

**REPORT ON PERFORMANCE OF BALLAST WATER
COLLECTION AND ANALYSIS DEVICES**

RV METEOR CRUISE M116/2

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Executive Summary

Promising approaches for ballast water sample collection and analysis have been developed, but require further study in the field to examine their utility for compliance monitoring. To address this gap, a voyage was undertaken by 20 international researchers on board the RV Meteor from June 4-15, 2015. During this time 28 trials were conducted to evaluate three ballast sampling devices (plankton net and 2 sampling skids) and a number of analytic devices (>200 μ m: 1 technique, \geq 50 μ m: 5 techniques, >10 μ m and <50 μ m: 10 techniques, bacteria: 6 techniques). Water samples were collected using paired sampling devices and analyzed in parallel by all analytic methods to determine whether results were similar between devices and whether quick, indicative methods offer comparable results to standard, time-intensive testing methods (e.g. microscopy) and high-end scientific approaches.

For sample collection, some differences were observed in the number of viable organisms collected by the various sampling devices (net, sampling skids in open and closed configurations), but these differences were not consistent across size classes and, in many cases, there was no significant difference between samples collected with a net or with a skid. For sample analysis, several promising indicative methods were identified that showed high correlation with microscopy results but allow much quicker processing.

This study is the first to concurrently test a large number of analytic tools and multiple sampling devices under operational conditions. Results are useful to identify the merits of each method and can serve as a basis for further improvement and development of these tools and methodologies for compliance monitoring.

1.0 Introduction

The Convention for the Control and Management of Ships' Ballast Water and Sediments, (2004; BWMC) aims to "prevent, minimize and ultimately eliminate the transfer of harmful aquatic organisms and pathogens". Ballast water is used to trim merchant vessels in order to enhance stability and to keep the propeller under the water line, but since it can contain organisms that are present in the water during ballasting, it can transfer organisms between regions. In fact, ballast water is considered one of the most prominent vectors for the transfer of marine non-indigenous species (Verling *et al.*, 2005). In this way, organisms reach foreign environments and may cause serious commercial, health and/or environmental damage (NRC 1996, Ruiz 2000, Williams 2013). Being aware of these hazards, the International Maritime Organization (IMO) began to address this problem at the beginning of the 1990s which resulted in the 2004 adoption of the BWMC. The BWMC requires compliance with certain standards limiting the number of living organisms of specified size classes discharged in ballast water (IMO 2008). These standards include restricting the concentration of organisms at discharge to (i) < 10 viable organisms per cubic meter ≥ 50 micrometers in minimum dimension, (ii) < 10 viable organisms per millilitre < 50 micrometers in minimum dimension and ≥ 10 micrometers in minimum dimension (hereafter, 10-50 μm), and the following concentrations of indicator microbes, as a human health standard: (iii) < 1 Colony Forming Unit (cfu) of Toxigenic *Vibrio cholerae* (serotypes O1 and O139) per 100 millilitres or per 1 gram (wet weight) of zooplankton samples, (iv) < 250 cfu of *Escherichia coli* per 100 millilitres, and (v) < 100 cfu Intestinal Enterococci per 100 millilitres. At present, most ships are expected to meet these standards through shipboard Ballast Water Management Systems (BWMS).

Much effort has been undertaken worldwide to develop BWMS, which usually consist of a filtration unit and a subsequent disinfection procedure that destroys or deactivates the remaining organisms. However, the BWMC is not yet in force. One reason non-subscribing States have been reluctant to ratify the BWMC is because there is some doubt about the reliability of the existing compliance monitoring methods. Ballast water compliance monitoring can be divided into two main parts: sample collection and sample analysis. Several promising approaches have been developed that could be applied during a "trial period", but these sampling and analysis methods need to be further studied in the field to understand their methodological differences, including benefits and drawbacks, and also assess their comparability, accuracy, and precision.

1.1 Sample collection devices

Traditionally, shipboard type approval testing has been conducted using an open collection system with plankton nets. Samples are collected using in-line, "L" shaped sampling probes (i.e. pitot tubes) installed in the vessel's ballast water piping. Ballast water sampled by each sampling probe is pressure-fed by the vessel's ballast system through connected piping and a flowmeter and into a conical plankton net with 35 μm mesh (49.497 μm in diagonal) within a wetted sample tub. Flowrates are adjusted to maintain approximately isokinetic flow (isokinetic according to IMO G-2 Guidelines). The sample retained inside the plankton net is

collected for analysis of organisms in the $\geq 50 \mu\text{m}$ size class, recognizing that the flexible nature of the mesh and many organisms may lead to some error in the capture rate. For organisms in the 10-50 μm size class, and water quality analyses, a composite sample totalling $\sim 5 \text{ L}$ is taken by collecting $\sim 400 \text{ ml}$ of water from the sample tubing (before or after water passes through the plankton net) every two to five minutes during the entire sampling duration. In general, 350-3000 L of water is collected for assessment of $\geq 50 \mu\text{m}$ size organisms at low density (US Coast Guard, 2010; Briski et al. 2014), so it is necessary to dispose of 'waste' water. 'Waste' water can be, for example, returned to the ship's ballast system downstream via a second purpose-built return port or an existing connection such as a drain valve (Briski et al. 2014), sent overboard using a submersible pump and hose, or deposited into the bilge to be processed and discharged by the ship, which is seldom the preferred option on board vessels.

More recently, collection systems (i.e. sampling skids) have been developed that enable filtration and sample collection of large volumes of water in a small space and, optionally, the ability to return filtered 'waste' water into the ship's ballast water pipe (closed systems). Again, the sampling skid connects to the ship's ballast system using in-line, "L" shaped sampling probes. The sampled ballast water flows through a filter housing with a filter basket having filter material sized according to the BWMC regulation (mesh size $50 \mu\text{m}$ in diagonal/diameter). Large size organisms ($\geq 50 \mu\text{m}$) are collected inside the filter assembly, and a bypass after the filter housing equipped with a valve allows for taking 10-50 μm plankton samples and bacterial samples as single samples with small volumes (e.g. 300ml) or drip samples across a longer period of time.

1.2 Analytic Methods

Standard procedures used for testing during type approval of BWMS include "detailed" analysis, such as microscopic examinations, that require extensive scientific expertise and equipment, and a timeframe generally too long for a compliance and enforcement scenario. However, as an alternative, a variety of rapid, easy, but mostly "indicative" analysis methods have been developed that do not directly count live organisms, but provide an indication of potential [gross] non-compliance with the BWMC discharge standards. Indicative methods rely on various indicators to assess the biomass and or viability of individuals in samples, including adenosine triphosphate (ATP) methods which detect the amount of cellular energy, pulse amplitude-modulation (PAM) methods which rely on the natural autofluorescence properties of the chlorophyll-protein complex present in algal cells, and fluorescein diacetate (FDA) methods which variously use FDA stain to measure enzymatic activity (group of esterase enzymes). Some indicative methods provide a calibration curve that allows an estimation of the number of individuals in samples based on a biomass estimate.

1.3 Project description and objectives

The RV Meteor is a 97.5 m research vessel operated by the German Research Foundation. The RV Meteor Cruise M116/2, which took place from June 4-15, 2015, was used to run a series of investigations to compare methods for ballast water sample collection and analysis by conducting replicated, comparative testing of water samples. During this voyage, 28

trials were conducted to evaluate three ballast sampling devices (plankton net, SGS skid, Triton skid NP 6007 TG 18) and a number of analytic tools (>200µm: 1 technique, ≥50µm: 7 techniques, 10-50µm: 9 techniques, <10 µm: 5 techniques; bacteria: 7 techniques). A full list of the analytic devices used on board, the targeted size class(es) for each device, and the participants responsible for each analysis are detailed in Table 1.

The METEOR experiments collected data to examine 4 main objectives: 1) Comparison of ballast water sample collection methods (plankton net, SGS sampling skid, TRITON sampling skid), 2) Comparison of ballast water analysis methods for measuring abundance of organisms ≥50 µm in the maximum dimension on the smallest axis, and 3) Comparison of ballast water analysis methods for measuring abundance of 10-50 µm organisms, and 4) Comparison of analysis methods for organisms <10 µm in the maximum dimension on the smallest axis (bacteria and phytoplankton). In addition, we obtained data to address 2 minor objectives: 1) Test potable water used as ballast for compliance with D-2 standard as per the request of the ship's management/operator, and 2) Examine if analysis methods are equally effective on treated and untreated ballast water. This study thus supports ongoing efforts to establish uniform methods for ballast water sampling and analysis under the Convention for the Control and Management of Ships' Ballast Water and Sediments adopted by the International Maritime Organization.

2.0 Methods

2.1 Test vessel and experimental design

All trials were conducted onboard the RV Meteor while in transit from Mindelo, Cape Verde to Hamburg, Germany. The RV Meteor is equipped with an Optimarin BWMS consisting of a filter and UV reactor, and multiple sampling ports to facilitate sample collection for compliance monitoring. The ballast water pipe system onboard the RV Meteor comprises DN10 galvanized steel pipes (diameter 100mm) and an uncompensated piston pump with a maximum capacity of 65m³/h. During the sampling experiments the system pressure ranged from 0.2 to 1.6 bar and the mean pump capacity was 56 m³/h resulting in a mean flow velocity of 1.98m/s. The variable pressure and periodic entrance of air into the ballast system presented a challenge for maintaining sub-isokinetic flow according to G-2.

Figure 1 gives a schematic overview of the BWMS with sampling points and valves that can be used to produce different flow paths through the ship's ballast system. Sample point A is located before the BWMS, sample port B is located after the BWMS, and two additional sampling points (C and D) are installed after the BWMS; port C is used for water collection and Port D is used for water return with a closed sampling system. The sampling ports A, B, and C installed in the ballast water pipes were equipped with an "L" shaped sampling probe with a leg facing upstream as required by the IMO Guidelines for Ballast Water Sampling (cf. IMO document MEPC.173(58), October 10th, 2008). At port D a return probe was installed with the opening facing downstream. The sampling probe had a diameter of 25.4mm.

A total of 28 trials were run with sampling devices used in pairs. The BWMS was turned off for 24 trials that focused on examining differences in organism density due to (i) sampling device and sampling port and (ii) analytic method used. During these tests, water was taken directly from the sea with no holding period (sea to sea). The BWMS was turned on for four trials which were used to (i) explore how analytic devices performed at high and low organism concentrations and (ii) examine the ability of analytic tools to rapidly detect the effects of UV treatment. One of these trials used water that had been treated and held in the ballast tank for two days before a second treatment upon discharge. The first UV trial was run with the UV system regulated and the remaining trials had unregulated UV treatment (see Table 2). When the system is run with regulated UV, a sensor evaluates the dose being achieved by the system and adjusts bulb output to achieve the required dose (i.e. if water has high DOC content, system increases bulb output, and in very clear water, system reduces bulb output). In trials with unregulated UV, the system operates at 100% UV power regardless of the water conditions. Unregulated UV was used in the final three trials since air bubbles were observed in the ballast sample collection systems (see Discussion) and it was unknown how these air bubbles might affect the UV regulation. Since our objectives were to examine the ability of the analytic tools to detect the effect of treatment, rather than examine the performance of the BWMS, this setting should not be important for our results. All trials using the BWMS were sampled using a net as the collection device both before and after treatment. Table 2 details sampling devices and water sources for each trial. Table A1 in Appendix A includes more detailed trial information including salinity, temperature, sampling time and locations, ballast water flow rate, and total volume of water that passed through the ballast system during the trial.

2.2 Sample collection

For each trial, the normal ballasting procedures onboard the RV Meteor were used to pump seawater through the ship's ballast water pipe system. The sampling ports already installed on the ballast water pipe system (described above) allowed for the simultaneous collection of paired samples of the same water at two different sampling ports with two different sampling techniques. Each of the three sampling devices have a 'cod' end (plankton net) or inbuilt filter (sampling skids), where the sample of organisms $\geq 50 \mu\text{m}$ is collected and concentrated using $50 \mu\text{m}$ mesh. For collection of $10\text{-}50 \mu\text{m}$ organisms, the devices have differing methods. For trials 1-5, the plankton net 'frequent grab' sample was taken by collecting 500 mL of unfiltered ballast water from the sample hose every two minutes for the duration of the collection. For trials 6-28, this water was collected directly from the containment drum after passing through the plankton net; this change was enacted following discussion in the on-board scientific meeting to eliminate a redundant filtration step during sample processing to separate $\geq 50 \mu\text{m}$ particles. For the SGS filter skid, a ball valve was installed through which a 'frequent grab' sample was collected from the water which has already passed through the $50 \mu\text{m}$ inbuilt filter. The Triton filter skid offers two options: (i) to collect a 'frequent grab' sample from the water that has already passed through the $50 \mu\text{m}$ inbuilt filter and (ii) to collect 'continuous drip' samples without the $50 \mu\text{m}$ filtration step; during the course of the voyage, option (i) was used. When possible, sampling devices were rotated

between sampling ports during testing. Since the closed filter skid systems can only be positioned at sample port (C) in order to return backflow water at (D), they were paired with an open method at port position (A). Based on the very short sections of straight pipe and number of bends in the ballast system, theoretically, the flow of ballast water at each sample port location was considered to be turbulent, such that upstream sampling would not affect downstream sampling (Richard et al. 2008). However, for all tests, the sampling port position was recorded to enable the statistical evaluation of any potential influence of sample port position. Devices used and their positions for each trial are detailed in Table 2.

For most trials, open ocean water was pumped through the ballast water pipe system while in transit, with the exception of two trials that tested organism densities in the ship's potable water, one trial that used Mindelo port water that had been held in a ballast tank for three days, and one trial that used treated ocean water that had been stored in a ballast tank for two days (see Table 2). The 'potable water testing' examined water that had been treated using the ship's potable water system and stored in ballast tanks for a period of time prior to testing to evaluate the use of potable water as ballast. During each trial, each collection device filtered ~1000 L of water for analysis of $\geq 50 \mu\text{m}$ size class that was condensed to 1 L (some exceptions; see Table A2); the actual volume of water filtered by each device was quantified and recorded so that appropriate densities could be back-calculated for device comparisons. The volume of water filtered was quantified using a Seametrics WMP104-100 magnetic flow meter for net samples, and built-in flow meters for the sampling skids. Additionally, each device collected between 10 and 16 L of water for analysis of 10-50 μm organisms and microbes.

2.3 Sample preparation

For each trial, a common batch of filtered seawater was prepared for use as rinse water by all participants during sample collection and sample analysis. Rinse water was prepared by filtering local seawater water obtained using the vessel's seawater taps through 1000 μm and 500 μm mesh. This filtrate was further sieved through 35 μm and 8 μm plankton mesh filters, and finally, passed through a 0.2 μm passive (gravity-fed) filter cartridge (Whatman Polycap TC).

For each trial, each participant received one sample bottle for each analysis method corresponding to the appropriate size fraction of water required. All sample collection, sample splitting, sample fractionation/sieving was completed in a uniform way, so that observed variability is more likely explained by analysis method rather than sample handling.

For water samples containing taxa $\geq 50 \mu\text{m}$, concentration was performed during sample collection, so post-collection processing was not required. To prepare individual sample bottles for each analysis method, each sample was mixed by inverting five times, and then sample bottles were half-filled (7 bottles, total volume 35-300 ml depending on analysis requirements). This procedure was repeated to fill the sample bottles. This splitting procedure (5x inversion, half fill, 5x inversion, fill remainder) was used to fill all sample bottles as detailed below (see also Sample Splitting SOP, Appendix B).

Water samples containing particles < 50 µm were processed to generate the fractions required for the remaining analyses (<50 µm, 10-50 µm, and <10 µm). First, the sample bottles for the < 50 µm fraction were filled (7 bottles, 50-600 ml). The remaining water was filtered on a 10 µm (diagonal) Sterlitech polyester track etch (PETE) membrane filter. The filtrate containing organisms < 10 µm was split into 8 sample bottles (125-500 ml), and the retained particles were resuspended in filter-sterile seawater with a final concentration up to 16x times the original volume (see Table A2). The concentrated sample was split into sample bottles for analysis of the 10-50 µm fraction (9 samples, 25-350 ml; see Sample Splitting SOP, Appendix B).

After each trial, all sampling gear and sample bottles were cleaned in a dilute (100-200 ppm) or concentrated (2500 ppm) commercial bleach bath (depending on equipment hardiness) to prevent cross-contamination of living organisms between tests. After bleaching, all equipment was rinsed with MilliQ water 3 times and nets were soaked in rinse water and hung to dry. Prior to re-use, all sample bottles were rinsed with filtered seawater 3 times to remove any residues.

2.4 Protocol for spiking ballast water samples

Since the numbers of IMO-relevant human pathogen bacteria levels are low in the open ocean, samples were spiked with bacteria in 4 trials in order to better compare analytic methods for bacteria. A stock culture of each *Escherichia coli* and *Enterococcus faecalis* were prepared from type cultures obtained from Public Health England, culture collections UK, by aseptically adding one Lenticule disc to a sterile bijoux tube containing 5 ml of sterile TSB medium. Cultures used were *E. coli*, NCTC 9001, Cat # CRM09001L, Batch 2037-15 and *E. faecalis*, NCTC 775, Cat # CRM00775L, Batch 2297-14. The culture was incubated for four hours to resuscitate the organisms under ideal conditions. After four hours, 1 ml of each organism suspension was inoculated into 20 ml of sterile Tryptic Soy Broth (TSB) medium prepared in a diluent of 75% reverse osmosis (RO) water and 25% filter-sterilised marine water and cultured overnight to acclimatise the organisms to high salt environments and reduce osmotic shock when spiking samples of marine water. The resulting cultures were used as “working stocks” and stored at 4 °C until required for spiking experiments. In parallel, these were assessed visually (experience was used to predict the number of organisms present based on turbidity) and serially diluted in sterile RO:marine water (75%:25%). 0.1 ml of the serial dilutions expected to contain between 10 and 100 cfu were plated onto Tryptose Soya Agar plates in triplicate and incubated overnight at 37 °C. These were counted and the mean result used to confirm the actual cfu value of the working stocks.

For ballast water trials, working stocks were serially diluted in sterile RO:marine water (25%:75%) to give target values in the bulk sample containers as indicated in the notes column of Table 2. Note that target values are affected by storage and handling of the working stocks, so the cfu values in the ballast water trials should be considered target values rather than exact numbers. Further, there is the potential that bacteria were killed by osmotic shock when mixed into the sample water; this is especially pertinent for trial 6 where bacteria were not acclimatized to the salinity before spiking.

2.5 Sample Analysis

Samples were analyzed in parallel using the analytic methods listed in Table 1. A short description of each method is provided in Table 3 and detailed methodology for each analytic method is provided in Appendix C. In order to minimize potential bias, all samples were provided to analysts in a 'blind' form (i.e. no information given about status as treated/untreated or sample collection method). From each sample bottle, participants were asked to draw three replicate subsamples for measurement. Samples were inverted five times before withdrawing each subsample to ensure samples were well mixed, and all steps of sample analysis were performed independently on each replicate sample. Due to time constraints and operational considerations (e.g. limited materials), not all analytic methods could be performed for all trials. Detailed information about the number of replicates analyzed for each trial by method is provided in Tables 4 through 7 for size classes $\geq 50 \mu\text{m}$, $10\text{-}50 \mu\text{m}$, $<10 \mu\text{m}$, and bacteria, respectively.

2.6 Statistical Analysis

All analyses were performed in the R statistical programming environment (R Core Team 2015). To account for any concentration steps performed by individual researchers (see Appendix C), values were standardized to equivalent concentrations in the raw sample where necessary. Further, since sample volumes collected by each sampling device varied, results were also standardized based on the total volume of water filtered by each sampling device (Table A1) for analyses involving sampling skids, ballast water treatment, and potable water testing.

2.6.1 Analytic Device Comparison

To compare results for each analytic device versus traditional microscopy, scatterplots were made that compared all measurements taken for each sample (1 sample per sampling port per trial (i.e. 2 samples per trial); 56 samples total) with replicates randomly paired. A line of best fit was generated using Deming's regression which accounts for error in both variables (Ripley and Thompson, 1987). Since Deming's regression does not provide a method to characterize strength of fit, the Pearson correlation coefficient was used to quantify the strength of the relationship between the two methods.

A model for methods comparisons was used to simultaneously compare results between analytic methods (Carstensen, 2010):

$$y_{mir} = \alpha_m + \beta_m(\mu_i + c_{mi}) + e_{mir}$$

where y_{mir} is the measured value for a given method (m), item (i) and replicate (r), α_m and β_m describe the linear relationship between the true value (μ_i) and the measurement made on item i by method m . The c_{mi} term is a random method by item effect ($c_{mi} \sim N(0, \tau_m^2)$) and e_{mir} represents the residual variation ($e_{mir} \sim N(0, \sigma^2)$). Note that the true value (μ_i) is estimated during the fitting process and is essentially a weighted mean across estimates by different

methods. Deming regression was used to verify model assumptions (constant variance and constant bias), and data were transformed when necessary to meet assumptions. Where logarithmic transformations are indicated, these refer to the natural log. Where bias was not constant (all analyses herein), Markov Chain Monte Carlo methods were used to fit the model which can account for linear bias between methods. Model validation was performed graphically by inspecting the traces and posterior densities for convergence. Note that not all methods could be analyzed using these methods due to inability to meet the assumptions of constant variance using transformation. These analyses were performed in R using the *MethComp* package (Carstensen et al. 2015).

2.6.2 Sampling Device Comparison

Sampling devices were compared using linear mixed effect models with fixed effects for sampling device and sampling port, and random effects for analytic device and trial. Measurement data from each analytic tool was z-transformed to standardize measurements from each device to mean = 0 and standard deviation =1 so that all devices influenced results equally (i.e. devices that report results with a high magnitude do not influence results more than those that report in units with a low magnitude). Models were run separately for each size class using *lme4* (Bates et al., 2015) in R (R Core Team, 2015). Variance structures were specified to account for different variances for both trials and analytic tools. Model selection was done using likelihood ratio tests and model assumptions were validated by visual inspection of residuals and using Levene's test. P-values for the effect of sampling port were obtained using likelihood ratio tests comparing models with and without sampling port included. P-values for differences between sampling devices were obtained by running pairwise Tukey contrasts using the general linear hypothesis testing function in the *Multcomp* package (Hothorn et al., 2008).

For all analyses, trials 1 and 2 were excluded due to errors in sample handling (see Table 2), and trials that compared water before and after treatment were excluded since treatment negates a paired comparison between collection devices. For the $\geq 50 \mu\text{m}$ size class, Welschmeyer ATP, bulk FDA, and Hach BW680 results were excluded from the model since they were used infrequently and caused the assumption of residual homogeneity to be violated. For the 10-50 μm size class, trials 1 through 5 were excluded since net samples for trials 1-5 did not exclude taxa $\geq 50 \mu\text{m}$.

2.6.3 Analysis of Samples before and after Treatment

In four trials, water was collected before and after treatment with a BWMS. One-way t-tests with Welch's correction for unequal variance were used to determine if each analytic method was able to detect a decrease in organism density immediately following treatment.

2.6.4 Potable Water Testing

One-way t-tests were used to determine whether the organism densities found in the tanks containing 'potable water' exceeded the IMO D-2 standards. For these tests, data from

all analysis methods and sampling devices were pooled, with the exception of data for which conversions to individuals by volume were unavailable (i.e. $\geq 50\mu\text{m}$: ATP, PAM, bulk FDA; 10-50 μm : ATP, PAM, bulk FDA).

3.0 Results and Discussion

All trials were conducted during transit from Mindelo, Cape Verde to Hamburg, Germany (Figure 2). Natural variation in the plankton communities in the water led to a great difference in the densities of individuals of each size class found throughout the voyage. The beginning of the cruise was mostly spent in oligotrophic water where biological variation was low and organism concentrations were at or below ballast discharge standards. Near the end of the cruise, very high densities were reached which were more suitable for testing water before/after treatment. Organism densities in the $\geq 50\mu\text{m}$ size class ranged between 1 individual/ m^3 and $\sim 800,000$ individuals/ m^3 (as estimated by microscopy) and organism densities in the 10-50 μm size class ranged between 0.3 and 60.3 individuals/mL (as estimated by microscopy after FDA staining). While the phytoplankton biomass varied largely, the phytoplankton viability, based on photosynthetic efficiency, remained fairly constant (based on flow cytometry results) and, with one exception (trial 7), the Fv/Fm ranged from a value of 0.3 to 0.65, indicative of healthy phytoplankton (Figure 3). The relative contribution of the 10-50 μm fraction was on average $\sim 10\%$ of the total phytoplankton counts (based on flow cytometry results).

For each trial, water samples containing organisms of varying size classes were collected and split for analysis. Due to random chance, it is not expected that every subsample measured would contain the exact same number of organisms. Instead, the true number of individuals in a sample is expected to be represented by a distribution of possibilities where the mean is equal to the true number of individuals and the variance equals the mean (i.e. Poisson distribution; Haigh, 1967). Variation in measurements between subsamples is therefore expected, and the amount of variation is expected to increase as the true population density increases. Importantly, as a result, observed differences between measurements may represent a combination of true differences between subsamples and measurement error.

3.1 Comparison of Analytic Devices

Information regarding the time requirements, costs, training requirements and portability of each analytic method tested is provided in Table 7.

3.1.1 Comparison of analytic devices for organisms $\geq 50\mu\text{m}$ in dimension

Eight methods were used to analyze water samples containing particles $\geq 50\mu\text{m}$:

- microscopy (visual inspection for motile organisms; staining for phytoplankton), Satake Pulse Counter, bulk FDA,
- two methods for PAM, measuring only phytoplankton,
 - Hach BW680

- Walz-Water PAM)
- two methods for ATP
 - Welschmeyer ATP method
 - SGS ATP (aqua-tools) method.

In general, most analytic methods were sensitive enough to detect organisms in the water samples at a range of densities (i.e. most analytic devices produced non-zero values where the microscope method detected live individuals; Figure 4; Deming regression coefficients are shown in Table 9). Since most measurement tools were unable to estimate the number of individuals in samples, it is not possible to determine whether the devices are equivalent to microscope measures. The Satake Pulse Counter is the only method which was able to provide density estimates in individuals/volume. This method tended to underestimate the density of individuals as compared to microscope counts (see Figure 4; most data points fall below 1:1 line). Notably, some other analytic methods used here (e.g. SGS ATP (aqua-tools)) may be able to estimate organism density in the future, but this is still under development.

A method comparison model was run to compare log+1 transformed data from SGS ATP (aqua-tools), microscopy, Walz-Water PAM, and the Satake Pulse Counter (Figure 5; Full model details in Appendix E.1); Hach BW 680, Welschmeyer ATP, and Bulk FDA methods were excluded due to limited data (see Table 4). The model allows measurement conversion between devices, but the confidence interval is wide due to uncertainty in the conversion. Note that while residual variation is reported by the model (Appendix E.1), it is not appropriate to draw conclusions on the precision of instruments based on these values since measurements are reported in different units.

An additional analysis was done to examine the results of the Optical Zooplankton Analyser (OZA) which counts zooplankton that are > 200 μm in size. Results were compared both to the microscope counts for zooplankton only and the total microscope counts (motile taxa and stained taxa). In both cases, the OZA underestimated organism densities (Figure 6), but correlation was much higher with zooplankton only microscope counts ($r=0.574$ vs 0.107).

3.1.2 Discussion of results for organisms $\geq 50 \mu\text{m}$ in dimension

During the voyage, it was observed that phytoplankton were present, often at high abundance, in the $\geq 50 \mu\text{m}$ size class. In response, the microscopy methods were adjusted to count phytoplankton $\geq 50 \mu\text{m}$ using FDA staining since movement is not a reliable indicator of viability for non-motile taxa. Essentially, a second count was added so that results included two sets of counts: (i) motile taxa counted visually, and (ii) non-motile taxa counted with FDA stain. Examinations of the efficacy of FDA stain for marine phytoplankton have focused on the 10-50 μm size class (e.g. Steinberg *et al.* 2011) and error rates for larger phytoplankton are unknown. Currently, most ballast water counting protocols do not add this extra step and instead count $\geq 50 \mu\text{m}$ phytoplankton at the same time as motile counts, with the assumption that intact cells are viable (e.g. First *et al.*, 2015). Based on results from this voyage, these two methodologies may yield very different results, suggesting that this issue should be considered further in future work.

The composition of the plankton communities is likely to affect the level of concordance between analytic methods. Since some methods used herein (e.g. PAM methods) are only able to detect phytoplankton, it is possible that results for total organism counts would be very different between phytoplankton-only methods and total organism methods if the samples had not been dominated by phytoplankton during this voyage. However, note that phytoplankton-only methods can indirectly detect zooplankton if phytoplankton have been consumed by the zooplankton.

3.1.3 Comparison of analytic devices for organisms in the 10-50 μm size class

Nine methods were used to analyze water samples containing 10-50 μm particles:

- microscopy (FDA staining); direct counts,
- Satake Pulse Counter; direct counts
- bulk FDA; indicative method,
- four methods based on different properties of the autofluorescence of the chlorophyll in phytoplankton
 - Hach BW680; indicative method converted into numbers
 - bbe 10cells; indicative method converted into numbers
 - BallastCheck2; indicative method converted into numbers
 - Walz Water PAM, indicative method
- flow cytometry; direct counts (counts both live and dead organisms), and
- Welschmeyer ATP; indicative method.

Five methods were able to estimate the number of individuals in samples: Hach BW680, 10cells, BallastCheck2, flow cytometry, and the Satake Pulse Counter. 10cells and the BallastCheck2 had the strongest correlation with microscopy results (Figure 7; Pearson correlation coefficient= 0.92 and 0.90 respectively). The regression line for the BallastCheck2 matched the 1:1 line most closely indicating that the device was neither systematically under- or over-estimating organism densities (Table 10). The Satake Pulse Counter underestimated organism densities as compared to microscope measurements (see Figure 7; most data points fall below 1:1 line) and flow cytometry overestimated organism densities as compared to microscopy (see Figure 7; most data points fall above the 1:1 line). The flow cytometer counts both live and dead organisms, so this is not unexpected. Many samples analysed by the Hach BW680 were below its detection limit; in 17 trials it did not detect a signal in any replicate where the microscope method detected viable organisms. In contrast, 10cells and BallastCheck2 methods reported zeros where the microscope method reported viable organisms at most once (i.e. in one replicate). For methods that did not report results in individuals/volume, the Walz-Water PAM had the strongest correlation with microscopy results (Pearson's correlation coefficient= 0.879).

Concentrations estimated by PAM devices are based on conversion factors which are particular to each device. To eliminate this source of variation, PAM devices were each compared to each other and to microscopy counts using their raw output, Fv (Figure 8). The Fv

values for these devices had high levels of correlation (range 0.75-0.96) with BallastCheck2 and 10cells showing the highest similarity. F_v values were also highly correlated with microscope densities ($r=0.82-0.87$; Figure 8).

A method comparison model was run to compare methods. The model compared log+1 transformed data from the 10cells, Hach BW680, BallastCheck2, Walz-Water PAM and microscopy (Figure 9; full model details in Appendix E.2). The slope of each conversion curve varies around 1 and the 95% confidence intervals show a much tighter fit than was observed for the $\geq 50 \mu\text{m}$ fraction indicating greater certainty in the conversion lines.

3.1.4 Discussion of results for organisms in the 10-50 μm size range

Results from the PAM fluorometers (i.e. 10cells, BallastCheck2, Walz-Water PAM and Hach BW680) were highly correlated with microscope results, but the fluorometers differed in their sensitivity (Figures 7, 8). PAM fluorometers measure F_o , total chlorophyll biomass, and F_m , total fluorescence after excitation and use these values to estimate F_v , which relates to live chlorophyll fluorescence ($F_v = F_m - F_o$). Chlorophyll biomass estimates based on F_v reduce the sensitivity of the instrument response, because the noise in each measure is combined making it easy to generate 'negative' values. Fluorometers in this category, such as the Hach BW680, are thus less sensitive. The 10cells also bases its estimates on F_v , but minimizes sensitivity loss by increasing signal strength through filtration.

PAM results (F_v , F_m , or F_o) can be converted to densities in cells/mL based on an internal calibration coefficient that is determined at the factory or by the end-user. The calibration constant is specific to each device, and consequently, different PAM devices can generate different density estimates even if they have the same fluorescence reading. This variation in calibration factors affects the slope between devices (Figure 7), and for this reason, results were analyzed both by looking at the raw fluorescence measurements (specifically, F_v ; Figure 8) and by looking at the calculated cell densities which can be compared to microscopy counts (Figure 7).

In reality, the true relationship between fluorescence and cell density varies between algal communities depending on chlorophyll cellular content (can vary by a magnitude of 5x due to photoadaptation and an additional 5x due to nutrient limitation/saturation) and the size of cells in the community (Veldhuis et al, 1997). Cell size in the 10-50 μm group represents a range of cell volumes (biomass) of potentially 125x (volume = $4/3 \pi r^3$); as such there is no 'standard' cell or community to which these devices are calibrated. During the METEOR voyage, the average cellular chlorophyll fluorescence of the entire phytoplankton community, and the 10-50 μm fraction in particular, varied by a factor of 2 to 3, with fluorescence increasing, in general, during the course of the voyage, with the exception of trials 10 through 14 when the average chlorophyll fluorescence was at its lowest (Figure 10). Variation in chlorophyll content per cell is a major source of error for estimating cell numbers on the basis of bulk chlorophyll. Simply, if cells have a higher chlorophyll concentration, fewer cells are needed for the same amount of chlorophyll fluorescence.

To examine this further, the number and size of phytoplankton cells and their chlorophyll fluorescence were determined by applying flow cytometry (Veldhuis & Kraay, 2000) to formalin-preserved samples. This data allows the determination of an independent chlorophyll fluorescence biomass (FCMchlor) which is distinct from that determined using standard fluorometry (e.g. WALZ Water PAM), and can be compared with the chlorophyll fluorescence properties (F_0) of the PAM-type of fluorometers. For the METEOR voyage, the total number of phytoplankton cells (all sizes and $< 10 \mu\text{m}$) show a reasonable correlation with the bulk fluorescence as measured with the WALZ-PAM. In contrast, the relationship between cell number and chlorophyll biomass for 10-50 μm phytoplankton is very poor (Figure 11). If the average cellular chlorophyll fluorescence of each cell is considered (recall that it varied throughout the voyage), we see a substantial increase in the relationship with total biomass, especially for the 10-50 μm fraction (i.e. the size class of interest; Figure 12). This implies that variation in size and therefore cellular chlorophyll content can have a significant effect on the relationship between fluorescence signal and cell number, and a simple conversion value for chlorophyll fluorescence to cell numbers will therefore not be completely reliable.

3.1.5 Comparison of analytic devices for taxa $< 10 \mu\text{m}$ (excl. bacteria)

Five methods were used to analyze water samples containing $< 10 \mu\text{m}$ particles: Walz Water PAM, BallastCheck2, bulk FDA, Hach BW680, and Welschmeyer ATP. Since microscopy data was not available, each method was compared to both Water PAM and BallastCheck2 since they were analyzed in all trials (Figure 13; Table 11). All methods showed some level of positive correlation with both Walz-Water PAM and BallastCheck2, but many samples registered below the detection limit of the Hach BW 680. A method comparison model was run to compare data for BallastCheck2, Bulk FDA and Welschmeyer ATP (Figure 14; full model details in Appendix E.3).

3.1.6 Discussion of results for taxa $< 10 \mu\text{m}$ (excl. bacteria)

While many methods were used to analyze the $< 10 \mu\text{m}$ fraction during the voyage, only PAM and BallastCheck2 were used consistently. There is a strong relationship between results for PAM and BallastCheck2, but there are a considerable number of outliers. More complete data from other methods would be useful to make inferences about these non-matching data points. Since all measurements are reported in different units, it is not possible to make inferences about the relative precision of each method.

3.1.7 Comparison of analytic devices for bacteria

Methods for measuring bacteria focused on either total bacteria (IDEXX Simplate and SGS ATP (aqua-tools), *Enterococcus* (IDEXX Enterolert, Speedy Breedy *Enterococcus*), or *E. coli* (Triton BW BacTest EC, IDEXX Colilert, Speedy Breedy *E. coli*). Bacteria levels were low throughout the voyage, with nearly all samples indicating levels of *E. coli* and *Enterococci* that were below the detection threshold for all measurement instruments except when samples were spiked (see methods). Analytic tools to detect total bacteria (IDEXX Simplate and SGS ATP (aqua-tools) were able to detect bacteria throughout the voyage, but there was low correlation

between measurements by each method (Figure 15; $r=0.239$). For many trials, SGS ATP (aquatools) detected bacteria when IDEXX Simplate readings were below the detection limit. Note that the detection limit of IDEXX Simplate varies depending on dilution used and that the SGS ATP (aquatools) methodology is designed to detect all 'living' ATP, whereas IDEXX Simplate is specific to bacteria that grow at 35°C.

Similarly, there was no clear relationship between the amount of *E. coli* measured by Speedy Breedy *E. coli* and Triton BW BacTest EC (Figure 16), though both devices detected *E. coli* in 3 of 4 trials where *E. coli* was spiked (trials 12, 21, and 22; note that bacteria may have been killed by osmotic shock in trial 6 because acclimation was not performed). In contrast, IDEXX Colilert measured all samples as below the detection limit with the exception of 1 sample in trial 4 where neither Speedy Breedy nor Triton BW BacTest EC detected *E. coli*.

Measurements of *Enterococcus* by IDEXX Enterolert and Speedy Breedy Enterococcus had a much stronger agreement (Figure 17; $r=0.765$) within their detection limits. Both devices detected *Enterococci* in trials 12, 21, and 22 (where it had been spiked) and IDEXX Enterolert additionally detected *Enterococci* in trial 6 (where it had been spiked) and trial 15 (at a low level).

3.1.7 Discussion of results for bacteria

Since bacteria levels were low throughout the voyage, we had limited data to use for comparison between these analytic methods. While bacteria spiking was used to ensure bacteria were present in some samples, there are at least two potential issues with this approach. First, it is expected that salinity shock killed bacteria in at least the first spiking experiment. While steps were taken to acclimate bacteria in subsequent trials (see methods), it is possible that salinity shock continued to be an issue and could influence differences between results depending on the length of exposure prior to analysis. Second, after the voyage, it was noticed that the strain of *E. coli* used for spiking may be lacking the glucuronidase enzyme needed for detection by IDEXX Colilert.

