

CRC for Food Agility NSW Oysters Transformation Project

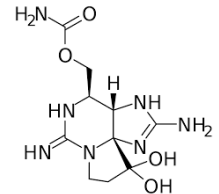
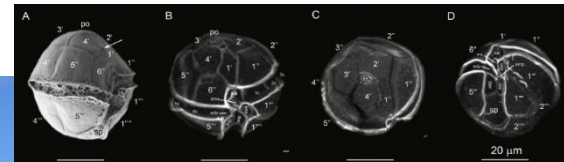


Shauna Murray, Penelope Ajani, Arjun Verma, Hazel Farrell, Anthony Zammit, the Yield, Mike Dove, Wayne O'Connor



Shellfish safety risks associated with water quality

- Harmful algal blooms (HABs)
- *E. coli*, coliforms, viruses such as Hepatitis, Norovirus, especially associated with land runoff after rain or sewage spills



Health warning renewed after two people treated in Tas hospital for shellfish poisoning

Updated 6 Oct 2015, 8:26pm

Two people have been hospitalised in Tasmania with paralytic shellfish poisoning after eating mussels they harvested from east coast areas affected by algal blooms.

A third person has also been treated.

All three became unwell after eating mussels from an area subject to a public health warning issued last week.

The Public Health department has advised against collecting or eating wild oysters, mussels, clams, pipis, scallops, abalone, rock lobster or crab from anywhere along the east coast.



PHOTO: People have been warned not to eat wild shellfish such as oysters, mussels and scallops from the affected east coast area. (Farrukh: Flickr)

Project Aims

- To reduce closure days for oyster harvesting in NSW
- To better predict and model harmful algal blooms, oyster disease and oyster growth

Through collecting and analysing detailed water and oyster data in relation to real-time temperature and salinity measurements in 13 estuaries

Project Overview

- **Detailed data:** Weekly sampling at 13 estuaries for 104 weeks
- **Citizen science :** EXCELLENT sample collection
- **Real time :** temperature and salinity sensors
- **Modelling :** *E.coli*, disease, oyster growth and HABs



Biological data

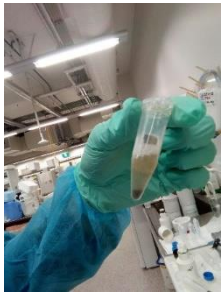


Physical data

Methods



Sample collection training



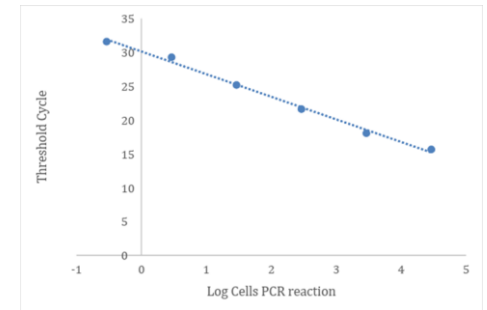
**Preserved
filter
samples**



**DNA
extraction
(automated)**



qPCR



Quantification

eDNA and qPCR for water quality assessment

- Detect rare species
 - Detect cryptic species and picoplankton
 - Quantitative
 - Detect functionally relevant genes, ie toxin production
-
- **Potentially very rapid (~1-2 hours)**
 - **Potentially low cost for assays and equipment**
 - **Potentially little need for expertise, ie can be done on site**



Results to date

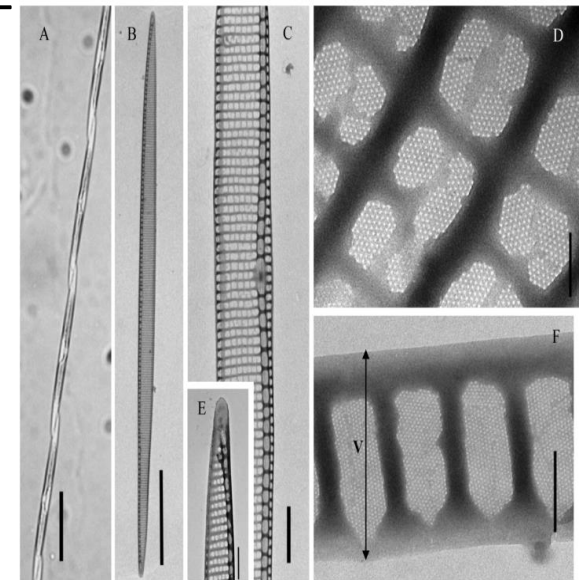
- ~2500 weekly water samples for bacteria and algae and ~1000 oysters already collected by growers across 13 estuaries.
- Review of Pambula management plan using data from the project
- Development of bacterial and HAB qPCR testing
- Comparison of qPCR vs high throughput sequencing for detecting pathogens and HABs
- Comparison of qPCR vs traditional plate counts

