

1 A workflow for the detection of antibiotic residues, measurement of water chemistry and
2 preservation of hospital sink drain samples for metagenomic sequencing

3

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23 **Structured summary**

24 **Background**

25 Hospital sinks are environmental reservoirs that harbour healthcare-associated (HCA)
26 pathogens. Selective pressures in sink environments, such as antibiotic residues, nutrient
27 waste and hardness ions, may promote antibiotic resistance gene (ARG) exchange between
28 bacteria. However, cheap and accurate sampling methods to characterise these factors are
29 lacking.

30 **Aim**

31 To validate a workflow to detect antibiotic residues and evaluate water chemistry using
32 dipsticks. Secondarily, to validate boric acid to preserve the taxonomic and ARG
33 ("resistome") composition of sink trap samples for metagenomic sequencing.

34 **Methods**

35 Antibiotic residue dipsticks were validated against serial dilutions of ampicillin, doxycycline,
36 sulfamethoxazole and ciprofloxacin, and water chemistry dipsticks against serial dilutions of
37 chemical calibration standards. Sink trap aspirates were used for a "real-world" pilot
38 evaluation of dipsticks. To assess boric acid as a preservative of microbial diversity, the
39 impact of incubation with and without boric acid at ~22°C on metagenomic sequencing
40 outputs was evaluated at Day 2 and Day 5 compared with baseline (Day 0).

41 **Findings**

42 The limits of detection for each antibiotic were: 3µg/L (ampicillin), 10µg/L (doxycycline),
43 20µg/L (sulfamethoxazole) and 8µg/L (ciprofloxacin). The best performing water chemistry
44 dipstick correctly characterised 34/40 (85%) standards in a concentration-dependent
45 manner. One trap sample tested positive for the presence of tetracyclines and
46 sulfonamides. Taxonomic and resistome composition were largely maintained after storage
47 with boric acid at ~22°C for up to five days.

48 **Conclusions**

49 Dipsticks can be used to detect antibiotic residues and characterise water chemistry in sink
50 trap samples. Boric acid was an effective preservative of trap sample composition,
51 representing a low-cost alternative to cold-chain transport.

52

53 **Keywords**

54 Hospital sinks, antibiotic residues, water chemistry, antimicrobial resistance (AMR)

55

56 **Introduction**

57 Antimicrobial resistance (AMR) is a significant healthcare challenge, and a global public
58 health threat [1-4]. Hospitals represent a major site for the emergence and dissemination of
59 multi-drug resistant (MDR) pathogens, such as carbapenemase-producing and extended-
60 spectrum β -lactamase (ESBL)-producing *Enterobacteriales* (CPE and ESBL-E, respectively),
61 particularly in critical care units [5-7]. These MDR pathogens can colonise healthcare-
62 associated (HCA) environmental reservoirs such as hospital sinks and contribute to
63 healthcare-associated infections (HAIs), with many studies linking HAIs to sink drains [8-10],
64 and successfully reducing HAI incidence via sink decontamination or removal [11, 12].

65

66 Metagenomics is increasingly used to characterise species and resistome diversity in
67 polymicrobial samples such as those from sink drains, but the results may be significantly
68 affected by sampling methodology, including storage conditions [13] and delays between
69 sample collection and processing such as those resulting from transportation to the
70 laboratory [14, 15]. Sample stabilisers, such as boric acid, which has been shown to limit
71 bacterial overgrowth in urine samples and is widely used for community urine sampling
72 [16], may offer a cheap and straightforward approach to maintaining sample microbial
73 composition for environmental surveys using metagenomics.

74

75 The impact of antibiotics on bacterial and AMR gene (ARG) persistence is of particular
76 concern in healthcare wastewater systems since these represent a confluence of patient
77 waste, antibiotic and chemical residues, and nutrients, creating a favourable environment
78 for ARG exchange in bacterial communities [17, 18]. For example, beta-lactam antibiotics
79 and their metabolites are excreted in many human fluid types, potentially exerting selective
80 pressures in disposal sites [18]. Moreover, polymicrobial biofilms in hospital sink drains
81 demonstrate high rates of ARG transfer [6, 19, 20]. Additionally, the presence of
82 disinfectants, such as chlorine and ethanol, non-antibiotic pharmaceuticals and heavy metal
83 pollutants including titanium dioxide can also promote ARG transfer [20-22].