3.2 Comparison of Sampling Devices

Since analytic tools reported measurements in various units (e.g. individuals/mL, pgATP/mL, fluorescein production rate) and all of this data was pooled and transformed to analyze the effect of sampling device (see methods), the outcome variable which relates to organism density is not readily interpretable; instead it represents a mean difference in measurements which can be attributed to sampling device. Thus, while it is possible to detect whether there are differences between the sampling devices, the amount of difference between the methods is unintelligible and we are unable to comment on whether a significant difference is operationally relevant.

3.2.1 Results for sampling devices

For the $\geq 50 \mu\text{m}$ size class, there was a significant effect of both port ($L = 9.8$ ($df=1$, $p<0.05$)) and sampling device ($L=23.4$ ($df=4$, $p<0.001$)). Densities of samples collected using the SGS skid (open or closed) and the Triton skid (closed) were not significantly different from samples collected using the net (Tukey contrasts, all $p>0.05$; Figure 18), however samples collected using the Triton skid in the open configuration were significantly lower than those collected using the net (Tukey contrast; $p<0.001$; Figure 18).

For the $10\text{-}50 \mu\text{m}$ size class, there was a highly significant effect of sampling device ($L=28.3$ ($df=4$, $p<0.001$)), but no significant effect of sampling port ($L=0.2$ ($df=1$, $p>0.05$)). Densities of samples collected using the SGS skid (closed configuration) and Triton skid (open and closed configuration) were not different from net samples (Tukey contrasts; all $p>0.05$). Organism densities were slightly higher in samples collected using the SGS sampling skid (open configuration) than samples collected using the net (Tukey contrast; $p<0.01$; Figure 19).

For the $< 10 \mu\text{m}$ size class, there was no significant effect of sampling device ($L=4.6$ ($df=4$, $p>0.05$)), but there was a significant effect of sampling port ($L=3.9$ ($df=1$, $p<0.05$)).

3.2.2 Discussion for sampling devices

Our experiments were designed to replicate the operational use of sampling skids as much as possible. While IMO rules state that isokinetic sampling is not strictly necessary, it is important to ensure representative sampling and to minimize stress on organisms. The ISO standards for ballast water sampling (2013) and a US Naval Research Lab report on this ISO standard (Drake *et al.*, 2015) require sampling probe diameters between 1.5 to 2.0 times the isokinetic diameter to facilitate sampling at sub-isokinetic speeds. As such, we attempted to sample accordingly throughout the voyage and we were largely successful. However, in three trials isokinetic sampling was not achieved. In trials 1 and 2, the ballast pump was pumping very slowly (17 and 29 m^3/hr ; compared to overall average of 57 m^3/hr during voyage). This was not recognized during sampling, so we were unable to alter our sampling rate to compensate. Resultantly both SGS and Triton sampled at super-isokinetic speeds (in trial 1 and trials 1 and 2, respectively), since pressure differences between the ballast system and the atmosphere vented through the sampling system as the path of least resistance (this is only possible when sampling skids are in the open configuration). Additionally, in trial 26 (net/net sampling), flow rates were super-isokinetic for both nets. At super isokinetic speeds, samples are expected to contain lower densities, but there should not be a difference between devices at similar velocities. These trials had already been excluded from the sampling device analysis due to methodology (trials 1 and 2, see table 2) or because they sampled using the same device (trial 26), so these violations of isokinetic sampling will not have any influence on our results.

In a related matter, the actual flow velocity in relation to the isokinetic velocity may be an important factor to consider. During the METEOR voyage, most sampling devices sampled at roughly the same rates (mean sampling velocities ranged between 43.53 m^3/h and 56.48 m^3/h for different sampling devices), but in some cases sampling rates were much lower (e.g. Triton closed system, mean 24.43 m^3/h , about 1/3 speed of the paired device). We were not able to

explicitly analyze the effect of sampling speed herein, but additional research may be warranted to determine whether it influences the density of organisms captured.

Operational challenges experienced during the course of the voyage may have affected the performance of the sampling devices. For example, during several trials, the filter cup of the Triton skid and the net sampling system were observed to contain a massive intrusion of micro-air bubbles. While the filter housing of the SGS skid is not transparent, it may be assumed that the SGS sampling system experienced the same issue. This would presumably have a considerable impact on the pressure regime in the BW pipe system, and could have exposed plankton organisms to hydrodynamic stress and impacted their viability (L. Schillak, pers. comm). This impact should have been comparable across sampling methods, so it should not influence our conclusions with respect to differences between devices. The air bubbles may have also had an effect on flow meter readings and since each device used a different type of flow meter (i.e. paddle wheel, magnetic, and positive displacement), these impacts may not be consistent across sampling devices. It is expected that any differences between flow meters would not have a large effect on the results (if correctly installed, max 2% error; C. Gianoli, pers. comm.).

Moreover, during several trials there was a high amount of sediment in the water. The IMO G2 regulations, Annex 3, para 6.2.3., page 5 state that "*the sampling protocol should take account of the potential for a suspended sediment load in the discharge to affect sample results*". Each skid developer has a different perspective on how high organism densities or high sediment load should affect sampling. From the SGS perspective, it is expected that samples with a high concentration of particles could be compliant and thus the SGS skid is designed to maintain operations even when particle loads are high. In contrast, Triton assumes that a blocked filter is a symptom of non-compliance and sampling should be stopped, since either a high sediment load or a high organism density during sampling would generate irreversible negative impacts on the vitality of the live organisms targeted for analysis. During the METEOR voyage, the filter of the Triton skid was clogged by very high organism densities and the filter cartridge jumped off its seat and became inoperational; this would be interpreted as a compliance failure.

3.3 Results and Discussion for Analytic Methods Before and After Treatment

A significant decrease in organism densities after treatment was detected by each analytic method in both size classes ($\geq 50 \mu\text{m}$ and $10\text{-}50 \mu\text{m}$; Figures 20, 21; one-way paired t tests on $\log+1$ transformed data with Welch's correction for unequal variance; all $p < 0.05$), with the exception of bulk FDA ($\geq 50 \mu\text{m}$ and $10\text{-}50 \mu\text{m}$), Welschmeyer ATP ($\geq 50 \mu\text{m}$), and flow cytometry ($10\text{-}50 \mu\text{m}$). Note that these methods did detect a decrease in organism densities, but due to limited usage may not have had enough statistical power to detect a difference. In particular, the PAM methods and the Satake Pulse Counter showed the greatest decrease in detection post-treatment.

For trials where treated water was held in the ballast tank for two days before being re-treated, all methods showed a decrease in organism density after both treatments (Figures 22,

23 for $\geq 50 \mu\text{m}$ and 10-50 μm , respectively), but some devices registered an increase in organism concentrations during the two-day hold period. This may be the result of a true increase in organism densities in tanks or it may be the result of leaky valves (see potable water testing results). Alternatively, since tanks were not cleaned before the trials, it is also possible that the increase is simply due to organisms already being present in the tank's residual ballast before the treated samples were added.

It is important to note the minimum detection limits (see Table 8) when comparing results, since instruments that are unable to detect low organism densities may appear to show a greater effect of treatment simply because they are registering zero values when only a few organisms remain.

3.4.1 Results and Discussion for Potable Water Testing

The 'potable water testing' trials examined water that had been treated using the potable water system and stored in ballast tanks for a period of time prior to testing. These trials were undertaken to evaluate the potential to use potable water as ballast (IMO, 2013). For organisms $\geq 50\mu\text{m}$, the D2-Standard requires a discharge of < 10 individuals per cubic metre of ballast water. Pooled data indicate that the organism concentration exceeded the D-2 standard (Figure 24; $t(23)=4.73$, $p<0.001$). Since density estimates were quite different between analytic devices (Table 12), we re-ran the analysis to determine if results would be the same if we were only analyzing the samples using traditional microscopy. Microscopy results also indicate that the organism concentration exceeded the D-2 standard ($t(11)=2.63$, $p=0.011$).

For 10-50 μm organisms, the D-2 standard requires a discharge of <10 individuals per milliliter of ballast water. Pooled data across all devices indicate that the organism concentration complies with the D-2 standard for this size fraction (Figure 24; $t(82)=-5.50$, $p>0.05$). Density estimates for each analytic device are shown in Table 13.

Importantly, salinity readings for these trials indicated that the water tested was brackish (trial 1= 13.8 ppt, trial 2=23.5 ppt), which is not consistent with potable water. As such, there is speculation that the water tested may have been a mix of potable water and ballast water, potentially due to leaking between tanks or because tanks were not completely empty when the potable water was introduced. Furthermore, in the second trial, the rinse water did not match the salinity of the test water (see Table 2). This may have caused stress to organisms in the $\geq 50 \mu\text{m}$ fraction, which may have resulted in death of some organisms, but this would not change the outcome of these results since taxa concentrations exceeded the threshold nonetheless.

Tables and Figures

Table 1. List of analysis methods conducted on the METEOR voyage, the size class targeted, and the participant(s) responsible for conducting the analysis.

Analysis Method/Type	Size Class (μm)	Participant
Optical zooplankton analysis	>200	Wouter van der Beek
Microscopy (movement + FDA staining)	≥ 50	Sarah Bailey
Satake Pulse Counter	≥ 50	Satake
MLML (steamlined) bulk FDA method	≥ 50	Nick Welschmeyer
ATP assay with improved extraction protocol	≥ 50	Nick Welschmeyer
SGS ATP (aqua-tools)	≥ 50	SGS
WALZ-Water PAM	<50	Marcel Veldhuis
Microscopy (FDA)	10-50	Julie Vanden Byllaardt
Ballast Check TM 2 (Turner fluorometer)	10-50	Lawrence Younan
10cells (PAM fluorometer)	10-50	André Zaake
Hach BW680 (PAM)	10-50	Nick Welschmeyer
Satake Pulse Counter	10-50	Satake
ATP assay with improved extraction protocol	10-50	Nick Welschmeyer
MLML (steamlined) bulk FDA method	10-50	Nick Welschmeyer
WALZ-Water PAM	10-50	Marcel Veldhuis
ATP assay with improved extraction protocol	<10	Nick Welschmeyer
MLML (steamlined) bulk FDA method	<10	Nick Welschmeyer
Hach BW680 (PAM)	<10	Nick Welschmeyer
WALZ-Water PAM	<10	Marcel Veldhuis
Flow cytometry after staining nuclear DNA	Bacteria	Marcel Veldhuis
IDEXX Simplate	Bacteria	SGS
SGS ATP (aqua-tools)	Bacteria	SGS
Speedy Breedy	<i>Enterococcus</i>	Derek Price
IDEXX Enterolert	<i>Enterococcus</i>	SGS
TRITON BW BacTest EC	<i>E. coli</i>	Lothar Schillak
IDEXX Colilert	<i>E. coli</i>	SGS
Speedy Breedy	<i>E. coli</i>	Derek Price

Table 2. Details for trials run on board the METEOR including the trial number (#), the sampling devices and ports used, the source for the water pumped through the ballast system and the destination for the water after being pumped through the ballast system, whether the OptiMarin BWTS was turned on (+) or off (-) and whether it was regulated/unregulated (see methods), and notes regarding spiking and any issues experienced during the trial.

#	Date	Sampling Device combination				Source	Destination	Treatment	Notes
		Port A	Port B	Port C	Port D				
1	4.6.2015	Triton		SGS		potable water tank 9	Ocean	-	Data only useful for comparison between analytic methods (not sampling methods), since size fractions for S2 were mixed up in splitting.
2		Triton		SGS		potable water tank 9	Ocean	-	Data only useful for comparison between analytic methods, since different rinse water was used in engine room for $\geq 50 \mu\text{m}$ samples (SGS used 13 ppt rinse water, TRITON used 38 ppt).
3	5.6.2015	Triton		Net		Ocean	Ocean	-	Net sample for the 10-50 fraction included all organisms >10 . This may introduce variation between results for this fraction.
4		Net		Net		Ocean	Ocean	-	Net sample for the 10-50 fraction included all organisms >10 .
5	6.6.2015	SGS		Net		Ocean	Ocean	-	Net sample for the 10-50 fraction included all organisms >10 . This may introduce variation between results for this fraction.
6	7.6.2015	Triton		Net		Ocean	Ocean	-	Bacteria samples were spiked with target densities of 500 cfu/100 ml E. coli & 100cfu/100ml E. faecalis in sample 1 and 100 cfu/100 ml E. coli & 500 cfu/100ml E. faecalis in sample 2.
7		Net		SGS		Mindelo water tank 9	Ocean	-	

8		SGS		Net		Ocean	Ocean	-	
9	8.6.2015	Triton		SGS - closed		Ocean	Ocean	-	
10		Net		SGS - closed		Ocean	Ocean	-	
11		Net		Net		Ocean	Ocean	-	
12	9.6.2015	SGS		Triton - closed		Ocean	Ocean	-	Bacteria samples were spiked with target densities of 500 cfu/100 ml <i>E. coli</i> & 50cfu/100ml <i>E. faecalis</i> in sample 1 and 50 cfu/100 ml <i>E. coli</i> & 500 cfu/100ml <i>E. faecalis</i> in sample 2.
13		Net		Triton - closed		Ocean	Ocean	-	
14		Net		Triton		Ocean	Ocean	-	
15	10.6.2015	Net	Net			Ocean	Tank 9	+	
16		Net	Net			Ocean	Tank 10	+	Regulated
17		Net		SGS - closed		Ocean	Ocean		Unregulated
18	11.6.2015	Net	Net			Ocean	Forepeak	+	
19		Triton		SGS		Ocean	Ocean	-	Unregulated
20		Net		SGS - closed		Ocean	Ocean	-	
21	12.6.2015	SGS		Triton - closed		Ocean	Ocean	-	Bacteria samples were spiked with target densities of 100 cfu/100 ml <i>E. coli</i> & 500cfu/100ml <i>E. faecalis</i> in sample 1 and 500 cfu/100 ml <i>E. coli</i> & 100 cfu/100ml <i>E. faecalis</i> in sample 2. Triton skid malfunctioned due to high densities causing clogging. Obtained <50µm samples from both sampling ports, but ≥50µm for SGS only.
22		Net		SGS - closed		Ocean	Ocean	-	Bacteria samples were spiked with target

Table 3. Brief description of analytic methods used on the METEOR voyage. Full description and SOP is available in Appendix C.

Analysis Method	Description
Optical zooplankton analysis (>200 μm)	The OZA method distinguishes viable zooplankton larger than 200 μm from dead organisms and debris based on their swimming capability by analyzing successive images. Samples are placed in the OZA device and analyzed by capturing images and processing them using MATLAB.
Microscopy (movement; $\geq 50 \mu\text{m}$)	Water samples are placed in a Bogorov chamber and live zooplankton (≥ 50) are enumerated by observing movement.
Microscopy (staining; $\geq 50 \mu\text{m}$ and 10-50 μm)	Samples are stained using FDA to identify live phytoplankton and counted using an epifluorescence microscope.
Satake Pulse Counter ($\geq 50 \mu\text{m}$ and 10-50 μm)	The Satake pulse counter employs pulse counting FDA method to estimate the number of viable organisms in ballast water samples by counting fluorescence pulses over specific threshold from FDA stained organisms. Samples are placed in the portable pulse counter system and an estimated number of viable organisms is displayed on the screen after one minute.
MLML (streamlined) bulk FDA method	The technique is a 'live' incubation. The organisms are captured on a GF/F filter (representing the 'volume filtered'). The filter is placed in an incubation fluid (tagged with FDA). the activity of the organisms converts the FDA to fluorescein and it is mixed and homogenized within the full volume of the incubation buffer (2 mL). We remove a small aliquot of the endpoint incubation buffer to determine the Fluorescein concentration within that 2 mL volume. From the final [fluorescein] concentration, taking into account the seawater volume filtered and the incubation volume we calculate the fluorescein production rate, ng fluorescein/(L h), and the concentration of live cells can be calculated.
Welschmeyer ATP	The technique parallels bulk FDA, but it is NOT an incubation; it is an extraction. Quantitative volumes of seawater are captured on the GF/F filter, the filter is immersed in a small volume (1.2 mL) of strong extraction fluid and after a 1 hour 'soak time' the extraction tubes were frozen (on the METEOR) and analyzed in batches after thawing. The extraction fluid is mixed thoroughly and measured for luminescence in the presence of luciferase enzyme; the luminescence produced is linearly proportional to ATP concentration, as standardized by ATP standards.
SGS ATP (aqua-tools)	Aqua-tools Ballast Water kit enable measuring in few minutes the whole living flora in collected samples ($\geq 50\mu\text{m}$; ≥ 10 and $< 50\mu\text{m}$; and bacteria indicators fractions) for a rapid assessment of your ballast water quality. This test kit allows a rapid estimation of all biological contaminant through the quantification of bioluminescent signal coming from the reaction of the Luminase TM with intracellular Adenosine TriPhosphate (cATP) – the energy carrier of any living cell.
WALZ-Water PAM	The WALZ-Water PAM is a desktop PAM device that is used to estimate phytoplankton biomass and photosynthetic activity. Measurements can be performed using whole water samples or size fractionated or otherwise collected water samples containing phytoplankton.

Ballast Check™ 2 (Turner fluorometer)	Turner Designs' Ballast Check-2 is a quick indicative compliance tool used for estimating the abundance and assessing the viability of phytoplankton from the 10-50 micron size class. This instrument uses the organism's fluorescence characteristics to provide a quick analysis of whether ballast water is in compliance with current discharge standards.
bbe 10cells (PAM fluorometer)	10cells is an indicative instrument for analyzing living cells based on variable fluorescence (Fv) of chlorophyll of living algae. Phytoplankton is filtered onto a filter paper which is placed inside the 10cells for measurement. The 10cells displays the estimated number of living cells per ml.
Hach BW680 (PAM)	Hach BW680 is a pocket-sized, battery operated fluorometer which uses PAM to determine the average variable fluorescence response. Water samples are deposited into a cuvette and the device displays BWI values and estimated risk. Live cell concentrations can be estimated based on BWI.
Bacteria- Flow cytometry after staining nuclear DNA	Bacterial DNA is stained using PicoGreen and samples are run through the flow cytometer. Flow cytometer counts for bacteria are calculated by using the size and presence/absence of chlorophyll to distinguish bacteria from phytoplankton.
IDEXX Simplate	SimPlate* for HPC method is used for the quantification of heterotrophic plate counts (HPC) in water. It detects viable bacteria in water by testing for the presence of key enzymes. The sample and media are added to a SimPlate, incubated, and then examined for fluorescing wells. The number of fluorescing wells corresponds to a Most Probable Number (MPN) of total bacteria in the original sample.
Speedy Breedy (Enterococcus and E. coli)	Speedy Breedy is a portable, sensitive, precision respirometer which detects and monitors microbial activity. Samples are added to a culture vessel containing a suitable nutrient medium and where present, contaminating microorganisms begin to grow. Speedy Breedy detects pressure transients due to metabolic processes where microbes are present.
IDEXX Enterolert	Enterolert* is based on IDEXX's patented Defined Substrate Technology* (DST*). When enterococci utilize their β -glucosidase enzyme to metabolize Enterolert's nutrient-indicator, 4-methyl-umbelliferyl β -D-glucoside, the sample fluoresces. Enterolert detects enterococci at 1 cfu per 100 mL sample within 24 hours
TRITON BW BacTest EC	The Triton BW Bac Test EC method was derived from PCR. Similar to PCR, primers designed for this test detect a group of genes within E. coli and induce the multiplication of an RNA with integrated fluorescein which gives a signal in a fluorometer.
IDEXX Colilert	Colilert-18 either simultaneously detects total coliforms and E. coli or fecal coliforms in water. It is based on IDEXX's patented Defined Substrate Technology*(DST*). When total or fecal coliforms metabolize Colilert-18's nutrient-indicator, ONPG, the sample turns yellow. When E. coli metabolize Colilert-18's nutrient-indicator, MUG, the sample fluoresces. Colilert-18 can simultaneously detect these bacteria at 1 cfu/100 ml within 18 hours even with as many as 2 million heterotrophic bacteria per 100 ml present.

Table 4. Total number of replicates run for each trial for each analytic device for measurement of organisms $\geq 50 \mu\text{m}$ in minimum dimension. Note that this number includes the sum total of replicates taken for both samples collected in the trial.

Trial #	Wels. ATP	SGS ATP (aqua-tools)	Bulk FDA	Hach BW680	Microscopy visual	Microscopy stain	Walz-Water PAM	Satake Pulse Counter
1	6	6	6	0	6	0	0	6
2	4	6	4	0	6	0	0	6
3	4	6	4	5	6	0	0	6
4	4	6	4	6	6	0	0	6
5	6	6	6	6	6	3	0	6
6	6	6	6	5	6	6	0	6
7	6	6	0	6	6	6	0	6
8	0	0	0	0	0	0	0	6
9	0	6	0	0	6	6	6	6
10	0	6	0	6	6	6	6	6
11	0	0	0	6	0	0	6	6
12	0	6	0	6	6	6	6	6
13	0	6	0	0	6	6	6	6
14	0	0	0	0	0	0	6	6
15	0	6	2	5	0	0	6	6
16	2	6	2	6	0	0	6	6
17	0	0	0	0	0	0	0	6
18	0	0	0	0	6	6	2	6
19	0	6	0	0	6	6	6	6
20	0	0	0	0	0	0	0	6
21b	0	3	0	0	3	3	3	3
22	0	6	0	0	6	6	6	6
23	0	6	0	0	0	0	0	6
24	0	6	0	0	6	6	6	6
25	0	6	0	0	6	6	6	6
26	0	6	0	0	0	0	6	6
27	0	6	0	0	6	6	6	6
28	0	6	0	0	6	6	6	6

Table 5. Number of replicates run for each trial for each analytic device for measurement of organisms >10 µm and <50 µm in minimum dimension. Note that this number includes the sum total of replicates taken for both samples collected in the trial.

Trial #	Wels. ATP	Ballast Check2	10cells	Bulk FDA	Flow cytometry	Hach	Microscopy	Walz-Water PAM	Satake Pulse Counter
1	6	6	6	6	2	6	6	6	6
2	4	6	6	4	2	6	6	6	6
3	3	2	6	4	2	6	6	6	5
4	4	3	6	4	2	6	6	6	4
5	6	4	6	6	2	6	6	6	6
6	6	5	6	6	2	3	6	6	6
7	6	4	6	0	2	2	6	6	6
8	0	2	6	0	2	0	0	6	5
9	6	6	6	6	2	6	6	6	6
10	6	4	6	6	2	6	6	6	6
11	6	5	6	6	2	4	0	6	6
12	4	6	6	4	2	6	6	6	6
13	0	6	6	0	2	0	6	6	6
14	0	6	6	0	2	0	0	6	6
15	6	6	6	6	2	8	0	6	6
16	6	6	6	6	2	6	0	6	6
17	0	6	6	0	2	0	0	6	6
18	6	6	6	6	2	6	6	6	6
19	0	6	6	0	2	0	6	6	6
20	0	6	6	0	2	0	0	6	6
21a	0	6	6	0	2	0	6	6	6
22	0	6	6	0	2	0	6	6	6
23	0	6	6	0	2	0	0	6	6
24	0	6	6	0	2	0	6	6	6
25	0	6	6	0	2	0	6	6	6
26	6	6	6	5	2	6	0	6	6
27	3	6	6	2	2	8	6	6	6
28	0	6	6	0	2	3	6	6	5

Table 6. Number of replicates run for each trial for each analytic device for measurement of organisms <10 µm in minimum dimension. Note that this number includes the sum total of replicates taken for both samples collected in the trial.

Trial #	Welschmeyer ATP	BallastCheck2	Bulk FDA	Hach	Walz-Water PAM	Flow cytometry
1	6	6	6	6	6	2
2	4	6	4	6	6	2
3	4	6	4	6	6	2
4	4	6	4	6	6	2
5	6	6	6	6	6	2
6	6	6	6	2	6	2
7	6	6	0	2	6	2
8	0	3	0	0	6	2
9	0	6	0	0	6	2
10	0	6	0	0	6	2
11	0	6	0	0	6	2
12	0	6	0	0	6	2
13	0	6	0	0	6	2
14	0	6	0	0	6	2
15	6	6	6	7	6	2
16	6	6	6	6	6	2
17	0	6	0	0	6	2
18	0	6	0	0	6	2
19	0	6	0	0	6	2
20	0	6	0	0	6	2
21a	0	6	0	0	6	2
22	0	6	0	0	6	2
23	0	6	0	0	6	2
24	0	6	0	0	6	2
25	0	6	0	0	6	2
26	0	6	0	0	6	2
27	0	6	0	5	6	2
28	0	6	0	0	6	2

Table 7. Number of replicates run for each trial for each analytic device for measurement of bacteria. Trials indicated with an asterisk were spiked for bacteria. Note that this number includes the sum total of replicates taken for both samples collected in the trial.

Trial #	Total bacteria		<i>Enterococcus</i>		<i>E coli</i>		
	IDEXX Simplate	SGS ATP (aqua-tools)	IDEXX Enterolert	Speedy Breedy	Triton BW BacTest EC	IDEXX Colilert	Speedy Breedy
1	6	6	6	6	6	6	6
2	6	6	6	6	6	6	6
3	6	6	6	6	6	6	6
4	6	6	6	6	6	6	6
5	6	6	6	6	6	6	6
6*	6	6	6	6	6	6	6
7	6	6	6	6	6	6	6
8	6	0	6	0	6	6	0
9	6	6	6	6	6	6	6
10	6	6	6	6	6	6	6
11	6	4	6	0	6	6	0
12*	6	6	6	6	5	6	6
13	6	6	6	6	6	6	6
14	6	6	6	0	6	6	0
15	6	6	6	6	6	6	6
16	6	6	6	0	6	6	0
17	6	0	6	0	6	6	0
18	6	6	6	0	6	6	0
19	6	6	6	0	6	6	0
20	6	6	6	0	6	6	0
21*	6	6	6	10	6	6	12
22*	6	6	6	6	5	6	5
23	6	6	6	0	6	6	0
24	0	6	6	0	6	6	0
25	0	6	6	0	6	6	0
26	0	6	6	0	4	6	0
27	0	6	0	0	5	0	12
28	0	6	0	0	6	0	0

Table 8. Comparison of analysis methods including cost, time, and training requirements.

Analysis Method	Size Class (µm)	Time Required		Cost		Detection limits (min/max)	Required training/ expert knowledge	Portable
		Active processing	Time to result	Acquisition	Running			
Optical zooplankton analysis	>200	10-30 min	10-30 min	Tool in early development stages				Yes
Microscopy (movement)	≥50	20-30 min	20-30 min	\$7000 CDN	NA	Lower limit: 0	Microscopy training and knowledge of zooplankton taxa required	Limited
Microscopy (FDA staining)	≥50 10-50	20 min	30 min	\$15000 CDN	\$0.02 CDN	Lower limit: 0	Microscopy training and some knowledge of phytoplankton taxa required	
Satake Pulse Counter	≥50 10-50	<5 min	10 min	Undecided		Lower limit: 0	Minimal	Yes
		<5 min	30 min			Lower limit: 0		Yes
MLML (streamlined) bulk FDA method	≥50 10-50 <10		1-2 hours					
Welschmeyer ATP	≥50 10-50 <10							
SGS ATP (aqua-tools)	≥50	50 min	50 min	7700 €	31.83 €	Lower limit: <0.01 pg ATP	Minimal	Yes
	10-50	50 min	50 min			Upper limit: Not applicable		
	bacteria	15 min	15 min			13.33 €		
Walz-Water PAM	≥50 <50 10-50 <10	2 min	2 min	15,000 €	5 €		Minimal training	Yes
Ballast Check™ 2 (PAM)	10-50	2 min	2 min				Minimal	Yes
bbe 10cells	10-50	2 min	2 min	4300 € (bulk)	1€		Minimal	Yes

(PAM)					ware version) 13800 € (advanced scientific version)								
Hach BW680 (PAM)	10-50	2 min	2 min		\$4907 CDN				7	Minimal		Yes	
Speedy Bready	bacteria	<5 min			3500€					Minimal		Yes	
IDEXX Simplate	bacteria	1 hour	1 hour		1000 €		3.36 €		Lower: 2 Upper: 738 (MPN/ml) *Assume 10x dilution	Minimal		No	
IDEXX colilert	E. coli	1 hour	1 hour		5500 €		5.02 €		Lower: 10 Upper: 2005 (MPN/100ml) *Assume 10x dilution	Minimal		No	
IDEXX enterolert	Enterococcus	1 hour	1 hour		5500 €		6 €		Lower: 10 Upper: 2005 (MPN/100ml) *Assume 10x dilution	Minimal		No	
TRITON BW BacTest EC	E. coli	25 min	25 min		9008€		0.8-1€			Minimal		Yes	

Table 9. Intercept, slope, and confidence intervals (CI) based on Deming regression of each method versus microscopy for organisms $\geq 50 \mu\text{m}$.

Method	Intercept	Lower 95% CI	Upper 95% CI	Slope	Lower 95% CI	Upper 95% CI
Satake Pulse Counter	-0.364	-0.694	-0.034	0.740	0.617	0.862
SGS ATP (aqua-tools)	7.623	6.533	8.713	0.722	0.474	0.971
Welschmeyer ATP	7.803	6.850	8.756	0.534	-0.112	1.181
Bulk FDA	6.902	5.193	8.611	0.486	-0.322	1.294
Hach BW680	2.599	1.428	3.769	1.453	0.974	1.932
Walz-Water PAM	0.052	-2.951	3.056	1.946	1.257	2.635

Table 10. Intercept, slope, and confidence intervals (CI) based on Deming regression of each method versus microscopy for 10-50 μm size class of organisms.

Method	Intercept	Lower 95% CI	Upper 95% CI	Slope	Lower 95% CI	Upper 95% CI
Hach BW680	-0.023	-0.440	0.395	0.862	0.599	1.125
bbe 10cells	-0.107	-0.289	0.075	1.187	1.097	1.276
BallastCheck2	0.098	-0.137	0.332	1.103	1.009	1.197
Flow cytometry	2.392	-0.278	5.062	0.588	-1.449	2.626
Satake Pulse Counter	0.086	-0.082	0.255	0.261	0.136	0.386
Walz-Water PAM	1.127	0.808	1.446	1.424	1.191	1.657
Welschmeyer ATP	-20.617	-129.141	87.906	34.886	-125.388	195.159
Bulk FDA	-8.540	-53.189	36.109	16.979	-53.376	87.334

Table 11. Intercept, slope, and confidence intervals (CI) based on Deming regression of each method versus BallastCheck2 and Walz-Water PAM for $<10 \mu\text{m}$ size class of organisms.

Method 1	Method 2	Intercept	Lower 95% CI	Upper 95% CI	Slope	Lower 95% CI	Upper 95% CI
BallastCheck2	Walz-Water PAM	-5.626	-9.099	-2.154	2.772	1.852	3.691
BallastCheck2	Bulk FDA	0.435	-1.099	1.970	1.173	0.679	1.667
BallastCheck2	Hach BW680	-12.591	-53.023	27.840	4.548	-6.022	15.118
BallastCheck2	ATP	-22.555	-96.469	51.359	9.188	-15.915	34.292
Walz-Water PAM	BallastCheck2	2.049	1.448	2.649	0.361	0.240	0.481
Walz-Water PAM	Bulk FDA	3.582	3.025	4.139	0.112	-0.008	0.233
Walz-Water PAM	Hach	11.331	1.882	20.780	-1.210	-2.952	0.532
Walz-Water PAM	Welschmeyer ATP	3.422	2.844	4.000	0.334	0.198	0.470

Table 12. Density of $\geq 50 \mu\text{m}$ organisms in potable water across both trials.

Analytic Device	Density (individuals/ m^3)
	Mean +/- -SD
Microscopy	89.6 +/- 104.9
Satake Pulse Counter	344.4 +/- 222.9

Table 13. Density of 10-50 μm organisms in potable water across both trials. (*) indicates that the individuals were non-viable. (**) indicates that all samples were below the detection limit for the device.

Analytic Device	Density (individuals/mL)
	Mean +/- -SD
BallastCheck2	2.9 +/- 2.5
10cells	0.2 +/- 0.1
Bulk FDA	6.5 +/- 6.0
Flow cytometry*	39.8* +/- 29.4
Hach fluorometer**	0.5 +/- 0.0
Microscopy	0.3 +/- 0.3
Satake Pulse Counter	1.3 +/- 2.2

Figure 1. Schematic view of the BWMS with sampling points at position (A), (B), (C) and (D).

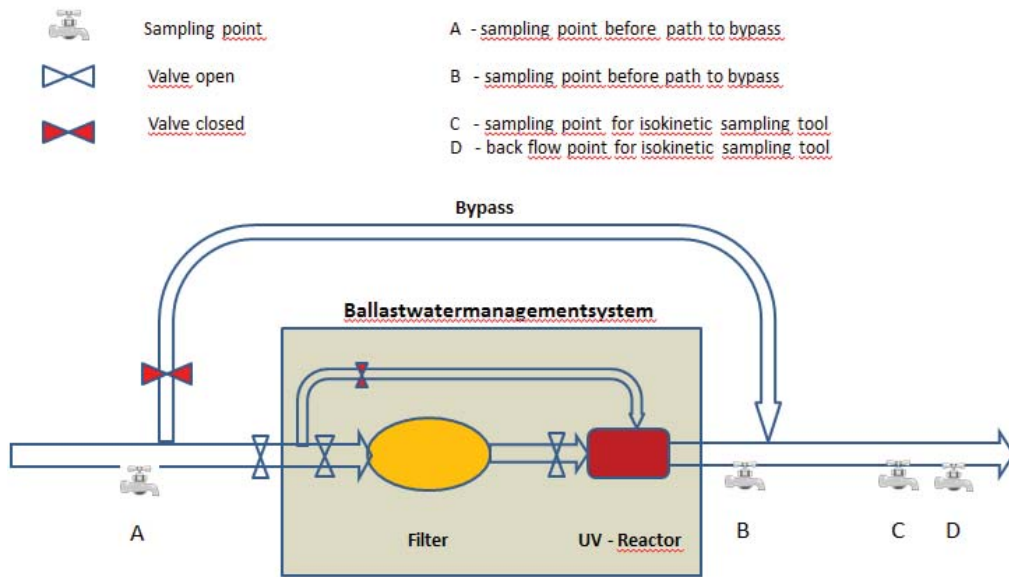


Figure 2. Map showing ship path and sampling locations for each trial.



Figure 3. Phytoplankton viability from Cape Verde Islands to Hamburg based on results from the Walz-Water PAM. Values between 0.3 and 0.6 are indicative of healthy phytoplankton.

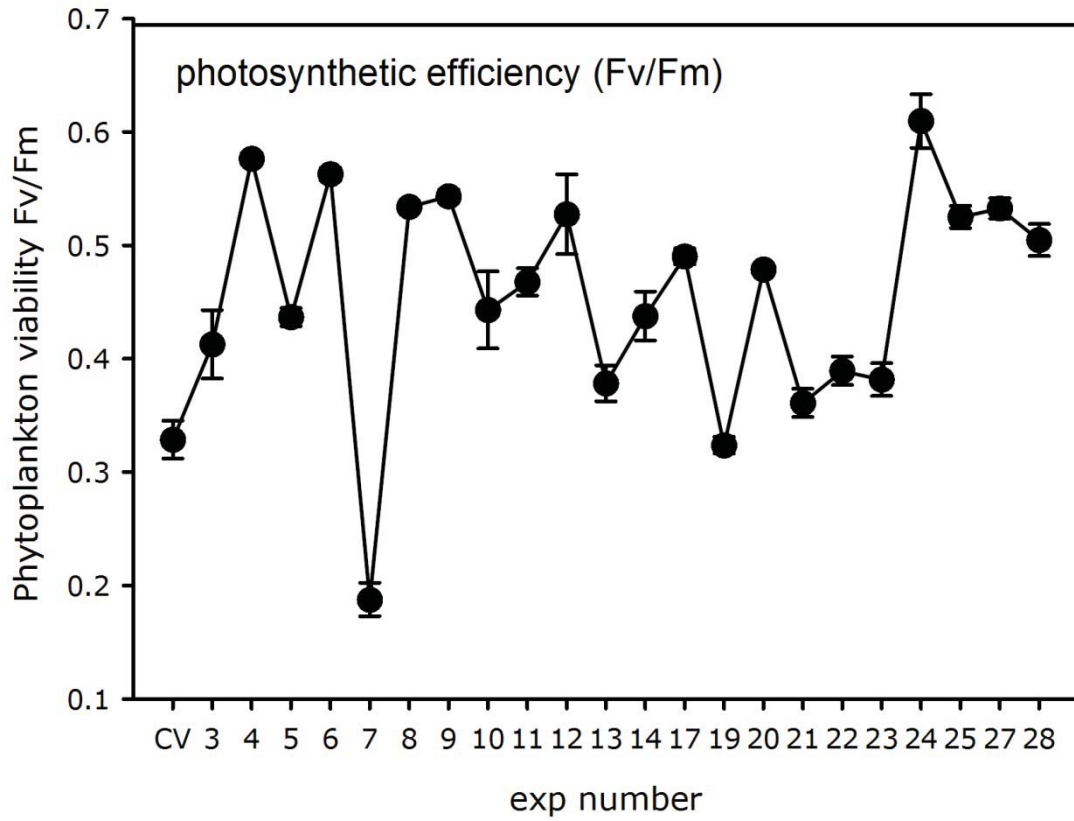


Figure 4. Scatterplots of each analytic tool for the $\geq 50 \mu\text{m}$ size class versus total microscopy counts. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. Red dots are used to distinguish samples that were treated with the ballast water management system. The solid line indicates the line of best fit found using Deming regression (full details in Table 8) and the dashed line indicates the 1:1 line for devices reporting values in the same units. The Pearson correlation coefficient for each plot is indicated above the figure. Note that coefficients should not be directly compared since plots differ in the number of data points. The shaded rectangles indicate a region where no data was available for a given technique (see Table 4).

