

The full-length gene transcript has been obtained using RACE, and aligns perfectly with genomic sequence surrounding the QTL marker. Efforts are currently underway to identify allelic variants in *P. japonicus* and other species that may have a significant effect on growth.

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Genetic relatedness of Asian arowana varieties: Introducing a new strain from Indonesia

W.C. Liew^a, A.K.W. Chang^{a,b}, W.K. Ang^{a,c}, K.C. Yap^d, L. Orban^{a,b}

^a Reproductive Genomics Group, Temasek Life Sciences Laboratory, Singapore

^b Department of Biological Sciences, The National University of Singapore, Singapore

^c Faculty of Veterinary Science, The University of Melbourne, Australia

^d Qian Hu Corporation Limited, Singapore

Bonytongues belong to one of the most ancient fish families (Osteoglossidae). At least one of the seven species is present on each Southern Hemisphere continent, except Antarctica. Besides being valuable ornamental fishes, several bonytongues are also valuable as research objects. The Asian arowana (*Scleropages formosus*) is the only member of the family with several colour varieties that show different geographic distribution across southeast Asia. The classification of these varieties – based primarily on morphometric measurements and visual observation – is under dispute. Since the original description of the red Asian arowana in 1844 (Schlegel and Müller), no other strain was identified in the Kapuas River (Kalimantan, Indonesia). Here we describe a new red variety, known locally as Menjuku, with different colour and other phenotypic traits compared to other Asian arowana strains. The genetic relationship of Menjuku to all known Asian arowana strains will be estimated by combining the power of AFLP assays, microsatellite genotyping and mtDNA analysis (control region, cytochrome *b* and NADH subunit 1). Our preliminary results with microsatellite genotyping indicate that the ancient Menjuku might have diverged from the common red variety soon after the ancestors of all reds separated from the other colour varieties.

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Factors affecting the maintenance of genetic variation in hatchery cultured silver-lipped pearl oysters (*Pinctada maxima*)

C.E. Lind, B.S. Evans, J.J.U. Taylor, J. Knauer, D.R. Jerry

Aquaculture Genetics Research Group School of Marine Biology and Aquaculture James Cook University Townsville, QLD 4811 Australia

Commercial hatchery processes were examined to highlight critical factors leading to the loss of genetic variation in artificially propagated silver-lipped pearl oyster (*Pinctada maxima*) populations. Microsatellite based DNA parentage analyses were employed to assess the practice of mass spawning as a contributor to significant genetic diversity loss. Here a communal spawning comprising 14 male and 9 female broodstock was performed in Bali, Indonesia, with the resulting cohort of larvae reared by commercial methods in 4 × 5000-l tanks. Initial broodstock contributions and subsequent relative family survival were estimated throughout larval development by sampling and genotyping at critical stages of morphological development (2, 8, 21 and 28 days post-fertilization), and as settled spat (35 days old). The results from this study and the implications of varying broodstock contributions and differential family survival on the genetic diversity of *P. maxima* will be discussed.

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Genetic structure and diversity of a high dispersal mollusc, *Pinctada maxima*, throughout Northern Australia and the Indo-West Pacific region

C.E. Lind^a, D.R. Jerry^a, B.S. Evans^a, J.J.U. Taylor^b, J. Knauer^b

^a Aquaculture Genetics Research Group School of Marine Biology and Aquaculture James Cook University, Townsville, Queensland 4811, Australia

^b Atlas Pacific Ltd. P.T. Cendana Indoparls Jalan Sekar Jepun V/21, Gatot Subroto Timur, Denpasar, Indonesia

The silver-lipped pearl oyster, *Pinctada maxima*, is the most important pearl producing species throughout northern Australia and Southeast Asia and due to its long planktonic larval phase has a large capacity to widely disperse. Currently very little information is known on the genetic structure and diversity of this