

ASI | Thoroughbred Oysters



Pacific
Oyster
Broodstock Catalogue

Edition 2 | Year Class 2013 | November 2015

Why ASI Thoroughbred Oysters?

The Australian Pacific oyster selective breeding program began in 1997 and in recent years has undergone some significant modifications to consistently produce greater than 4% per year genetic gains.

A computer model of the Pacific oyster production system has been used to identify the genetic traits that influence profitability.

The model, developed by researchers from CSIRO's Food Futures National Research Flagship, and validated using actual farm data, has been used to simulate and evaluate potential selection strategies.

Five traits – growth rate, shell width index, time to reach market condition, mortality and uniformity – have been shown to equally affect grower profitability.

Growth rate, shell width index and time to reach market condition are now used as part of routine breeding decisions. Some South Australian mortality data are also employed and the inclusion of uniformity is a subject of ongoing research.

Meanwhile, the number of families produced each year has increased to 80. This strategy of using economic weighing of traits and increased numbers of families is capable of delivering genetic gains in the breeding population of over 8.5% per generation, or 4% per year, while maintaining inbreeding at

acceptable levels. ASI's practical breeding plan produces high numbers of high quality, two-year-old Thoroughbred Oyster broodstock, increasing commercial selection options and allowing hatcheries to combine desirable traits.

Contact ASI to find out how Thoroughbred Oyster broodstock can help to increase your profitability.

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How are ASI Thoroughbred Oysters selected?

ASI conducts extensive, annual progeny testing of its Thoroughbred Oyster broodstock families. Replicate groups of oysters from each family are grown out under commercial conditions from ~6 mm size, at up to five sites in three States (Tasmania, South Australia and New South Wales).

Data on live counts, size (length, width and depth), whole weight, meat weight, meat composition and shell weight, as well as a POMS resistance, are collected at intervals throughout grow-out.

The resulting extensive data set is input to a rapidly growing database. At present the database contains more than 214,000 individual measurement records and this figure is set to increase by more than 20,000 per year.

The database is housed at CSIRO where data analysis is conducted by a specialist team of quantitative geneticists, mathematicians and computer programmers. It yields information on the extent of the genetic contribution to a trait (the heritability), and its potential for improvement through selection (a combination of heritability and variability for the trait).

This work employs best-practice analytical systems identical to those employed elsewhere in the selective breeding of livestock (such as dairy cattle) and plants (such as plantation timber). It also uses custom systems, such as an “Inbreeding Calculator” which manages genetic

diversity in the ASI stock.

The combination of heritability and variability is used to predict the amount of change in a trait that a family may be expected to yield: the Estimated Breeding Value (EBV) of the family for the trait. Further combination of data on all traits of interest and their relative economic weights generates a single index value.

This value indicates the potential change in profitability associated with a family. ASI uses this index value, and knowledge of how each trait contributed to it, when recommending families for commercial spat production, and when selecting families to produce the next generation of Thoroughbred Oyster broodstock.

YC13 Broodstock Selection



YC13.01



YC13.02



YC13.07



YC13.31



YC13.48



YC13.52



YC13.60



YC13.66



YC13.85

The 2013 broodstock have been picked based on quantitative values, such as live counts, size (length, width and depth), whole weight, meat weight and shell weight, as well as POMS resistance. The following is an exposition on each animal line, their raw data and characteristics.



YC13.01

This family is characterised by a heavy dark red shell with a good growth profile. It has performed well in POMS field trials and has the best survival rate in SA conditions relative to other broodstock.

YC13.02

This line exhibits a very dark shell with a symmetrical shape. The family grows well. It displays a good POMS resistance and moderate survival in SA.





YC13.07

This family is predominantly black with a single white stripe feature. It is wider and deeper than it is long. It has above average resistance to POMS and good survivorship in SA conditions.

YC13.31

This line is also predominantly black with a single white stripe feature. However, it has more length compared to YC13.07. It has high POMS resistance and lower survivorship in SA conditions.



YC13.48

A predominantly red shelled oyster with white striations. Typified by a wide, deep shell, this family displays moderately good growth. Its POMS resistance is at the lower end of the spectrum. However, it has a good survival in SA conditions and a high conditioning value.



YC13.52

This line displays variable colourations with a good growth profile. It has the widest shell out of the selected brood-stock and has moderate POMS resistance and good survivorship in SA conditions.





YC13.60

This family is the fairest one of them all with slight red-brown striations. It also has a good length to width ratio and is a fast grower. It has a good POMS resistance and does well in SA conditions.

YC13.66

This family has variable colour with a great shape and moderate growth rate. It has a deep shell and conditions well. Its POMS survivorship is moderate and does well in SA conditions.





YC13.85

These animals display variable colour with a great shape. It has shown to be a fast grower and has the highest POMS survivorship and conditions well in SA waters.



Data Table Legend

CODE	DEFINITION
FAMILY_ID	Family ID
SIRE_FAM	Sire Family ID
DAM_FAM	Dam family ID
F	Inbreeding coefficient
POM_%	POMS survival (% change in juvenile survival)
SAMS_%	SAMS survival (% change in juvenile survival)
LEN_%	Length % gain
WI_%	Width Index % gain
DI_%	Depth Index % gain
WT_%	Total weight % gain
CON_%	Condition Index % gain

YC13 Year Class Data

FAMILY_ID	SIRE_FAM	DAM_FAM	F	POM_%	SAMS_%	LEN_%	WI_%	DI_%	WT_%	CON_%
2013001	2011033	2011022	0.025543	47.1%	12.6%	2.5%	0.1%	4.3%	13.2%	-2.5%
2013002	2012016	2011022	0.029617	36.2%	9.4%	2.8%	4.0%	3.3%	14.1%	-8.0%
2013007	2011048	2011033	0.038879	29.0%	10.4%	-13.8%	12.4%	18.9%	-3.0%	0.8%
2013031	2011006	2011027	0.033169	41.3%	7.5%	2.7%	2.9%	-3.9%	-1.2%	1.5%
2013048	2011033	2011041	0.02565	17.3%	10.1%	-6.9%	11.0%	6.4%	-2.3%	1.1%
2013052	2011001	2011041	0.011791	25.0%	11.7%	-5.7%	13.2%	7.0%	1.5%	0.1%
2013060	2009027	2011022	0.02951	50.6%	7.2%	3.0%	3.3%	2.7%	13.2%	-4.1%
2013066	2011027	2011033	0.031067	17.9%	10.8%	-3.2%	7.7%	6.0%	3.3%	2.3%
2013085	2011022	2011006	0.023296	50.8%	9.0%	8.6%	-2.4%	-3.3%	13.7%	-2.4%

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