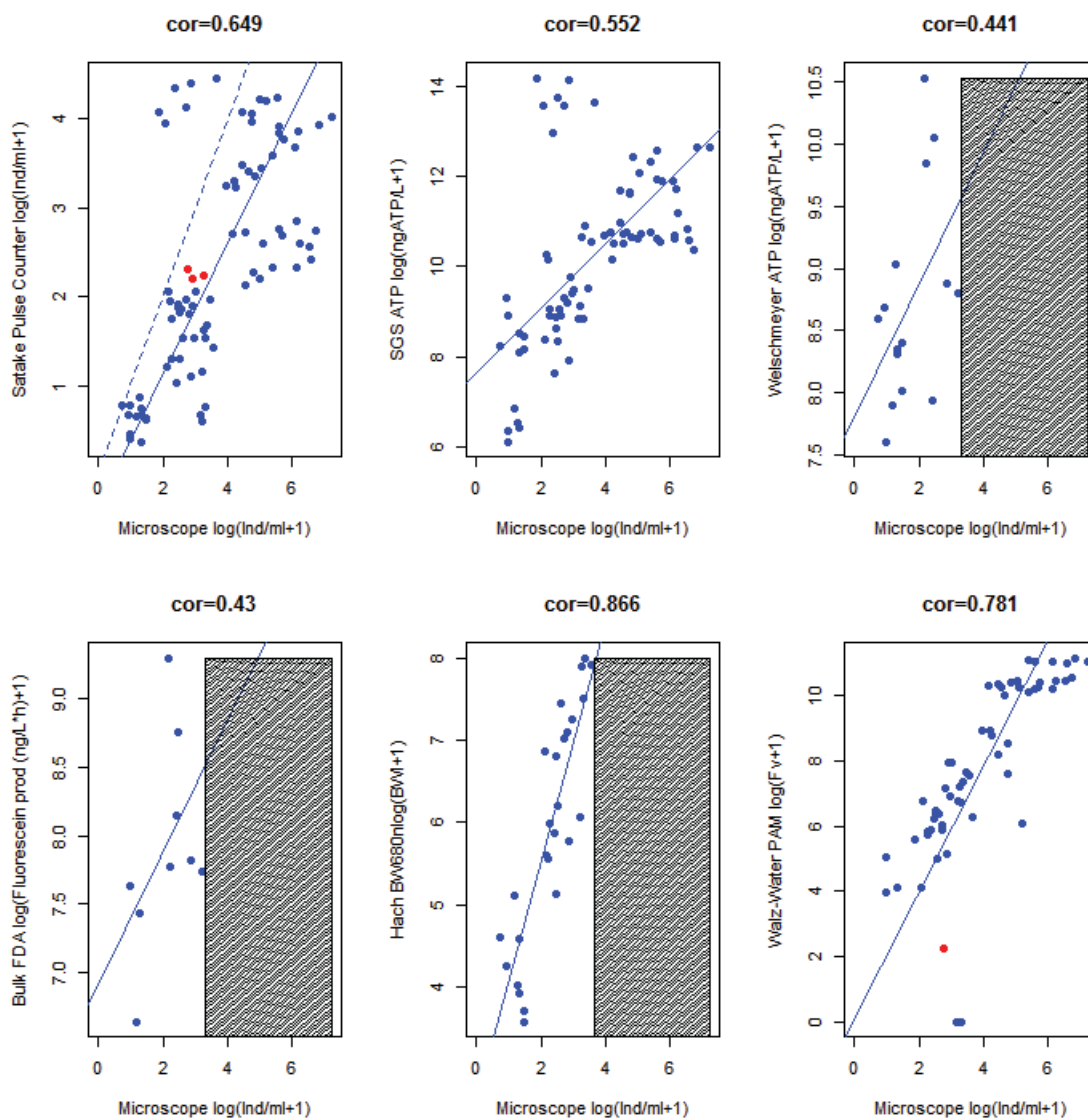


Figure 5. Estimated conversion lines (thick black line) and 95% confidence intervals (thin black lines) to convert between measurements made using different analytic devices for $\geq 50 \mu\text{m}$ organisms. Data points are indicated as black dots; all values are standardized to raw sample concentration to account for any concentrations performed by individual researchers and log+1 transformed to satisfy model requirements. Full model data is available in Appendix E.1.

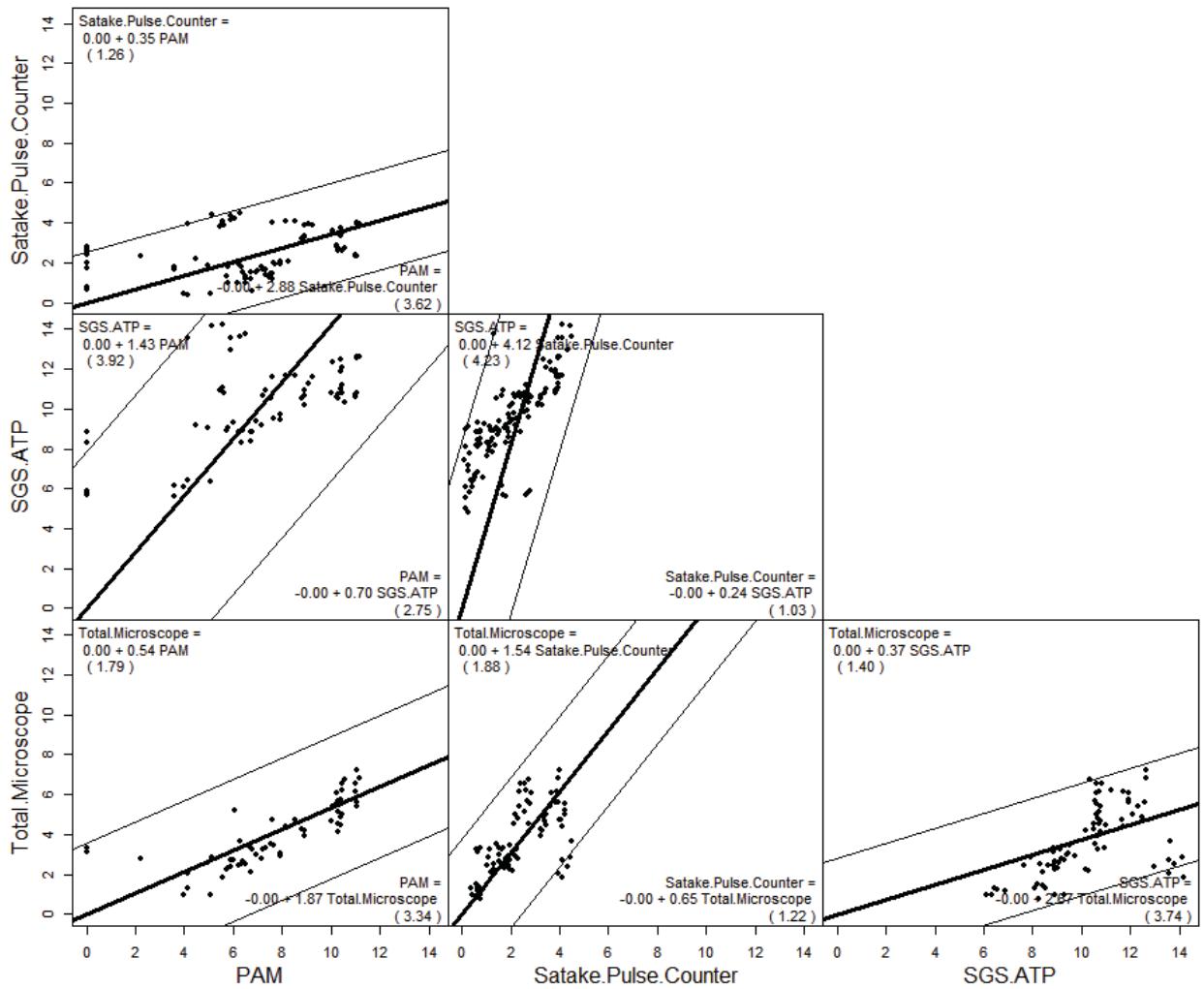


Figure 6. Scatterplots of each results for the Optical Zooplankton Analyzer (>200 μm) versus motile and total microscopy counts. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. The solid black line indicates the line of best fit found using Deming regression and the dashed line indicates the 1:1 line. The Pearson correlation coefficient for each plot is indicated above the figure.

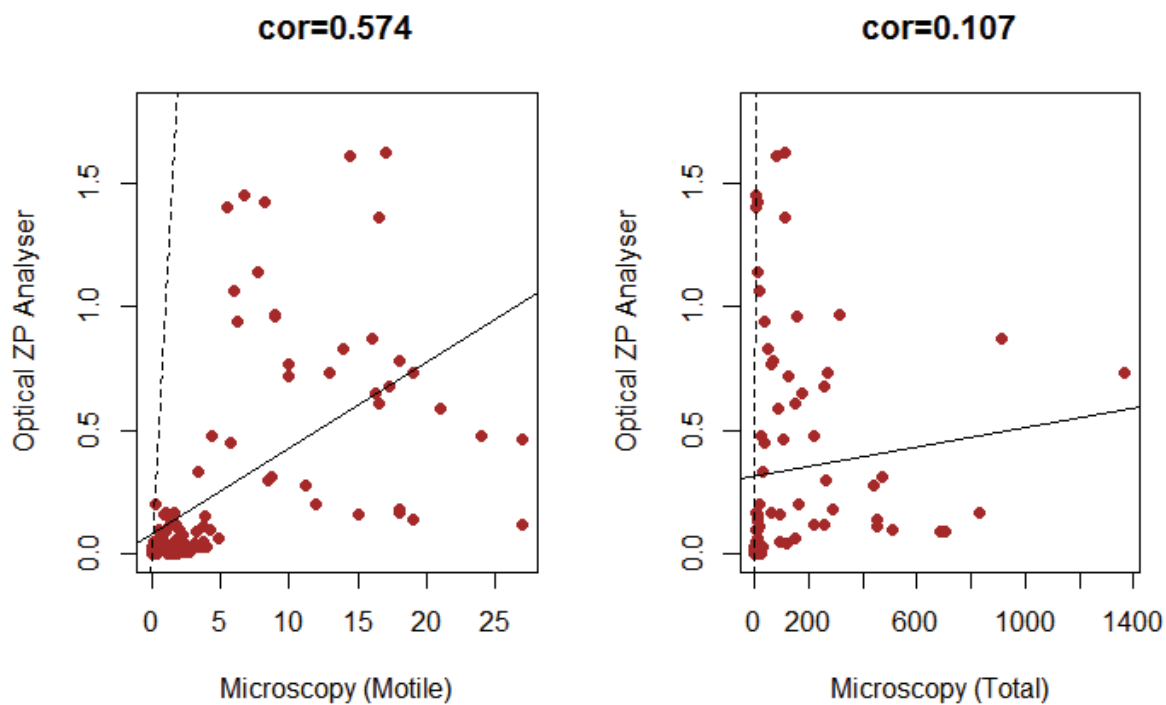


Figure 7. Scatterplots of each analytic tool for the 10-50 μm size class versus total microscopy counts. Red points are used to distinguish samples that were treated with the ballast water management system. Grey points indicate values that were below the detection range of the Hach BW680 and were plotted assuming the minimum detection limit. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. The solid line indicates the line of best fit found using Deming regression and the dashed line indicates the 1:1 line for devices reporting values in the same units. The Pearson correlation coefficient for each plot is indicated above the figure. Note that coefficients should not be directly compared since plots differ in the number of data points. The shaded rectangles indicate a region where no data was available for a given technique (see Table 5).

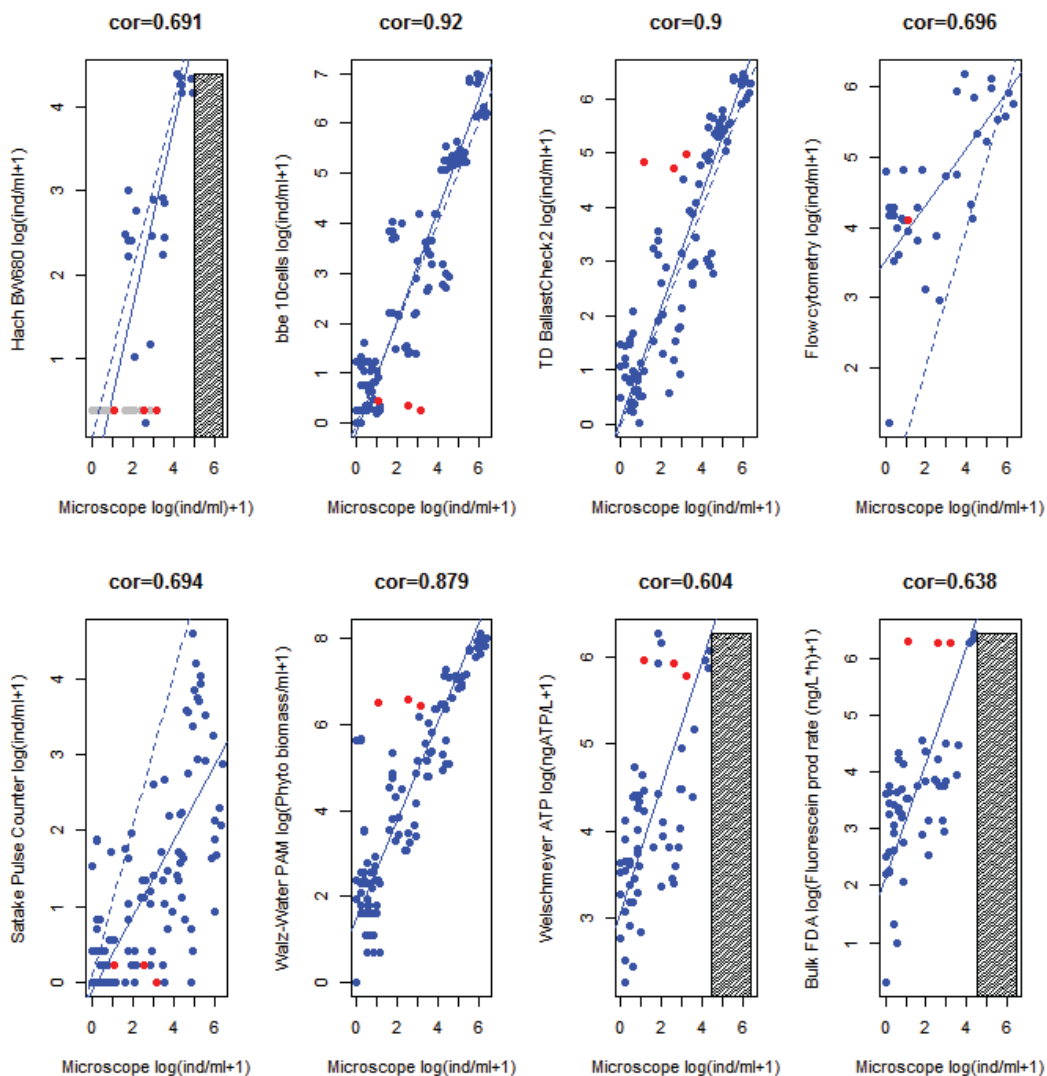


Figure 8. Pairwise scatterplots of Fv values for each PAM tool and microscopy counts (ind/mL) for the 10-50 μm size class. The boxes above the diagonal show the Pearson correlation coefficient (r) for each pair.

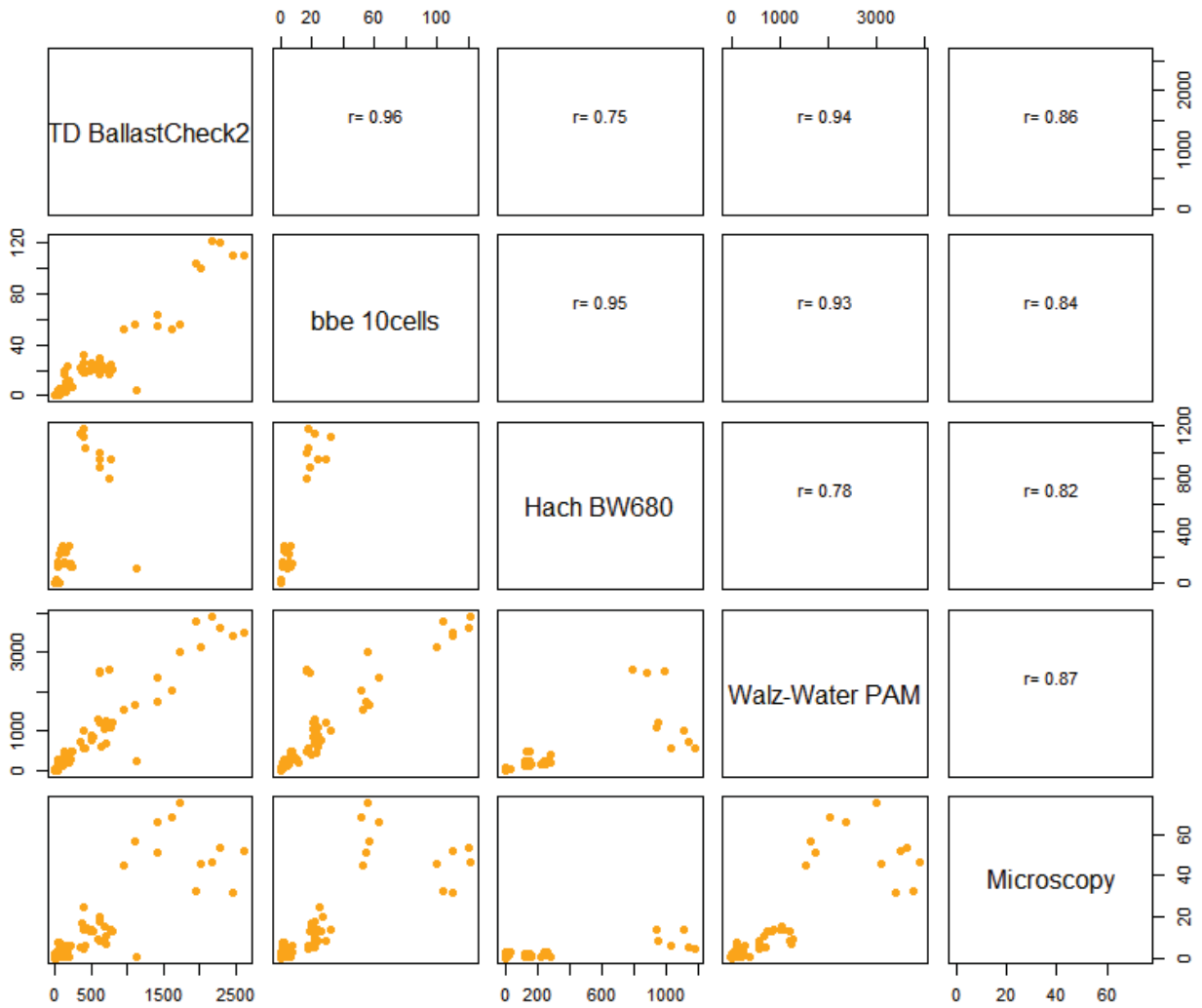


Figure 9. Estimated conversion lines (thick line) and 95% confidence intervals (thin lines) convert between measurements made using different analytic devices for 10-50 μm organisms (bbe 10cells, Hach BW680, BallastCheck2, Walz-Water PAM (labelled PAM) and Microscopy). Data points are indicated as black dots. Full model data is available in Appendix E.2.

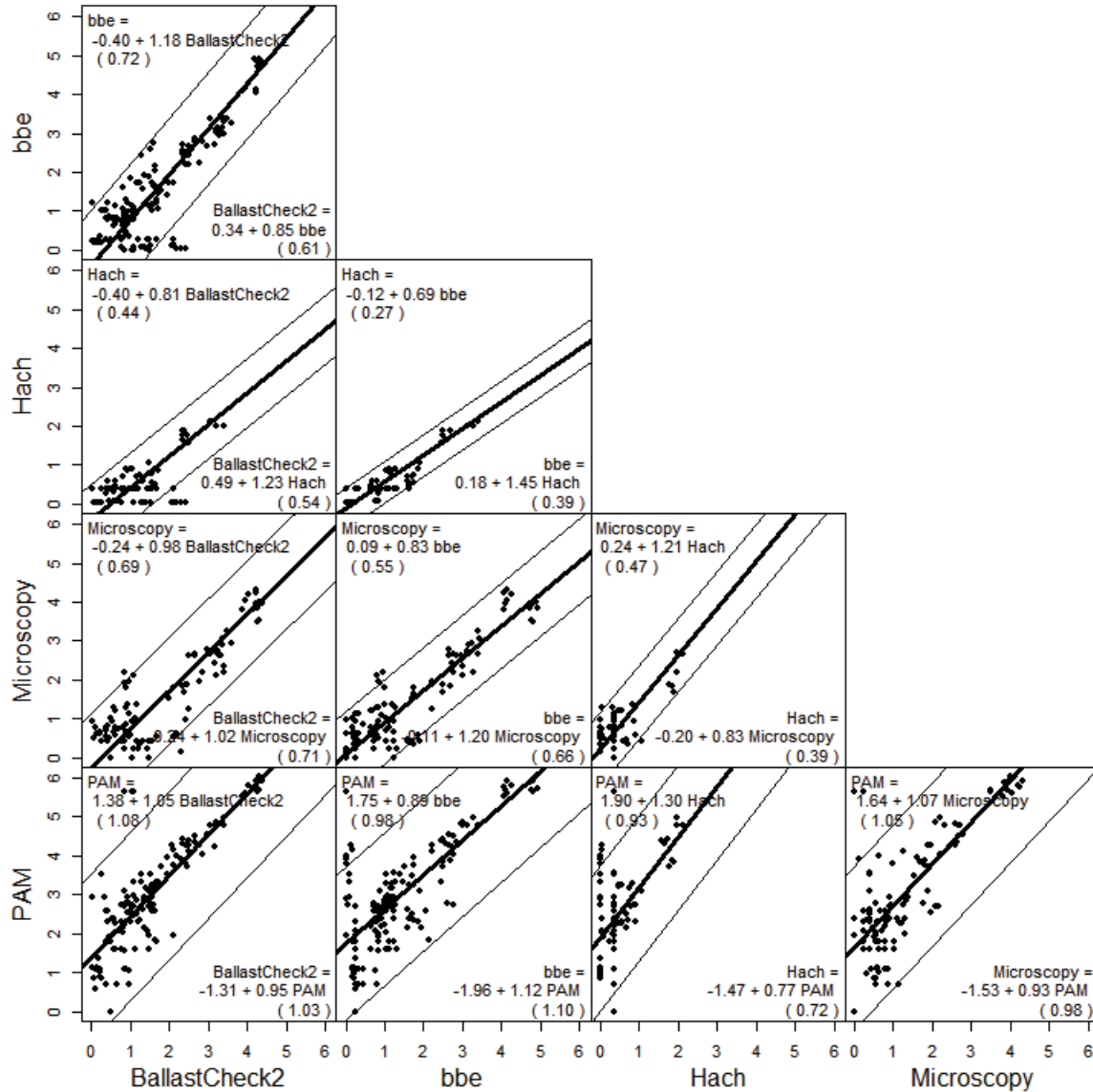


Figure 10. Average chlorophyll fluorescence per cell for total phytoplankton (2 – 50 μm ; black dots) and 10-50 μm cells (blue dots) based on the mean of 2 replicates measured using the Walz-Water PAM. Note different scales on the y-axes.

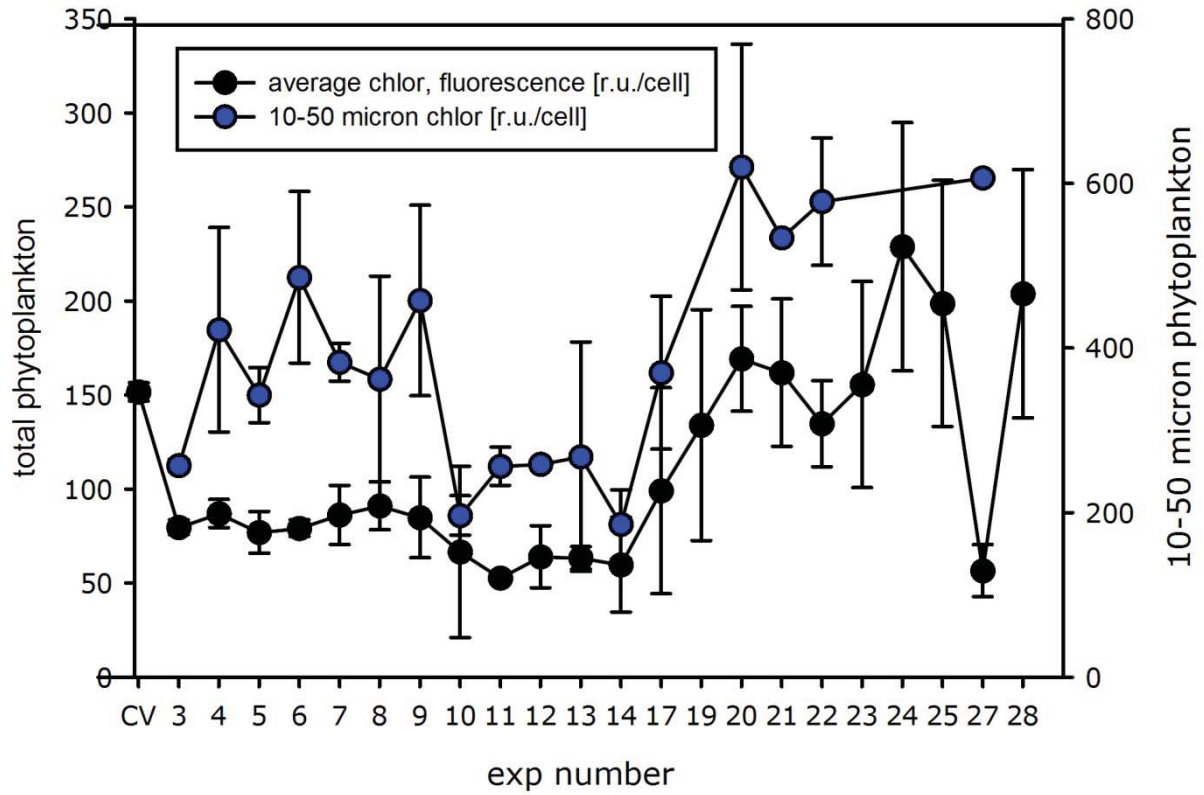


Figure 11. Cell number as estimated by flow cytometry versus WALZ-Pam chlorophyll fluorescence for total phytoplankton (blue diamonds), 10-50 μm phytoplankton (red squares) and < 10 μm phytoplankton (green triangles). Linear regression equations and coefficient of determination (R^2) are shown for each group.

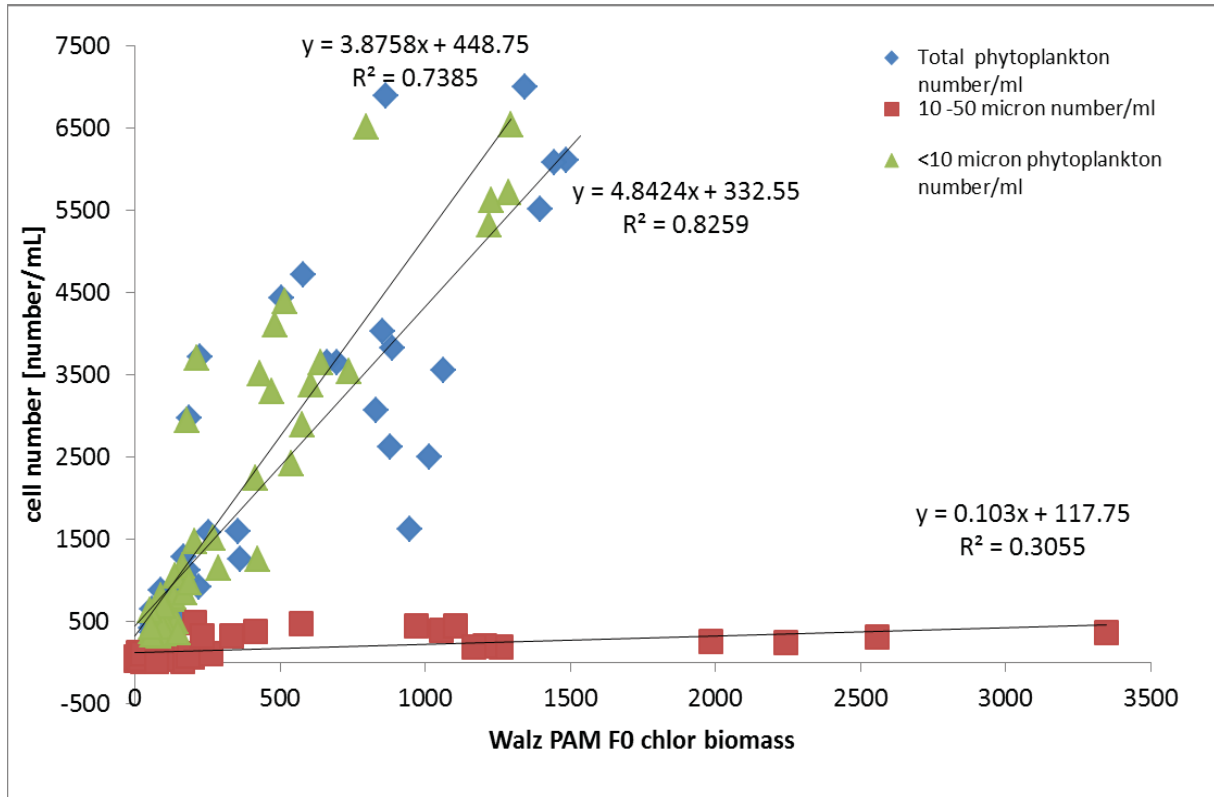


Figure 12. Integrated chlorophyll biomass of the phytoplankton (FCMchlor = flow cytometer counts * cellular chlorophyll fluorescence) versus WALZ-Pam chlorophyll fluorescence for total phytoplankton (blue diamonds), 10-50 μm phytoplankton (red squares) and < 10 μm phytoplankton (green triangles). Linear regression equations and coefficient of determination (R^2) are shown for each group.

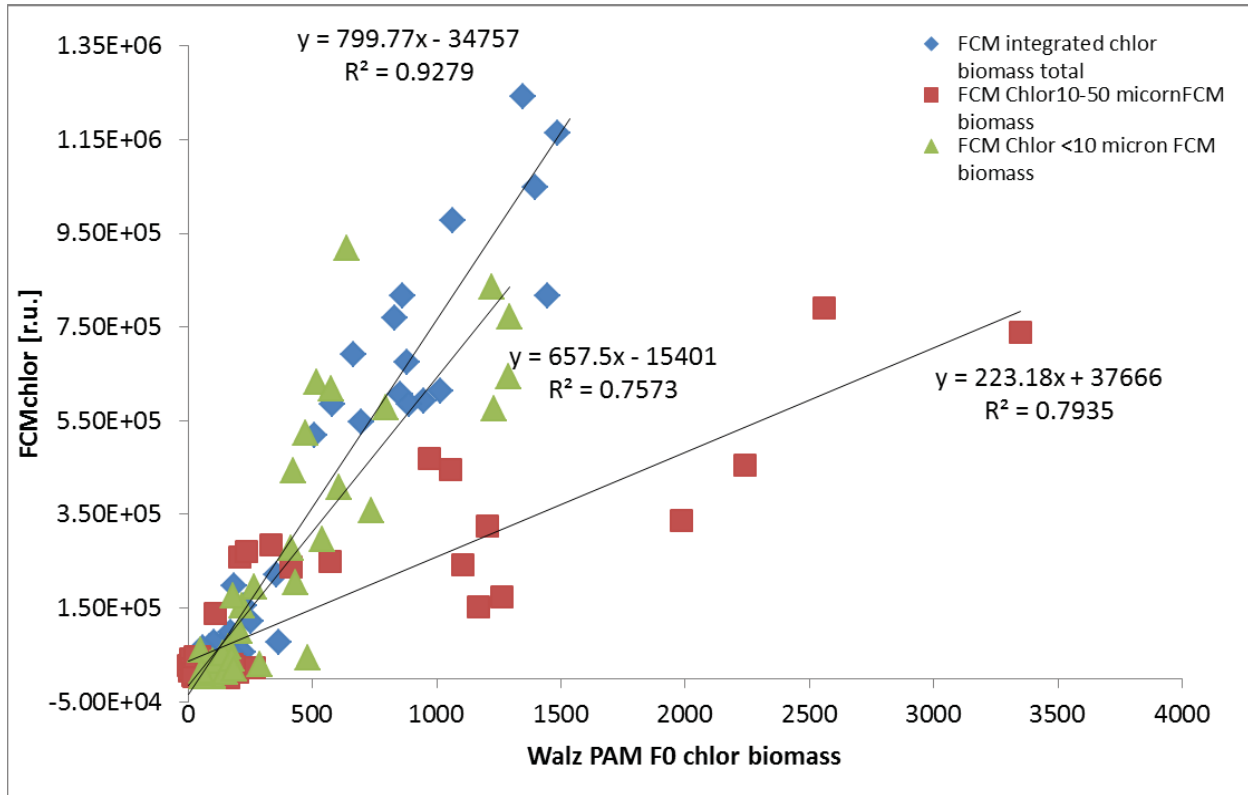


Figure 13. Scatterplots of each analytic tool for the < 10 μm size class versus BallastCheck2 (top row) and Walz-Water PAM (bottom row). Red points are used to distinguish samples that were treated with the ballast water management system. Grey points indicate values that were below the detection range of the Hach BW680, and are plotted assuming the minimum detection limit for points below the detection limit. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. The blue line indicates the line of best fit found using Deming regression. The Pearson correlation coefficient for each plot is indicated above the figure. Note that coefficients should not be directly compared since plots differ in the number of data points (see Table 6).

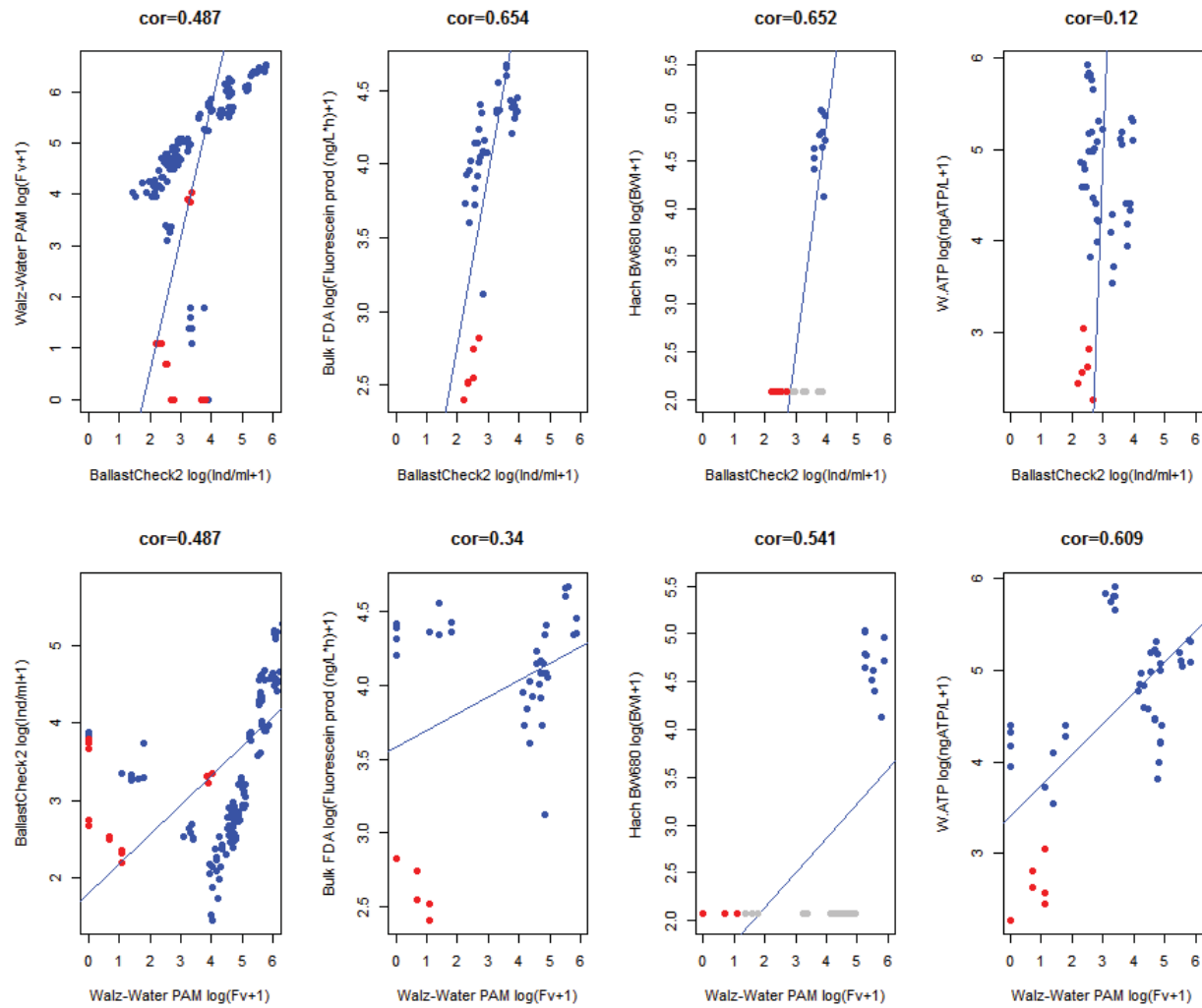


Figure 14. Estimated conversion lines (thick line) and 95% confidence intervals (thin lines) to convert between measurements made using different analytic devices for < 10 μm size class (BallastCheck2, Welschmeyer ATP, and bulk FDA). Data points are indicated as black dots. Full model data is available in Appendix E.3.