Results: Pambula Lake – salinity only management

- Modelling of the real time salinity compared to current management on rainfall and *E.coli* at Pambula
- ~3 fewer harvest area closures per year if Pambula adopted salinity only management = 9 days over 3 years.
- A real time, high frequency monitoring temperature and salinity sensor can be used to manage closures in Pambula Lake harvest area.
- During the initial implementation of such a management plan change, rainfall events would continue to be monitored

Results: *Pseudo-nitzschia* bloom in Wagonga

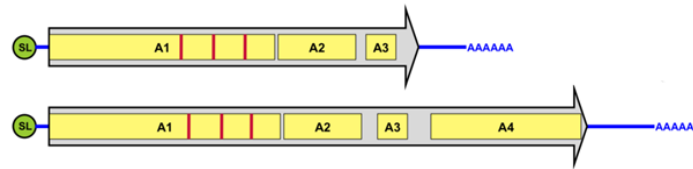
- 8 April 2019 Wagonga Inlet - Site 1 *P. cuspidata* (25.4 pg DA cell⁻¹)
- *Pseudo-nitzschia delicatissima* group - 430,000 cells/L (PAL 50,000 cells/L), however no positive biotoxins
- 4 species were isolated and are growing in the laboratory at UTS identified as *P. cuspidata*, *P. hasleana*, *P. fraudulenta* and *P. multiseries*
- *P. cuspidata* the most toxic of all *Pseudo-nitzschia*'s tested from NSW; responsible for the bloom in 2010 which lasted 16 weeks
- awaiting toxin results for all four species
- Examining the cause of the bloom



Ajani et al. 2013

On farm HAB and *E. coli* detection using qPCR

- qPCR assay developed for **on farm use**
- Cost effective, rapid
- Amplifies functional gene *sxtA* from any HAB species



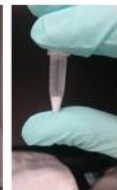
Seawater
Filtration



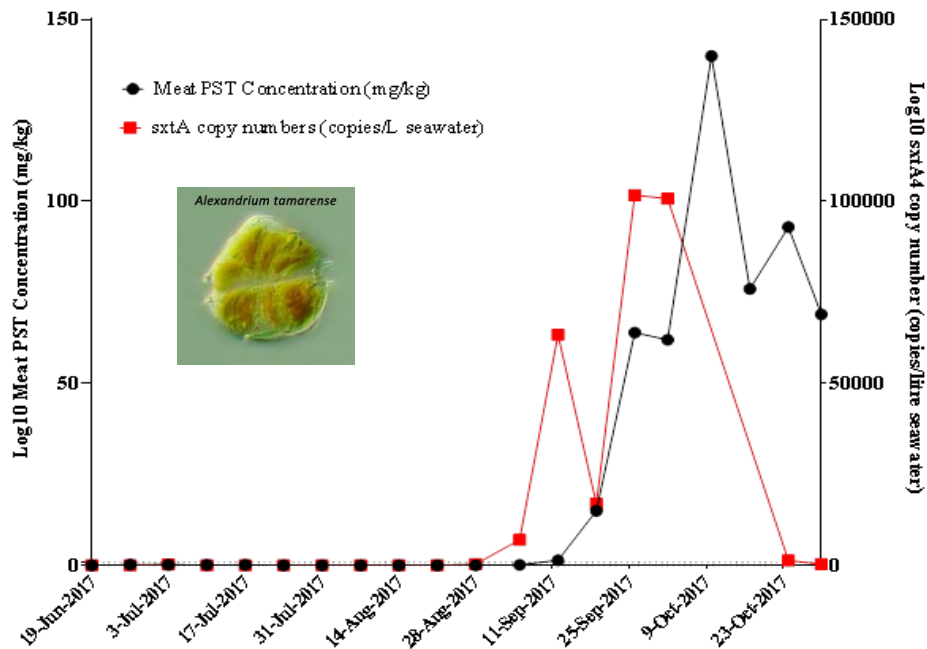
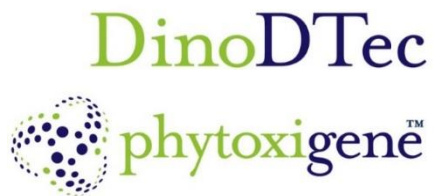
DNA Sample
Processing



qPCR



On farm HAB detection assay



Poster: Rendy Ruvindy,



Acknowledgements

- Mark van Asten
- Rendy Ruvindy
- Allen Lo
- Matt Tesoriero
- Luke Clay
- Kate McLennan
- Dr. Nahshon Siboni



Diagnostic
TECHNOLOGY



Climate
Change
Cluster

- Dr. Hazel Farrell
- Dr. Wayne O'Connor
- Dr. Michael Dove
- Kyle Johnston
- Aiden Mellor
- Ashley Rootsey



Department of
Primary Industries
Food Authority



Department of
Primary Industries



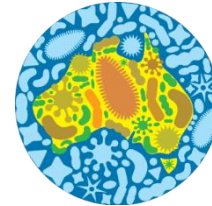
Huge thanks to all sample collectors over the past year!

