ABSTRACTS

SESSION 5: INDUSTRY USE OF GENETICS

GENETIC IMPROVEMENT IN TASMANIAN ATLANTIC SALMON *SALMO SALAR* AFTER 14 YEARS OF SELECTIVE BREEDING

Kube P.D.[a §], Verbyla K.L.[b], Evans B.S.[c]

[a] *CSIRO Agriculture and Food, Hobart, 7000, Australia*
[b] *CSIRO Data61, Canberra, 2601, Australia*
[c] *Tassal Operations, Hobart, 7000, Australia*

Abstract

The Tasmanian Atlantic salmon selective breeding program commenced in 2004 and now, after the production of 14 year classes, this is a mature breeding program and it is a central element to the sustainability of the Tasmanian salmon industry. The primary goals have been to improve growth rate and the resistance to amoebic gill disease (AGD), a disease which is endemic to the Tasmanian growing environment and which adds significantly to the cost of production. Secondary goals have been to ensure that there is no decline in carcass quality and to maintain the rate of marine maturation at current levels. Initial research focused on breeding for resistance to AGD, for which there was no prior information, and this has proven to be moderately heritable and responsive to selection. Genetic selection has resulted in demonstrable gains which increase by approximately 3.5% per year and genetic management is now considered a key element of disease management. This has been done whilst achieving a similar rate of rate in growth rate and largely meeting the goals of no adverse change in secondary traits. The selective breeding activities have provided a large population that has provided sound estimates of genetic parameters for all traits which will be summarised, together with the details of genetic gains. Future work is focusing on genomic selection and this in now part of the operational genetic evaluation for this breeding program. The details of the implementation, together with the challenges and gains, are given in a separate presentation (Verbyla, Kube and Evans).

Keywords: Atlantic salmon, selective breeding, amoebic gill disease, heritability

[§] Corresponding author. Tel.: +61 3 62325241
E-mail address: peter.kube@csiro.au

IMPLEMENTATION OF GENOMIC SELECTION IN TASMANIAN ATLANTIC SALMON

K. L. Verbyla[a§], P. D. Kube[b], B. S. Evans[c]

[a] DATA61, CSIRO, Canberra, 2601, Australia
[b] Agriculture & Food, CSIRO, Hobart, 7004, Australia
[c] Tassal Operations, Hobart, 7001, Australia

Abstract

Genomic information was included for the first time in the prediction of breeding values for Atlantic salmon within the Australian Salmon Enterprises of Tasmania Pty Ltd selective breeding program in 2016. The high potential of within family selection to accelerate genetic gain, something not possible using the traditional pedigree based approach, provided the impetus for implementation. The ability to implement such a scheme began with the design of a custom 50K SNP array. Subsequent genotyping revealed extensive persistence of linkage disequilibrium, resulting in high accuracies of both imputation and genomic breeding values when using imputed data. Consequently, a low-density novel 3K genotype-by-sequence assay was devised. Through the use of the two genotyping platforms all individuals in future year classes are now being genotyped on at least one platform. Progeny data from genomic selection decisions is currently limited and, therefore, the potential gains in accuracy achieved through the implementation of genomic selection were evaluated for a suite of marine-environment traits using a cross validation approach to replicate the typical data structure of the population. Genomic derived breeding values were found to provide significant increases in accuracy for all traits.

Keywords: genomic selection, Atlantic salmon, applied breeding.

[§] Corresponding author. Tel: +61 2 6216 7256
Email address: klara.verbyla@csiro.au

PIPETTE AND PAPER: COMBINING MOLECULAR AND GENEALOGICAL METHODS TO ASSESS A NILE TILAPIA (OREOCHROMIS NILOTICUS) BREEDING PROGRAM

Maria G. Nayfa[a], **David B. Jones**[a,^], **Curtis E. Lind**[b], **John A.H. Benzie**[b], **Dean R. Jerry**[a], **and Kyall R. Zenger**[a]

[a]*Centre for Sustainable Tropical Fisheries and Aquaculture, College of Science and Engineering, James Cook University, Townsville, QLD, 4811 Australia*
[b]*WorldFish, Penang, 11960, Malaysia*
[^]*Current Address: Département Ressources Biologiques Environnement, Centre Ifremer du Pacifique, Vairao, 98725, French Polynesia*