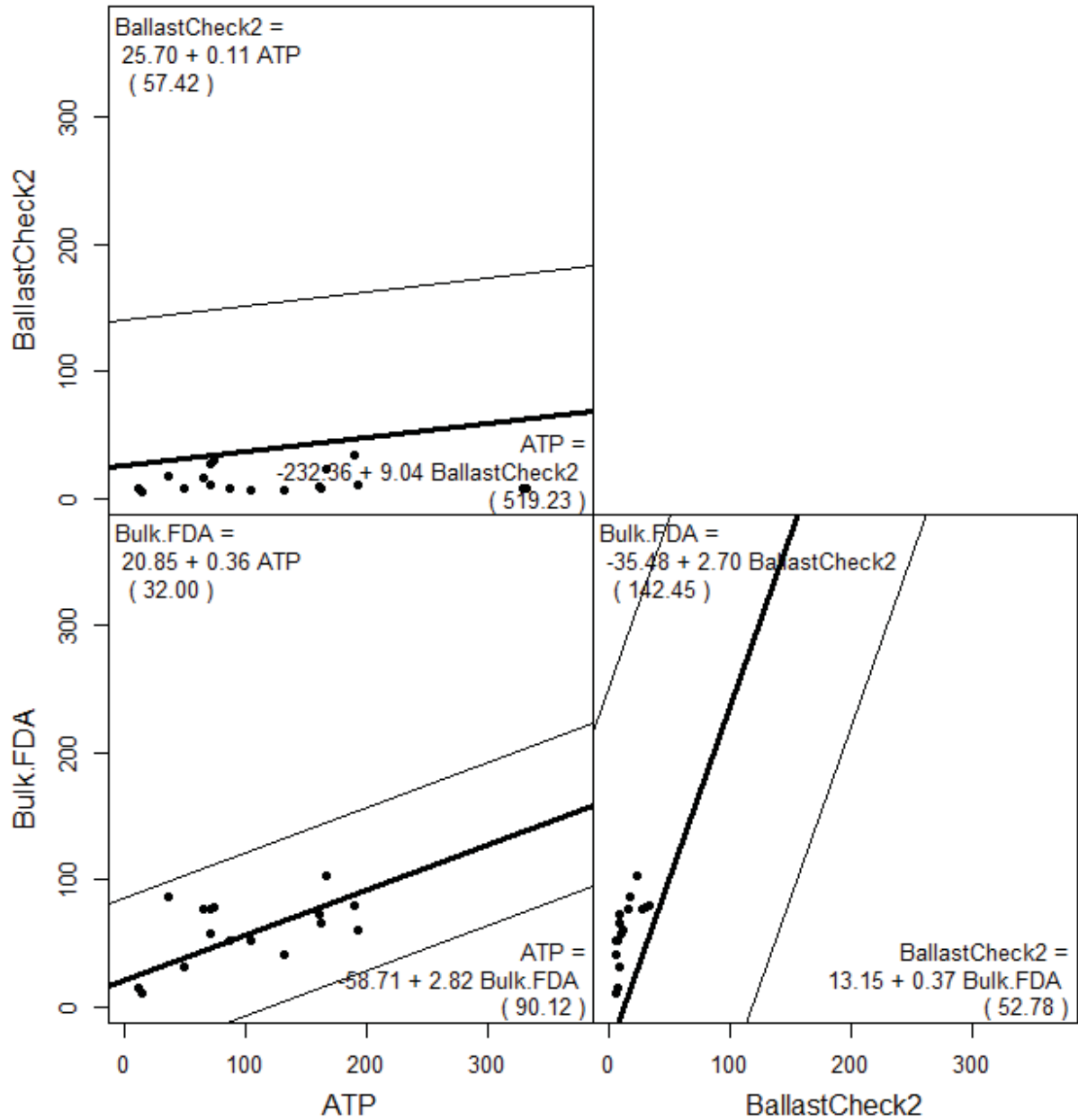


Figure 15. Scatterplot of estimated bacterial densities by IDEXX Simplate and SGS ATP (aqua-tools). Green points represent points where a measurement was given for each device and blue points represent values that were below the detection limit of IDEXX Simplate. Blue points were plotted assuming zero values for measurements below detection limit. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. The green line indicate the line of best fit found using Deming regression and the Pearson correlation coefficient is indicated above the figure; both are based only on points where true measures were obtained from both devices.

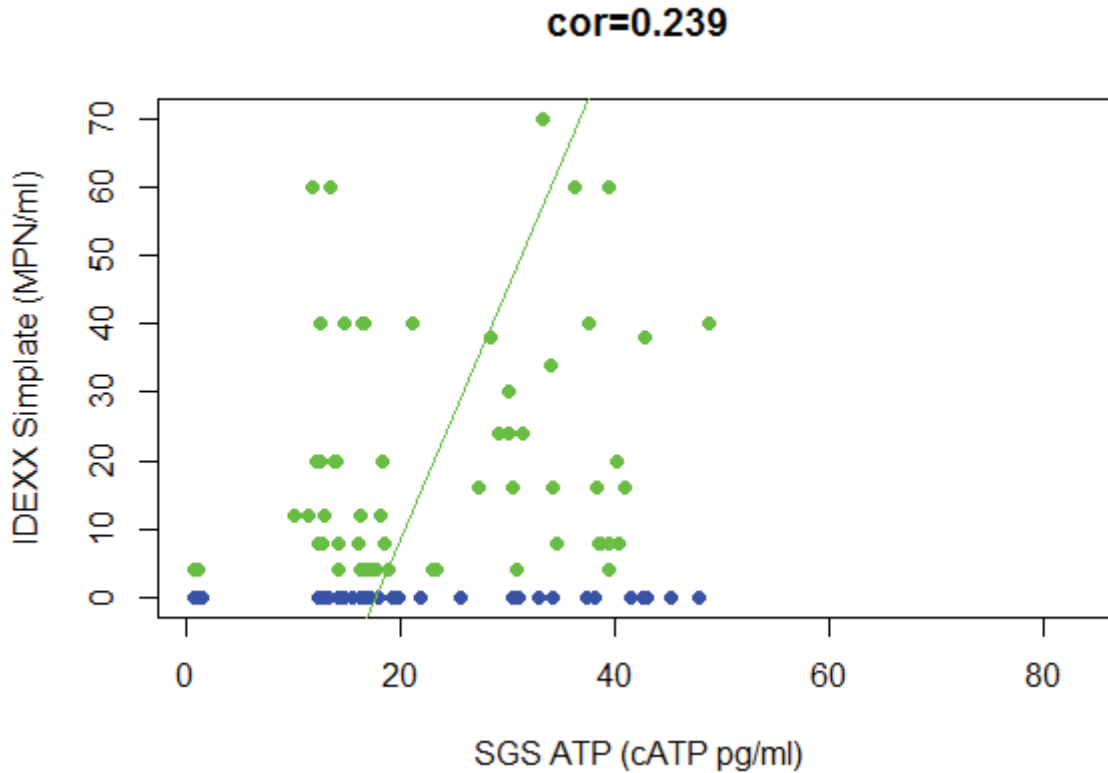


Figure 16. Scatterplot of estimated *E. coli* densities by Triton BW BacTest EC and Speedy Breedy. Green points represent points where a measurement was given for each device and blue points represent values that were under the detection range of Triton BW BacTest EC. Blue points were plotted assuming the zero values for samples below the detection limit. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. The green line indicate the line of best fit found using Deming regression and the Pearson correlation coefficient is indicated above the figure; both are based only on points where true measures were obtained from both devices.

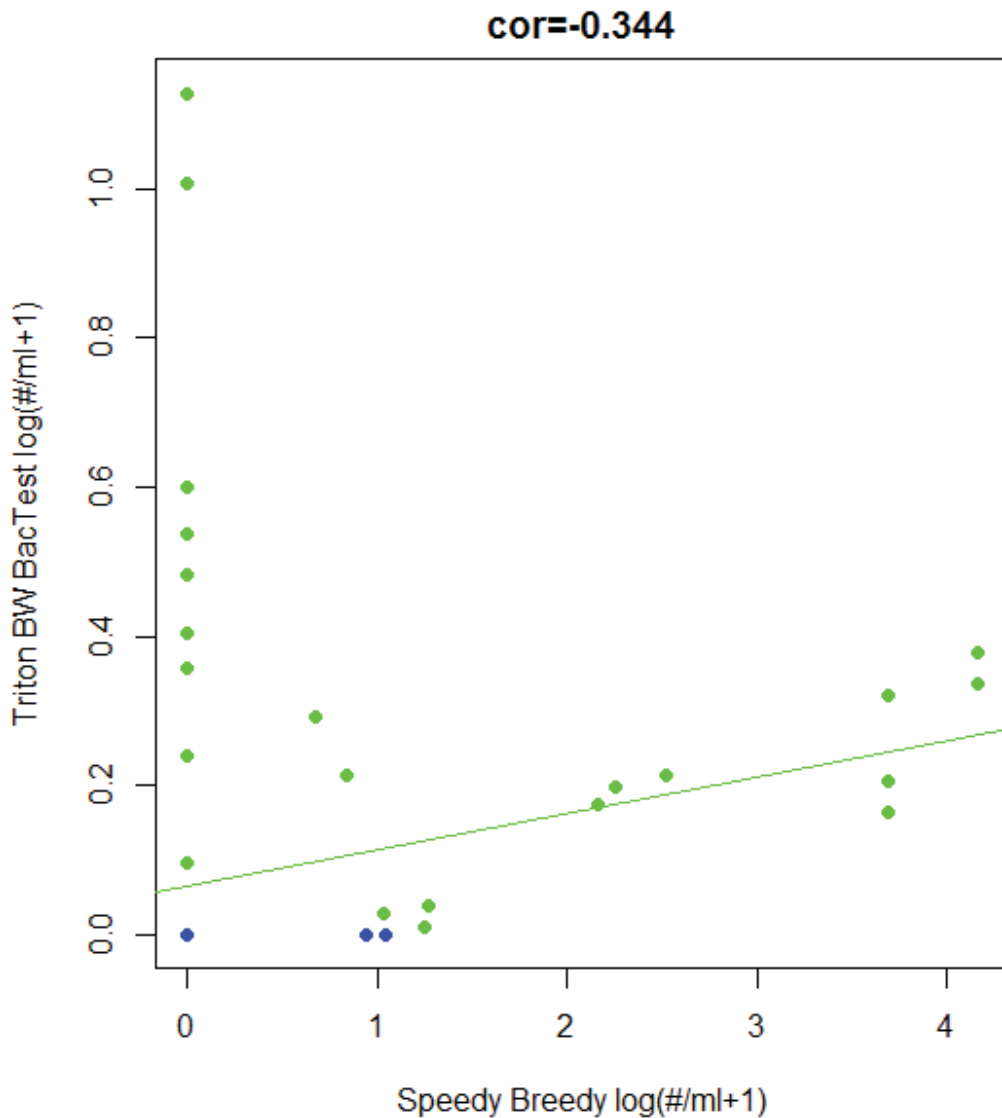


Figure 17. Scatterplot of estimated *Enterococcus* densities by IDEXX Enterolert and Speedy Breedy. Green points represent points where a measurement was given for each device and blue points represent values that were over the detection range of IDEXX Enterolert. Blue points were plotted assuming the maximum detection limit for points above the detection limit. All values are standardized to raw sample concentration to account for any concentrations performed by individual researchers. The green line indicate the line of best fit found using Deming regression and the Pearson correlation coefficient is indicated above the figure; both are based only on points where true measures were obtained from both devices.

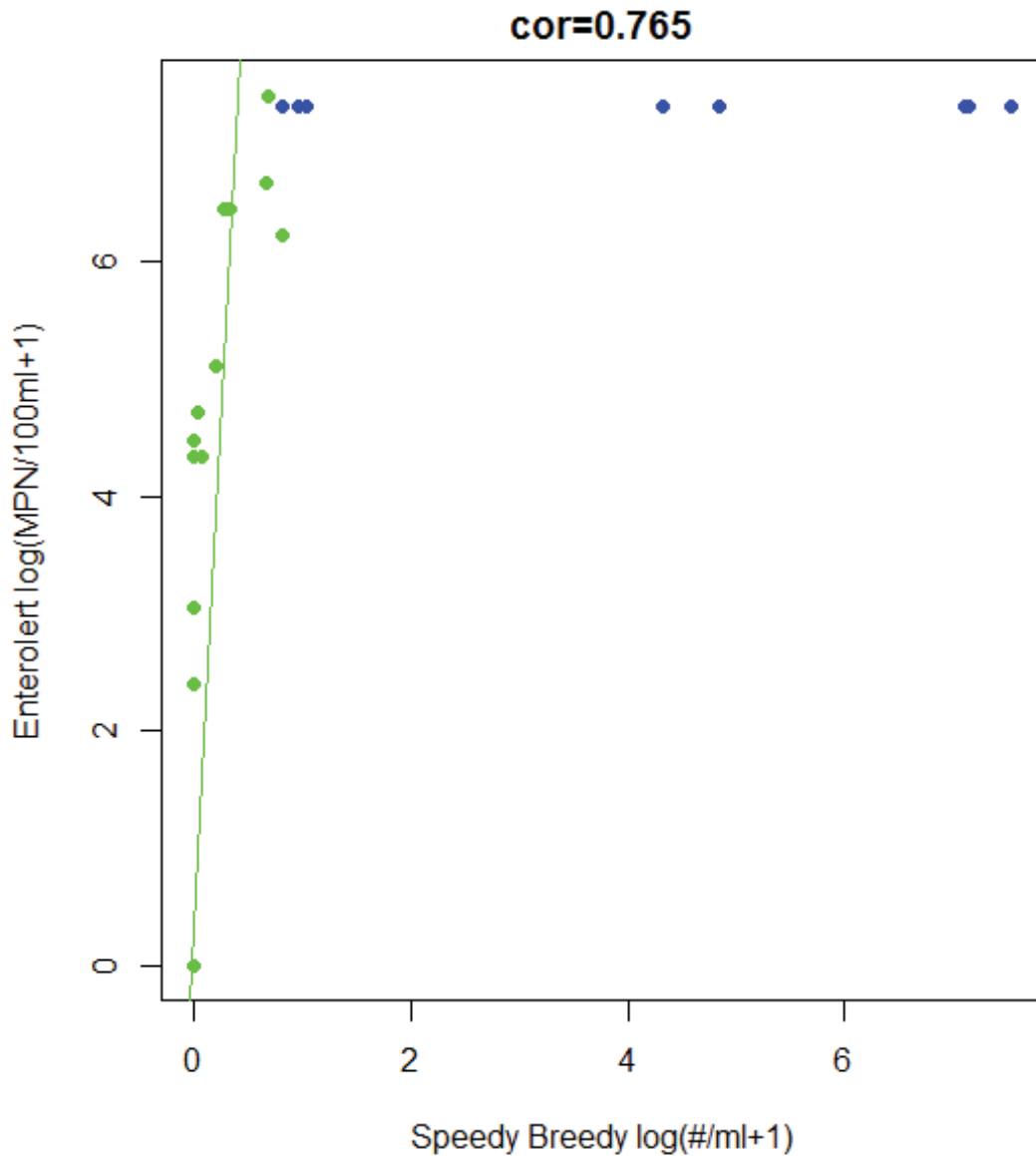


Figure 18. Results of Tukey pairwise contrasts for measurements made on samples collected using different collection devices for organisms $\geq 50 \mu\text{m}$. The dot indicates the expected difference between samples collected using the devices indicated based on a linear mixed model (see methods and results) and the lines show the 95% confidence interval. There is no significant difference between collection devices where the confidence interval overlaps the vertical dashed line.

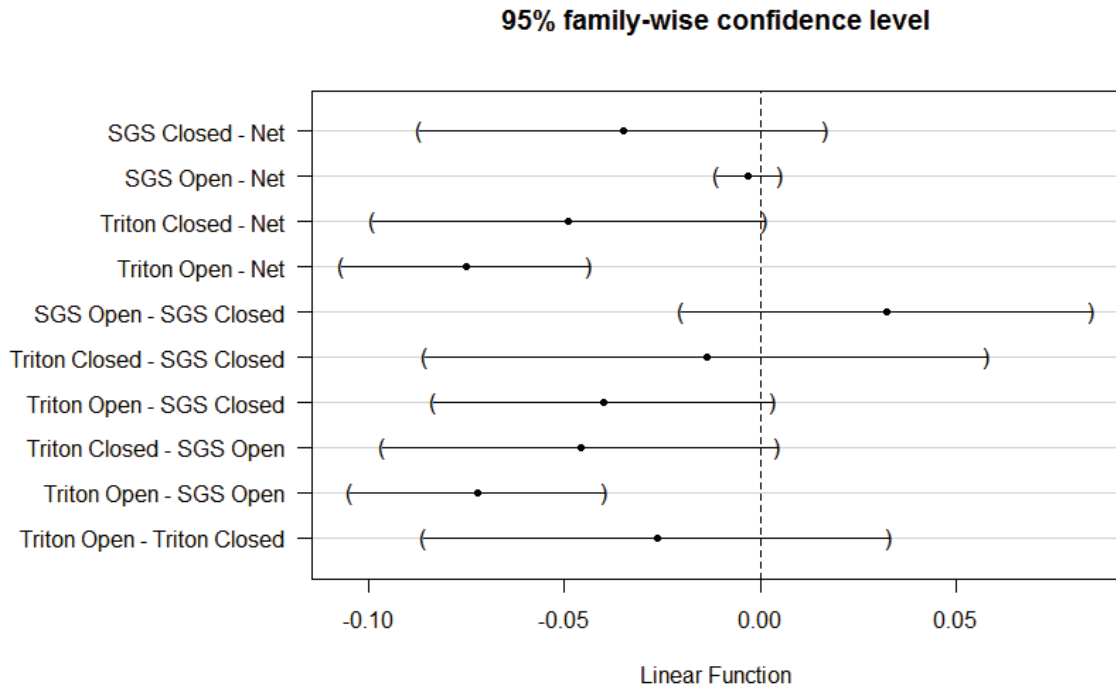


Figure 19. Results of Tukey pairwise contrasts for measurements made on samples collected using different collection devices for 10-50 μm organisms. The dot indicates the expected difference between samples collected using the devices indicated based on a linear mixed model (see methods and results) and the lines show the 95% confidence interval. There is no significant difference between collection devices where the confidence interval overlaps the vertical dashed line.

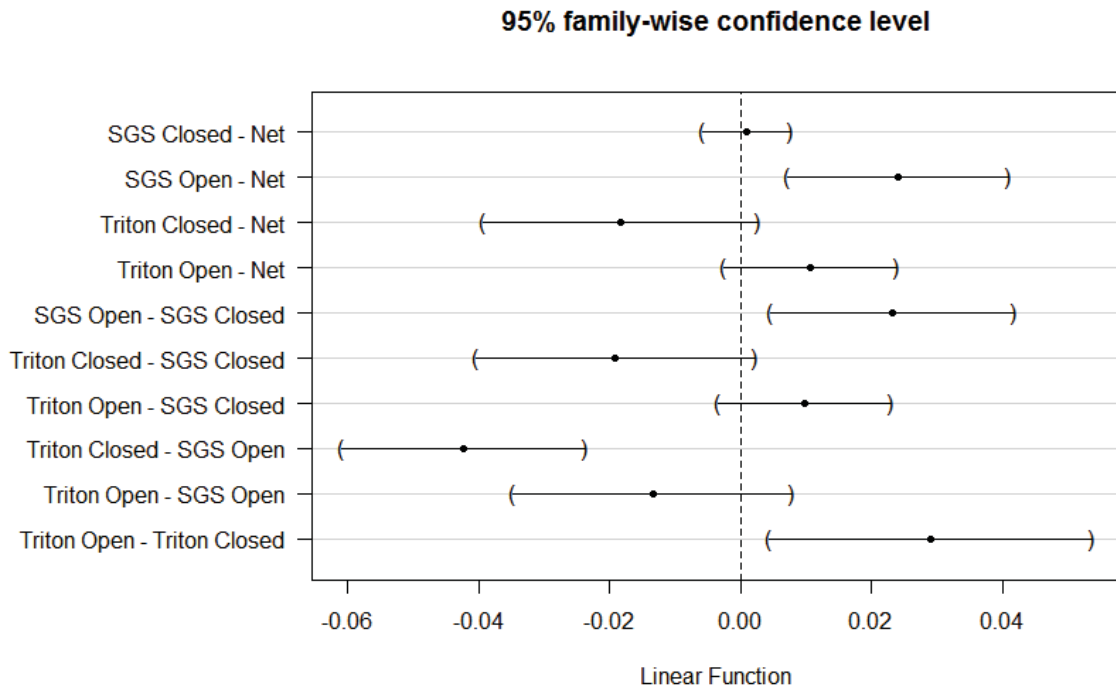


Figure 20. Bar graphs of estimated mean densities (\pm SD) before and after treatment with the OptiMarin BWMS for organisms $\geq 50 \mu\text{m}$. Red bars show estimated densities before treatment, and blue bar shows densities after treatment. All values are standardized to raw ballast concentration. (*) indicates that only 1 replicate was run during trials. A significant decrease in densities were seen for all analytic devices except bulk FDA and Welschmeyer ATP (One-way paired t tests on log+1 transformed data with Welch's correction for unequal variance; all $p < 0.05$).

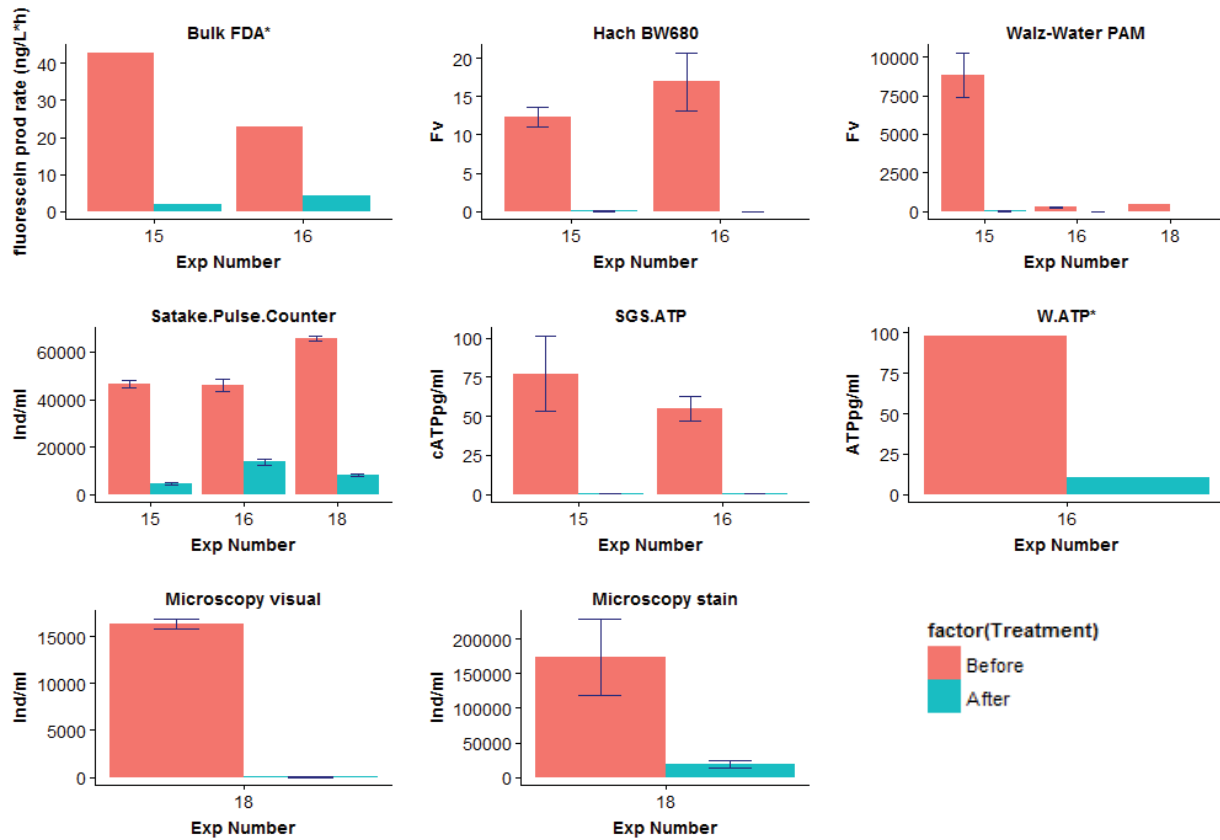


Figure 21. Bar graphs of estimated mean densities (\pm SD) before and after treatment with the OptiMarin BWMS for 10-50 μ m organisms. Red bars show estimated densities before treatment, and blue bars show densities after treatment. All values are standardized to raw ballast concentration. Only 1 replicate was run per trial for flow cytometry. A significant decrease in densities were seen for all analytic devices except flow cytometry and bulk FDA (One-way paired t tests on log+1 transformed data with Welch's correction for unequal variance; all $p < 0.05$).

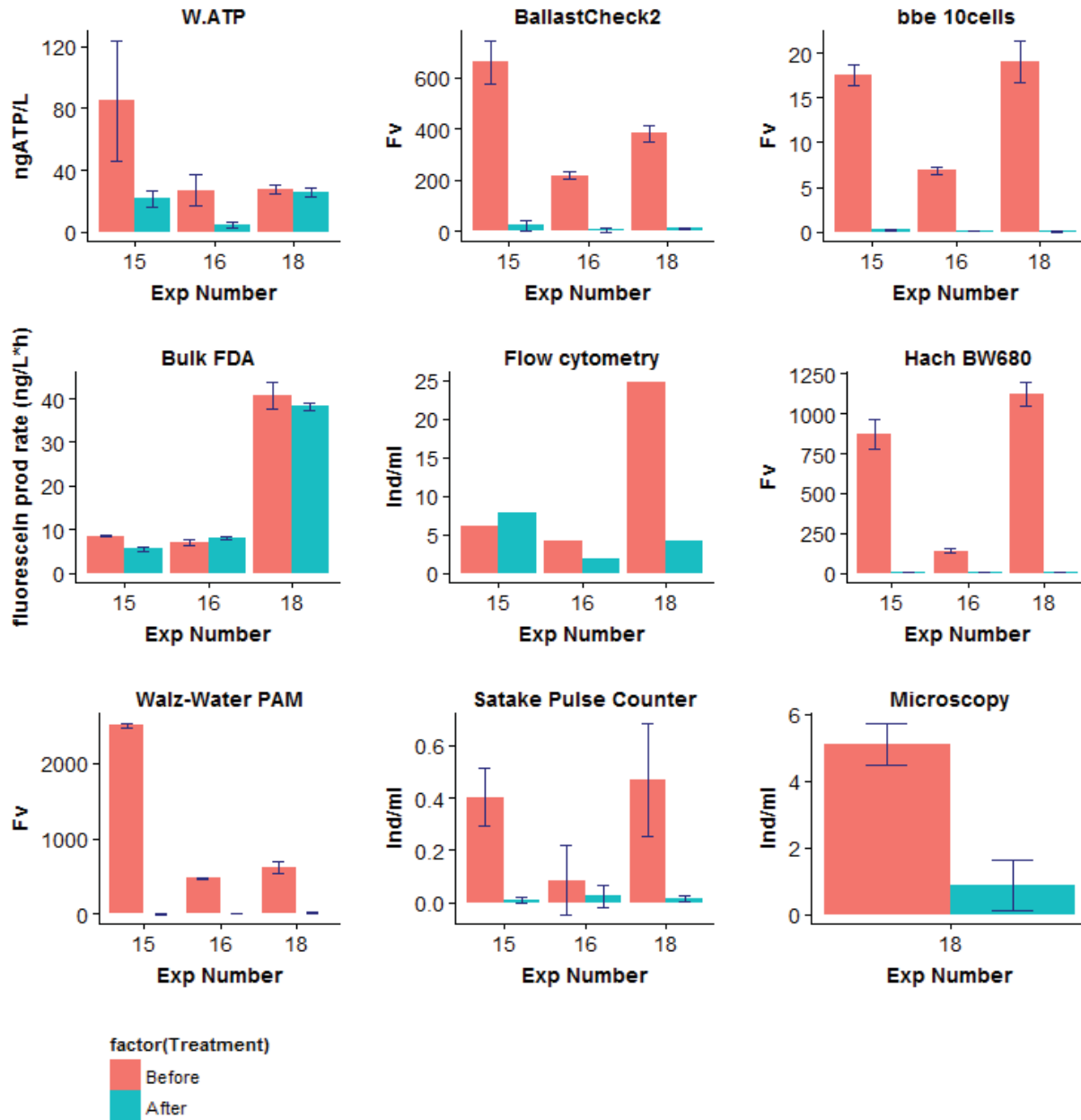


Figure 22. Bar graph of estimated mean densities (\pm SD) for $\geq 50 \mu\text{m}$ organisms in water that was treated using the OptiMarin BWMS and retreated after being held in a ballast tank for 2 days. All values are standardized to raw ballast concentration. (18, Before) shows estimated densities before treatment, (18, After) shows densities after the first treatment, (26, Before) shows densities before the second treatment, and (26, After) shows densities after the second treatment.

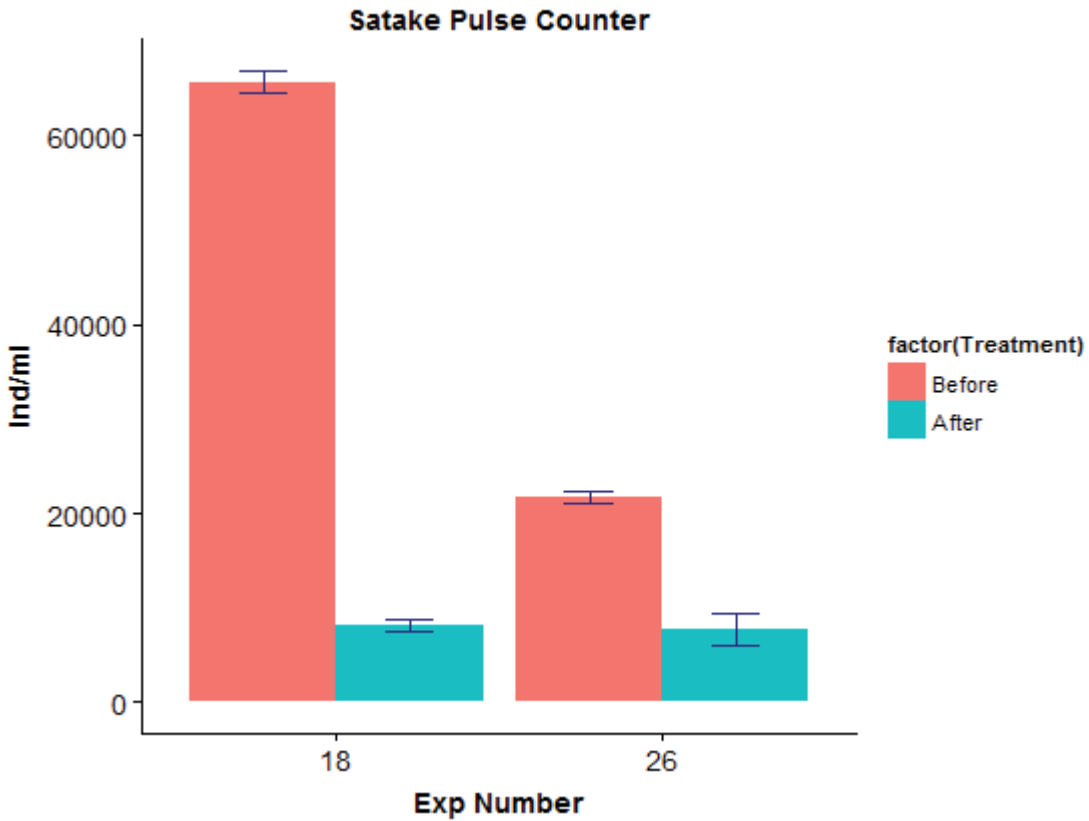


Figure 23. Bar graphs of estimated mean densities (\pm SD) for 10-50 μ m organisms in water that was treated using the OptiMarin BWMS and retreated after being held in a ballast tank for 2 days. All values are standardized to raw ballast concentration. (18, Before) shows estimated densities before treatment, (18, After) shows densities after the first treatment, (26, Before) shows densities before the second treatment, and (26, After) shows densities after the second treatment.

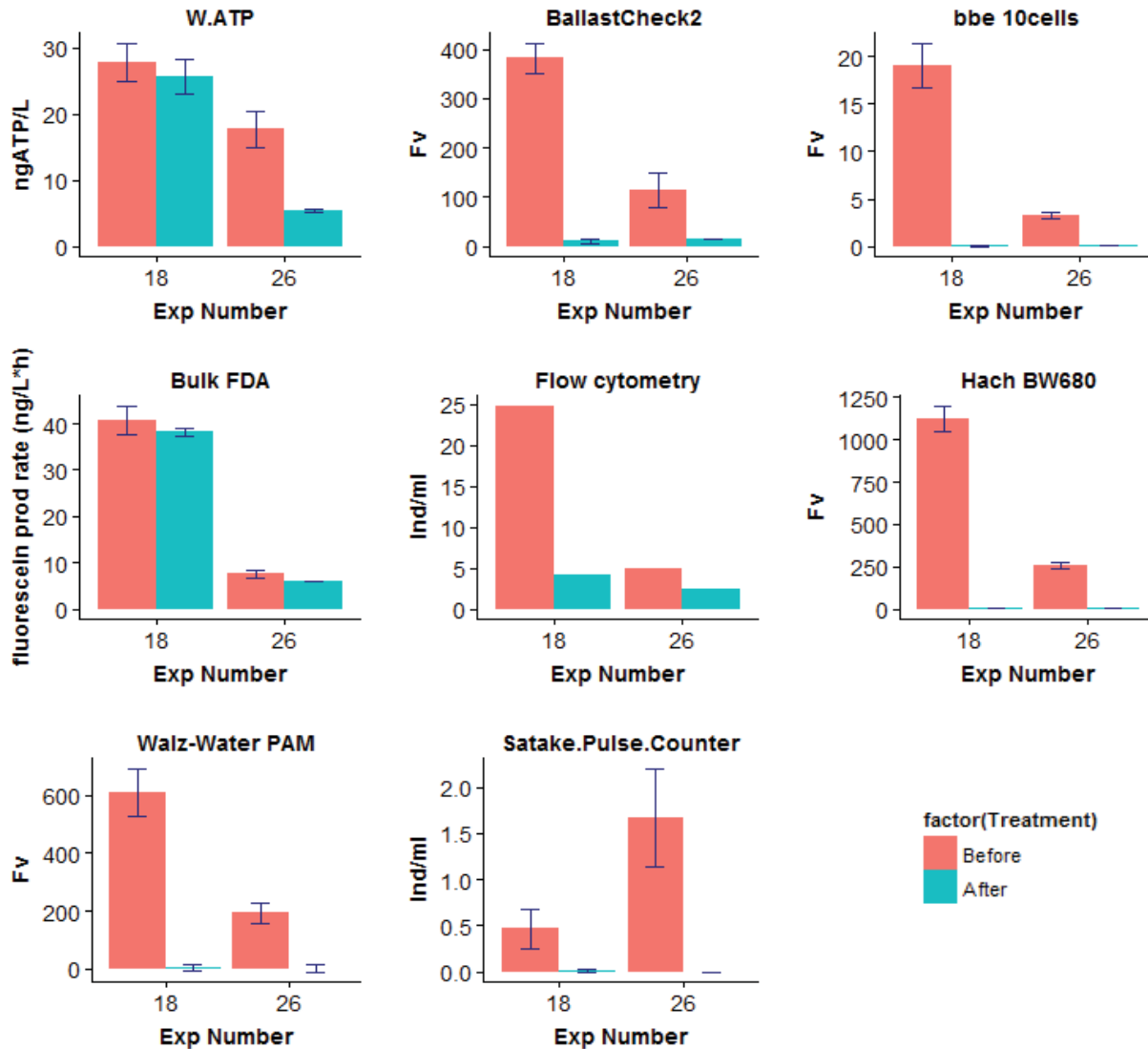
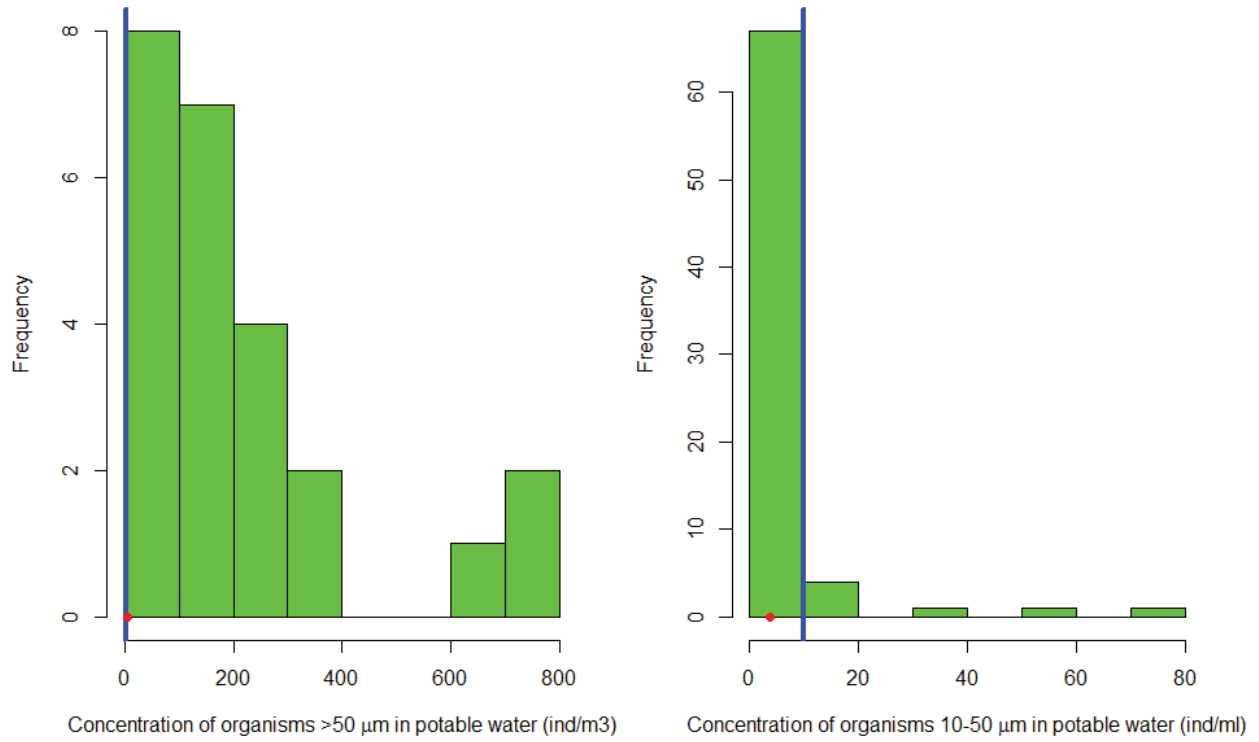


Figure 24. Histogram of the concentration of organisms $\geq 50\mu\text{m}$ in individuals/ m^3 (left panel) and organisms 10-50 μm in individuals/mL (right panel) in potable water samples. The vertical blue line indicates the D2-standard and the red dot on the x-axis marks the mean.



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APPENDICES

Appendix A: Detailed sampling information.

Table A1: Detailed sample collection information. Columns detail the total ballast volume that passed through the ship's ballast pipes during sampling, the pumping rate of the ballast water, the start and end time of each trial, the salinity and temperature of sampled water, the ship starting and ending position, and the source of water used for the trial.