84

85 Understanding how healthcare-associated environmental drivers such as antibiotic residues
86 and water chemistry contribute to the selection and dissemination of MDR pathogens
87 within the hospital estate is a prerequisite to optimising infection prevention and control
88 (IPC) and improving patient outcomes. However, rapidly and accurately evaluating these
89 environmental drivers has been considered costly and challenging owing to the need for
90 specialised analytical methods, and time-sensitive sample deterioration. Portable, cheap
91 and easy-to-use dipstick approaches to measuring antibiotic concentrations and water
92 chemistry would be of benefit.

93

94 In this study we piloted an easy-to-use workflow using dipsticks to detect the presence of
95 antibiotic residues and evaluate water chemistry in hospital sink traps and water chemistry
96 of hospital tap water. In addition, we validated the use of boric acid to preserve the
97 taxonomic and resistome composition of hospital sink trap samples during transport prior to
98 metagenomic sequencing.
99

100 **Methods**

101 *Antibiotic residue dipstick evaluation*

102 The QuaTest BTSQ 4-in-1 (Beta/Tetra/Sulfa/Quino) rapid test kit (Ringbio, China) was
103 validated according to the manufacturer's instructions using serial dilutions of ampicillin
104 (Cambridge Bioscience, UK), doxycycline (Merck Life Science, UK), sulfamethoxazole (Insight
105 Biotechnology Ltd, UK) and ciprofloxacin (Cambridge Bioscience, UK) from 1 mg/ml (acting
106 as a positive control) to the limits of detection (LoD) for each antibiotic. This dipstick was
107 chosen as it evaluates antibiotics commonly used in human healthcare settings.
108

109 *Water chemistry dipstick evaluation*

110 Three water quality dipstick kits (Bebapanda Upgrade 14-in-1 reagent strips [China],
111 SaySummer 16-in-1 reagent strips [China] and Qguai 9-in-1 test strips [China]) were
112 evaluated using calibration standard dilutions of: copper, chloride, nitrate, nitrite, hardness,
113 pH and alkalinity (Merck Life Science, UK). A fourth dipstick, Sensafe Boris's Silvercheck
114 strips (USA), was validated using silver calibration standard dilutions (Merck Life Science,
115 UK).

116
117 For dipsticks that performed best on the calibration standards we conducted a "real-world"
118 dipstick evaluation. Three hospital sink traps (A, B & C) were aspirated (50mls/trap) as
119 described previously [23] and tested using the Bebapanda Upgrade 14-in-1 reagent strips,
120 Sensafe Boris's Silvercheck strips and the QuaTest BTSQ 4-in-1 test kit. Aliquots of tap water
121 were collected from each sink after running each tap for 30 seconds, then tested using both
122 the Bebapanda and Sensafe Silvercheck dipsticks.
123

124 *Validation of boric acid as a preservative of microbial composition in samples*

125 Following dipstick evaluations, the three trap aspirates were also used to validate boric acid
126 as a preservative of microbial diversity. Three timepoints were evaluated: baseline (Day 0),
127 and at days 2 (Day 2) and 5 (Day 5) processed with and without boric acid (n=5 samples per
128 sink). For the baseline samples DNA was extracted immediately using the PowerSoil kit
129 (Qiagen); the day 2 +/- boric acid and day 5 +/- boric acid samples were incubated at ~22°C
130 for two and five days respectively prior to metagenomic DNA extraction. Metagenomes
131 (n=15) were sequenced on the Illumina MiSeq (v3 kit, 2x300bp). Metagenome taxonomic
132 and resistome profiles were generated with ResPipe (v.1.6.1) [24]. To address the difference
133 in sequencing effort across samples, all samples were randomly subsampled to 475,190
134 reads (the minimum observed). Mean absolute percentage error (MAPE) and Bray-Curtis
135 dissimilarity of genera were used to assess preservation of baseline taxonomy and sample-
136 level dissimilarity respectively. Normality was confirmed using the Shapiro-Wilk test before
137 paired sample t-testing to evaluate for statistically significant differences in taxonomic and
138 ARG distributions (p<0.05) between samples.

139

140 **Results**

141 *Antibiotic residues can be detected with dipsticks, with varying limits of detection (LoD)*
142 The LoDs for the QuaTest BTSQ 4-in-1 test kit for each antibiotic were: 3 µg/L (ampicillin), 10
143 µg/L (doxycycline), 20 µg/L (sulfamethoxazole) and 8 µg/L (ciprofloxacin). No cross-reactivity
144 nor false positive results were observed, and control lines were present in each test
145 ensuring validity of each result.

