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ORIGINAL ARTICLE

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Fitness costs associated with carriage of a large staphylococcal plasmid are reduced by subinhibitory concentrations of antiseptics

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Abstract

Staphylococcus aureus carries a collection of mobile genetic elements that often harbor virulence and antimicrobial resistance genes. Since the introduction of antibiotics, plasmids have become a major genetic element responsible for the distribution of antimicrobial resistance. Under antimicrobial selection, resistance plasmids are maintained within bacterial populations as a means to ensure survival. However, in the absence of selection, large plasmids can be lost due to the fitness costs associated with harboring these genetic elements. pC02 is a previously identified multidrug resistance, conjugative plasmid that is found in S. aureus. In addition to antibiotic resistance, pC02 also carries genes known to be associated with antiseptic resistance. Among these, we previously characterized the contribution of qacA to pC02 mediated reduced chlorhexidine susceptibility. Herein, we demonstrate that pC02 also mediates triclosan resistance, likely due to the presence of *fabl*, a known triclosan resistance gene. Moreover, we demonstrate that conjugative transfer of pC02 increases triclosan resistance in recipient cells. Competition assays demonstrated a fitness cost associated with carriage of the large pC02 plasmid. However, subinhibitory concentrations of either chlorhexidine or triclosan abrogated this fitness cost. Given the widespread use of these antiseptics, both of which accumulate in wastewater and other environmental reservoirs, indiscriminate use of antiseptics likely imposes a constant selective pressure that promotes maintenance of antimicrobial resistance factors within S. aureus.

KEYWORDS

antibiotic resistance, bacterial plasmids, mobile genetic elements, Staphylococcus

1 | INTRODUCTION

Infections caused by multidrug-resistant *S. aureus* continue to result in therapeutic failure and extended hospital stays. The evolution of multidrug resistance in bacteria is associated with

nonessential antibiotic applications and improper administration of these agents (Andersson and Hughes, 2010; Foster, 2017; Munita & Arias, 2016; Ventola, 2015). Today, it is not uncommon for pathogens to be resistant to multiple antibiotics. Antibiotic resistance is commonly attributed to large plasmids, which have

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accumulated resistance genes over time. In addition to antibiotic resistance genes, plasmids can also harbor biocide and heavy metal resistance genes (McCarthy & Lindsay, 2012). When found on the same genetic element, this collection of resistance genes can provide protection against a wide variety of compounds, any one of which can provide a selective pressure to maintain the entire genetic element; this phenomenon is known as coselection (Gullberg, Albrecht, Karlsson, Sandegren, & Andersson, 2014; Pal, Bengtsson-Palme, Kristiansson, & Larsson, 2015). Given the increased awareness of the need to reduce unnecessary antibiotic prescriptions, some coselective pressures are being minimized. However, increased utilization of antiseptics, such as quaternary ammonium compounds and chlorhexidine, in common use household products have increased their abundance in environmental reservoirs. To this end, little is known about the coselective pressures imposed by subinhibitory concentrations of antiseptic compounds on multidrug resistance plasmids in S. aureus.

In our previous work, we identified and characterized a large multidrug resistance conjugative plasmid in S. aureus called pC02 (Johnson et al., 2015; LaBreck, Li, Gibbons, & Merrell, 2019; LaBreck et al., 2018). In the prior characterization study, pC02 was shown to be a fusion between at least two theta replicating plasmids: one plasmid containing the conjugative gene cluster and the other harboring antibiotic resistance genes (erythromycin, beta-lactam resistance), a heavy metal resistance gene (cadmium resistance), and biocide resistance genes (LaBreck et al., 2019). For biocide resistance, pC02 harbors qacA and fabl, which offer reduced susceptibility to chlorhexidine and triclosan, respectively. We previously demonstrated that pC02 gacA mediates reduced susceptibility to chlorhexidine (LaBreck et al., 2018). Herein, we demonstrate that pC02 also mediates reduced triclosan susceptibility. To further dissect the implications of carrying these biocide resistance genes, we analyzed the potential of subinhibitory concentrations of antiseptics to coselect for other resistance genes on pC02.