Exp Num	Total ballast volume (m ³)	Flow Rate (m ³ /hr)	Start Time	End Time	Sample Salinity (psu)	Sample Temp (C)	Start Position Longitude	Start Position Latitude	End Position Longitude	End Position Latitude	Water Source
1	6.57	17	17:22:00	17:45:00	13.84	23.12	18.08	-24.47	18.14	-24.44	Tank 0.7
2	14.02	29	09:42:00	10:11:00	23.5	22.3	20.97	-23.19	21.04	-23.13	Tank 0.7
3	17.7	58	13:20:00	13:38:00	35.75	22.2	21.61	-22.92	21.67	-22.89	Ocean
4	16.15	57	09:15:00	09:32:00	34	21.7	24.86	-21.46	24.90	-21.43	Ocean
5	17.73	56	13:01:00	13:20:00	34.86	22.8	25.43	-21.19	25.49	-21.17	Ocean
6	16.43	58	08:59:00	09:16:00	35.57	20.81	28.73	-19.66	28.77	-19.64	Ocean
7	14.4	48	12:47:00	13:12:00	35.63	20.97	29.35	-19.36	29.42	-19.33	Tank 0.9
8	17	60	15:40:00	15:57:00	36.07	20.74	29.83	-19.13	29.88	-19.11	Ocean
9	22.23	58	08:14:00	08:37:00	36.15	20.22	32.66	-17.76	32.72	-17.73	Ocean
10	21.85	57	12:23:00	12:46:00	35.09	19.32	33.34	-17.36	33.40	-17.32	Ocean
11	18.37	58	15:13:00	15:32:00	35.36	19.27	33.81	-17.07	33.86	-17.03	Ocean
12	16.5	55	08:24:00	08:44:00	35.59	19.2	36.69	-15.21	36.75	-15.17	Ocean
13	18.15	55	12:15:00	12:35:00	34.95	18.47	37.31	-14.80	37.36	-14.77	Ocean
14	24.75	55	15:28:00	15:55:00	34.78	18.77	37.83	-14.46	37.91	-14.41	Ocean
15	16.8	56	08:30:00	08:48:00	35.06	17.13	40.40	-12.71	40.43	-12.69	Ocean
16	16.15	57	12:25:00	12:42:00	34.79	17.07	40.75	-12.47	40.78	-12.45	Ocean
17	22.8	57	15:45:00	16:09:00	34.94	16.7	41.14	-12.20	41.18	-12.17	Ocean
18	16.8	56	08:15:00	08:33:00	34.93	15.75	43.23	-10.71	43.28	-10.68	Ocean
19	17.7	59	12:18:00	12:38:00	35.08	16	43.82	-10.24	43.87	-10.20	Ocean
20	21.47	56	15:35:00	15:58:00	34.51	15.81	44.32	-9.80	44.38	-9.74	Ocean
21a	16.8	56	08:44:00	09:02:00	35.2	15.52	47.22	-7.08	47.27	-7.03	Ocean
21b	15.87	56	09:27:00	09:44:00	34.95	15.1	47.35	-6.97	47.40	-6.92	Ocean
22	16.5	55	12:25:00	12:43:00	34.65	14.11	47.90	-6.46	47.96	-6.41	Ocean

23	15.87	56	15:48:00	16:05:00	34.42	14.9	48.49	-5.90	48.53	-5.86	Ocean
24	21.46	56	08:25:00	08:48:00	34.07	13.19	50.12	-1.15	50.14	-1.04	Ocean
25	17.3	56	12:19:00	12:38:00	33.96	13.12	50.29	-0.12	50.30	-0.04	Ocean
26	15	50	15:46:00	15:59:00	34.31	13.77	50.45	0.81	50.46	0.87	Tank 0.1
27	15.87	56	08:35:00	08:52:00	34.02	13.7	52.80	4.18	52.84	4.22	Ocean
28	16.5	55	12:20:00	12:40:00	33.29	13.79	53.29	4.64	53.34	4.68	Ocean

Table A2: Sample volumes and concentrations for $\geq 50 \mu\text{m}$ and $< 50 \mu\text{m}$ samples.

Exp Num	Port	Collection Device	Total volume filtered ($\geq 50 \mu\text{m}$)	Condensed Volume ($\geq 50 \mu\text{m}$)	Total Volume Collected ($< 50 \mu\text{m}$)	Concentration Factor ($< 50 \mu\text{m}$) (Total / Condensed volume)
1	A	Triton Open	1001	1	10	1
1	C	SGS Open	1020	1	10	1
2	A	Triton Open	1417	1	10	1
2	C	SGS Open	729	1	10	1
3	A	Triton Open	1001	1	10	1
3	C	Net	1036	1	10	1
4	A	Net	1048	1	10	1
4	C	Net	1014	1	10	1
5	A	SGS Open	1003	1	10	1
5	C	Net	1135	1	10	1
6	A	Triton Open	1001	1	10	1
6	C	Net	1032	1	10	1
7	A	Net	1003	1	11	1
7	C	SGS Open	1073	1	10	1
8	A	SGS Open	1000	1	10	1
8	C	Net	1059	1	10	1
9	A	Triton Open	1157	1	15	6.5
9	C	SGS Closed	1005	1	15	6
10	A	Net	1264	1	15	14.5
10	C	SGS Closed	1001	1	15.5	15.5
11	A	Net	1020	1	16	16
11	C	Net	1060	1	15	14
12	A	SGS Open	1072	1	15	12
12	C	Triton Closed	307	1	15	14
13	A	Net	1114	1	15	11.5
13	C	Triton Closed	231	1	15	13.5
14	A	Net	1568	1	15	14
14	C	Triton Open	1002	1	15	14
15	A	Net	1051	1	15	14
15	B	Net	1017	1	15	13.6
16	A	Net	1025	1	15	14
16	B	Net	1005	1	15	14
17	A	Net	1172	1	15	15
17	C	SGS Closed	1002	1	15	14
18	A	Net	1019	1	15	14
18	B	Net	1040	1	15	14
19	A	Triton Open	1000	1	15	14

19	C	SGS Open	1129	1	15	14
20	A	Net	1203	1	15	14
20	C	SGS Closed	1001	1	15	14
21a	A	SGS Open	1069	1	15	8
21a	C	Triton Closed	835	1	10	8
21b	A	SGS Open	854	1	NA	NA
21b	C	Triton Closed	NA	1	NA	NA
22	A	Net	1102	1	15	8
22	C	SGS Closed	1001	1	15	8
23	A	Net	1009	1	15	10
23	C	Net	1013	1	15	10
24	A	Net	1162	1	15	8
24	C	SGS Closed	1001	1	15	8
25	A	Net	1038	1	15	8
25	C	Net	1017	1	15	8
26	A	Net	1012	1	15	14
26	B	Net	1052	1	15	14
27	A	SGS Open	1001	1	15	10
27	C	Net	1021	1	15	10
28	A	Net	1058	1	15	10
28	C	SGS Closed	662	1	15	10

Appendix B: Sample Splitting Procedure

The following procedure was used to split samples collected into the engine room into sample bottles for each individual method:

≥50 μm (1 L)

1. Gently invert the 1-L bottle 5 times.
2. Half-fill 1 bottle of each AA, AB, AC, AD, AE, AF and “extra.”
3. Gently invert the 1-L bottle 5 times and top up the volumes.

<50 μm (15 L)

1. Gently invert the 10-L carboy 5 times.
2. Half-fill 1 bottle of each DD, DE, DG, DJ, BK, BC-1 and “extra.”
3. Gently invert the 10-L carboy 5 times and top up the volumes.
4. Filter remaining water on a 10 μm (diagonal) Sterlitech polyester track etch (PETE) membrane filter.
5. Resuspend retained particles in 1.5L sterile seawater for 10-50 μm fraction.
6. Retain ~3L filtrate containing organisms in the smaller than 10 μm size fraction.

> 10 < 50 μm (1.5 L)

1. Gently invert the carboy containing the resuspended particles 5 times.
2. Half-fill 1 bottle of each BB, BC-2, BD, BE, BF, BG, BH, and BJ.
3. Gently invert the carboy 5 times and top up the volumes.

< 10 μm (~3 L)

1. Gently invert the carboy 5 times.
2. Half-fill 1 bottle of each DH, DI, BC-3, CC, CD, CE, CF and CG.
3. Gently invert the carboy 5 times and top up the volumes.
4. Rinse the carboy with filtered seawater 5 times and allow to drip-dry.

Appendix C: Protocols for Analytic Methods

Optical Zooplankton Analysis (OZA)

Size Class: >200 μ m

Researcher: Wouter van de Beek

Description: The OZA method distinguishes viable zooplankton larger than 200 μ m from dead organisms and debris based on their swimming capability. An LED in the OZA device projects shadows of the organisms in the sample onto a partially transparent projection screen. To ensure very sharp projections of the organisms, the light coming from the LED must approach perfect light collimation. To do so, the divergent light coming from the LED is collimated by a lens and the collimation is further optimized using mirrors to make the distance from lens to sample as long as possible. Two successive images of the projection are captured by camera and loaded in Matlab for analysis. Matlab subtracts one image from the other (analyzed image from reference image), so that every object that has the same location in both images disappears. Resultantly, the only objects that remain are those that have moved: swimming, viable zooplankton. The final image is made binary and the number of objects are automatically counted.

Methods:

1. A 200 mL sample is poured into a sample bottle and filled to the top with the same salinity water (diluting); this reduces movement in the sample caused by the ship's movement.
2. The sample is placed in the OZA device and left for 15 minutes to allow debris to settle and ensure debris that is still settling does so at a lower speed than detectable.
3. The camera is focused manually and 2 pictures are captured.
4. The camera is removed from the device and connected to a computer. Images are downloaded and converted from RAW to TIFF for Matlab analyses.
5. Images are placed in chronicle order and filenames are input to MATLAB code for processing. The MATLAB script takes approximately 10-15 seconds to display the results which include the analyzed image with the motile organisms identified as purple dots, and organism counts, which are displayed above the image. This process is repeated after reversing the order of the images (i.e. analyzed image becomes reference image), and the average is taken of these two results to get the final result.
6. Steps 3-5 are repeated in triplicate for each sample. Note that the waiting time is only necessary for the first run, since the same 200mL is used for all three tests.

Microscopy

Size class: $\geq 50 \mu\text{m}$; $10 \mu\text{m} > x > 50 \mu\text{m}$

Researchers: Julie Vanden Byllaardt, Johanna Bradie, Sarah Bailey

Description: Microscopy is the historical standard for the analysis of ballast water samples.

Methods ($\geq 50 \mu\text{m}$):

1. Initially, a 50 ml sample [AA] of the $\sim 1000\text{L}$ concentrated water was received for enumeration of live organisms greater than $50 \mu\text{m}$. Due to very low densities of large motile invertebrates at the beginning of the voyage, this was increased to 200ml beginning with test run #4. The density of large motile invertebrates varied widely as the vessel sailed – when required, the sample received was further concentrated up to 20x using $50 \mu\text{m}$ (in diagonal) plankton mesh to achieve a target range of 20-50 motile invertebrates per ml. The concentration factor utilized was recorded for each sample such that an estimate of densities in the unprocessed raw water could be calculated.
2. Each [concentrated] sample was well mixed by gentle inversion five times.
3. Three one ml subsamples were drawn using a $1000 \mu\text{l}$ Eppendorf Research® pipette. The end of the pipette tip was cut shorter by approximately 5 mm to enlarge the diameter of the tip opening to facilitate capture of larger organisms.
4. To facilitate counting at sea, we modified standard Bogorov chambers by adding plexiglass blocks in each curve, dividing the chamber into five channels, each having one ml capacity. Each subsample was deposited into a channel for analysis under a Nikon SMZ800N dissecting microscope at 30x magnification.
5. All organisms retained in the sample were assumed to be larger than $50\mu\text{m}$ in minimum dimension since the sample had been processed 2 or 3 times on $50 \mu\text{m}$ mesh – however, protists obviously smaller than $50\mu\text{m}$ were occasionally observed and omitted from counts. Motile organisms were counted if they exhibited any movement autonomously or in response to gentle nudging using an insect pin. Non-motile organisms, such as diatoms, were counted using FDA stain as described for organisms in the $10\text{-}50 \mu\text{m}$ size range.
6. Three additional one ml subsamples were taken from the [concentrated] sample for staining, with 0.25 or 0.5 ml examined under an epifluorescence microscope, depending on density.

All counts were completed within 6 hours of the start of sample collection.

Methods ($10 \mu\text{m} > x > 50 \mu\text{m}$):

1. Each [concentrated] sample was well mixed by slow inversion of the sample bottle 5 times.
2. In triplicate, 5 ml of the water was drawn using a $5000 \mu\text{l}$ Eppendorf Research® pipette, placed in a 20 ml glass scintillation vial and stained with $10 \mu\text{l}$ of 2.5 mM fluorescein diacetate (FDA; in solution with dimethyl sulfoxide) to create a final concentration of $5 \mu\text{M}$ FDA.
3. Stained subsamples were dark incubated for 10 minutes, after which 1 ml was loaded into a gridded 1mm^2 Sedgewick-Rafter counting chamber.

4. Fluorescing cells were enumerated at 200x magnification using a Zeiss Axio Vert.A1 inverted epifluorescence microscope fitted with a blue light excitation-green bandpass emission filter cube (FITC; excitation 465 - 495 nm, dichoric 505 nm, barrier 515 - 555 nm) and light-emitting diode (LED) illumination.
5. Due to the low concentration of algae in the sample water, the entire chamber was viewed and fluorescing cells were counted if any dimension was greater than 10 μm , using the gridded line thickness of 18 μm as a size reference. Individuals that were only partly fluorescing were counted as viable. Cells within colonies were only included in counts if the individual cell had a dimension greater than 10 μm . Stained aliquots were examined within 20 minutes of dark incubation and all samples were processed within 4 hours of the start of sample collection. FDA stain was kept frozen and in the dark when not in use.

Satake Pulse Counter

Size Class: $\geq 50\mu\text{m}$ and $10\mu\text{m} < x < 50\mu\text{m}$

Researchers: Akiko Nakata and Jianjun He, Satake Corporation

Description: The Satake pulse counter, which employs pulse counting FDA method, estimates the number of viable organisms in ballast water samples by counting fluorescence pulse over specific threshold from FDA stained organisms in short time. This system consists of main body (detection unit, touch panel display and CPU), sample cell, portable casing and AC adapter. This system is small enough to be carried on board by one person, and therefore suitable for PSC inspection. Figure A1-1 shows a schematic diagram of the detection unit of the Satake pulse counter. The detection unit consists of LEDs, a stirrer, a detector, and optical filters. The LED has an excitation light source that provides blue light with a specific wavelength which makes stained organisms fluorescent. A photomultiplier tube is used as a detector in order to detect weak fluorescence. The optical filters are employed to cut stray light in order to enhance sensitivity. Figure A1-2 shows an image of detected pulse signals. When fluorescence intensity from one organism exceeds a pre-fixed threshold, the number of organisms which pass on the monitoring area will be counted.

Methods:

1. L size plankton ($x \geq 50 \mu\text{m}$) measurement
 - Unfreeze “Reagent L” (FDA) at room temperature.
 - Put the stirring bar into sample cell.
 - Add 100 mL of sampling water into sample cell
 - Add “Reagent L” (FDA) to sample cell
 - Wait for ten minutes.
 - Switch on, then press “L size” button on screen.
 - Set sample cell in the body, and press start button.
 - Estimated number of viable organisms will be displayed on the screen.

2. S size plankton ($10 \sim 50 \mu\text{m}$) measurement
 - Unfreeze “Reagent S” (FDA) at room temperature.
 - Add sampling water into “Reagent S” bottle up to 5 mL scale line using a dropper.
 - Wait for thirty minutes.
 - Put the stirring bar into sample cell.
 - Transfer 5 mL stained sampling water to sample cell.
 - Add more sampling water without FDA staining up to 100 mL.
 - Switch on, then press “S size” button on screen.
 - Set sample cell in the body, and press start button.
 - Estimated number of viable organisms will be displayed on the screen.

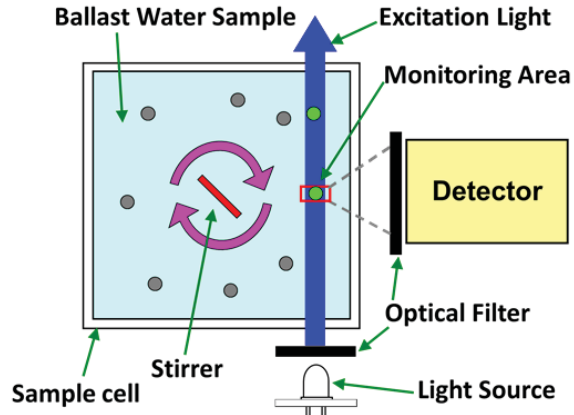


Figure A1-1: Schematic diagram of detection unit of Satake pulse counter

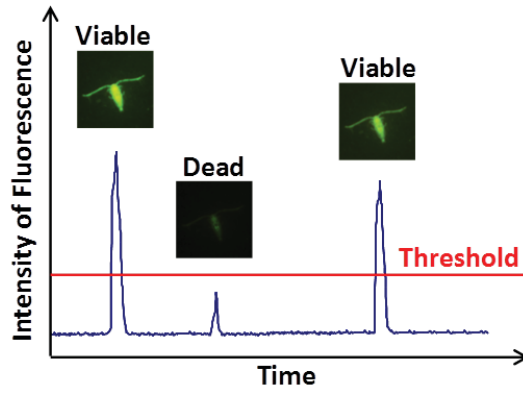


Figure A2-2: Image of detected pulse signals

bbe 10cells (PAM)

Size Class: 10µm>x>50µm

Researcher: André Zaake, bbe

Description: bbe 10cells is an indicative Instrument for analyzing living cells in ballast water. It is based on variable fluorescence (Fv) of chlorophyll of living algae. During a filtration step, the algae are placed on a filter inside a bbe filter kit. This filter will be placed in the instrument and a measurement can be started. By changing the volume of filtration or filter size it can be adapted to different environments and requirements. It is easy to use, takes approx. 1 min and no chemicals are needed.

Methods:

1. Switch the instrument on by pressing "Power".
2. Optionally, filter sample using a 50µm pre filter.
3. Fill a 10ml syringe to 10ml with sample.
4. Pull the syringe to fill 2ml additional air in it.
5. Take a bbe 8µm filter kit and push/screw the syringe on.
6. Press the syringe gently while holding the syringe with filter kit vertically. Press until the syringe is completely empty (include air).
7. Pull the filter kit to release from syringe.
8. Open filter kit by open latch.
9. Remove filter strip while holding it horizontally.
10. Dry filter by pressing a tissue on bottom of filter.
11. Insert filter into 10cells and close cap.
12. Press start.
13. Wait approximately 1min --> result will be displayed on screen.
14. Remove filter strip.

Turner Designs' Ballast-Check 2 (PAM)

Size Class: 10µm>x>50µm

Researcher: Lawrence Younan, Turner Designs

Description: Turner Designs' Ballast Check-2 is a quick indicative compliance tool used for estimating the abundance and assessing the viability of phytoplankton from the 10-50 micron size class. This high precision instrument uses the organism's fluorescence characteristics to provide a quick analysis of whether ballast water is in compliance with current discharge standards. The Ballast Check-2 is a small, lightweight, durable instrument operated by four AAA batteries. It can store up to 1000 data points, which can be viewed using the instrument's display or downloaded directly to your computer. Factory set, it is ready for use right out of the box, no calibration necessary.

Methods:

All Standard Operating Procedures pertaining to calibration check, sample processing, measurement, and maintenance/cleaning can be found in the Ballast-Check 2 User's Manual; sections referenced for each procedure.

Sample Analysis:

For each trial, analysis was completed on 3 size fractionated samples (< 50 µm, 10-50 µm, and < 10 µm) in triplicate from each collection device (S1 and S2). All measurements were corrected for blank using rinse water that was available for each sampling event. All subsamples (fractionated samples) were analyzed independently, using rinse water as a blank value, to calculate individual cells per milliliter and associated activity of those cells. The final analysis used both the < 50 micron and < 10 micron samples, using the < 10 micron filtrate sample as a blank, to calculate individual cells per milliliter, activity of those cells, and the risk associated with the water collected for that sampling event, for that sampling method (S1 or S2).

Sample Measurement:

The following procedure was used to analyze the three subsamples independently:

- 1) The sample bottle was gently inverted 5x
- 2) A 1-cm square glass cuvette was rinsed 3x using the mixed sample
- 3) 3.5 milliliters of sample was transferred into the cuvette using a 5 ml pipet
- 4) Cuvette walls were wiped using KIMTECH Kimwipes
- 5) Cuvette was inserted into the Ballast Check-2
- 6) Sample was measured
 - a. If a 10 micron filtered sample was not required, sample analysis was done and results were logged
 - b. If a 10 micron filtered sample was requested, a secondary 1-cm glass cuvette containing rinse water was inserted into the Ballast Check-2 and read in place of the 10 micron sample, then sample analysis was done and results were logged
- 7) Steps 1-6b were repeated 3x for each subsample provided
- 8) Logged results were downloaded and transcribed into provided data sheets

The following procedure was used to run a final analysis using 2 of the three subsamples provided (< 50 micron and < 10 micron samples):

- 1) Both sample bottles were gently inverted 5x
- 2) Two 1-cm square glass cuvette were rinsed 3x using the mixed sample (one cuvette for the < 50 micron sample and one cuvette for the < 10 micron sample)
- 3) 3.5 milliliters of each sample was transferred into its respective cuvette using a 5 ml pipet
- 4) Cuvette walls were wiped using KIMTECH Kimwipes
- 5) The < 50 micron sample cuvette was inserted into the Ballast Check-2
- 6) Sample was measured
 - a. If a 10 micron filtered sample was not required, sample analysis was done and results were logged
 - b. If a 10 micron filtered sample was requested, the < 10 micron sample cuvette was inserted into the Ballast Check-2 and measured, then sample analysis was done and results were logged
- 7) Steps 1-6b were repeated 3x for each sampling method (S1 and S2)
- 8) Logged results were downloaded and transcribed into provided data sheets

Calibration Check Procedure (See section 2.3 in the Ballast-Check 2 Manual)

Sampling Procedure (See section 2.5 in the Ballast-Check 2 Manual)

Data Download Procedure (See section 2.7 in the Ballast-Check 2 Manual)

Calculations

There are two gain states that may be used to read a sample depending on the sample's fluorescence intensity. If the sample read has a high amount of fluorescence, the 1x gain state is used for the measurement. For low fluorescing samples, the 10x gain state is used. The Ballast-Check 2 will log the gain state used for each sample measured so the appropriate blank and calibration values can be applied when manually calculating Abundance.

Abundance is calculated as:

$$\text{Abundance} = [(\text{Unfiltered } F_o - \text{Blank}) - (10\text{micron filtered } F_o - \text{Blank})] * [(\text{Cal Val})/(\text{Cal RFU})]$$

where "Blank" and "Cal RFU" are gain specific

The Activity calculation requires a blank to be subtracted from the Unfiltered F_o and F_m values to accurately estimate algal viability. To manually calculate Activity, the gain state the sample was read in needs to be known so the appropriate blank can be applied.

If the sample did not require filtration, then Activity is calculated as:

$$\text{Activity} = (\text{Unfiltered } F_m - \text{Blank } 10x) - (\text{Unfiltered } F_o - \text{Blank } 10x) \quad (\text{Unfiltered } F_m - \text{Blank } 10x)$$

If the sample required filtration, then Activity is calculated as:

$$\text{Activity} = (\text{Unfiltered } F_m - 10\text{micron filtered } F_m) - (\text{Unfiltered } F_o - 10\text{micron filtered } F_o) \\ (\text{Unfiltered } F_m - 10\text{micron filtered } F_m)$$

Walz-Water Pulse-Amplitude-Modulation (PAM)

Size Class: $10\ \mu\text{m} < x < 50\ \mu\text{m}$; $\geq 50\ \mu\text{m}$; $< 10\ \mu\text{m}$

Researcher: M.Veldhuis, MEA-nl, RUG

Description: The aim of PAM is to estimate the phytoplankton biomass as chlorophyll (in terms of autofluorescence) and the photosynthetic activity (as estimate of viability) of phytoplankton. Measurements can be performed using whole water samples or size fractionated or otherwise collected water samples containing phytoplankton.

Principle: Chlorophyll a fluorescence, particularly F_v/F_m , which has shown to be a sensitive indicator of photosynthetic performance (Krause & Weis, 1991). Modulated fluorometry (Schreiber et al., 1986) allows the recording of photosynthetic performance parameters that are obtained using saturation pulses applied during fluorescence induction by an actinic light source (Heraud & Berdall, 2000). The PAM fluorometer measures different stages of the fluorescence of the chlorophyll-protein complex of phytoplankton. After dark adaptation the measured fluorescence is the auto, minimum or ground fluorescence signal (F_0).

During the activation the sample is illuminated with light saturation pulses by means of pulse amplitude modulation (PAM). During process the maximum yield of photochemical energy conversions will be measured of the chlorophyll-protein complex (F_m). The difference between both fluorescence signals is the variable fluorescence (F_v). This variable fluorescence is an indicator of the efficiency of the photosynthetic activity of the chlorophyll-protein complex of the algal cell. In healthy and fast growing phytoplankton cells the difference is high but in stressed or dead phytoplankton cells the both values of fluorescence signals are nearly identical, hence difference is only minimal.

Definitions

Actinic light: light that will facilitate photosynthesis or stimulate light sensitive species

PAM: Pulse Amplitude Modulation

r.u.: relative unit

F_0 : total chlorophyll biomass, estimated in relative units (r.u.)

F_m : chlorophyll fluorescence after excitation (r.u.)

F_v : variable chlorophyll fluorescence: $F_v = F_m - F_0$

F_v/F_m : photosynthetic efficiency of the phytoplankton community. Typical values range between 0 and ca 0.8



Figure 1: PAM fluorometry; a fast method to determine (bulk) phytoplankton biomass and the photosynthetic activity of the phytoplankton. Left Universal Control Unit, right Water ED/B

Reagents and consumables

- Sample water (GF/F or 0.2 µm filtered)
- Mili Q or equivalent water

Equipment and tools

- PAM-Universal-Control unit, WALZ
- WATER-ED/B Emitter-Detector-Unit, WALZ
- Water-K, Quartz glass cuvette
- PC or laptop with WALZ measurement software (PAM WALZ Win-Control v3.23)

Sampling and sample handling

Obtain different water samples during the sampling and fractionation procedure and store them in the dark prior to analysis. Avoid bright light and high temperatures. Analyse samples as soon as possible after receiving the bottles.

Procedure

5.1. Processing

- Analysis of the samples can be done when samples were stored in the dark for at least 30 min.

5.2. Analysis

- Start the computer and the software program for the PAM (=Wincontrol version 3.23).
- Prior to this measurement the operator should be familiar with the procedures as described in the PAM control manual (PAM control unit and Water PAM manual).
- Program selects automatically last save protocol for given set of measurements.
- First a Blank sample needs to be measured; fill (at least 2-3 mL) the PAM cuvette with filtered sample water (0.2 micron) or challenge water and cover the cuvette with the lid.
- The Ft signal needs to stabilize for at least 30 seconds.
- To increase the stability highlight ML-F-high, this will increase the number of saturation pulses
- Mix water sample gently and fill a cuvette with a sample (2-3 mL)
- The Ft signal needs to stabilize for at least 30 seconds.
- Note: Ft measurement is not reliable when the value is below 100 r.u. or above 1000 r.u. If this is the case, increase or decrease the PM-Gain, respectively. Note the PM-Gain down (10, 15 or 20). Make sure to calibrate settings again for zero with filtered water sample
- Press the F0, Fm button to activate saturation light pulse for reading of F0, Fm and yield (Fv/Fm) (Saturation pulse intensity reaches up to 3000 µmol quanta m⁻²s⁻¹).
- Note the values of F0, Fm and Fv/Fm ratio as well as the run number
- Data should be saved (floppy icon) using a date and unique identification code
- Repeat the whole procedure three times, a higher gain may be needed when measuring treated water samples with low phytoplankton biomass and photosynthetic efficiency
- When analysis with the PAM is finished, rinse the PAM cuvette with mili Q water.
- Save data, close the program on the computer and turn off the computer and the PAM control.

Calculation and Report

F0 fluorescence of dark adapted phytoplankton
Fm maximum fluorescence yield after saturated light induction
Fv variable amount of fluorescence = Fm-F0

Phytoplankton photosynthetic efficiency $Fv/Fm = (Fm - F0) / Fm$ (no unit, ratio)
With a dark-adapted sample: $\Delta F/Fm = (Fm-F0)/F = Fv/Fm$, corresponding to the maximal yield of photochemical energy conversion.

Raw data are presented as chlorophyll biomass (F0), not corrected for instrument settings. Viability is presented as a quantitative measurement ranging from 0 to approximately 0.8 as the sample measured and can be compared for the different fractions.

To convert the raw data into a number (viable) cells a set of specific calibration curves need to be made for each size class of phytoplankton and is because of its complexity outside the scope of this exercise.

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Hach BW680 (PAM)

Researcher: Nick Welschmeyer

Size classes: $\geq 50 \mu\text{m}$; $10 \mu\text{m} < x < 50 \mu\text{m}$; $< 10 \mu\text{m}$

Summary: The determination of variable chlorophyll *a* (chl) fluorescence from natural, whole-cell phytoplankton serves as a rapid method to assess relative ballast water compliance. The Standard Operating Procedure (SOP) here provides details on the application of variable chl *a* fluorometry to ballast water compliance testing (see Protocol Overview). The method is specifically configured to yield easily measured data that scales proportionally with the total living phytoplankton biomass within the 10 - 50 μm size class. A calibrated conversion factor allows simple calculation of the equivalent numerical live count for purposes of compliance evaluation against published ballast water discharge standards (BWDSs).

Scope and Application: The protocol described here utilizes modulated fluorescence instrumentation to measure variable chl *a* fluorescence for the rapid evaluation of ballast water compliance. The method is based on simple, whole-cell evaluation of small sample volumes (2.5 mL) without the requirement for reagents nor biological incubations. The method is rapid (<2 min) and requires no special training. The method does have its limitations for direct comparison to ballast water discharge standards because the detection response is restricted to autotrophic, chl-containing organisms only, thus ignoring heterotrophs. The trade-off, however, lies in the 1) *speed* (1-2 min), 2) *simplicity* (no reagents) and *convenience* (portable, pocket-sized instrumentation) of the procedure; these are considered ideal traits for rapid ballast water compliance monitoring.

To our knowledge, the method, as described here, could be executed by any of the currently marketed variable chl fluorometers capable of delivering stable measurements of F_v (Schrieber et al. 2000) at levels of chlorophyll approximating those concentrations expected for successfully treated ballast water (see Protocol Overview). The list of vendors include BBE Moldaenke, Schwentinental, Germany; Chelsea Instruments, Ltd., West Molesey, United Kingdom; Hach Corp, Loveland, CO USA; Hansatech, Ltd., Pentney, United Kingdom; Heinz Walz GmbH, Effeltrich, Germany; Opti-Sciences, Hudson, NH USA; Photon Systems, Inc., Brno, Czech Republic; Qubit Systems, Inc., Kingston Ontario, Canada; Satlantic Instruments, Dalhousie, Canada; Turner Designs, Inc., Sunnyvale CA USA.

In the SOP here, we describe the use of the pocket-sized, battery operated BW680 fluorometer, originally developed by PSI Inc. (Czech Republic) and now modified and marketed for ballast water work by Hach Corporation (USA). The instrument is preprogrammed with repetitive flash sequences, utilizing both blue and red excitation energy (to optimally cover fluorescence excitation of all algal taxa, including cyanophytes) yielding a single averaged variable fluorescence response, termed the Ballast Water Index (BWI). The BWI response shares all the characteristics of F_v , the standardized term for 'variable fluorescence' generated by all variable chl fluorescence instruments (Schrieber et al. 2000). The convenient features of the BW680 instrument for rapid ballast water testing relate to its simplicity: 1) no instrument blanking is required, 2) the wide dynamic range of the detector requires no gain adjustments from its

minimum detection level of 0.05 µg Chl *a*/L to over 40 µg Chl *a*/L, and 3) no user-based programming manipulations are required (nor offered); it operates on the push of a single button.

Methods:

- Hold filter-fractionated samples in the dark for a minimum of 3 minutes before making measurements. The correct determination of BWI (also Fv) must be made on dark-adapted samples. A room temperature darkened cabinet/drawer is sufficient; conversely, samples can be held in darkened, amber sample bottles, held out of direct sunlight.
- Pipet or decant 2.5 mL dark-adapted sample water into a clean, plastic, fluorometer cuvette. Keep volumes consistent, since changes in volume level will affect optical environment within the cuvette chamber.
- Place sample cuvette in the instrument sample chamber, close the lid and press 'MEASURE'; the BWI response will be displayed in ca. one minute.
- Measure the unprocessed sample. Record measurement; data are also stored in internal memory, accessed by USB data downloads.
- The programmed flash sequence will expose sample water to high saturating levels of light that may require some recovery time; the same cuvette fluid should not be measured twice. Therefore, replicate measurements, if desired, should be made on fresh sample additions.
- Calculate estimated numeric concentration of cells using Eq. 1 below; compare to ballast water discharge standards of 10 live cells/mL for the 10-50 µm size class.

Calculation of equivalent numeric cell concentration

Equations 1 and 2, below, provides the means to estimate the equivalent numeric concentration of live cells corresponding to the measured BWI signal (or Fv) of any unknown ballast water sample, processed as described above. The exponentially-weighted mean cell size of the 10-50 µm plankton size class is calculated to be 15 µm ESD (Welschmeyer 2013) based on organism size distribution models for coastal systems, characterized by a Log biomass vs. Log cell volume slope of -0.1 (Vidondo et al. 1997). A cell specific BWI response factor (RF) of 14.98 BWI/(cell mL⁻¹) for the 15 µm ESD cell size was determined empirically, and specifically, for the BW680 fluorometer from sized-based analysis of several freshwater and marine phytoplankton species; data shown in Fig. 1 (from Welschmeyer 2013). The BWI signal for the 10-50 µm size category is calculated by subtracting Fraction 2 (<10 µm) from Fraction 1 (<50 µm):

$$\text{Eq. 1: } BWI(10-50\mu\text{m}) = BWI(<50\mu\text{m}) - BWI(<10\mu\text{m})$$

As noted above, the calculated 15 µm mean cell diameter refers to the 10-50 µm size category. The estimate of live autotrophic cells within the 10-50 µm size class is then calculated as:

$$\text{Eq. 2: Live cells/mL}(10-50\mu\text{m}) = \text{Sample } BWI(10-50\mu\text{m}) / (14.98 \text{ BWI}/(\text{cell mL}^{-1}))$$

NOTE: The Response Factor (RF) for 'Fv' determined on modulated fluorometers from other manufacturers must be determined empirically, as in Fig. 1, due to unique characteristics for each manufacturer's optical design and detector responses (e.g., raw fluorescence signals). Eq. 2 is specific to the BW680 (Hach Corrp.)

Method detection limits

0.05 µg Chl/L, equivalent to ca. 5 live cells/mL for 15 µm ESD cells.

List of Abbreviations

BWI Ballast Water Index (fluorescence parameter)

Chl Chlorophyll *a*

CV Coefficient of Variation

ESD Equivalent Spherical Diameter

RF Response Factor

Health and Safety

No health and safety issues.

Interferences

Turbidity greater than 20 NTU will cause decreases in BWI

Personnel Qualifications and Responsibilities

Non-technical personnel can execute all aspects of the method; no special training or practice is required.

Special Equipment and Materials

- Hach BW680 handheld modulated fluorometer (or equivalent).
- Disposable plastic 1 cm cuvettes; 4 sides clear, standard VIS transparency.
- Pipet capable of dispensing 2.5 mL sample volume.
- Extra AAA batteries (4) or USB data cord for drawing computer power. New batteries will last several days under full time use.
- 10 µm syringe filters (Pall Life Sciences, Acrodisc Versapor Membrane, 10 µm, PN AP-4001T).
- 50 µm nylon sieve filter (50 µm on diagonal); this coarse filter can be reused after rinsing.

Equipment and Supplies

- Instrument carry case
- Squeeze bottle for rinsing cuvettes (distilled water)
- Plastic waste receptacle for fluids.
- Test tube rack to hold samples (50 mL each, nominal)
- Sample tubes.
- 10 µm syringe filters

Quality Control

The instrument sensitivity is calibrated at the factory. Once calibrated, the solid state, fixed-optics fluorometer is not expected to drift, unless physically mishandled (e.g., dropped on steel deck). Warm up time (<5 sec) is factory programmed into the startup procedure when the instrument is turned on. Instrument will be supplied with a permanent solid standard to check for sensitivity drift.

Flow Cytometry

Size Class: $2 \mu\text{m} < x < 50 \mu\text{m}$

Researcher: M.Veldhuis, MEA-nl, RUG;

Author of methods: L. Douwes

Summary: This SOP describes the procedure which should be followed when measurements of the total number of phytoplankton in the size range from $2 \leq \text{cell diameter} < 50 \mu\text{m}$ are needed. Phytoplankton numbers are determined based on the presence of their red fluorescence caused by the presence of chlorophyll. SOP-317.

Aim: The aim of this SOP is to describe sampling, sample storage and analysis of phytoplankton in the size range $2 \leq \text{cell diameter} < 50 \mu\text{m}$ and using flow cytometry (FCM). Of each individual particle, size, optical density and three different fluorescent properties are analysed and stored for detailed analysis. Size class differentiation can be made on basis of filter fractionation or using an internal standard.

Definitions:

Total phytoplankton cells: total number of free phytoplankton cells with cell size varying from $2 \leq d < 50 \mu\text{m}$ present in the water per mL based on counting cells possessing chlorophyll auto-fluorescence.

Calibration of flow cytometer: see 'Coulter XL basic training manual'. This calibration procedure provides estimate of sample flow rate ($\mu\text{L/s}$)

Conversion of actual counts to absolute counts :

Run numbers are unique and linked to a control, treatment activity, and date of intake or discharge.

Absolute Counts = (counted cells – blank) * 1000/counted volume (mL)

Phytoplankton numbers/mL counted cells: number of chlorophyll containing phytoplankton cells

Blank: number of chlorophyll containing phytoplankton cells counted in 0.2 micron filtered sample (average over whole sample set)

Absolute number of cells is averaged of the 3 samples bottles.

Information of Green, Orange auto fluorescence is additional data not immediately necessary. In addition, when present same data of subpopulations can be added to the data sheet.