146

147 *Chemistry dipsticks performed differently, with variable limits of detection*

148 Overall, the Bebapanda Upgrade strips correctly characterised 34/40 (85%) of calibration
149 standard concentrations whereas the SaySummer and Qguai strips were less reliable,
150 correctly characterising only 23/40 (56%) of the biochemistry calibration standard
151 concentrations (Table 1). Incorrect classifications were at the lower end of the
152 concentration ranges, consistent with varying LoDs, with Bebapanda incorrectly classifying
153 copper 1 mg/L, residual chlorine 0.5 mg/L, nitrate 10 mg/L, and nitrite 1, 5 and 10 mg/L.
154 SaySummer and Qguai strips incorrectly classified copper 1 and 10 mg/L, residual chlorine
155 0.5, 1 and 3 mg/L, nitrate 10, 25 and 50 mg/L, nitrite 1, 5 and 10 mg/L, hardness 25 and 50
156 mg/L (plus 125 mg/L SS only), pH 7.0 (Q only), and finally alkalinity 40, 80 and 120 mg/L.
157 Sensafe Boris's Silvercheck strips correctly characterised all 6 silver dilutions (0, 0.05, 0.1,
158 0.25, 0.5 and 1.0 mg/L).

159

160 *Dipsticks can be used on “real-life” sink trap and water samples*

161 Dipsticks were easy-to-use on the “real-life” sink trap samples. The trap aspirate from sink C
162 tested positive for the presence of tetracycline and sulfonamide antibiotic classes, denoted
163 as the absence of a test line and/or line colour intensity less than that of the control line
164 (Figure 1). Chemical indicators varied across sink trap aspirates and tap water samples to
165 some extent, highlighting that measuring these parameters may provide valuable context in
166 an epidemiological survey. Alkalinity values appropriately mirrored pH values, and one sink
167 drain (sink C) demonstrated a low pH and the presence of bromine and chlorine, possibly
168 consistent with the application of a cleaning agent (Table 2).

169

170 *Boric acid preserves the microbial taxonomic and AMR gene composition of sink trap
171 samples for metagenomics*

172 Boric acid significantly preserved the microbial composition of sink trap aspirates.
173 Proteobacteria dominated all samples, but apparent overgrowth was prevented in samples
174 supplemented with boric acid (Figure 2, top panel). 1-MAPE scores (with higher scores
175 indicating greater similarity with baseline samples) indicated baseline (Day 0) taxonomic
176 diversity and abundance were most closely preserved in samples containing boric acid, with
177 significant divergence from baseline in sink A samples without boric acid ($p=0.01$) (Figure 2,
178 bottom panel). Samples without boric acid diverged from baseline by Day 2 whereas
179 samples with boric acid still resembled baseline at Day 5; however, decreasing 1-MAPE
180 between days 2 and 5 was observed for all samples even with boric acid, indicating that the
181 preservative effect of boric acid on composition is time-sensitive (Figure 2, bottom panel).

182

183 The preservative effect of boric acid was less evident for the resistome, possibly due to
184 limited sensitivity in detecting ARGs in these samples at this sequencing depth, as
185 demonstrated by the low numbers of sequencing reads matching AMR gene targets (Figure
186 3, top panel). In sink A, no ARGs were detected at baseline, making it impossible to calculate
187 1-MAPE scores. In sink B, where aminoglycoside resistance genes were detected at baseline,

188 sulfonamide resistance genes were also detected by Day 5, with proportionally more
189 divergence observed in the sample without boric acid, likely consistent with the overgrowth
190 of a sulfonamide resistant species (Figure 3, top panel). For sink C, both samples showed a
191 similar degree of divergence from baseline by Day 2, regardless of the presence or absence
192 of boric acid. There was a slight increase in the 1-MAPE score for Day 5 with boric acid
193 compared to the sample without boric acid, consistent with better preservation of ARG
194 composition over time using boric acid. Anecdotally but of interest, the number of reads
195 matching to ARG targets was highest for the sink C drain sample, which was also the sample
196 in which antibiotic residues were identified. Overall, clustering patterns based on Bray-
197 Curtis dissimilarities were observed for both taxonomy and resistome data, with distinct
198 separation based on the sink sampled, and broadly closer clustering for cases with boric acid
199 and baseline (Supplementary figure 1).