Abstract

Traditionally, genealogical data has been utilized to monitor inbreeding rates, relatedness, and co-ancestry within selective breeding programs. Within genealogical records, incorrect parental assignments are often as high as 15% in terrestrial selective breeding programs; however, error rates within aquatic breeding programs are not widely reported. Due to large family sizes, short generation intervals, and low traceability in juvenile stages, pedigree errors within aquatic breeding programs have the potential to be higher than terrestrial programs. The Abbassa Selection Line (ASL) is a product of a controlled selective breeding program of Nile tilapia (*Oreochromis niloticus*) that until recently has been managed solely based on genealogical data. To assess the accuracy of recorded ASL genealogical data, 1,040 genome-wide SNPs were used in a three-tiered approach to assign parentage. To determine the level of genetic diversity within ASL, genetic indices were calculated using 6,163 stringently filtered SNPs. These SNPs were also used to determine pedigree genetic structure and the number of families present. Inbreeding coefficients and founder contributions were calculated from two founding events for 11 generations of the ASL using molecularly corrected pedigree records. A comparison between genealogical records and molecular data revealed that on average, 61.2% of ASL genealogical records were erroneous (over 4x the error rate observed in terrestrial records). These genealogical errors have likely contributed to the low levels of genetic gain (3.8%) per generation observed within this line. The ASL aims to retain 100-120 families per generation; however, only 28 family lines were identified based on genotyping 57.1-63.9% of broodstock in generations 9-11. This suggests that the selected 100-120 families may not be genetically distinct. An assessment of founder contribution to the ASL revealed that only 35 founders comprise over 81.6% of available genetic material within the ASL. This indicates that founder contribution has eroded within the ASL, and that optimal founder contribution should be taken into consideration in future management strategies to preserve genetic diversity. This study highlights the importance of using molecular data to ensure that genealogical records are accurate so that aquatic selective breeding programs can optimize both the retention of genetic diversity and genetic gain.

Keywords: selective breeding, farm management, pedigrees, genome-wide markers, SNPs

Corresponding author. Tel.: +61 421 651 075 ; E-mail address: maria.nayfa@my.jcu.edu.au

NEW ZEALAND AQUACULTURE SELECTIVE BREEDING AND INDUSTRY APPLICATION

Symonds J.E.[a§], King N.[a], Camara M.D.[b], Walker S.P.[a], Roberts R.[c], Malpot E.[d], Preece M.[e], Amer P.R.[f], Hely F.S.[f], Clarke S.M.[g], Dodds K.G.[g], Tate M.[h], Buxton P.[h]

[a]Aquaculture Group, Cawthorn Institute, Nelson 7010, New Zealand
[b]DairyNZ, Newstead, Hamilton 3240, New Zealand
[c]SPATNZ, Nelson 7071, New Zealand
[d]Moana New Zealand, Nelson 7071, New Zealand
[e]The New Zealand King Salmon Co. Ltd, Picton 7220, New Zealand
[f]AbacusBio, Dunedin 9016, New Zealand
[g]Invermay Agricultural Centre, AgResearch, Mosgiel 9053, New Zealand
[h]Sanford Limited, Kaitangata 9281 New Zealand

Abstract

Aquaculture is an important primary industry for New Zealand (NZ) and the three-flagship species, Greenshell™ mussels (*Perna canaliculus*), Pacific oysters (*Crassostrea gigas*), and Chinook salmon (*Oncorhynchus tshawytscha*), currently produce over NZD $400 million p.a. in export revenue. Aquaculture of all three species began in the 1960-70s and it was not until the 1990s that selective breeding was initiated. A challenge was to develop programmes that overcame biological obstacles (such as early larval mortality in shellfish) and operated cost-effectively on a relatively small scale while still providing significant industry gains. The first Chinook salmon family breeding programme was established in 1994 by Southern Ocean Seafood Ltd. The Cawthron Institute initiated a Pacific oyster family-based breeding programme in 1999. In 2002 Cawthron produced the first Greenshell™ mussel families using wild parents and have since established a family-based breeding programme, now operated and managed by SPATNZ and BreedCo Ltd. In 2007, the second largest NZ salmon farming company, Sanford Ltd., decided to move away from mass selection and has since developed a combined between- and within-family selection programme. The breeding programmes are designed so that the families are evaluated on one or more commercial farms, either in mixed family groups or as separate replicated families. The initial focus was improved growth, and moderate to high heritabilities were estimated for the growth traits in all three species. As a result, time to harvest was significantly reduced. As the industry has developed, more emphasis has been placed on quality and yield traits and the development of multi-trait selection indices. The breeding programmes have also allowed the industry to respond effectively to new challenges, such as the mass mortalities of Pacific oysters, which first occurred in 2010 due to a highly pathogenic variant of the oyster herpes virus (OsHV-1 µvar). Moderate heritability for resilience to the virus in lab and field challenges has led to family selection for this trait and improved survival on the farms. We are now developing genomic resources based on SNP genotyping (genotyping-by-sequencing and SNP chip approaches) to evaluate the potential commercial benefits of genomic selection in all three species.

Keywords: Industry benefits, selection, Chinook salmon, shellfish

[§] Corresponding author. Tel.: +64 3 548 2319; E-mail address: jane.symonds@cawthron.org.nz