Principle

To determine the number of phytoplankton in the size range $2 \leq \text{cell diameter} < 50 \mu\text{m}$ and using flow cytometry (FCM).

Reagents and consumables

- Sampling water
- Prefiltered sampling water ($0.2 \mu\text{m}$ prefiltered)
- Sample tubes

Equipment and tools

- Dark sample bottles (500 – 1000 mL)
- Pipettes and pipette tips (1-10 mL)
- Beckman Coulter EPICS XL-MCL flow cytometer
- Refrigerator or cool-box

Sampling and handling

Obtain water samples, this can be freshly collected samples or samples preserved and stored in the freezer. Fresh samples should be stored in a cool box or equivalent container in the dark and cool until analysis. Measurements should be conducted within 4 hours after samples. In the case of preserved samples, samples should be thawed (avoid exposure to light) and measured within 2 hours.

Procedure

1. Mix sample gently prior to taking subsample.
2. A volume of 2.5 – 3.0 mL subsample is pipetted in a clean flow cytometer sample tube of 5 mL (1- 3 replicates). No additions are made to the sample.

Analysis

1. Sample tubes are transferred to manual or carousel of the flow cytometer for analysis.
2. Start up, maintenance and preparatory phase to calibrate the flow cytometer is described in 'Coulter XL basic training manual'.
3. Blank sample is taken prior to the analysis of actual samples (0.2 micron filtered sample).
4. In case of carousel 6 – 12 samples are in the carousel to avoid heating of the sample. This number may vary depending on ambient water temperature of the water samples.
5. Add ND 10 filter in front of FS detector to reduce sensitivity.
6. Analyse sample in the flow cytometer, by manual or through the carousel using test protocol (usually Phyto-10NDX). X may vary for water type or type of treatment.
7. Raw analysis is stored as 3.0 FCM list mode data file and includes setting of flow cytometer parameters for scatter and different fluorescence wavelengths, each sample has unique number (xxxxxxx.lmd).
8. Stored RAW data file is analysed with commercially available software package FCS Express V3 (DeNovo version 3 or higher) using predefined protocol (MEA-Phyto-10ND-vX.fey). Phytoplankton cells are separated from other particles based on scatter and the red fluorescence of the chlorophyll present in the phytoplankton cell (PMT4, > 610 nm emission). The higher limit of the size range of phytoplankton is determined using 10 micron size spherical beads as an internal standard. Phytoplankton numbers of collective phytoplankton community and each subpopulation are collected in spread sheet and converted into absolute counts are correcting for flow rate and sample dilution factors (when appropriate).

Calculation and Report

Absolute number (unit mL) = (counted number of phytoplankton)* f1 = phytoplankton > 10 micron number/mL

f1: (Conversion factor * counted number of phytoplankton) / counting time (seconds)

Conversion factor = number of seconds to analyse 1 mL of sample

Absolute number of phytoplankton in the size range from 2 – 10 micron is average of 1-3 replicates. In addition to the number of phytoplankton cells, the size of cells (in relative units) and auto-fluorescence of the chlorophyll (FL4) and, when present, phycoerythrin (PE) fluorescence (FL2) are measured. PE is a photopigment typically present in cyanobacteria.

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Bulk FDA Viability Assay

Researcher: Nick Welschmeyer

Size classes: $\geq 50 \mu\text{m}$; $10\mu\text{m} > x > 50\mu\text{m}$; $< 10\mu\text{m}$

Summary The bulk FDA viability assay is a cuvette based fluorometric technique that provides quantitative measurements of total living biomass contained in ballast water samples (freshwater, brackish or marine). The method relies on the active conversion of fluorescein diacetate (FDA) to its fluorescent by-product fluorescein, by natural enzyme activity in live cells. The bulk FDA assay responds to all living organisms, whether autotrophic or heterotrophic, and produces low, nearly undetectable signals when cells are dead (Welschmeyer and Maurer, 2011).

Scope and Application Here we describe a technique to measure total living biomass based on enzyme-activated fluorescein production derived from the substrate, FDA (Welschmeyer and Maurer 2011). The method relies on the capture of particulate matter on selective size filters followed by incubation of the particles in a sterile buffer solution that is quantitatively tagged with FDA. The intracellular, live-cell production of FDA-derived fluorescein is diffusively passed to the extracellular fluid in the buffer suspension, and the concentration of fluorescein is determined fluorometrically in standard 1 cm fluorometer cuvettes. The procedure described here is applied to the 10-50 μm size class of ballast water organisms using simple size-fractionation filter capture. The method utilizes syringe-based manipulations for 1) filtration, 2) reagent addition and 3) incubation, thus reducing potential shipboard contamination and providing pipet-free protocol execution. The expected production rate of fluorescein for cell sizes characteristic of the 10-50 μm range is known (see below). Therefore, the nominal concentration of live cells responsible for the measured fluorescein production rate can be calculated. Measurement of ballast water with unknown live cell concentrations can thus be tested for compliance relative to defined, numeric Ballast Water Discharge Standards (BWDS).

Methods

1. Collect sample water by passing the desired volume through a 50 μm sieve, thus removing organisms $> 50 \mu\text{m}$. Nominally, 500 mL is adequate for up to three replicate assays.
2. Filter 100 mL sample water through a 10 μm pore size, 2.5 cm diameter, sealed syringe filter (Pall Life Sciences, Acrodisc Versapor Membrane, 10 μm pore, PN AP-4001T), using a clean 140 mL plastic syringe. Discard filtrate.
3. Remove syringe filter from large sample syringe. Replace with empty, but fully depressed, 5 ml plastic syringe/plunger on top of sealed syringe filter, fasten luer lock connection. Place empty 5 mL FDA syringe barrel (w/ female connector) on bottom of sealed syringe filter, fasten luer lock connection.
4. Invert syringe pair and decant pre-measured volume (2.5 mL) of Reagent A Buffer into empty FDA injection syringe barrel; add one drop FDA Reagent. Cap barrel with syringe plunger gently to seal, preventing pressurized loss of fluid through filter. Mix solutions.

5. Invert syringe pair so that top of sealed filter faces upwards and slowly inject Reagent A+B mixture upward through the bottom of the syringe filter, fully depressing the plunger. Keep this vertical orientation (see Note 2 below).
6. Store syringe pair vertically in a darkened, room temperature environment (cabinet), with fluid on top. Incubate for 1 hour; record ambient temperature. Sealed filter should be facing up.
7. Plunge fluid downward through filter, depressing plunger fully. Invert syringe pair and again plunge fluid downward through filter, depressing plunger fully. This step ensures well-mixed incubation fluid. Syringe-pair will now be upside-down, with FDA syringe on top, receiver syringe on the bottom.
8. Draw the plunger of the bottom receiver syringe down slightly (ca. 0.5 cm) to relieve pressure within syringe. Remove empty top syringe (female connector, FDA syringe) from the sealed syringe filter. Invert remaining syringe and syringe filter and dispense reaction fluid through syringe filter into a clean 1 cm fluorometer cuvet.
9. Add two drops finishing solution to cuvette contents, cap and mix gently (invert 3 times).
10. Measure fluorescence on hand-held calibrated fluorescein fluorometer.

Calculation of equivalent numeric cell concentration

Equation 1 below provides the means to estimate the equivalent numeric concentration of live cells corresponding to the measured fluorescein production rate of any unknown ballast water sample, processed as described above. This assumes the sample was captured by filter size fractionation corresponding to the 10-50 μm size class and was incubated at 20 C. The exponentially-weighted mean cell size of the 10-50 μm plankton size class is calculated to be 15 μm ESD (Welschmeyer and Maurer 2013) based on organism size distribution models for coastal systems, characterized by a Log biomass vs. Log cell volume slope of -0.1 (Vidondo et al. 1997). A cell-specific response factor of 2.86 (μg fluorescein cell⁻¹ h⁻¹) for the 15 μm ESD cell size (at 20 C) was determined empirically from sized-based analysis of several freshwater and marine phytoplankton species; data shown in Fig. 1 (from Welschmeyer and Maurer 2013).

$$\text{Eq. 1. } \frac{\text{live cells}}{\text{ml}} = \frac{\text{sample fluorescein } \frac{\mu\text{g}}{\text{L}} \cdot \text{cuvette volume (mL)}}{\frac{2.86 \mu\text{g fluorescein}}{\text{cell} \cdot \text{hr}} \cdot \text{volume filtered (L)} \cdot \text{incubation time (h)}}$$

Method Detection Limits

0.5 μg fluorescein/L (equivalent to ca. 5 live cells per mL, nominal 15 μm equivalent spherical diameter, assuming 100 mL filtration, 2.5 mL incubation reagent, 1 hour incubation)

List of Abbreviations

BWDS Ballast Water Discharge Standard
 ESD Equivalent Spherical Diameter
 FDA Fluorescein diacetate
 RF Response Factor

Health and Safety

FDA solubilized in DMSO (flammable; 5 mL per stock vial; refrigerated, thus frozen). MSDS posted at <http://biooce.mlml.calstate.edu/home/resources/>

Cautions

Avoid skin contact with DMSO solution.

Interferences

If ballast treatment includes UV inactivation of cells, there may be residual enzyme activity in the treated cells for several days after the last UV exposure, thus yielding residual fluorescein production. Bulk FDA response will be reduced relative to uptake water (control) but may indicate numeric equivalent live cell concentrations higher than actual.

Personnel Qualifications and Responsibilities

Non-technical personnel can execute all aspects of the method, but practice with tap water is recommended for syringe manipulations to avoid leaks and spills and, thus, sample loss.

Special Equipment and Materials

- Turner AquaFluor handheld fluorometer (or equivalent); 480 nm/520 nm, excitation/emission.
- Disposable plastic 1 cm cuvettes; 4 sides clear, standard VIS transparency.
- Sealed syringe filter, 10 μ m pore (Pall Life Sciences, Acrodisc Versapor Membrane, 10 μ m, PN AP-4001T).
- Reagent A (Incubation Buffer), Reagent B (FDA Solution), Reagents are available in trial kits from Moss Landing Marine Laboratories until a distribution network is established.
- 10 μ g/L fluorescein standard in capped 1 cm fluorometer cuvette.

Equipment and Supplies

- Clean sampling bottles, preferably polycarbonate (nominal 500 mL).
- Squeeze bottle of distilled water for rinsing, or equivalent
- 2 – 5 mL clean plastic syringes (male/female) per sample
- 1 – 140 mL (or equivalent) plastic syringe for initial sample filtration.
- 1 – 10 cm x 10 cm 35 μ m (50 μ m on the diagonal) prefilter nylon mesh to remove >50 μ m organisms.
- Plastic waste receptacle for fluids.
- Test tube rack or open container to hold sample syringe-pair vertical during incubation.
- Thermometer (\pm 1 C) for determination of mean incubation temperature.

Quality Control

Calibrate the Turner AquaFluor fluorometer, using the sealed 10 μ g/L fluorescein standard provided (see instrument instructions). Once calibrated, the solid state, fixed-optics fluorometer is not expected to drift, unless physically mishandled (e.g., dropped on steel deck). Warm up time (<5 sec) is factory programmed into the startup procedure when the instrument is turned on. Reagents may be stored at refrigerated temperature for 6 months; up to one year if frozen.

References

- Welschmeyer, N. and B. Maurer. 2011. A portable, sensitive plankton viability assay for IMO shipboard ballast water compliance testing. In: Proceedings of the Global R&D Forum on Compliance Monitoring and Enforcement – Ballast Water Management Systems, Istanbul, Turkey, p117-130, Eds. A. Olgun, F.T. Karokoc and F. Haag.
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- Vidondo, B., Y.T. Prairie, J.M. Blanco and C.M. Duarte. 1997. Some aspects of the analysis of size spectra in aquatic ecology. *Limnol. Oceanogr.* 42:184-192.

SGS ATP (aqua-tools)

Size Class: $\geq 50 \mu\text{m}$; $10\mu\text{m} > x > 50\mu\text{m}$; bacteria

Researcher: Sebastien Peuchet

Description: ATP (adenosine triphosphate) have a long history on determination of bacteria concentration; development of new generation of ATP analysis answer to the necessity to have an on-board system on the ship that is robust, reliable and non-expensive. AQUA-TOOLS, in collaboration with SGS Group (Switzerland) and LuminUltra (Canada), has developed a full, easy and rapid method to ensure that ballast water treatment system are compliant. Ballast Water Treatment Monitoring Kit by ATP 2G can give fast and accurate results in few hours compare to the traditional methods for the different fractions of organisms ($\geq 50\mu\text{m}$, $10\text{-}50\mu\text{m}$ and total bacteria). Aqua-tools Ballast Water kit enable measuring in few minutes the whole living flora in collected samples ($\geq 50\mu\text{m}$; ≥ 10 and $< 50\mu\text{m}$; and bacteria indicators fractions) for a rapid assessment of your ballast water quality. This test kit allows a rapid estimation of all biological contaminant through the quantification of bioluminescent signal coming from the reaction of the LuminaseTM with intracellular Adenosine TriPhosphate (cATP) – the energy carrier of any living cell. This kit dedicated to ballast water analysis is based on second generation of ATP test kit, providing quantitative results without interferences thanks to adapted protocol and calibration solution.

Methods:

Calibration (All size classes)

1. Rehydrate Luminase with the Luminase buffer. Gently mix from time to time.
2. Put 100 μL of Luminase in a luminometer tube.
3. Measure the background noise. If $> 15\text{RLU}$, discard the tube and prepare a new one.
4. After the measure add 2 drop of UltraCheck1 and measure the signal.
5. Subtract the noise value from the signal and record it (RLUuc1).

Protocol ($> 50 \mu\text{m}$):

1. After mixing the AE bottle (200mL), pour 60mL into a graduated 100mL Becher
2. Filter that volume through the $36\mu\text{m}$ mesh handfilter
3. Rinse the 100mL Becher with the “Rinse” water
4. Rinse the handfilter with the “Rinse” water
5. Regroup the organisms in define area and transfer them into a small 10mL Becher using the “Rinse” water
6. Measure the volume of concentrated sample (noted as RV50)
7. Homogenize and take 1mL and transfer it into a grinding tube
8. Add 5mL of Modified UltraLyse30 solution into the grinding tube
9. Switch on the grinder and set it in mode 2, speed 9, for 50 sec (6000rpm; 50sec)
10. Attach the tube and push start
11. When the rotation stops, remove the tube, shake it, re-attached the tube, and push the start button again.

12. When the rotation stops, remove the tube, shake it, re-attached the tube, and push the start button again. (it's not a copy and paste mistake I really do that 2 times)
13. When the rotation stops, remove the tube and let it on the table still for 5min
14. (During this time, clean Becher and filtration equipment, and start filtrating replicate 2)
15. After the incubation time, take 100µL and transfer it into a 5mL UltraLute tube
16. Mix the UltraLute tube and finish the replicate2 and 3 filtration / extraction
17. Take a luminometer tube, put 100µL of Luminase inside and measure the background noise tube (RLUempty ; if >15RLU discard the tube and prepare a new one)
18. After the measure, add 100µL of the UltraLute tube into the same luminometer and measure the signal (RLUcATP50)
19. Ask for the volume of ballast water that has been filtrated through the filtration device and put the value in the table (ZV)

Protocol (10µm>x>50µm):

1. After mixing the BI bottle (350mL), pour 100mL into a graduated 100mL Becher
2. Filter that volume through the 7µm mesh handfilter.
3. Rinse the 100mL Becher with the "Rinse" water
4. Rinse the handfilter with the "Rinse" water
5. Regroup the organisms in define area and transfer them into a small 10mL Becher using the "Rinse" water
6. Measure the volume of concentrated sample (noted as RV10-50)
7. Homogenize and take 1mL and transfer it into a grinding tube
8. Add 5mL of Modified UltraLyse30 solution into the grinding tube
9. Switch on the grinder and set it in mode 2, speed 9, for 50 sec (6000rpm; 50sec)
10. Attach the tube and push start
11. When the rotation stops, remove the tube, shake it, re-attached the tube, and push the start button again.
12. When the rotation stops, remove the tube, shake it, re-attached the tube, and push the start button again. (it's not a copy and paste mistake I really do that 2 times)
13. When the rotation stops, remove the tube and let it on the table still for 5min
14. (During this time, clean Becher and filtration equipment, and start filtrating replicate 2)
15. After the incubation time, take 100µL and transfer it into a 5mL UltraLute tube
16. Mix the UltraLute tube and finish the replicate2 and 3 filtration / extraction
17. Take a luminometer tube, put 100µL of Luminase inside and measure the background noise tube (RLUempty ; if >15RLU discard the tube and prepare a new one)
18. After the measure, add 100µL of the UltraLute tube into the same luminometer and measure the signal (RLUcATP10-50)
19. Ask for the volume of ballast water that has been filtrated through the filtration device and put the value in the table (PV)

Blank measurement (>50 and 10-50µm)

1. Homogenize the "Rinse" water take 1mL and transfer it into a grinding tube
2. Add 5mL of Modified UltraLyse30 solution into the grinding tube
3. Switch on the grinder and set it in mode 2, speed 9, for 50 sec (6000rpm; 50sec)

4. Attach the tube and push start
5. When the rotation stops, remove the tube, shake it, re-attached the tube, and push the start button again.
6. When the rotation stops, remove the tube, shake it, re-attached the tube, and push the start button again. (it's not a copy and paste mistake I really do that 2 times)
7. When the rotation stops, remove the tube and let it on the table still for 5min
8. (During this time, clean Becher and filtration equipment, and start filtrating replicate 2)
9. After the incubation time, take 100 μ L and transfer it into a 5mL UltraLute tube
10. Mix the UltraLute tube
11. Take a luminometer tube, put 100 μ L of Luminase inside and measure the background noise tube (RLUempty ; if >15RLU discard the tube and prepare a new one)
12. After the measure, add 100 μ L of the UltraLute tube into the same luminometer and measure the signal (RLUartesa)

Protocol (Bacteria)

1. Take a 60mL syringe, remove it from the packaging, discard the paper part and use the plastic part to lay the disassembled syringe (plunger and barrel)
2. Attach the 2.7 μ m disc filter to the barrel, attach the 0,7 μ m disc filter to the other disc
3. Pour 50mL of DH sample into the barrel, add the plunger and filter ONLY the liquid, not the air
4. Remove the two filters, remove the plunger, reattach the filters, pour 50mL of DH sample add the plunger and filter ONLY the liquid, not the air.
5. Remove the filters, remove the plunger, discard the 2.7 μ m disc filter, reattach the 0,7 μ m filter directly to the barrel.
6. Open a 9mL UltraLute tube and put the syringe on the top
7. Take 1mL of UltraLyse7 solution and transfer it into the barrel, add the plunger and filter the entire content of the barrel (liquid and air)
8. Mix the UltraLute tube to dilute the ATP extract correctly
9. Take a luminometer tube, put 100 μ L of Luminase inside and measure the background noise tube (RLUempty ; if >15RLU discard the tube and prepare a new one)
10. After the measure, add 100 μ L of the UltraLute tube into the same luminometer and measure the signal (RLUcATPbact)

Welschmeyer ATP

Size Class: $\geq 50 \mu\text{m}$; $10\mu\text{m} > x > 50\mu\text{m}$; bacteria

Researcher: Nick Welschmeyer

No methods have been provided.

Triton BW BacTest EC

Size Class: Bacteria

Researcher: Lothar Schillak, Triton Marine Science&Consult, Germany

Description: The Triton BW Bac Test EC was especially designed for the analysis of the concentration of *Escherichia coli* in ballast water. The basic method is derived from the Polymerase Chain Reaction-PCR method. Similar to the PCR, primers with their codons, especially developed for this test, detect a predefined group of genes within the genome of *Escherichia coli*. When the primer binds to this group of genes it induces the multiplication of the RNA and with integrated fluorescein the multiplication gives a signal in a fluorometer. However, different to the PCR the reaction is held on an isothermal level.

The development of the multiplication follows the enzymatic kinetics of a sigmoid curve, in which the inflection point, for the Triton BW Bac Test EC set to 5.000 fluorescence units (F), is defined as “positive”. Since the multiplication develops exponentially, the inflection point 5 kF is trespassed the earlier the higher the concentration of *Escherichia coli* is in the sample.

The fluorometer software is adapted to the Triton BW Bac Test EC and data can be transferred and stored in a laptop using an respective laptop Triton BW Bac Test EC software.

Materials: (to perform analysis of 1 ballast water sample in triplicate)

- Water, sterile filtered 0.2 µm, approximately 200mL
- Buffer tube (available from *Triton Marine Science and Consult*)
- Lyophilisate teststrips (8 wells; available from *Triton Marine Science and Consult*)
- Triton fluorometer with Triton Data Processing Software (available from *Triton Marine Science and Consult*)
- Heating block for tubes
- Laptop
- 2 plankton filters (35µm mesh and 7µm mesh)
- 3 beakers (600ml, 500ml, 250ml)
- 2 syringes, luer-lock (140ml and 60ml)
- Fibre glass syringe luer-lock filter, 1-2µm nominal mesh, Ø 23mm (*winlab* no. 101265251)
- Syringe filter holder, Ø 13mm (*Sartorius stedim biotech* no. 80238-004-50)
- Cellulose nitrate membrane filter, 0,45 pore size Ø 13mm (*Sartorius stedim biotech* no. 11306—13-----N)
- Vario pipette (Eppendorf „research plus“, 10-100µl)
- Pipette tips, 100µl (*StarLab* no. S1120-1840)
- Tube rack for tubes
- Tweezers

Methods:

1. Place cellulose nitrate filters into syringe filter holders
2. Filter 600ml of ballast water sample through a 35µm mesh filter
3. Filter filtrate from step 2 through a 7µm mesh filter

4. Take 140ml of filtrate from step 3 into syringe 140ml, attach fibre glass filter to syringe and filter into a beaker 250ml, discard filter
5. Take 100ml of filtrate from step 4 into syringe 140ml, attach syringe filter holder and filter 100ml through the cellulose nitrate membrane filter inside the filter holder, detach filter holder
6. Take 20ml water sterile filtered 0,2µm into syringe 60ml, attach filterholder from step 5 to syringe 60ml, push the 20ml water through the cellulose nitrate membrane filter inside the filter holder, detach filter holder
7. Open filter holder and carefully take out the cellulose nitrate membrane filter from inside the filter holder with tweezers, place it into a buffer tube, gently destroy the filter inside the buffer tube
8. Repeat step 4 to step 7 for triplicates 2 and 3. The triplicate buffer tubes 1,2 and 3 are stable for several days (store at 4°C)
9. Set-up analysis programme in the fluorometer as instructed on the fluorometer screen
10. Place triplicate buffer tubes 1,2 and 3 into heating block, incubate 2 minutes at 99°C. Let tubes return to ambient room temperature
11. Take 25µl from each buffer tube 1,2 and 3 into wells nos. 1, 2 and 3 of a test strip
12. Take 25µl from buffer tube no. 3 into well number 4 (control) of the test strip, make sure all wells are closed
13. Place test strip into the pre-set slot of the fluorometer and start analysis
14. The sigmoid curves of wells 1, 2, 3 and 4 are shown on the screen of the fluorometer until completion of the analysis
15. The analysis is followed by an annealing and multiplication rate control
16. After termination of the analysis, transfer the respective analysis file to the laptop, start data programme and transfer readings of sigmoid curves into cfu/100ml as instructed by the programme.

Figure 1: BW Bactest EC: fluorometer with two slots for test strips

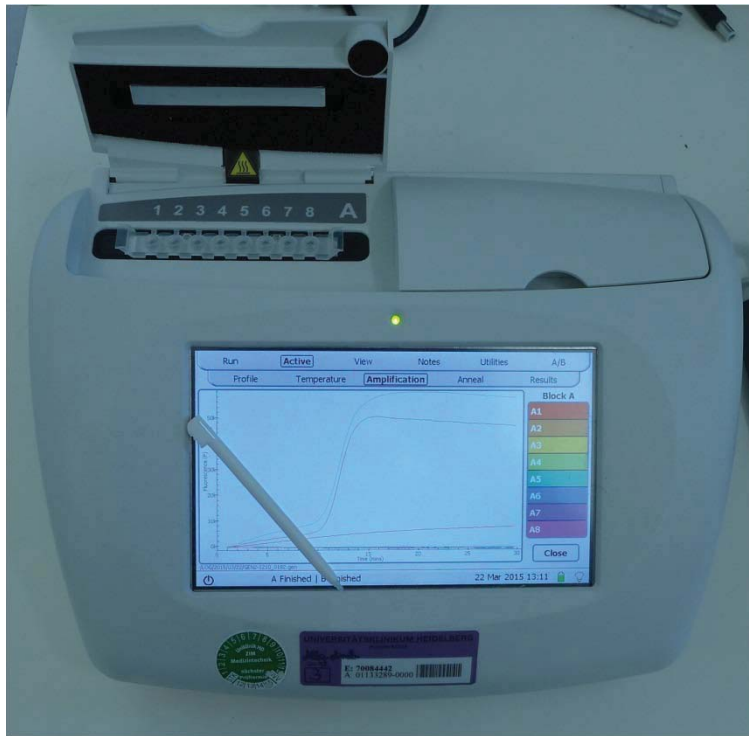
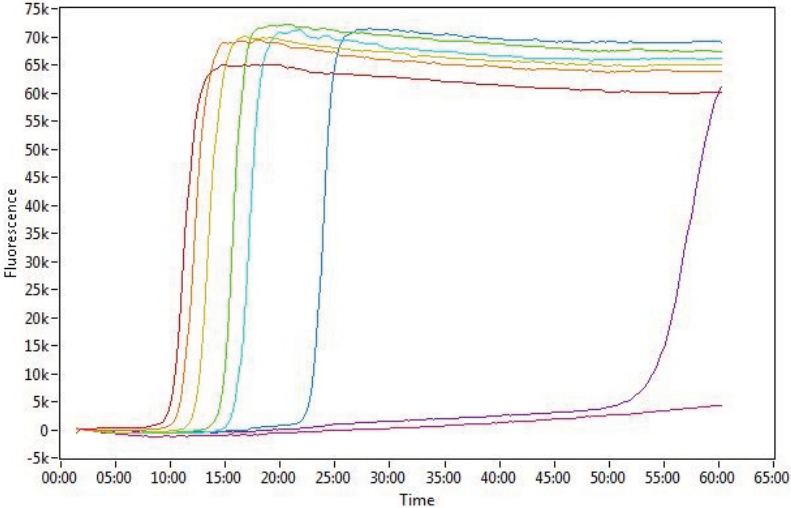


Figure 2: BW Bactest EC: test strip



Figure 3: BW Bactest EC: typical graphs for determination of final value



Bacteria quantification by flow cytometry after staining nuclear DNA

Size Class: Bacteria

Researcher: Marcel Veldhuis

The cellular DNA content of the phytoplankton community was analyzed with the green nuclear stain PicoGreen (MP, P-7581) according to the method described by Veldhuis et al. (1997, J. Phycol. 33, 527-541) on a flow cytometer (COULTER-Elite-ESP, 75mW laser power, 488 nm excitation wavelength). The method used differed in that RNase and Triton X100 were not added prior to analysis. Although it increased the peak width of the DNA signal slightly the chlorophyll signal could be better separated from the DNA signal. Flow cytometer counts for bacteria were calculated by using the size and presence/absence of chlorophyll to distinguish bacteria from phytoplankton.

Speedy Breedy – By Bactest

Size Class: Bacteria

Researcher: Derek Price

Description: Speedy Breedy is a portable, sensitive, precision respirometer which detects and monitors microbial activity. Detection of microbial activity is determined as a consequence of pressure transients relating to gaseous exchanges within a closed culture vessel of 50 ml working volume, as a result of microbial respiration. Samples are added to a culture vessel containing a suitable nutrient medium and where present, contaminating microorganisms begin to grow. Speedy Breedy has advanced mixing technology that homogenises the culture conditions for rapid growth of microbes and efficiently converts gaseous changes in the culture medium into pressure variances in the headspace, therefore allowing detection of pressure transients due to metabolic processes where microbes are present. Time to detection is indicative of the degree of contamination in the sample.


Methods: Testing for E. coli or Enterococcus in potable or marine ballast water.


It is recommended to wear latex gloves while processing samples, cleaning them before and after the procedure with medical wipes or 70% ethanol in water.

1. Filter sterilise 45 ml of milli Q water (using a 0.2 um syringe filter) directly into a new sterile Speedy Breedy culture vessel.
For E. coli tests use vessels pre-filled with MacConkey Broth capsules.
For Enterococcus tests use vessels pre-filled with M-Enterococcus Broth capsules.
2. Using a sterile 5 ml syringe, remove 5 ml of sample from its container.
3. Using aseptic technique and touching only the outer rim, remove the filling cap from the culture vessel by rotating it anticlockwise and fill the vessel with the 5 ml sample.
4. Replace the cap and make sure it is firmly located by turning it clockwise to engage it. A small arrow on the top of the vessel indicates the correct closed position.
5. Note: an alternative method is to dilute the sample 1 in 10 in a large sterile container and add 50 ml of this diluted sample to the Speed Breedy vessel.
6. Ensure that the Speedy Breedy instrument is plugged in and press the “on” button (first button on the central display).
7. When you first switch on your Speedy Breedy in test mode, you will see the message “Speedy Breedy Booting” followed by “Speedy Breedy by Bactest” and finally “MAIN MENU: Setup Test” appear on the display.

To start a test:

1. To begin a test using Speedy Breedy, select “Set up test” from the Main Menu using the arrow buttons, and confirm by pressing the Select (⏏) button.
2. You will then be prompted to SELECT PROTOCOL. Scroll through Protocols present on the device’s SD card by pressing the arrow keys and then confirm the Protocol you would like to use for your test by pressing the Select (⏏) button.
3. Once a test Protocol is selected, Speedy Breedy prompts the user to select which chamber(s) you wish to conduct a test in. Test Protocols typically allow the user to

select one or both of the test chambers. To select which chamber you wish to use, cycle through options using the arrow buttons, and confirm using the Select () button

4. Once you have chosen the chamber(s) you wish to run a test in, Speedy Breedy prompts you to BEGIN TEST. It is at this point that Speedy Breedy Culture Vessels should be introduced into the test chamber(s). Speedy Breedy will not allow a test to begin without a vessel present in the chamber(s) and without the lid closed.
5. Once you have introduced the Culture Vessel and closed the lid, press the Select () button to begin your test.
6. Speedy Breedy will indicate contamination by a change of colour of the flashing LED on the central display from green to red. If no red LED is seen and the protocol completes its time course, the sample is not contaminated.
7. If a PC or lap top is connected via USB to Speedy Breedy, results can be visualised as pressure curves. The time to detection is found by placing the cursor over the (red) detection line on the graph. If the protocol is linked to a calibration curve (some supplied) then the degree of contamination in the original sample is also indicated.

SimPlate* for HPC

Unit Dose

English

Introduction

SimPlate* for HPC method is used for the quantification of heterotrophic plate counts (HPC) in water. It is based on IDEXX's patented Multiple Enzyme Technology*, which detects viable bacteria in water by testing for the presence of key enzymes known to be present in these organisms. It uses multiple enzyme substrates that produce a blue fluorescence when metabolized by waterborne bacteria. The sample and media are added to a SimPlate, incubated, and then examined for fluorescing wells. The number of fluorescing wells corresponds to a Most Probable Number (MPN) of total bacteria in the original sample. The MPN values generated by the SimPlate for HPC method correlate with the Pour Plate method using Total Plate Count Agar incubated at 35°C for 48 hours as described in *Standard Methods for the Examination of Water and Wastewater*¹.

Contents

- 25 sterile media tubes for 10 mL samples
- 25 sterile SimPlate plates with lids
- MPN table
- This insert

Storage

Store at 2–30°C and away from light. Expiration date is printed on the box of media tubes.

Test Procedure

1. Add 10±0.2 mL of sample to a media tube, re-cap and shake to dissolve. See image #1.
2. Pour the contents of the tube onto the center of the plate base. See image #2.
3. Cover the plate with the lid and gently swirl to distribute the sample into all the wells. See image #3.
NOTE: Air bubbles in the wells do not interfere with the test.
4. Tip the plate 90–120° to drain excess sample into the absorbent pad. See image #4.
5. Invert the plate and incubate for 48 hours at 35±0.5°C. See image #5.
6. Count the number of wells showing any fluorescence by holding a 6-watt, 365-nm UV light 5 inches above the plate. Direct light away from your eyes and towards the sample. Alternatively, you may read fluorescent wells through the back of the inverted SimPlate base.
7. Refer to the MPN table provided to determine the Most Probable Number of heterotrophic plate count bacteria in the original sample. The table takes into account the sample/media poured off in step #4 above.

Procedural Notes

1. Follow aseptic technique.
2. Chlorinated samples should be treated with sodium thiosulfate prior to testing.
3. Results can be read from 45 to 72 hours after start of incubation.
4. Dispose of sample and media in accordance with Good Laboratory Practices.
5. Samples may be diluted before adding to the media as long as the final volume (sample plus sterile diluent) is 10±0.2 mL. Adjust the MPN result to reflect dilutions. For example, if 1 mL of sample and 9 mL of sterile diluent are tested (a 10-fold dilution), multiply the MPN table number by 10 to find the correct MPN/mL.

Quality Control Procedure

The following procedure is recommended for each lot of SimPlate for HPC product:

1. A. Positive Control: IDEXX-QC HPC/TVC²: *Enterococcus faecalis*.
B. Negative Control/Blank: Use 10 mL of rehydrated HPC media.
2. Follow steps 1–7.
3. Negative Control/Blank wells should not fluoresce after incubation.

For technical support, please call:

North/South America: +1 207 556 4496 or +1 800 321 0207

Europe: +00800 4339 9111

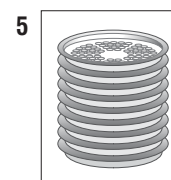
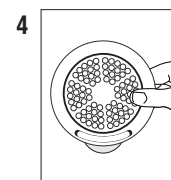
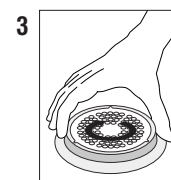
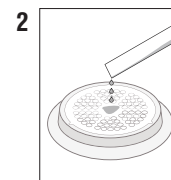
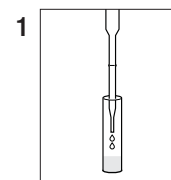
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idexx.com/water



¹ Eaton, AD, Clesceri, LS, Greenberg, AE, Rice, EN. *Standard Methods for the Examination of Water and Wastewater*. American Public Health Association, 2005. Washington, DC.

² IDEXX-QC HPC/TVC, IDEXX Catalog #UN3373-WQC-HPC.

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Patent information: idexx.com/patents.

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IDEXX

One IDEXX Drive
Westbrook, Maine 04092 USA

**Unit Dose
SimPlate For HPC
Most Probable Number (MPN) Table**

# Positive Wells	MPN	95% confidence limits	
		lower	upper
0	<0.2	<0.03	<1.4
1	0.2	0.0	1.4
2	0.4	0.1	1.6
3	0.6	0.2	1.9
4	0.8	0.3	2.2
5	1.0	0.4	2.5
6	1.2	0.6	2.7
7	1.5	0.7	3.0
8	1.7	0.8	3.3
9	1.9	1.0	3.6
10	2.1	1.1	3.9
11	2.3	1.3	4.2
12	2.6	1.5	4.5
13	2.8	1.6	4.8
14	3.0	1.8	5.1
15	3.3	2.0	5.4
16	3.5	2.2	5.8
17	3.8	2.3	6.1
18	4.0	2.5	6.4
19	4.3	2.7	6.7
20	4.5	2.9	7.0
21	4.8	3.1	7.4
22	5.1	3.3	7.7
23	5.3	3.5	8.0
24	5.6	3.8	8.4
25	5.9	4.0	8.7
26	6.2	4.2	9.1
27	6.5	4.4	9.4
28	6.8	4.7	9.8
29	7.1	4.9	10.2
30	7.4	5.1	10.6
31	7.7	5.4	10.9
32	8.0	5.6	11.3
33	8.3	5.9	11.7
34	8.6	6.2	12.1
35	9.0	6.4	12.6
36	9.3	6.7	13.0
37	9.7	7.0	13.4
38	10.0	7.3	13.9
39	10.4	7.6	14.3
40	10.8	7.9	14.8
41	11.2	8.2	15.2
42	11.6	8.5	15.7

# Positive Wells	MPN	95% confidence limits	
		lower	upper
43	12.0	8.8	16.2
44	12.4	9.1	16.7
45	12.8	9.5	17.3
46	13.2	9.8	17.8
47	13.7	10.2	18.3
48	14.1	10.6	18.9
49	14.6	10.9	19.5
50	15.1	11.3	20.1
51	15.6	11.7	20.7
52	16.1	12.1	21.3
53	16.6	12.5	22.0
54	17.1	13.0	22.7
55	17.7	13.4	23.4
56	18.3	13.9	24.1
57	18.9	14.4	24.9
58	19.5	14.9	25.7
59	20.2	15.4	26.5
60	20.9	15.9	27.3
61	21.6	16.5	28.2
62	22.3	17.1	29.2
63	23.1	17.7	30.2
64	23.9	18.3	31.2
65	24.8	19.0	32.3
66	25.7	19.7	33.5
67	26.6	20.4	34.7
68	27.6	21.2	36.1
69	28.7	22.0	37.5
70	29.9	22.9	39.0
71	31.1	23.8	40.7
72	32.4	24.8	42.5
73	33.9	25.8	44.4
74	35.5	27.0	46.6
75	37.2	28.2	49.1
76	39.2	29.6	51.9
77	41.4	31.1	55.1
78	44.0	32.8	58.9
79	47.0	34.8	63.6
80	50.7	37.1	69.5
81	55.5	39.8	77.5
82	62.3	43.2	89.9
83	73.8	47.6	114.6
84	>73.8	>47.6	>114.6

MPN is per mL of the 10 mL sample added to the media tube (pour-off is accounted for).

SimPlate* for HPC

Méthode SimPlate* pour HPC • Dose Unitaire

Française

Introduction

La méthode SimPlate* pour HPC est utilisée pour la quantification de la flore totale revivable dans l'eau ("heterotrophic plate counts" ou HPC). Ce test repose sur la technologie multienzymatique (Multiple Enzyme Technology*) d'IDEXX breveté qui détecte les bactéries viables dans l'eau en recherchant les enzymes clés, connues pour être présentes dans ces microorganismes. Cette méthode utilise plusieurs substrats enzymatiques produisant une fluorescence bleue lorsqu'ils sont métabolisés par les bactéries présentes dans l'eau. L'échantillon et le milieu nutritif sont déposés sur la plaque SimPlate. L'ensemble est incubé puis examiné sous UV pour compter les puits fluorescents. Le nombre de puits fluorescents correspond au nombre le plus probable ("Most Probable Number" ou MPN) de bactéries totales présentes dans l'échantillon original. Les valeurs NPP générées par la méthode SimPlate pour HPC sont conformes à la méthode en boîte de Pétri utilisant une numération totale sur plaque en milieu gélosé à une incubation de 35°C pendant 48 heures, tel que décrit dans *Standard Methods for the Examination of Water and Wastewater*¹ (Méthodes traditionnelles pour l'analyse de l'eau et des eaux usées).

