natural selection on locally adapted natural populations.

Poster 3016

Title Towards selective breeding of the Silver-lip pearl oyster (*Pinctada maxima*) understanding genotype by environment (GxE) interactions

Presenting Author: Dean R. Jerry, Aquaculture Genetics Research Program, School of Marine and Tropical Biology, James Cook University, Townsville, Qld 4810, Australia

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Abstract:
Before selective breeding involving a new aquaculture species it is important to identify populations/strains to be used as a founder genetic base and that possess "superior" characteristics for commercial production. Also of interest is an understanding of how phenotypic expression of important traits is influenced by local environmental conditions (genotype by environment interactions). Currently, there is interest in the selective breeding of the silver-lipped pearl oyster *P. maxima* in Indonesia. Before a breeding programme commences for this species we need to identify populations on which to base the founder stock and because improved oysters will be grown at multiple sites, determine the influence local environmental conditions have on the expression of oyster growth and pearl quality. In this experiment we produced spat from 27 full-sib families derived from three wild Indonesian *P. maxima* populations (Bali, Raja Empat, Aru) and communally stocked them at two different grow-out sites. Microsatellite-based DNA parentage analyses were used to assign oysters to their family and population of origin and growth and morphometric data obtained at 6,12 and 18 months. Results from this experiment will be presented and the implications of possible genotype by environment interactions on a future selective breeding programme for *P. maxima* discussed.

Poster 3017

Title: Status of Channel Catfish Genomics

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Abstract:
Channel catfish production is now the leading aquaculture species in the U.S., with 600 millions pounds processed annually. To support selective breeding programs, molecular tools are being developed to help characterizing the catfish genome and identify genomic regions that control important production traits. Briefly, framework genetic linkage maps have been produced based on microsatellite loci and Amplified Fragment Length Polymorphism loci. 400,000 Expressed Sequence Tags have been identified from several tissues and cell lines, and will be clustered and annotated in the Gene Index Project. One cDNA microarray and one high density

oligonucleotide array have been developed for global gene expression studies. Three large-insert catfish Bacterial Artificial Chromosome (BAC) libraries have been produced. More than 57,000 BAC ends have been sequenced. A physical map has been generated to integrate the genetic map with catfish chromosomes, allowing for fine mapping of phenotypic trait alleles such as Quantitative Trait Loci, effective positional cloning of genes controlling economically important traits to improve germplasm and for comparative genomic analyses. The physical map will also provide a minimal tiling path for a whole genome sequencing project.

Poster 3018

Title: **Developing genomic resources for new and emerging aquaculture species in New Zealand**

Presenting Author: P. J. Fisher, Invermay Agricultural Centre, Private Bag 50034, Mosgiel 9053, New Zealand

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Abstract:
Commercial aquaculture, with notable exceptions, has been slower than terrestrial livestock industries to invest in selective breeding. Recognizing the value of aquaculture genetics, NIWA has initiated a program to build broodstock resources for three high value species: yellowtail kingfish (*Seriola lalandi*), groper (*Polyprion oxygeneios*) and paua (abalone, *Haliotis iris*). The goal is to identify and select high performing broodstock individuals by evaluating their offspring through multiple crosses. Key performance traits of commercial value such as growth, product quality and yield, will be assessed in these families. Species specific methodologies are being developed to manage genetic diversity within the broodstock and identify the parentage of the evaluated offspring. For paua, individual controlled 1:1 family crosses have been established and one significant issue is whether these families should be reared separately or pooled. For large marine finfish such as kingfish and groper, communal spawning is standard, but this provides little control over individual matings. Therefore, determining parentage (with DNA markers) is essential for all three species. We describe the identification of highly variable microsatellites in each species (using long read, single pass 454 sequencing technology) and the downstream procedures for developing them into parentage testing panels.

Poster 3019

Title: Preliminary linkage map of *Haliotis midae* based on AFLP and microsatellite markers

Presenting Author: Rouvay Roodt-Wilding, Department of Genetics, University of Stellenbosch, Stellenbosch, South Africa

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2. Peizheng Wang

Abstract:
This study presents first-generation preliminary linkage maps for *Haliotis midae*, the only commercially important abalone species found in South Africa. Linkage maps were constructed using AFLP and microsatellite markers segregating in a F1 family following a pseudo-testcross mapping strategy. Twelve AFLP primer combinations, which produced 573 segregating bands and 10 microsatellite markers, were genotyped in the parents and 108 progeny of the mapping family. Of the 573 segregating AFLP peaks genotyped, 241 segregated in a 1:1 ratio and 332 in a 3:1 ratio. Of these AFLP markers, 90 segregated according to the expected 1:1 Mendelian ratio and 164 segregated according to the expected 3:1 Mendelian ratio at the P = 0.05 level and were used for linkage analysis. Of the 10 microsatellite markers genotyped, nine were informative for linkage mapping analysis. A total of 12 and 10 linkage groups were detected for the female (601.6cM; 41 markers) and male map (431.9cM; 33 markers). This linkage map forms a starting point for more detailed study of the *H. midae* genome and will act as a scaffold for basic and applied studies in abalone and initiate the mapping of quantitative trait loci (QTL) of commercially important traits and future marker assisted selection (MAS) selective breeding programmes.

Poster 3020

Title: QTL for resistance against Infectious Pancreatic Necrosis in Atlantic salmon.

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Abstract:

A genome scan was used to identify QTL for resistance to Infectious Pancreatic Necrosis (IPN) in Atlantic salmon, a major cause of mortalities and losses in the salmon farming industry and a potential target for marker-assisted selection. The disease affects fry as well as post-smolt. The genome scan, performed on 10 large full-sib families of challenge-tested post-smolt, revealed a single major QTL explaining 80 % of the genetic variation, in addition to one other experiment-wide significant QTL (1 % of genetic variation). The major QTL was highly significant in 10 of 20 mapping parents and was mapped to a 3 cM interval. Challenge-tested fry, siblings of the investigated post-smolt, were used to show that the QTL had the same effect on fry as on post-smolt. Subsequently, ~100 full-sib groups off fry were genotyped for a larger set of markers, in order to fine-map the QTL, possibly detecting population-level associations, and to determine linkage phases in QTL heterozygous broodstock animals. The results from fine-mapping will be presented at the conference. The QTL is identical to the one detected by Houston et al. (Genetics 2008), and has been implemented in the breeding programme of Aqua Gen Ltd as of 2007.