200

201 Discussion

202 In this pilot study we validated an easy-to-use workflow to both monitor hospital sink drains
203 for commonly used antibiotic classes and evaluate water chemistry in sink traps and tap
204 water, demonstrating the QuaTest BTSQ 4-in-1 antibiotic dipstick and Bebapanda Upgrade
205 14-in-1 and SenSafe Boris's Silvercheck strips may be suitable for this purpose. Additionally,
206 we validated the use of boric acid to preserve the microbial composition of hospital sink
207 drain aspirates, mitigating transport-associated compositional changes, and facilitating
208 more representative taxonomic and resistome profiling using metagenomics. We sampled
209 three sinks in a healthcare setting to characterise ease of use and generate some example
210 data.

211

212 The presence of antibiotics in hospital sink drains may facilitate persistence of AMR genes,
213 horizontal gene transfer and emergence of MDR bacteria. Previously, Voigt *et al* [17]
214 identified high concentrations of antibiotics from hospital sink drains, shower drains and
215 toilets within oncology and neurological clinics, suggesting the presence of antibiotic
216 residues in hospital wastewater corresponds to heavy antibiotic usage typical in such clinics.
217 Effective and cheap monitoring of such environmental selection pressures could be of
218 relevance to mitigating AMR selection in the environment. The easy-to-use QuaTest
219 qualitative dipstick is a lateral flow immunochromatographic assay rapidly indicating
220 antibiotic presence in a sample by the absence of a line for the corresponding antibiotic, or
221 a line with a lower intensity in comparison to the control line. This assay identifies the
222 presence of 40 beta-lactams, tetracyclines, sulfonamides and quinolones. Our validation
223 against serial dilutions of known antibiotic concentrations indicates good sensitivity and
224 specificity for all four classes of antibiotics.

225

226 Four different dipstick brands were used to measure water chemistry, including one
227 specifically for silver concentrations. Although all dipsticks performed well in quantifying
228 water chemistry at higher concentrations, the Bebapanda Upgrade 14-in-1 strips worked
229 best at the lower concentrations of the eight diluted standards evaluated, and the SenSafe
230 Boris's Silvercheck strips accurately characterised silver concentrations. When applied to
231 sink trap and tap water samples from three hospital sinks, some differences were noted.
232 Piped water is generally hard in our region (~260-280 mg/L) [25] as it contains large
233 amounts of magnesium and calcium, but testing in our sinks demonstrated results lower
234 (sinks A, B) and higher than this (sink C). Sinks A and B could perhaps be supplied from a

235 different water source. For sink C, it may be that the tap from this particular sink was
236 infrequently cleaned and a mineral plaque inside the tap was contributing to the hardness
237 value sampled. Fluoride is not added to the water supply in this region but occurs naturally
238 in drinking water supplies, as reflected in the results, whereas the water is chloraminated or
239 chlorinated [25], but we were only able to detect free chlorine in trap aspirate from sink C
240 which may have been from a cleaning product. The presence of lead is perhaps from lead
241 service pipes or an inaccuracy in the dipstick colour chart given this analyte was not
242 evaluated as part of our standard dilutions. Bromine, an oxidant which can be used as a
243 sanitiser or disinfectant, was only detected in the trap aspirate of sink C which may again
244 have been residual post-cleaning.

245

246 Biologically active environmental samples such as sink trap aspirates may undergo
247 compositional changes during transport, potentially impacting the accuracy of subsequent
248 analyses and interpretation. Factors such as temperature fluctuation, nutrient depletion,
249 incubation time, residual disinfectants or cleaning products and handling practices can lead
250 to shifts in microbial populations and DNA degradation. Although these issues can be
251 predominately mitigated through immediate deep freezing and cold-chain transport
252 practices, these approaches incur significant cost and present a logistical challenge. Our
253 study demonstrates that boric acid is an effective short-term preservative of the taxonomic
254 composition and probably resistome of sink trap samples for 2-5 days at room temperature,
255 although our observations on preservation of the resistome were less clear, probably driven
256 by the relatively low numbers of reads mapping to ARG targets at the sequencing depth
257 used. Interestingly, most samples clustered by the sampled sink regardless of boric acid
258 status for both taxonomic and resistome ordinations, suggesting sink-level differences (e.g.
259 location, usage, design) are stronger drivers of variation than composition shifts occurring
260 over five days storage. However, this observation needs to be considered with caution given
261 the small numbers of sink traps evaluated.