Contenu

- 25 tubes de milieu stériles pour échantillons de 10 ml
- 25 plaques SimPlate stériles avec couvercles
- Tableau des valeurs NPP
- Cette notice

Conservation

Conserver entre 2–30°C, à l'abri de la lumière. La date de péremption est imprimée sur la boîte.

Procédure de test

1. Ajouter 10±0,2 ml d'échantillon dans un tube de milieu nutritif, remettre le bouchon puis agiter pour mélanger. Voici l'illustration n° 1.
 2. Verser le contenu du tube au centre de la plaque. Voici l'illustration n° 2.
 3. Recouvrir la plaque avec le couvercle puis répartir l'échantillon dans tous les puits en effectuant un mouvement circulaire à la plaque. Voici l'illustration n° 3.
- REMARQUE:** Les bulles d'air présentes dans les puits n'interfèrent pas avec le test.
4. Incliner la plaque à 90–120° pour verser l'excès de liquide dans le tampon absorbant. Voici l'illustration n° 4.
 5. Retourner la plaque et laisser incubé pendant 48 heures à 35±0,5°C. Voici l'illustration n° 5.
 6. Compter le nombre de puits présentant une fluorescence en tenant une lampe à UV (6 W, 365 nm) à 12,5 cm au-dessus de la plaque. Diriger la lampe vers l'échantillon et non vers les yeux. Egalement, vous pouvez lire des puits fluorescents quand vous inversez le SimPlate.
 7. Consulter le tableau des valeurs NPP fourni pour déterminer le nombre le plus probable de bactéries présentes dans l'échantillon original. Le tableau tient compte de l'échantillon/du milieu éliminé à l'étape 4 ci-dessus.

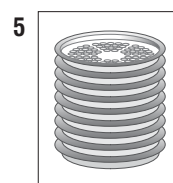
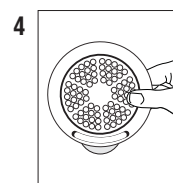
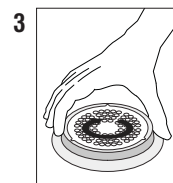
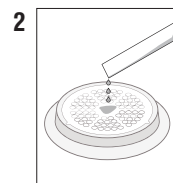
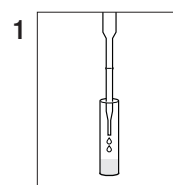
Notes concernant la procédure de test

1. Respecter une technique aseptique.
2. Les échantillons chlorés doivent être traités au thiosulfate de sodium avant le test.
3. Les résultats doivent être lus entre 45 et 72 heures après le début de l'incubation.
4. Éliminer l'échantillon et le milieu conformément aux Bonnes Pratiques de Laboratoire.
5. Les échantillons peuvent être dilués avant leur addition au milieu tant que le volume final (échantillon plus diluant stérile) est de 10±0,2 ml. Ajuster le résultat NPP pour tenir compte des dilutions. Par exemple, si 1 ml d'échantillon et 9 ml de diluant stérile sont testés (dilution de 1:10), il faut multiplier par 10 la valeur donnée dans le tableau des valeurs NPP pour obtenir le NPP/ml correct.

Contrôle de qualité

La procédure suivante est recommandée pour chaque lot de produit Simplate pour HPC:

1. A. Contrôle positif: IDEXX-QC HPC²: *Enterococcus faecalis*.
B. Contrôle négatif/à blanc: utiliser 10 ml de milieu HPC réhydraté.
2. Suivre les étapes 1 à 7.
3. Les puits de contrôle négatif/blanc ne doivent pas être fluorescents après l'incubation.



Pour obtenir l'assistance technique, veuillez appeler :

Europe: +00800 4339 9111

idexx.fr/eau

¹ Eaton, AD, Clesceri, LS, Greenberg, AE, Rice, EN. *Standard Methods for the Examination of Water and Wastewater* (Méthodes traditionnelles d'analyses de l'eau et des eaux usées), American Public Health Association, 2005, Washington, DC.

² HPC/TVC d'IDEXX-QC, IDEXX Catalogue n° UN3373-WQC-HPC.

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IDEXX

One IDEXX Drive
Westbrook, Maine 04092 USA

**Dose Unitaire
SimPlate pour HPC
Tableau des valeurs MPN**

# Puits Positifs	MPN	Limites de confiance à 95%	
		minimum	maximum
0	<0,2	<0,03	<1,4
1	0,2	0,0	1,4
2	0,4	0,1	1,6
3	0,6	0,2	1,9
4	0,8	0,3	2,2
5	1,0	0,4	2,5
6	1,2	0,6	2,7
7	1,5	0,7	3,0
8	1,7	0,8	3,3
9	1,9	1,0	3,6
10	2,1	1,1	3,9
11	2,3	1,3	4,2
12	2,6	1,5	4,5
13	2,8	1,6	4,8
14	3,0	1,8	5,1
15	3,3	2,0	5,4
16	3,5	2,2	5,8
17	3,8	2,3	6,1
18	4,0	2,5	6,4
19	4,3	2,7	6,7
20	4,5	2,9	7,0
21	4,8	3,1	7,4
22	5,1	3,3	7,7
23	5,3	3,5	8,0
24	5,6	3,8	8,4
25	5,9	4,0	8,7
26	6,2	4,2	9,1
27	6,5	4,4	9,4
28	6,8	4,7	9,8
29	7,1	4,9	10,2
30	7,4	5,1	10,6
31	7,7	5,4	10,9
32	8,0	5,6	11,3
33	8,3	5,9	11,7
34	8,6	6,2	12,1
35	9,0	6,4	12,6
36	9,3	6,7	13,0
37	9,7	7,0	13,4
38	10,0	7,3	13,9
39	10,4	7,6	14,3
40	10,8	7,9	14,8
41	11,2	8,2	15,2
42	11,6	8,5	15,7

# Puits Positifs	MPN	Limites de confiance à 95%	
		minimum	maximum
43	12,0	8,8	16,2
44	12,4	9,1	16,7
45	12,8	9,5	17,3
46	13,2	9,8	17,8
47	13,7	10,2	18,3
48	14,1	10,6	18,9
49	14,6	10,9	19,5
50	15,1	11,3	20,1
51	15,6	11,7	20,7
52	16,1	12,1	21,3
53	16,6	12,5	22,0
54	17,1	13,0	22,7
55	17,7	13,4	23,4
56	18,3	13,9	24,1
57	18,9	14,4	24,9
58	19,5	14,9	25,7
59	20,2	15,4	26,5
60	20,9	15,9	27,3
61	21,6	16,5	28,2
62	22,3	17,1	29,2
63	23,1	17,7	30,2
64	23,9	18,3	31,2
65	24,8	19,0	32,3
66	25,7	19,7	33,5
67	26,6	20,4	34,7
68	27,6	21,2	36,1
69	28,7	22,0	37,5
70	29,9	22,9	39,0
71	31,1	23,8	40,7
72	32,4	24,8	42,5
73	33,9	25,8	44,4
74	35,5	27,0	46,6
75	37,2	28,2	49,1
76	39,2	29,6	51,9
77	41,4	31,1	55,1
78	44,0	32,8	58,9
79	47,0	34,8	63,6
80	50,7	37,1	69,5
81	55,5	39,8	77,5
82	62,3	43,2	89,9
83	73,8	47,6	114,6
84	>73,8	>47,6	>114,6

Le résultat final est exprimé en NPP/ ml (résultat final qui tient compte des 10ml analysés et du volume d'échantillon absorbé).

SimPlate* for HPC

Metodo SimPlate* per HPC • Dosaggio Unitario

Italiano

Introduzione

Metodo SimPlate* per HPC è utilizzato per la quantificazione HPC (conte in piastra di batteri eterotrofi) nell'acqua. Si basa su una tecnologia IDEXX (Multiple Enzyme Technology*) brevettata, che rileva i batteri vitali nell'acqua testando la presenza di enzimi chiave la cui presenza in questi organismi è certa. Utilizza substrati enzimatici multipli che sviluppano una fluorescenza blu allorché metabolizzati dai batteri contenuti nell'acqua. Il campione e il terreno vengono posti in una piastra SimPlate, incubati e quindi esaminati alla ricerca di pozzetti fluorescenti. Il numero di pozzetti SimPlate fluorescenti corrisponde all'MPN (Most Probable Number, numero più probabile) di batteri totali nel campione originario. I valori MPN generati mediante il metodo SimPlate per HPC sono correlati con il metodo Pour Plate utilizzando Total Plate Count Agar incubato a 35°C per 48 ore, come illustrato in *Standard Methods for the Examination of Water and Wastewater [Metodi standard per l'esame dell'acqua e delle acque di scarico]*¹.

Contenuto

- 25 provette di terreno sterile per campioni di 10 ml
- 25 piastre SimPlate con relativo coperchio
- Tabella MPN
- Il presente foglietto illustrativo

Conservazione

Conservare a 2–30°C, al riparo dalla luce. La data di scadenza è stampata sulla scatola.

Procedura del test

1. Versare 10±0,2 ml di campione in una provetta di terreno, ritappare e agitare per sciogliere. Vedere la Figura 1.
2. Versare il contenuto della provetta al centro della base della piastra. Vedere la Figura 2.
3. Chiudere la piastra con il coperchio e agitarla delicatamente per distribuire il campione in tutti i pozzetti. Vedere la Figura 3.
NOTA: le bolle d'aria eventualmente presenti nei pozzetti non interferiscono con il test.
4. Eliminare l'eccesso dei campioni inclinando la piastra con un angolo di 90–120° sulla spugnetta. Vedere la Figura 4.
5. Capovolgere la piastra e incubare per 48 ore a 35±0,5°C. Vedere la Figura 5.
6. Contare il numero di pozzetti che presentano fluorescenza tenendo una lampada UV da 6-watt, 365 nm, 12,5 cm al di sopra della piastra. Rivolgere la lampada verso il campione, non verso gli occhi. Diversamente, si può effettuare la lettura della fluorescenza attraverso il retro della base del SimPlate.
7. Consultare la tabella MPN allegata alla confezione per determinare l'MNP delle conte in piastra di batteri eterotrofi nel campione originario. La tabella tiene conto del campione/terreno versato al punto 4 della presente procedura.

Note procedurali

1. Adottare una tecnica asettica.
2. Prima del test, trattare con tiosolfato di sodio i campioni clorati.
3. E' possibile leggere i risultati nell'arco di tempo da 45 a 72 ore dall'inizio dell'incubazione.
4. Smettere il campione e il terreno in conformità alle procedure standard di laboratorio.
5. E' possibile diluire i campioni prima di aggiungerli al terreno fino ad ottenere un volume finale (campione più diluente sterile) di 10±0,2 ml. Regolare l'MNP in modo da riflettere le diluizioni. Per esempio, in caso di test condotto su 1 ml di campione e 9 ml di diluente sterile (una diluizione di dieci volte), moltiplicare il numero riportato nella tabella MPN per 10 per trovare l'MPN/ml corretto.

Procedura di controllo di qualità

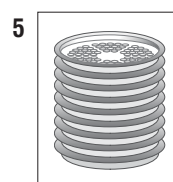
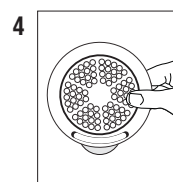
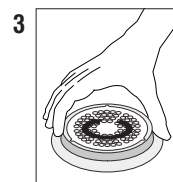
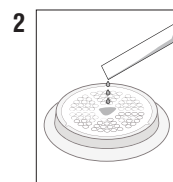
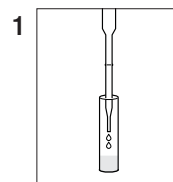
Per ciascun lotto di SimPlate per il prodotto HPC è raccomandata una delle seguenti procedure:

1. A. Controllo positivo: HPC IDEXX-QC: *Enterococcus faecalis*.
B. Controllo negativo/in bianco: usare 10 ml di terreno colturale HPC reidratato.
2. Seguire i passaggi da 1 a 7.
3. I pozzetti per il controllo negativo/in bianco non dovrebbero diventare fluorescenti dopo l'incubazione.

Per ricevere assistenza tecnica contattare:

Europa: +3902 31920351

idexx.it/acqua



¹ Eaton, AD, Clesceri, LS, Greenberg, AE, Rice, EN. *Standard Methods for the Examination of Water and Wastewater*. American Public Health Association, 2005. Washington, DC.

² HPC/TVC IDEXX-QC, Catalogo IDEXX N. UN3373-WQC-HPC.

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IDEXX

One IDEXX Drive
Westbrook, Maine 04092 USA

**Dosaggio Unitario
SimPlate per HPC
Tabella MPN**

# Pozzetti positivi	MPN	Limiti fiduciali del 95%	
		inferiore	superiore
0	<0,2	<0,03	<1,4
1	0,2	0,0	1,4
2	0,4	0,1	1,6
3	0,6	0,2	1,9
4	0,8	0,3	2,2
5	1,0	0,4	2,5
6	1,2	0,6	2,7
7	1,5	0,7	3,0
8	1,7	0,8	3,3
9	1,9	1,0	3,6
10	2,1	1,1	3,9
11	2,3	1,3	4,2
12	2,6	1,5	4,5
13	2,8	1,6	4,8
14	3,0	1,8	5,1
15	3,3	2,0	5,4
16	3,5	2,2	5,8
17	3,8	2,3	6,1
18	4,0	2,5	6,4
19	4,3	2,7	6,7
20	4,5	2,9	7,0
21	4,8	3,1	7,4
22	5,1	3,3	7,7
23	5,3	3,5	8,0
24	5,6	3,8	8,4
25	5,9	4,0	8,7
26	6,2	4,2	9,1
27	6,5	4,4	9,4
28	6,8	4,7	9,8
29	7,1	4,9	10,2
30	7,4	5,1	10,6
31	7,7	5,4	10,9
32	8,0	5,6	11,3
33	8,3	5,9	11,7
34	8,6	6,2	12,1
35	9,0	6,4	12,6
36	9,3	6,7	13,0
37	9,7	7,0	13,4
38	10,0	7,3	13,9
39	10,4	7,6	14,3
40	10,8	7,9	14,8
41	11,2	8,2	15,2
42	11,6	8,5	15,7

# Pozzetti positivi	MPN	Limiti fiduciali del 95%	
		inferiore	superiore
43	12,0	8,8	16,2
44	12,4	9,1	16,7
45	12,8	9,5	17,3
46	13,2	9,8	17,8
47	13,7	10,2	18,3
48	14,1	10,6	18,9
49	14,6	10,9	19,5
50	15,1	11,3	20,1
51	15,6	11,7	20,7
52	16,1	12,1	21,3
53	16,6	12,5	22,0
54	17,1	13,0	22,7
55	17,7	13,4	23,4
56	18,3	13,9	24,1
57	18,9	14,4	24,9
58	19,5	14,9	25,7
59	20,2	15,4	26,5
60	20,9	15,9	27,3
61	21,6	16,5	28,2
62	22,3	17,1	29,2
63	23,1	17,7	30,2
64	23,9	18,3	31,2
65	24,8	19,0	32,3
66	25,7	19,7	33,5
67	26,6	20,4	34,7
68	27,6	21,2	36,1
69	28,7	22,0	37,5
70	29,9	22,9	39,0
71	31,1	23,8	40,7
72	32,4	24,8	42,5
73	33,9	25,8	44,4
74	35,5	27,0	46,6
75	37,2	28,2	49,1
76	39,2	29,6	51,9
77	41,4	31,1	55,1
78	44,0	32,8	58,9
79	47,0	34,8	63,6
80	50,7	37,1	69,5
81	55,5	39,8	77,5
82	62,3	43,2	89,9
83	73,8	47,6	114,6
84	>73,8	>47,6	>114,6

Il Numero Più Probabile é riferito ad 1 ml dei 10 ml di campione aggiunto alla fiala di reagente (tenendo in acconto l'eccesso).

SimPlate* for HPC

Método SimPlate* para RPH • Dosis Unitaria

Español

Introducción

El método SimPlate* para RPH se usa para la cuantificación de recuentos de plaquetas heterotróficas (RPH) en agua. Se basa en la tecnología de enzimas múltiples de IDEXX patentado (Multiple Enzyme Technology*), que detecta bacterias viables en el agua comprobando la presencia de enzimas clave que se sabe existen en esos organismos. Se vale de sustratos de enzimas múltiples que producen una fluorescencia azul al ser metabolizados por la bacteria que se encuentra en el agua. La muestra y el medio se añaden a una placa SimPlate, se incuban y luego se examinan para determinar la presencia de pocillos fluorescentes. El número de pocillos fluorescentes corresponde al Número Más Probable (NMP) de bacteria total en la muestra original. Los valores del MPN generados por la SimPlate para el método de recuento de heterótrofos en placa (Heterotrophic Plate Count, HPC) coinciden con el método de vertido en placa utilizando agar para el recuento total en placa incubado a 35 °C durante 48 horas según se describe en la publicación *Standard Methods for the Examination of Water and Wastewater*¹.

Contenido

- 25 probetas de medio, esterilizadas, para muestras de 10 ml
- 25 placas SimPlate, esterilizadas y con tapa
- Tabla de NMP
- Este folleto

Conservación

Conservar entre 2–30°C y fuera del alcance de la luz. La fecha de caducidad es en la caja.

Procedimiento de prueba

1. Agregue 10 ± 0,2 ml de muestra a una probeta de medio, ponga la tapa y agite para disolver. Vea la imagen N° 1.
2. Vierta el contenido de la probeta en el centro de la base de la placa. Vea la imagen N° 2.
3. Cubra la placa con la tapa y agite suavemente para distribuir la muestra en todos los pocillos. Vea la imagen N° 3.
NOTA: las burbujas de aire en los pocillos no interfieren con la muestra
4. Coloque la placa en un ángulo de 90° a 120° para verter el exceso en el paño absorbente. Vea la imagen N° 4.
5. Invierta la placa e incube durante 48 horas a 35 ± 0,5°C. Vea la imagen N° 5.
6. Cuente el número de pocillos que tienen fluorescencia: sujete una bombilla de 6 wats, 365 nm de luz UV a una distancia de 12,5 cm por encima de la placa. Apunte la bombilla hacia la muestra. Alternativamente, usted puede leer los pozos fluorescentes a través de la parte posterior de la base invertida del SimPlate.
7. Consulte la tabla de NMP (MPN) proporcionada para determinar el número más probable de bacteria de recuento de plaqueta heterotrófica en la muestra original. La tabla tiene en cuenta la muestra/medio eliminado en el paso 4.

Notas del procedimiento

1. Proceda con técnica aséptica.
2. Las muestras clorinadas se deben tratar con tiosulfato de sodio antes de hacer la prueba.
3. Los resultados se pueden leer desde 45 hasta 72 horas después de iniciada la incubación.
4. Elimine la muestra y el medio siguiendo buenas prácticas de laboratorio.
5. Las muestras se pueden diluir antes de agregar al medio siempre que el volumen final (muestra más diluyente esterilizado) sea 10 ± 0,2 ml. Ajuste el NMP para reflejar las diluciones. Por ejemplo, si se ponen a prueba 1 ml de muestra y 9 ml de diluyente estéril (dilución de 1:10), multiplique el número de la tabla de NMP por 10 para encontrar el NMP/ml correcto.

Procedimiento de control de calidad

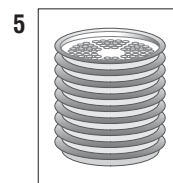
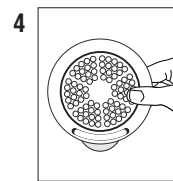
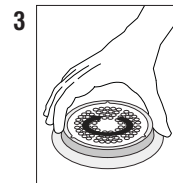
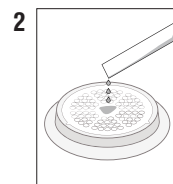
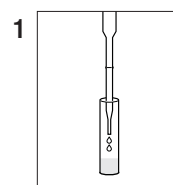
El siguiente procedimiento se recomienda para cada lote de SimPlate para productos sometidos al HPC:

1. A. Control positivo: IDEXX-QC HPC²: *Enterococcus faecalis*.
B. Control negativo/blanco: use 10 ml de medios de HPC rehidratados.
2. Siga los pasos del 1 al 7.
3. Los pocillos de control negativo/blanco no deben quedar fluorescentes después de la incubación.

Contacte con el servicio técnico en los siguientes teléfonos:

Europa: +00800 4339 9111

idexx.es/agua



¹ Eaton, AD, Clesceri, LS, Greenberg, AE, Rice, EN. *Standard Methods for the Examination of Water and Wastewater (Métodos estándares para el análisis del agua y las aguas residuales)*. American Public Health Association (Asociación Americana de Salud Pública), 2005. Washington, DC.

² IDEXX-QC HPC/TVC, IDEXX Catalog #UN3373-WQC-HPC.

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IDEXX

One IDEXX Drive
Westbrook, Maine 04092 USA

**Dosis Unitaria
SimPlate de RPH
Tabla de NMP**

# Pocillos positivos	NMP	Límites de confianza del 95%	
		inferior	superior
0	<0,2	<0,03	<1,4
1	0,2	0,0	1,4
2	0,4	0,1	1,6
3	0,6	0,2	1,9
4	0,8	0,3	2,2
5	1,0	0,4	2,5
6	1,2	0,6	2,7
7	1,5	0,7	3,0
8	1,7	0,8	3,3
9	1,9	1,0	3,6
10	2,1	1,1	3,9
11	2,3	1,3	4,2
12	2,6	1,5	4,5
13	2,8	1,6	4,8
14	3,0	1,8	5,1
15	3,3	2,0	5,4
16	3,5	2,2	5,8
17	3,8	2,3	6,1
18	4,0	2,5	6,4
19	4,3	2,7	6,7
20	4,5	2,9	7,0
21	4,8	3,1	7,4
22	5,1	3,3	7,7
23	5,3	3,5	8,0
24	5,6	3,8	8,4
25	5,9	4,0	8,7
26	6,2	4,2	9,1
27	6,5	4,4	9,4
28	6,8	4,7	9,8
29	7,1	4,9	10,2
30	7,4	5,1	10,6
31	7,7	5,4	10,9
32	8,0	5,6	11,3
33	8,3	5,9	11,7
34	8,6	6,2	12,1
35	9,0	6,4	12,6
36	9,3	6,7	13,0
37	9,7	7,0	13,4
38	10,0	7,3	13,9
39	10,4	7,6	14,3
40	10,8	7,9	14,8
41	11,2	8,2	15,2
42	11,6	8,5	15,7

# Pocillos positivos	NMP	Límites de confianza del 95%	
		inferior	superior
43	12,0	8,8	16,2
44	12,4	9,1	16,7
45	12,8	9,5	17,3
46	13,2	9,8	17,8
47	13,7	10,2	18,3
48	14,1	10,6	18,9
49	14,6	10,9	19,5
50	15,1	11,3	20,1
51	15,6	11,7	20,7
52	16,1	12,1	21,3
53	16,6	12,5	22,0
54	17,1	13,0	22,7
55	17,7	13,4	23,4
56	18,3	13,9	24,1
57	18,9	14,4	24,9
58	19,5	14,9	25,7
59	20,2	15,4	26,5
60	20,9	15,9	27,3
61	21,6	16,5	28,2
62	22,3	17,1	29,2
63	23,1	17,7	30,2
64	23,9	18,3	31,2
65	24,8	19,0	32,3
66	25,7	19,7	33,5
67	26,6	20,4	34,7
68	27,6	21,2	36,1
69	28,7	22,0	37,5
70	29,9	22,9	39,0
71	31,1	23,8	40,7
72	32,4	24,8	42,5
73	33,9	25,8	44,4
74	35,5	27,0	46,6
75	37,2	28,2	49,1
76	39,2	29,6	51,9
77	41,4	31,1	55,1
78	44,0	32,8	58,9
79	47,0	34,8	63,6
80	50,7	37,1	69,5
81	55,5	39,8	77,5
82	62,3	43,2	89,9
83	73,8	47,6	114,6
84	>73,8	>47,6	>114,6

El NMP es por ml de los 10 ml de la muestra añadida al reactivo en tubo (teniendo en cuenta el producto que se pueda derramar).

SimPlate* for HPC

SimPlate* Methode für HPC • Einheitsdosis

Deutsch

Einführung

Die SimPlate* Methode für HPC wird zur quantitativen Bestimmung der Zahl heterotropher Bakterien (HPC, heterotrophic plate counts) in Wasser verwendet. Der Test beruht auf der zum Patent angemeldeten Mehrfach-Enzymtechnologie von IDEXX (Multiple Enzyme Technology*). Mit dieser Methode können lebensfähige Bakterien in Wasser nachgewiesen werden, indem sie auf die Anwesenheit wichtiger Enzyme, die in diesen Organismen bekanntermaßen vorhanden sind, getestet werden. Dabei werden mehrere Enzymsubstrate verwendet, die blau fluoreszieren, wenn sie durch im Wasser vorhandene Bakterien metabolisiert werden. Probe und Medien werden auf eine SimPlate Platte gegeben, inkubiert und anschließend auf fluoreszierende Vertiefungen überprüft. Die Zahl der fluoreszierenden Vertiefungen entspricht einer Wahrscheinlichsten Gesamtbakterienzahl (MPN, most probable number) in der ursprünglichen Probe. Die von der SimPlate for HPC-Methode erzeugten MPN-Werte korrelieren mit der Pour-Plate-Methode, bei der Total Plate Count Agar verwendet wird, der 48 Stunden bei 35°C wie in *Standard Methods for the Examination of Water and Wastewater*¹ beschrieben inkubiert wurde.

Inhalt

- 25 sterile Medienröhrchen für 10-ml-Proben
- 25 sterile SimPlate Platten mit Deckel
- MPN-Tabelle
- Die vorliegende Packungsbeilage

Lagerung

Bei 2–30°C vor Licht geschützt aufbewahren. Das Verfallsdatum ist auf dem Kasten aufgedruckt.

Testverfahren

1. 10±0,2 ml Probe in ein Medienröhrchen geben, Verschluss wieder aufsetzen, und zur Auflösung schütteln. Siehe Abb. 1.
2. Inhalt des Röhrchens in die Mitte einer Platte gießen. Siehe Abb. 2.
3. Platte mit Deckel verschließen und vorsichtig kreisförmig bewegen, um die Probe gleichmäßig auf alle Vertiefungen zu verteilen. Siehe Abb. 3.
HINWEIS: Luftblasen in den Vertiefungen beeinflussen den Test nicht.
4. Platte 90–120° kippen, damit die überschüssige Flüssigkeit von dem Schwamm absorbiert wird. Siehe Abb. 4.
5. Platte umdrehen und 48 Stunden bei 35±0,5°C inkubieren. Siehe Abb. 5.
6. Die Zahl der fluoreszierenden Vertiefungen bestimmen, indem eine UV-Lampe mit einer Leistung von 6-Watt bei einer Wellenlänge von 365 nm etwa 12,5 cm über die Platte gehalten wird. Dabei das Licht von den Augen weg und zur Platte hinrichten. Sie können alternativ die fluoreszierenden Vertiefungen auch durch die Rückwand der SimPlate ablesen.
7. Die Wahrscheinlichste Zahl (MPN) der heterotrophen Bakterien in der ursprünglichen Probe wird mit Hilfe der mitgelieferten MPN-Tabelle bestimmt. Die Tabelle berücksichtigt die in Schritt 4 abgossene Probe inkl. Medium.

Verfahrenshinweise

1. Aseptisch arbeiten.
2. Chlorierte Proben müssen vor dem Testen mit Natriumthiosulfat behandelt werden.
3. Die Ergebnisse können 45 bis 72 Stunden nach Beginn der Inkubation abgelesen werden.
4. Proben und Medien müssen in Übereinstimmung mit anerkannten Laborverfahren entsorgt werden.
5. Proben können vor Zugabe zum Medium verdünnt werden, solange das endgültige Volumen (Probe plus steriles Verdünnungsmittel) 10±0,2 ml beträgt. Der MPN-Wert muss dann entsprechend korrigiert werden, um die Verdünnung zu berücksichtigen. Werden z.B. 1 ml Probe und 9 ml steriles Verdünnungsmittel getestet (10 fache Verdünnung), muss der aus der MPN-Tabelle bestimmte Wert mit 10 multipliziert werden, um den korrekten MPN-Wert pro ml zu erhalten.

Qualitätskontrollverfahren

Das folgende Verfahren wird für jede SimPlate for HPC-Produktcharge empfohlen:

1. A. Positivkontrolle: IDEXX-QC HPC²: *Enterococcus faecalis*.
B. Negativkontrolle/Blindprobe: 10 ml rehydriertes HPC-Medium verwenden.
2. Schritte 1 bis 7 durchführen.
3. Die Wells der Negativkontrolle/Blindprobe dürfen nach der Inkubation keine Fluoreszenz aufweisen.

Telefonnummern des technischen Supports:

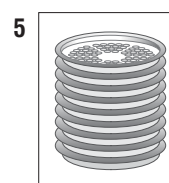
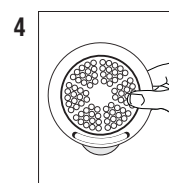
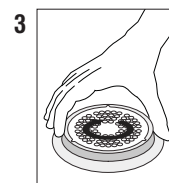
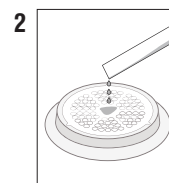
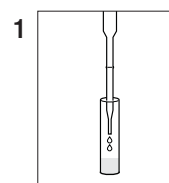
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idexx.de/wasser

¹ Eaton, AD, Clesceri, LS, Greenberg, AE, Rice, EN. *Standard Methods for the Examination of Water and Wastewater (Standardverfahren für die Wasser- und Abwasseruntersuchung)*. American Public Health Association, 2005. Washington, DC, USA.

² IDEXX-QC HPC/TV, IDEXX Bestellnr. UN3373-WQC-HPC.

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IDEXX

One IDEXX Drive
Westbrook, Maine 04092 USA

**Einheitsdosis
SimPlate für HPC
MPN - Tabelle**

# Positiven Vertiefungen	MPN	95% Vertrauensgrenze	
		Untere	Obere
0	<0,2	<0,03	<1,4
1	0,2	0,0	1,4
2	0,4	0,1	1,6
3	0,6	0,2	1,9
4	0,8	0,3	2,2
5	1,0	0,4	2,5
6	1,2	0,6	2,7
7	1,5	0,7	3,0
8	1,7	0,8	3,3
9	1,9	1,0	3,6
10	2,1	1,1	3,9
11	2,3	1,3	4,2
12	2,6	1,5	4,5
13	2,8	1,6	4,8
14	3,0	1,8	5,1
15	3,3	2,0	5,4
16	3,5	2,2	5,8
17	3,8	2,3	6,1
18	4,0	2,5	6,4
19	4,3	2,7	6,7
20	4,5	2,9	7,0
21	4,8	3,1	7,4
22	5,1	3,3	7,7
23	5,3	3,5	8,0
24	5,6	3,8	8,4
25	5,9	4,0	8,7
26	6,2	4,2	9,1
27	6,5	4,4	9,4
28	6,8	4,7	9,8
29	7,1	4,9	10,2
30	7,4	5,1	10,6
31	7,7	5,4	10,9
32	8,0	5,6	11,3
33	8,3	5,9	11,7
34	8,6	6,2	12,1
35	9,0	6,4	12,6
36	9,3	6,7	13,0
37	9,7	7,0	13,4
38	10,0	7,3	13,9
39	10,4	7,6	14,3
40	10,8	7,9	14,8
41	11,2	8,2	15,2
42	11,6	8,5	15,7

# Positiven Vertiefungen	MPN	95% Vertrauensgrenze	
		Untere	Obere
43	12,0	8,8	16,2
44	12,4	9,1	16,7
45	12,8	9,5	17,3
46	13,2	9,8	17,8
47	13,7	10,2	18,3
48	14,1	10,6	18,9
49	14,6	10,9	19,5
50	15,1	11,3	20,1
51	15,6	11,7	20,7
52	16,1	12,1	21,3
53	16,6	12,5	22,0
54	17,1	13,0	22,7
55	17,7	13,4	23,4
56	18,3	13,9	24,1
57	18,9	14,4	24,9
58	19,5	14,9	25,7
59	20,2	15,4	26,5
60	20,9	15,9	27,3
61	21,6	16,5	28,2
62	22,3	17,1	29,2
63	23,1	17,7	30,2
64	23,9	18,3	31,2
65	24,8	19,0	32,3
66	25,7	19,7	33,5
67	26,6	20,4	34,7
68	27,6	21,2	36,1
69	28,7	22,0	37,5
70	29,9	22,9	39,0
71	31,1	23,8	40,7
72	32,4	24,8	42,5
73	33,9	25,8	44,4
74	35,5	27,0	46,6
75	37,2	28,2	49,1
76	39,2	29,6	51,9
77	41,4	31,1	55,1
78	44,0	32,8	58,9
79	47,0	34,8	63,6
80	50,7	37,1	69,5
81	55,5	39,8	77,5
82	62,3	43,2	89,9
83	73,8	47,6	114,6
84	>73,8	>47,6	>114,6

Der MPN Wert ist pro 1 ml der 10 ml Probe, welche zum Reagenzröhrchen dazugegeben wird.

SimPlate^{*} for HPC

HPC用SimPlate^{*}・Unit Dose

日本語版

商品の紹介

HPC用SimPlate^{*}は、水中の従属栄養細菌数(HPC)の定量検査用キットです。これは、IDEXXが特許を取得した「Multiple Enzyme Technology^{*}」を基にしています。この技術は、細菌の存在の指標である主な酵素の有無を調べることによって、水中の生菌を検出します。水中の細菌による代謝によって青い蛍光を発する複数の酵素基質を利用しています。検体と培地はSimPlate平板で培養し、蛍光を発するウェルの数を数えます。蛍光を発するウェルの数から、検体中の全細菌の最確数(MPN値)を求めます。HPC用SimPlateで求められた最確数(MPN値)は、「Standard Methods for the Examination of Water and Wastewater¹」(水および排水標準検査法)に掲載されている、35°Cで48時間培養された標準寒天培地を使用した混釈平板法と相関があります。

内容

- 10ml用滅菌培地チューブ25本
- 滅菌SimPlate25枚(蓋付き)
- MPN表
- 使用説明書

保存

直射光を避け、2~30°Cで保管してください。使用期限は培地チューブの箱に印字されています。

操作手順

1. 培地チューブに10 ± 0.2 mlの検体を加え、蓋を開けて振り、ゆっくり混ぜてください。図1を参照。
2. SimPlateの中央に培地チューブ内の検体を全て注入してください。図2を参照。
3. SimPlateに蓋をし、全ウェルに検体が分注されるよう、水平に動かしてください。図3を参照。
注:ウェル内に気泡があっても、結果には影響はありません。
4. SimPlateを90°~120°に傾け、余分な検体を吸収パッドに吸引させてください。図4を参照。
5. SimPlateを逆さまにし、35 ± 0.5°Cで48時間培養してください。図5を参照。
6. 蓋を外し、SimPlateの上5インチ(13 cm)に6W・365nm UVランプを置き、蛍光を発するウェルの個数を数えてください。光が目に向けないように注意し、検体に向けてください。また、シンプレート逆さまにして、裏側から蛍光発色をカウントすることもできます。
7. 専用MPN表を参照して、検体中の従属栄養細菌の最確数(MPN値)を求めてください。この表は、上記ステップ4で吸引した検体や培地を考慮しています。

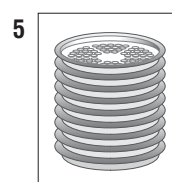
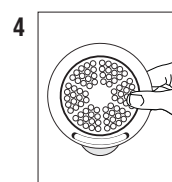
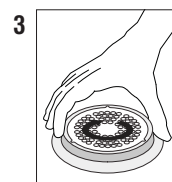
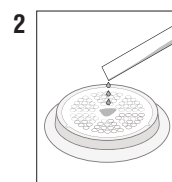
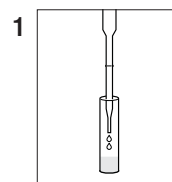
操作上の注意

1. 無菌操作を行ってください。
2. 塩素処理した検体は、検査前に、チオ硫酸ナトリウムで処理してください。
3. 培養開始後、45~72時間で結果判定できます。
4. 検体と培地はGLPに従って廃棄してください。
5. 最終的な量(検体と培地の合計)が10 ± 0.2 mlであれば、ごく少量の検体を検査することができます。その際は、使用した検体の量に応じて、MPN値を調整します。例えば、1 mlの検体と9 mlの培地を使用した場合、MPN表の数値は、0.1 ml当たりの数値です。1 ml当たりのMPNに換算するには、その数値を10倍します。

品質管理手順

HPC用SimPlateの各ロット毎に次の操作手順を行うことをお勧めします。

1. A. 陽性対照:IDEXX-QC HPC/TVC²:Enterococcus faecalis(フェカリス菌)。
B. 陰性対照/ブランク:再水和されたHPC培地10 mlを使用。
2. 手順1~7を実施してください。
3. 陰性対照/ブランクウェルは、培養後に蛍光を発しないはずで。



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idexx.co.jp/water

アイデックス ラボラトリーズ株式会社東京都三鷹市北野3-3-7

1. Eaton, AD, Clesceri, LS, Greenberg, AE, Rice, EN. *Standard Methods for the Examination of Water and Wastewater*. American Public Health Association, 2005. Washington, DC.
2. IDEXX-QC HPC/TVC, IDEXX カタログ番号 UN3373-WQC-HPC.