Molecular genetic tools for estuarine water quality assessment

1. Molecular barcoding or metagenomics using eDNA



BIOPLATFORMS
AUSTRALIA



- Detect rare species
- Detect cryptic species and picoplankton
- Characterise entire community
- Detect functionally relevant genes, ie toxin production

BUT: for many organisms, ie microalgae, not quantitative*

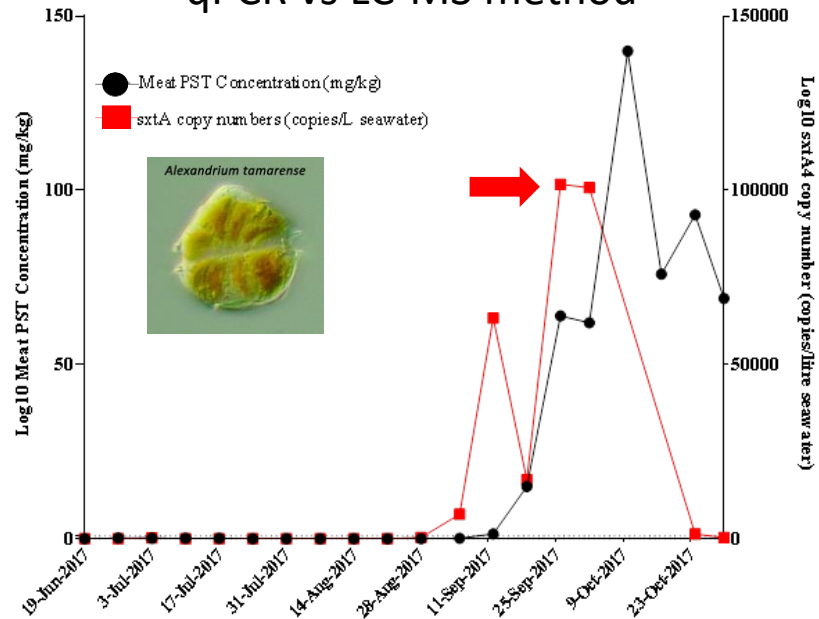
Time frame: ~several weeks

Requires sophisticated and expensive equipment

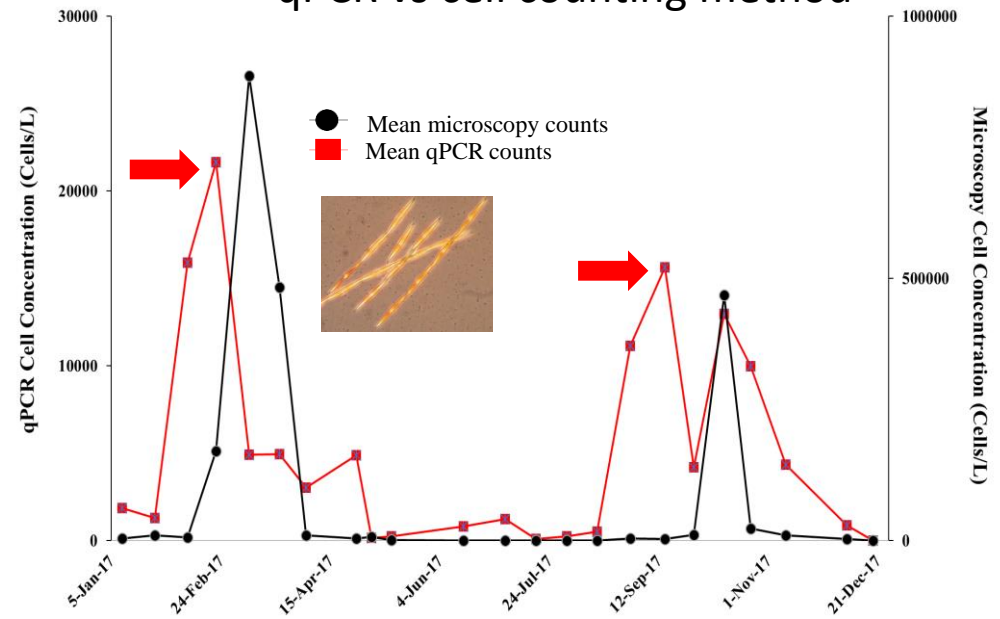
Source: * Smith et al 2017 and references therein

Proof of concept

qPCR vs LC-MS method



qPCR vs cell counting method



- Early detection and similar trends compared to traditional monitoring methods
- Gene copy number issues (Large genomes, inter-strain variation)