262

263 In addition to the small number of sink trap/tap samples analysed, there were several
264 limitations to this study. We assessed dilutions of standards for only 8 of the 14 chemicals
265 evaluated on the chemistry dipsticks, as standards for the other analytes were not readily
266 available. Dilution was undertaken in sterile purified water rather than a matrix mimicking a
267 sink trap or tap water sample, as these matrices would be difficult to simulate and using
268 real-life samples means that background concentrations of these chemicals may already be
269 present. For the antibiotic dipstick a downside is that it gives a binary, qualitative result that
270 does not differentiate between antibiotics within each of the four classes or any indication
271 of the detection of multiple antibiotics within each class.

272

273 **Conclusions**

274 This study evaluated and piloted easy-to-use dipsticks to detect the presence of four classes
275 of antibiotic residues and measure water chemistry parameters from sink trap aspirates and
276 tap water. Taxonomic and resistome composition of hospital trap samples were largely
277 maintained after storage with boric acid at ~22°C for up to five days, facilitating the
278 collection of environmental samples for multi-site studies. Performing simple dipstick tests
279 to detect antibiotic residues and measure water chemistry parameters in hospital
280 wastewater and accurately evaluating pathogen and AMR gene burden in sink reservoirs

281 may contribute to strategies to monitor and mitigate the impact of AMR selection in
282 hospital environments.

283

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285

286 **Conflict of Interest statement**

287 All authors declare no conflict of interest in this study.

288

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Analyte	Bebapanda Upgrade 14-in-1	SaySummer 16-in-1	Qguai 9-in-1 test strips
Copper (mg/L)			
0			
1			
10	+		
30	+	+	+
100	+	+	+
300	+	+	+
Residual chlorine (mg/L)			
0			
0.5			
1	+		
3	+		
5	+	+	+
10	+	+	+
20	+	+	+
Nitrate (mg/L)			
0			
10			
25	+		
50	+		
100	+	+	+
250	+	+	+
500	+	+	+
Nitrite (mg/L)			
0			
1			
5			
10			
20	+	+	+
40	+	+	+
80	+	+	+
Hardness (mg/L)			
0			
25	+		
50	+		
125	+		+
250	+	+	+
425	+	+	+
pH			
7.0	+	+	
Alkalinity (mg/L)			
0			
40	+		
80	+		
120	+		
180	+	+	+
240	+	+	+

380

381 **Table 1.** Results of the dipstick tests on calibration standards of the chemical analytes being
 382 tested. “+” denotes cases where the analyte was detected with the dipstick, a blank value
 383 cases where the analyte was not detected with the dipstick.

384

385

Analyte	Sink trap A	Tap A	Sink trap B	Tap B	Sink trap C	Tap C
Alkalinity (mg/L)	240	180	240	180	0	120
pH	8.4	7.8	8.4	7.8	6.2	7.2
Hardness (mg/L)	125	125	125	125	425	425
Fluoride (mg/L)	25	25	25	25	25	0
Sulfite (mg/L)	0	0	0	0	0	0
Nitrite (mg/L)	0	0	0	0	0	0
Nitrate (mg/L)	0	25	25	25	0	25
Bromine (mg/L)	0	0	0	0	20	0
Free chlorine (mg/L)	0	0	0	0	5	0
Mercury (mg/L)	0	0	0	0	0	0
Chromium (mg/L)	0	0	0	0	5	0
Iron (mg/L)	0	0	0	0	5	5
Copper (mg/L)	0	0	0	1	1	0
Lead (mg/L)	20	20	20	20	20	20
Silver (mg/L)	0	0	0	0	0	0

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Table 2. Sink trap aspirate and tap water sample chemistry measurements using Bebapanda Upgrade 14 in 1 reagent dipsticks and Sensafe Boris's Silvercheck dipsticks

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Figure 1. Antibiotic residues of tetracycline and sulfonamide classes of antibiotics detected in sink trap sample C. A control line indicates the dipstick is performing; antibiotics are characterised as present if the antibiotic-specific line is less dark than the control line or absent.