^{*}SimPlateはBioControl Systems, Inc.の商標または登録商標であり、IDEXXがBioControl Systems, Inc.の許可を得て使用しています。
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IDEXX

One IDEXX Drive
Westbrook, Maine 04092 USA

Unit Dose
HPC用SimPlate
 最確数 (MPN) 表

陽性ウェル の数	MPN	95%信頼限界	
		下限	上限
0	<0.2	<0.03	<1.4
1	0.2	0.0	1.4
2	0.4	0.1	1.6
3	0.6	0.2	1.9
4	0.8	0.3	2.2
5	1.0	0.4	2.5
6	1.2	0.6	2.7
7	1.5	0.7	3.0
8	1.7	0.8	3.3
9	1.9	1.0	3.6
10	2.1	1.1	3.9
11	2.3	1.3	4.2
12	2.6	1.5	4.5
13	2.8	1.6	4.8
14	3.0	1.8	5.1
15	3.3	2.0	5.4
16	3.5	2.2	5.8
17	3.8	2.3	6.1
18	4.0	2.5	6.4
19	4.3	2.7	6.7
20	4.5	2.9	7.0
21	4.8	3.1	7.4
22	5.1	3.3	7.7
23	5.3	3.5	8.0
24	5.6	3.8	8.4
25	5.9	4.0	8.7
26	6.2	4.2	9.1
27	6.5	4.4	9.4
28	6.8	4.7	9.8
29	7.1	4.9	10.2
30	7.4	5.1	10.6
31	7.7	5.4	10.9
32	8.0	5.6	11.3
33	8.3	5.9	11.7
34	8.6	6.2	12.1
35	9.0	6.4	12.6
36	9.3	6.7	13.0
37	9.7	7.0	13.4
38	10.0	7.3	13.9
39	10.4	7.6	14.3
40	10.8	7.9	14.8
41	11.2	8.2	15.2
42	11.6	8.5	15.7

陽性ウェル の数	MPN	95%信頼限界	
		下限	上限
43	12.0	8.8	16.2
44	12.4	9.1	16.7
45	12.8	9.5	17.3
46	13.2	9.8	17.8
47	13.7	10.2	18.3
48	14.1	10.6	18.9
49	14.6	10.9	19.5
50	15.1	11.3	20.1
51	15.6	11.7	20.7
52	16.1	12.1	21.3
53	16.6	12.5	22.0
54	17.1	13.0	22.7
55	17.7	13.4	23.4
56	18.3	13.9	24.1
57	18.9	14.4	24.9
58	19.5	14.9	25.7
59	20.2	15.4	26.5
60	20.9	15.9	27.3
61	21.6	16.5	28.2
62	22.3	17.1	29.2
63	23.1	17.7	30.2
64	23.9	18.3	31.2
65	24.8	19.0	32.3
66	25.7	19.7	33.5
67	26.6	20.4	34.7
68	27.6	21.2	36.1
69	28.7	22.0	37.5
70	29.9	22.9	39.0
71	31.1	23.8	40.7
72	32.4	24.8	42.5
73	33.9	25.8	44.4
74	35.5	27.0	46.6
75	37.2	28.2	49.1
76	39.2	29.6	51.9
77	41.4	31.1	55.1
78	44.0	32.8	58.9
79	47.0	34.8	63.6
80	50.7	37.1	69.5
81	55.5	39.8	77.5
82	62.3	43.2	89.9
83	73.8	47.6	114.6
84	>73.8	>47.6	>114.6

MPNは、培地チューブに添加した検体10 ml中のml単位の値です（吸収した検体や培地を考慮しています）。

EnteroBERT® Test Kit

Introduction

EnteroBERT® detects enterococci such as *E. faecium* and *E. faecalis* in liquid or semi-liquid water. It is based on ISO 24691 (previously defined as ISO 15701), which uses a 4-methylumbelliferyl-D-glucuronide (4-MUG) substrate to detect enterococci. The test is based on the ability of enterococci to hydrolyze 4-MUG, releasing fluorescent 4-methylumbelliferone (4-MU) from the substrate.

1. Add contents of one packet to 100 mL sample in a sterile, clear plastic cup.
2. Cover and shake.
3. Incubate at 41-43.5°C for 24 hours.
4. Read results according to Result Interpretation table below.

Quant-iTay® Enumeration Procedure

1. Add contents of one packet to 100 mL water sample in a sterile vessel.
2. Cap vessel and shake until dissolved.
3. Pour sample/liquid mixture into a Quant-iTay® or Quanti-Tay® (2000) and seal in.
4. Incubate at 41-43.5°C for 24 hours.
5. Read results according to the Result Interpretation table below. Count the number of positive wells, and refer to the MPN table, provided with the trays to obtain a Most Probable Number (MPN).

Result Interpretation

Appearance	Result
Blue fluorescence	Negative for enterococci
Red fluorescence	Positive for enterococci

- Look for fluorescence with a 6-well, 360 mL UV light within 5 inches of the sample in a dark environment. Flip light away from your eyes and towards the sample.
- A clear result is a definition of 24-28 hours. In addition, possible to enterococci observed within 24 hours and negatives observed after 28 hours are observed.

Precedural Notes

- Marine water samples must be diluted at least 10-fold with sterile fresh water. Multiply the MPN value by the dilution factor to obtain the final MPN.
- Use only sterile, nonfluorescent, nonred-water for dilutions.
- For comparison a water blank can be used when interpreting results.
- This test may not reflect your local regulations. For compliance testing, be sure to follow appropriate regulatory procedures.
- EnteroBERT® can run in any multiple tube format. Standard Methods for the Examination of Water and Wastewater® MPN tables are available for a primary water test. EnteroBERT® performance characteristics do not apply to samples allowed by any pre-enrichment or concentration.
- Aseptic technique should always be followed when using EnteroBERT®. Dispose of in accordance with Good Laboratory Practices.

Quality Control Procedures

1. One of the following quality control procedures is recommended for each lot of EnteroBERT®:
 - A. ISO 24691: Enterococcus faecalis, Enterococcus faecium, and Streptococcus faecalis.
 - B. I. For each of the American Type Culture Collection (ATCC) bacterial strains (Enterococcus faecium ATCC-29282, Streptococcus faecalis ATCC-29518, and Streptococcus faecalis ATCC-29519), streak 10 µL of each into a labeled TSA or Staph-Agar plates and incubate at 35-37°C for 18-24 hours.
 - i. For each bacterial strain, both a sterile 1/4 L inoculating loop to inoculate a colony and use it to inoculate a labeled test tube containing 5 mL of sterile deionized water. Close cap and shake thoroughly.
 - ii. For each bacterial strain, take a 1/4 L loop from the test tube and use it to inoculate a labeled vessel containing 100 mL of sterile deionized water. Close your controls.
 3. Results should match the Result Interpretation table above.

1. Eaton, B., Clayton, L., Rice, R., Goring, G., Frazar, M., et al. Standard Methods for the Examination of Water and Wastewater, 21st ed. Washington, DC: American Public Health Association, 2005.
2. ISO 24691:2006. Enterococcus faecalis and Enterococcus faecium in water.
3. American Type Culture Collection. ATCC 29282, ATCC 29518, ATCC 29519, ATCC 35061, ATCC 35067, ATCC 35068, ATCC 35069, ATCC 35070, ATCC 35071, ATCC 35072, ATCC 35073, ATCC 35074, ATCC 35075, ATCC 35076, ATCC 35077, ATCC 35078, ATCC 35079, ATCC 35080, ATCC 35081, ATCC 35082, ATCC 35083, ATCC 35084, ATCC 35085, ATCC 35086, ATCC 35087, ATCC 35088, ATCC 35089, ATCC 35090, ATCC 35091, ATCC 35092, ATCC 35093, ATCC 35094, ATCC 35095, ATCC 35096, ATCC 35097, ATCC 35098, ATCC 35099, ATCC 35100, ATCC 35101, ATCC 35102, ATCC 35103, ATCC 35104, ATCC 35105, ATCC 35106, ATCC 35107, ATCC 35108, ATCC 35109, ATCC 35110, ATCC 35111, ATCC 35112, ATCC 35113, ATCC 35114, ATCC 35115, ATCC 35116, ATCC 35117, ATCC 35118, ATCC 35119, ATCC 35120, ATCC 35121, ATCC 35122, ATCC 35123, ATCC 35124, ATCC 35125, ATCC 35126, ATCC 35127, ATCC 35128, ATCC 35129, ATCC 35130, ATCC 35131, ATCC 35132, ATCC 35133, ATCC 35134, ATCC 35135, ATCC 35136, ATCC 35137, ATCC 35138, ATCC 35139, ATCC 35140, ATCC 35141, ATCC 35142, ATCC 35143, ATCC 35144, ATCC 35145, ATCC 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Appendix D: Description of Sampling Skids

Triton NP 6007 TG 18 ballast water sampling system

The Triton NP 6007 TG 18 ballast water sampling system has a modular design and consists in minimum of five major elements: a diaphragm valve, a filter housing equipped with filter cartouche and a transparent filter cup, an isokinetic bypass (elbow), a volume count and a ball valve. The material of all elements fulfil international quality requirements for pipe installations in the food industry and in the clinical sector. With the installation of a diaphragm valve at the intake and a ball valve at the outlet the Triton NP 6007 TG 18 sampling system fulfils the IMO Guidelines for Ballast Water Sampling (cf. IMO document MEPC.173(58), October 10th, 2008)

In its minimal composition the footprint of the Triton NP 6007 TG 18 sampling system is 40x40x45cm.

The Triton NP 6007 TG 18 can be operated as an open sampling system (i.e. the waste water is collected in a container or is directed into the bilge of the ship) or as a closed sampling system (i.e. the waste water is re-directed into the ballast water main pipe). With the NP 6007 TG 18 two different types of ballast water samples can be generated: (i) frequent grab samples and (ii) drip samples.

Connected to a sampling port the diaphragm valve of the NP 6007 TG 18 allows for the regulation of the flow volume through the NP 6007 TG 18 and with shutting both valves, the diaphragm valve and the ball valve, the NP 6007 TG 18 is completely cut off from the ballast water main pipe.

The ballast water diverted from the main pipe enters the transparent filter housing and passes through a filter cartouche with a filter material that has been developed especially for the sampling of plankton organisms $\geq 50\mu\text{m}$ from ballast water onboard ships. Having passed the filter housing the water is directed through an isokinetic elbow, which, equipped with a small ball valve, allows for the sampling of ballast water for the analysis of plankton organisms $<50\mu\text{m}$ and of bacteria, too. After the isokinetic elbow the waste water finally passes a digital volume count, which allows for the monitoring of flow volume, total volume and flow velocity.

Depending on the flow velocity in the ballast water main pipe and the flow volume through the NP 6007 TG 18 the time for sampling of $1,0\text{m}^3$ of ballast water can be easily calculated.

At the start of the sampling procedure both valves, the diaphragm valve and the ball valve, are fully opened and the flow volume through the NP 6007 TG 18 is adjusted with the diaphragm valve to a value which ensures that the sensitive plankton organisms $\geq 50\mu\text{m}$ are not impacted by the filtration process itself. While the ballast water passes through the NP 6007 TG 18 additional samples can be taken through the small ball valve of the isokinetic elbow for the analysis of plankton organisms $<50\mu\text{m}$ and bacteria.

After the termination of the sampling process both valves are closed. To retrieve the plankton organisms retained in the filter cartouche the transparent cup of the filter housing is screwed off. The filter cartouche can easily be removed from the filter head by a half turn of the cartouche. Since the filter cartouche is closed with a funnel and a small ball valve at its lower

end, the plankton organisms trapped inside the filter cartouche can easily be rinsed into a beaker for further sample processing and analysis.

Figure D.1: Triton NP 6007 TG 18 skid: basic set of elements



Figure D.2: Triton NP 6007 TG 18 skid: installations during Meteor cruise



Figure D.3: Triton NP 6007 TG 18 skid: installation during hydraulic tests



SGS BWS 1

1 THE SGS BWS1

The SGS Ballast Water Sampler (SGS BWS1) has a footprint of 45x25 cm and weighs 6.5 kg. Figure 1 shows the SGS BWS1 with the sampling pipe, filter housing containing the steel filter, two pressure gauges to monitor differential pressure across the filter, bypass sampling port and the volume count at the discharge connection. In certain configurations the discharge connection will also be equipped with an L-shaped pipe.



Figure 1: The SGS Ballast Water Sampler v02. The parts are numbered in the order that the water passes through the sampler. 1: Sampling pipe. 2: Filter housing. 3: Pressure gauges. 4: Bypass sampling port. 5: Volume count.

The ballast water enters the sampling system via the sampling pipe and is directed into the large filterhousing, in which the plankton organisms $\geq 50\mu\text{m}$ are retained. The water then leaves the filterhousing through a straight pipe section, in which a small isokinetic bypass sampling port (figure 2) allows for the sampling of ballast water for analysis of plankton organisms $\geq 10\mu\text{m} < 50\mu\text{m}$ and bacteria.



Figure 2: The isokinetic bypass sampling port, dismantled (left) and installed (right)

The different parts, like hoses, volume count and sampling pipes are connected by a system of clamps (figure 3), which allows for easy dismantling and cleaning.



Figure 3: The connecting system and additional ball valves

The flange which fixes the sampling pipe into the ship's main ballast water pipe can is of DN100 size, in line with the ISO 11711-1:2013 standard for ballast water sampling connections and the recommendations by the USCG for modifying this standard (USNRL Report 3900 6130/1550). Figure 4 shows the parts of the sampling pipe assembly; figure 5 shows the completed assembly.

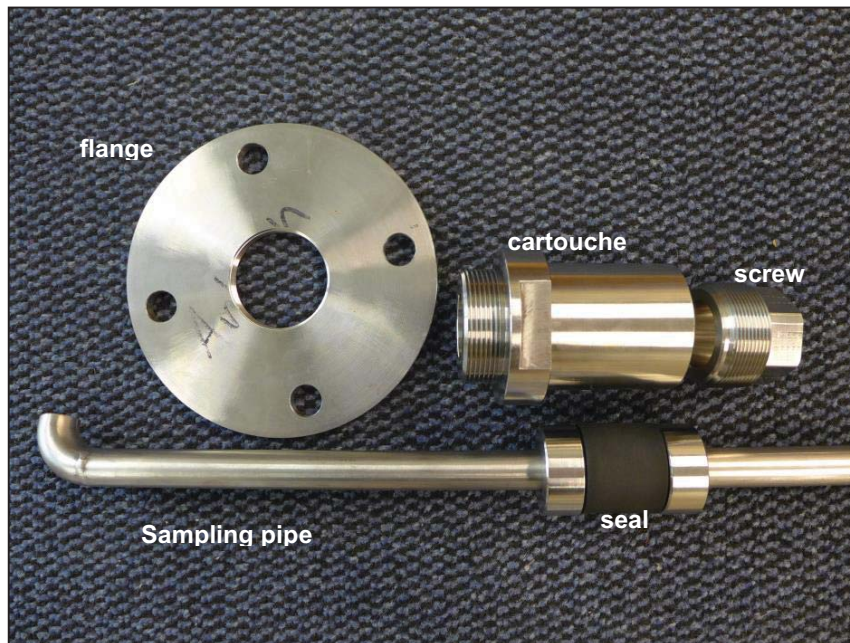


Figure 4: The components of the sampling pipe. The sampling pipe is mounted inside the cartouche and fastened in place with the screw. The seal prevents leaking. This assembly is then screwed into the flange so it can be attached to the piping on-board.

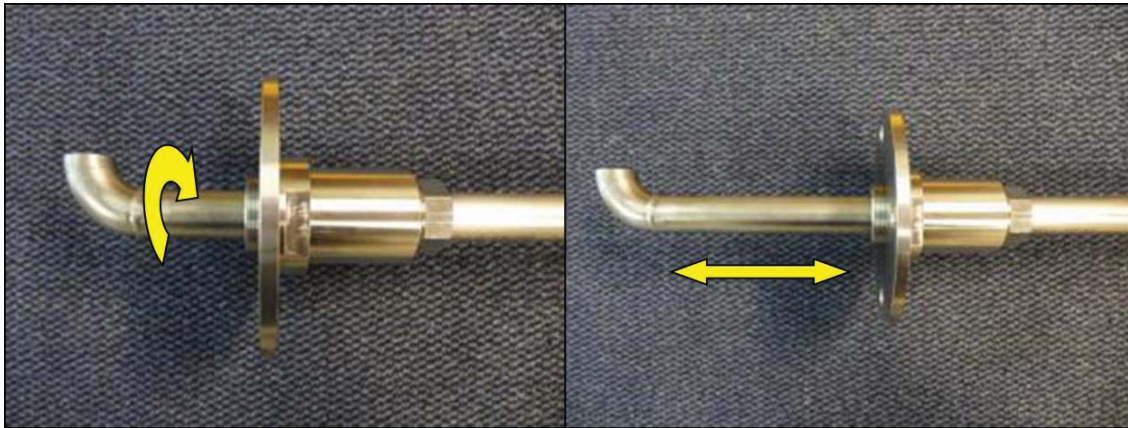


Figure 5: The complete sampling pipe assembly, arrows indicate the possibilities to adjust the position of the sampling pipe

Once the flange with the cartouche and the sampling pipe are fixed to the main ballast water pipe, the position of the sampling pipe inside the main ballast water pipe can easily be adjusted. Figure 5 presents the mounted cartouche with yellow arrows indicating the possibilities to adjust the sampling pipe inside the main ballast water pipe, i.e. the opening of the sampling pipe inside the main ballast water pipe is positioned concentrically and faces upstream.

Attaching the SGS BWS1 directly to a flange on the ballast water discharge pipe is only possible if the pipe is empty. Since this is often not the case on ships, the sampling pipes are designed to be able to fit through a ball valve (figure 6). The flange with the sampling pipe can be attached while the ball valve is closed. When the ball valve is opened the sampling pipe can then be inserted into the ballast water pipe. Using this configuration the sampling pipe can be inserted without emptying the ballast water discharge line.

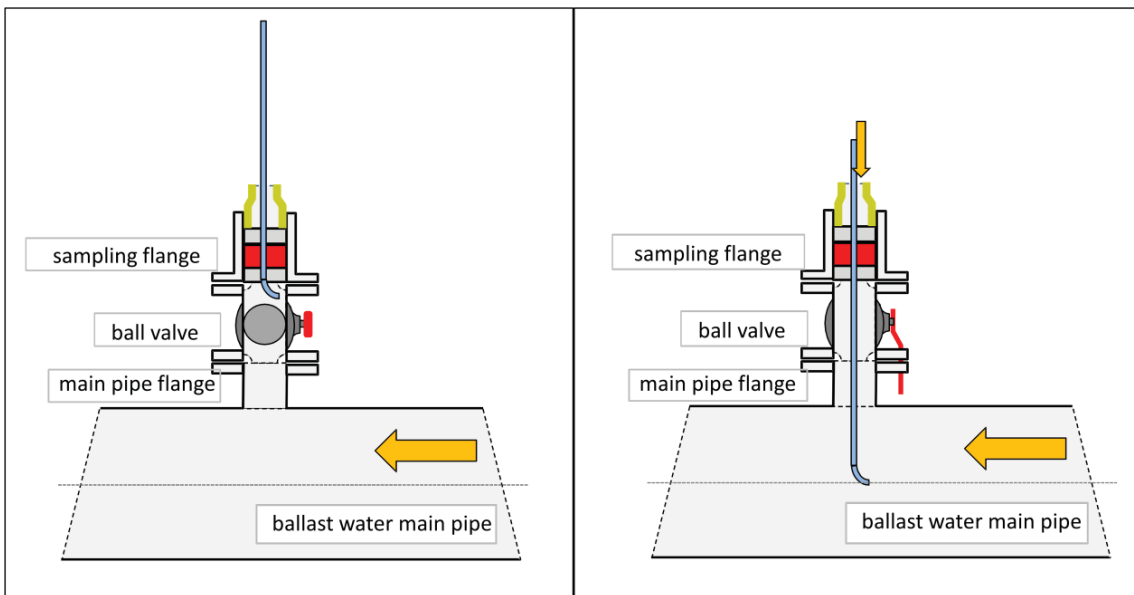


Figure 6: Installation of the isokinetic pipe into main ballast water pipes on-board ships without emptying the main ballast water pipe

The SGS BWS1 is equipped with a steel filter screen with laser-perforations of 50 μm (figure 7 and 8). In addition to being extremely sturdy, it also has a very smooth surface which is very suitable for washing particles and organisms down to the collection tap. Cleaning of the filter is also a fast and easy process.



Figure 7: The stainless steel screen filter inlet of the SGS BWS1, the rubber ring at the top prevents water and organisms from bypassing the filter. The valve at the bottom allows easy collection of the sample.

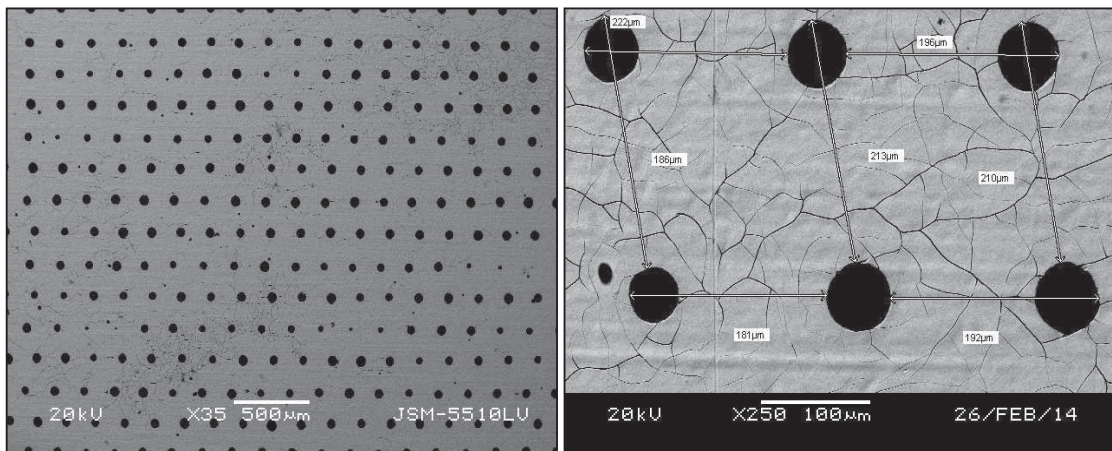


Figure 8: Scanning Electron Microscopy pictures of the steel filter screen.

The SGS BWS1 can be used in either closed loop (figure 9) or open loop configuration (figure 10). The configurations are very similar, in open loop no return port is used.

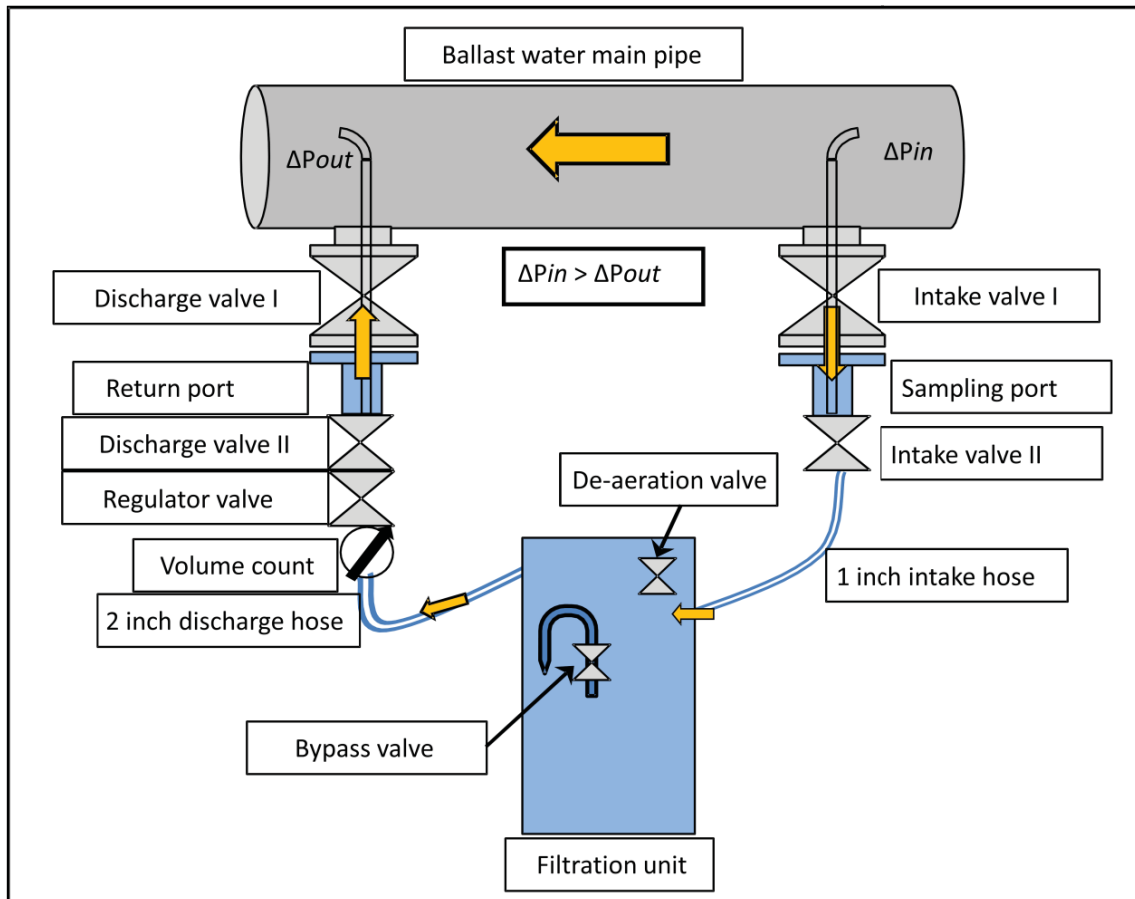


Figure 9. Schematic of the sampling system configuration in closed loop.

Since the main connecting valves (intake valve I and discharge valve I) cannot be closed when the sampling probes are inserted, closing the sampler off from the main system is done by the additional valves that come with the system (intake valve II and discharge valve II).

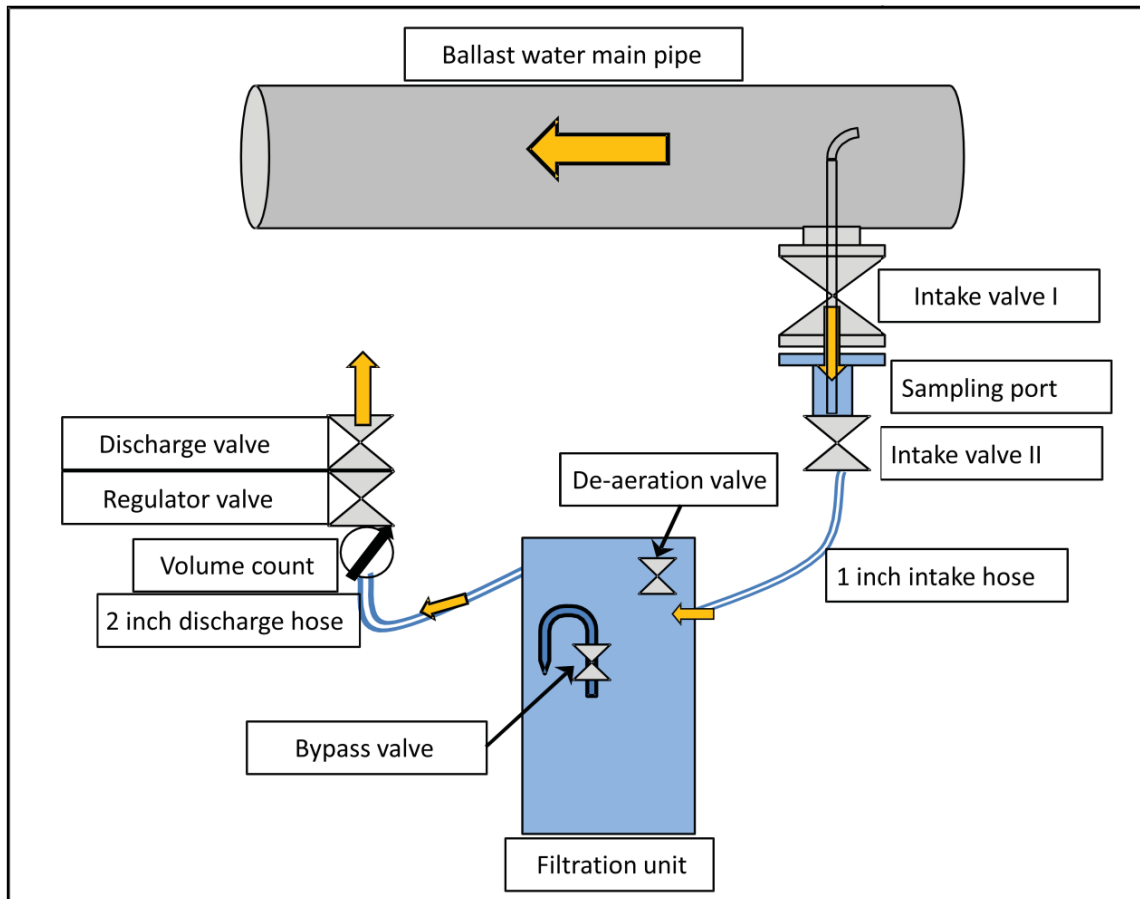


Figure 10. Schematic of the sampling system configuration in open loop.

In both configurations the correct flow for safe sampling of plankton is maintained using the regulator valve.

All recommendations and terminology in this document is in line with ISO 11711-1:2013 and the US Naval Research Institute report: 'Ballast Water Sample Ports, Sample Probes, and Sample Collection Devices: Recommendations for Standardization' (Report 3900 6130/1550).

Appendix E: Method Comparison Statistics results

Appendix E.1: G50 Method Comparison Results: SGS ATP, Microscopy, PAM, and Satake Pulse Counter: log+1 transformed data

Conversion between methods:

To:	From:	alpha	beta	sd.pred	int(t-f)	slope(t-f)	sd(t-f)
PAM	PAM	0.000	1.000	4.151	0.000	0.000	4.151
	Satake.Pulse.Counter	4.595	0.885	2.994	4.875	-0.122	3.176
	SGS.ATP	0.352	0.645	3.088	0.428	-0.431	3.754
	Total.Microscope	3.131	0.974	3.284	3.173	-0.027	3.328
Satake.Pulse.Counter	PAM	-5.191	1.130	3.365	-4.875	0.122	3.160
	Satake.Pulse.Counter	0.000	1.000	0.360	0.000	0.000	0.360
	SGS.ATP	-4.710	0.717	0.991	-5.487	-0.330	1.154
	Total.Microscope	-1.482	1.063	1.447	-1.437	0.061	1.403
SGS.ATP	PAM	-0.545	1.550	4.766	-0.428	0.431	3.738
	Satake.Pulse.Counter	6.570	1.395	1.388	5.487	0.330	1.159
	SGS.ATP	0.000	1.000	1.805	0.000	0.000	1.805
	Total.Microscope	4.505	1.485	2.340	3.625	0.390	1.883
Total.Microscope	PAM	-3.216	1.027	3.323	-3.173	0.027	3.278
	Satake.Pulse.Counter	1.394	0.941	1.384	1.437	-0.061	1.426
	SGS.ATP	-3.033	0.673	1.596	-3.625	-0.390	1.907
	Total.Microscope	0.000	1.000	1.861	0.000	0.000	1.861

Variance components (sd):

Method	IXR	MXI	res
PAM	0	2.734	1.056
Satake.Pulse.Counter	0	0.239	0.088
SGS.ATP	0	1.079	0.678
Total.Microscope	0	1.263	0.361

Variance components with 95 % cred.int.:

method	PAM	Satake.Pulse.Counter	SGS.ATP	Total.Microscope		
qnt	50%	2.5%	97.5%	50%	2.5%	97.5%
SD	IXR	0.000	0.000	0.000	0.000	0.000
	MXI	2.734	1.904	3.784	0.239	0.012
	res	1.056	0.888	1.287	0.088	0.077
	tot	2.935	2.173	3.930	0.255	0.087
					1.276	0.938
					1.608	1.263
					1.457	0.893
					0.361	0.304
					1.316	0.964
					1.811	1.811

Mean parameters with 95 % cred.int.:

alpha[Satake.Pulse.Counter.PAM]	50%	2.5%	97.5%	P(>0/1)
	-5.192	-61.703	-0.367	0.008

alpha[SGS.ATP.PAM]	-0.543	-79.066	5.674	0.472
alpha[Total.Microscope.PAM]	-3.208	-55.646	1.226	0.126
alpha[PAM.Satake.Pulse.Counter]	4.594	0.893	6.984	0.992
alpha[SGS.ATP.Satake.Pulse.Counter]	6.561	5.354	7.421	1.000
alpha[Total.Microscope.Satake.Pulse.Counter]	1.396	-0.241	2.689	0.958
alpha[PAM.SGS.ATP]	0.353	-8.542	6.229	0.528
alpha[Satake.Pulse.Counter.SGS.ATP]	-4.716	-7.073	-2.799	0.000
alpha[Total.Microscope.SGS.ATP]	-3.033	-6.944	0.549	0.049
alpha[PAM.Total.Microscope]	3.139	-3.261	6.682	0.874
alpha[Satake.Pulse.Counter.Total.Microscope]	-1.480	-6.217	0.158	0.042
alpha[SGS.ATP.Total.Microscope]	4.505	-1.729	6.612	0.951
beta[Satake.Pulse.Counter.PAM]	1.130	0.420	9.395	0.565
beta[SGS.ATP.PAM]	1.550	0.642	12.876	0.778
beta[Total.Microscope.PAM]	1.027	0.364	8.595	0.513
beta[PAM.Satake.Pulse.Counter]	0.885	0.106	2.383	0.435
beta[SGS.ATP.Satake.Pulse.Counter]	1.395	1.037	1.933	0.985
beta[Total.Microscope.Satake.Pulse.Counter]	0.941	0.435	1.544	0.414
beta[PAM.SGS.ATP]	0.645	0.078	1.558	0.222
beta[Satake.Pulse.Counter.SGS.ATP]	0.717	0.517	0.964	0.015
beta[Total.Microscope.SGS.ATP]	0.673	0.317	1.066	0.051
beta[PAM.Total.Microscope]	0.974	0.116	2.746	0.487
beta[Satake.Pulse.Counter.Total.Microscope]	1.063	0.648	2.296	0.586
beta[SGS.ATP.Total.Microscope]	1.485	0.938	3.152	0.949

Note that intercepts in conversion formulae are adjusted to get conversion formulae that represent the same line both ways, and hence the median intercepts in the posterior do not agree exactly with those given in the conversion formulae.

Appendix E.2: 10-50 Method Comparison Results: BallastCheck2, bbe, Hach BW680, Microscopy

Note: Response transformed by: function (y) { log(y + 1)}

Conversion between methods:

To:	From:	alpha	beta	sd.pred	int(t-f)	slope(t-f)	sd(t-f)
BallastCheck2	Ba11astCheck2	0.000	1.000	0.750	0.000	0.000	0.750
	bbe	0.338	0.849	0.616	0.366	-0.163	0.666
	Hach	0.488	1.232	0.546	0.437	0.208	0.489
	Microscopy	0.242	1.020	0.709	0.239	0.020	0.702
bbe	Ba11astCheck2	-1.313	0.950	1.026	-1.347	-0.052	1.053
	bbe	-0.398	1.178	0.723	-0.366	0.163	0.664
	Hach	0.000	1.000	0.511	0.000	0.000	0.511
	Microscopy	0.178	1.453	0.390	0.145	0.369	0.318
Hach	Ba11astCheck2	-0.109	1.203	0.659	-0.099	0.184	0.598
	bbe	-1.955	1.120	1.094	-1.844	0.113	1.032
	Hach	-0.396	0.812	0.441	-0.437	-0.208	0.487
	Microscopy	-0.122	0.688	0.269	-0.145	-0.369	0.318
Microscopy	Ba11astCheck2	0.000	1.000	0.117	0.000	0.000	0.117
	bbe	-0.198	0.829	0.389	-0.217	-0.187	0.426
	Hach	-1.468	0.772	0.720	-1.657	-0.257	0.812
	Microscopy	-0.237	0.980	0.693	-0.239	-0.020	0.700
PAM	Ba11astCheck2	0.091	0.832	0.549	0.099	-0.184	0.600
	bbe	0.239	1.207	0.471	0.217	0.187	0.427
	Hach	0.000	1.000	0.641	0.000	0.000	0.641
	Microscopy	-1.532	0.932	0.974	-1.586	-0.070	1.008
PAM	Ba11astCheck2	1.383	1.053	1.084	1.347	0.052	1.056
	bbe	1.745	0.893	0.981	1.844	-0.113	1.037
	Hach	1.902	1.295	0.934	1.657	0.257	0.813
	Microscopy	1.644	1.073	1.051	1.586	0.070	1.014
PAM	PAM	0.000	1.000	1.306	0.000	0.000	1.306

Variance components (sd):

Method	s.d.	IxR	MxI	res
Ba11astCheck2	0	0.489	0.204	
bbe	0	0.341	0.119	
Hach	0	0.064	0.052	
Microscopy	0	0.385	0.238	
PAM	0	0.875	0.294	

Appendix E.3: <10 Method Comparison Results

Conversion between methods:		alpha	beta	sd.pred	int(t-f)	slope(t-f)	sd(t-f)
To:	From:						
ATP	ATP	0.000	1.000	95.792	0.000	0.000	95.792
	Ba11astCheck2	-232.360	9.043	514.574	-46.275	1.602	102.479
	Bu1k.FDA	-58.713	2.816	106.476	-30.773	0.952	55.807
Ba11astCheck2	ATP	25.696	0.111	57.421	46.275	-1.602	103.407
	Ba11astCheck2	0.000	1.000	74.953	0.000	0.000	74.953
	Bu1k.FDA	13.146	0.371	55.044	19.183	-0.919	80.324
Bu1k.FDA	ATP	20.851	0.355	32.005	30.773	-0.952	47.235
	Ba11astCheck2	-35.477	2.699	142.448	-19.183	0.919	77.025
	Bu1k.FDA	0.000	1.000	28.261	0.000	0.000	28.261

Variance components (sd):

Method	s.d.	IxR	MxI	res
ATP	0	65.320	17.343	
Ba11astCheck2	0	52.912	2.915	
Bu1k.FDA	0	19.023	6.051	

Variance components with 95 % cred.int.:

method	ATP	Ba11astCheck2	Bu1k.FDA
qnt	50%	50%	50%
SD	0.000	0.000	0.000
IxR	65.320	1.577	162.364
MxI	17.343	13.556	22.873
res	67.735	16.256	163.363
tot	0.000	0.000	0.000
	2.250	67.894	19.023
	2.585	3.352	6.051
	3.768	67.951	19.984
	0.000	0.000	0.000
	2.5%	97.5%	97.5%
	0.000	0.000	0.000
	1.502	1.502	35.962
	4.659	4.659	8.204
	6.103	6.103	36.445