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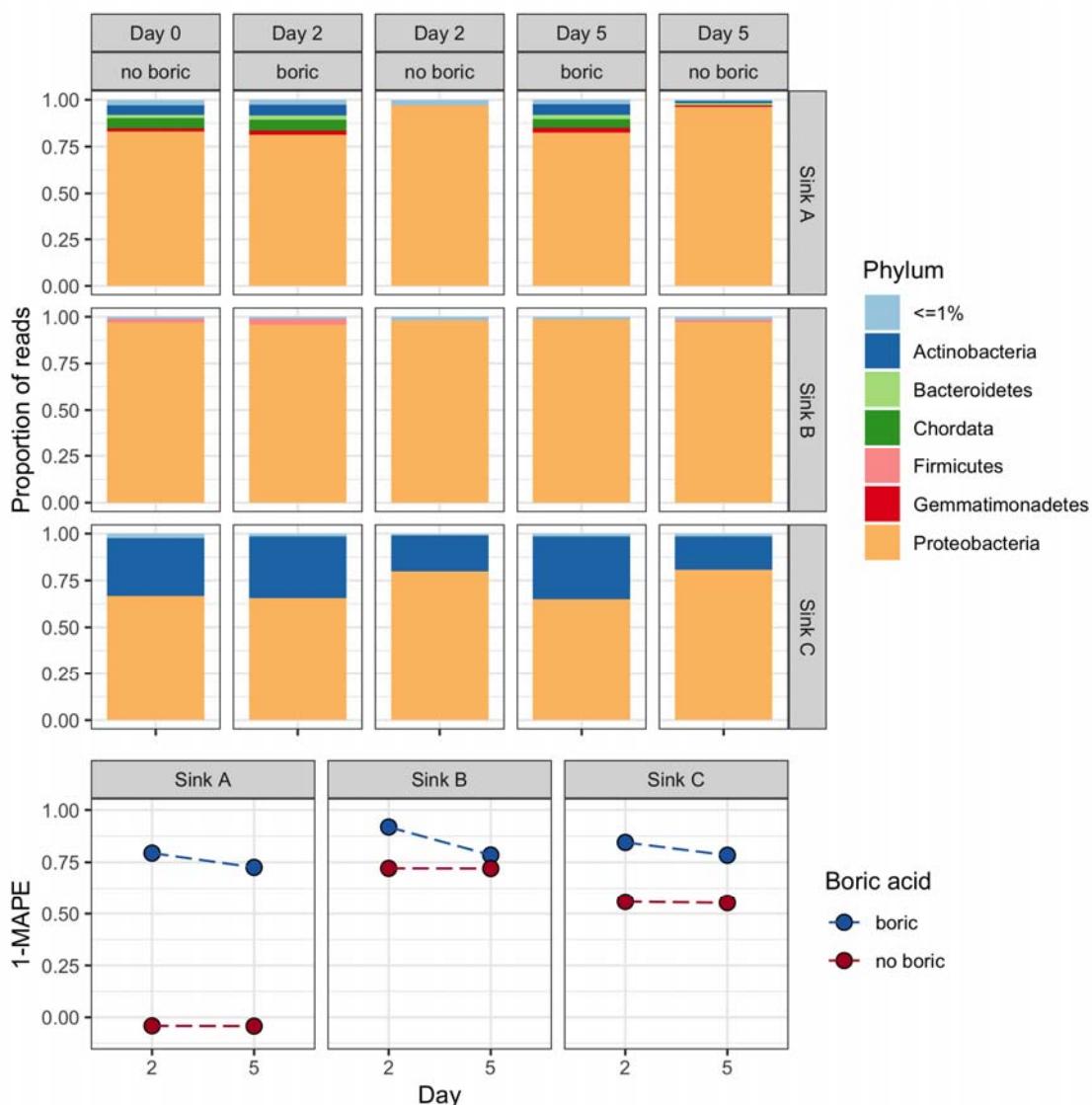
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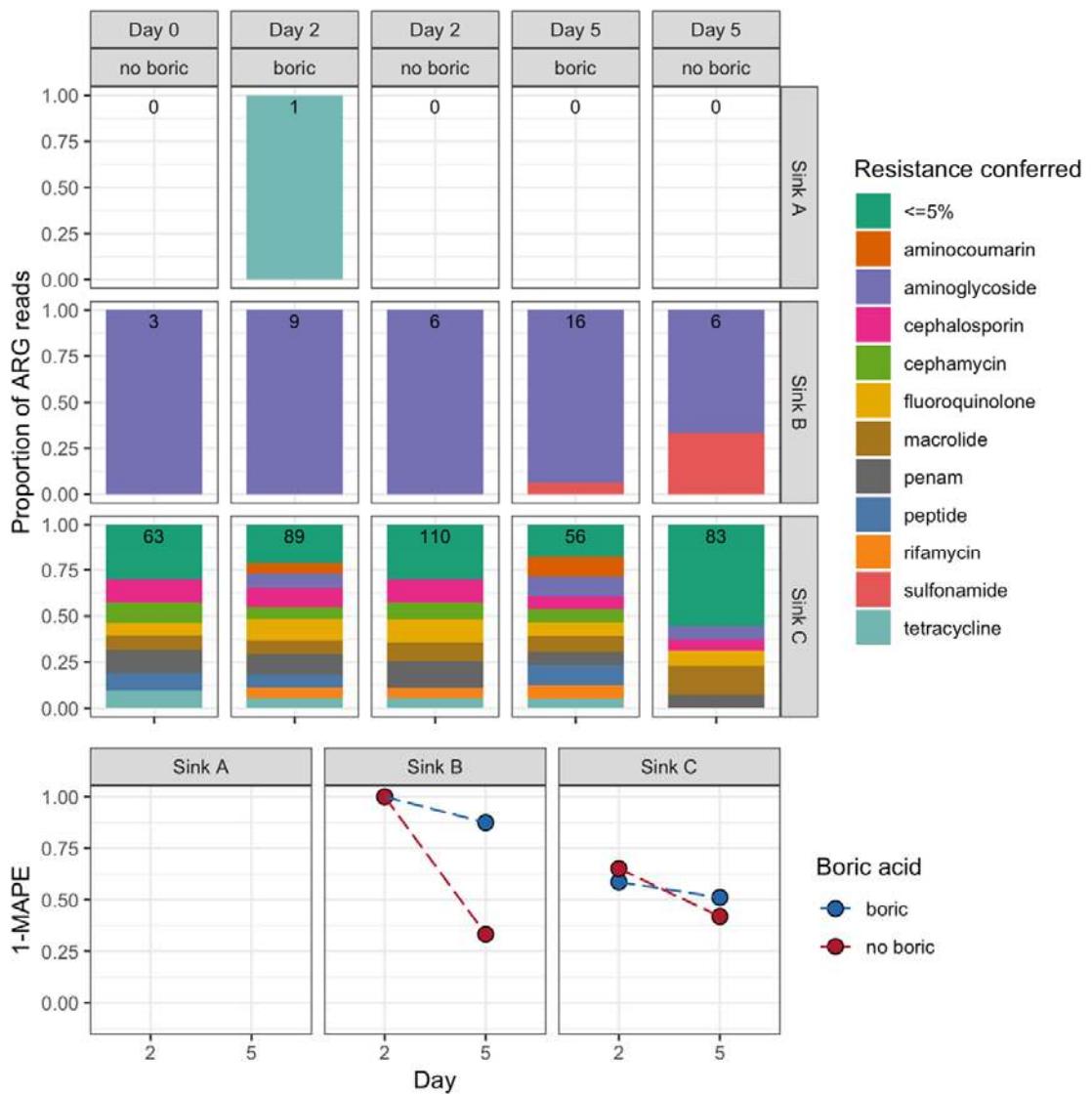
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Figure 2. Taxonomic distributions in samples with and without boric acid. (Top panel) Relative abundances of phyla across sink samples faceted by sink (A, B, C), processing day and use of boric acid as a preservative. <= represents phyla under 0.01 proportion of reads. (Bottom panel) Mean absolute percentage error (MAPE) of taxonomic abundances between baseline (Day 0) and processing day faceted by sink and stratified by whether boric acid was used as a preservative, where $1-\text{MAPE}=1$ indicates perfect preservation of baseline taxonomic distributions.



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Figure 3. Antimicrobial resistance gene (ARG) presence in samples with and without boric acid. (Top panel) ARG reads identified in sink samples A-C by day of evaluation and with/without boric acid, represented as the proportion of reads conferring resistance to a given antimicrobial class, with the number of reads identified in each facet. <= represents resistances under 0.05 proportion of reads. (Bottom panel) Mean absolute percentage error (MAPE) of abundances between baseline (Day 0) and processing day faceted by sink sample A-C and stratified by whether boric acid was used as a preservative, where 1-MAPE=1 indicates perfect preservation of baseline ARG proportions.

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