2 | MATERIALS AND METHODS

2.1 | Bacteria and growth conditions

Staphylococcus aureus 2014.C02 (S. aureus C02), S. aureus C02-M2, S. aureus C02-RN, and S. aureus RN TC (pC02F) were previously described (LaBreck et al., 2019, 2018). Briefly, S. aureus C02 harbors the conjugative plasmid pC02 (GenBank: CP012121.2). S. aureus C02-M2 is an isogenic variant of S. aureus C02 that has been cured of pC02. S. aureus C02-RN is a spontaneously resistant rifampin and novobiocin-resistant strain that was derived in the S. aureus C02-M2 background. S. aureus C02-RN TC (pC02F) is a transconjugant derivative of a mating between S. aureus C02 and C02-RN wherein C02-RN obtained pC02 by conjugation. The strains are archived in our strain collection under the following

DSM numbers: *S. aureus* 2014.C02 (DSM 1418), *S. aureus* C02-M2 (DSM 1552), *S. aureus* C02-RN (DSM1553), and *S. aureus* C02-RN TC (pC02F) (DSM1699). All strains were grown in Mueller Hinton Broth II (Becton Dickinson). For solid media, MHB was supplemented with 1.7% agar.

2.2 | Triclosan susceptibility testing

The MIC of triclosan was tested in a macrobroth dilution assay as previously described (Johnson et al., 2015; LaBreck et al., 2018) with minor modifications. Briefly, approximately 5.0×10^4 colony forming units (CFU) were inoculated into 2 ml of MHB containing increasing concentrations (0.2 µg/ml to 1.0 µg/ml in increments of 0.2 µg/ml, or 0.002 µg/ml to 0.01 µg/ml in increments of 0.002 µg/ml) of purified (≥97.0%) Irgasan (Sigma). The cultures were grown at 37°C degrees overnight, shaking at 220 rpm. The MIC was determined by visual analysis of the culture's turbidity. Similarly, the MIC of chlorhexidine for C02-RN was tested by microbroth dilution as previously described (Johnson et al., 2015; LaBreck et al., 2018).

2.3 | pC02 fitness cost

Strains of C02 and C02-M2 (C02 cured of pC02) were grown overnight in 2 ml of Muller Hinton Broth (MHB). The following day, approximately 2.5×10^4 CFU of each strain was combined in 2 ml of MHB. About 10 µl was taken from the mixed culture for input CFU determination, and the culture was grown shaking at 37°C for 24 hr. CFU for CO2 were determined by plating on MHA supplemented with cadmium chloride; CFU for C02-M2 were determined by plating on MHA followed by subtraction of the total CFU determined for C02. The following day, CFU for C02 and C02-M2 were determined from the 24-hr mixed culture, and the culture was passaged as approximately 1×10^5 CFU into 2 ml of fresh MHB. The culture was repeatedly passaged as described above, and CFU were determined at 48, 72, and 96 hr as a means to determine the competitive fitness, as represented by a competition index, of C02 and C02-M2 over time. A similar protocol was followed for experiments that were conducted with subinhibitory concentrations of antiseptics with minor modifications. Briefly, strains were grown overnight without selection in MHB, the following day equal CFU of the strains were added to 2 ml of MHB supplemented with either 0.1 µg/ml, 0.5 μ g/ml, or 0.01 μ g/ml chlorhexidine or 0.003 μ g/ml, 0.0015 μ g/ ml, or 0.00075 µg/ml triclosan. Antiseptic selection was maintained throughout the multiple passages. The spread in the gathered data was likely attributed to the plating method used to determine total CFU of the bacteria; 10 µl streak dilutions were used. The subinhibitory antiseptic concentrations were empirically selected based on strain MIC values, which are shown in Table 1 (Buffet-Bataillon, Tattevin, Bonnaure-Mallet, & Jolivet-Gougeon, 2012).

TABLE 1 Antiseptic MIC for C02 strains

	Triclosan		Chlorhexidine ^a	
Strain	Median ^b	Max	Median	Max
C02	1	1	0.9	1
C02-M2	0.006	0.006	0.3	0.4
C02-RN	0.008	0.01	0.2	0.2
C02-RN TC (pC02F)	1	1	0.5	0.5

^aData for chlorhexidine MIC for C02, C02-M2, and C02-RN TC (pC02F) are taken from LaBreck et al. (2018).

 b Values are concentrations in $\mu g/ml.$ Data were obtained from at least 3 biologically independent experiments.

The competitive index was calculated using the following formula: Output (CFU C02-M2/CFU C02)/Input (CFU C02-M2/CFU C02).

3 | RESULTS AND DISCUSSION

On pC02, *fabl* is found on the TnSha1 element (Furi et al., 2016) (Figure 1). To determine the extent of triclosan resistance mediated

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by this element, we measured the triclosan MIC of strain CO2 and a plasmid cured variant of CO2, CO2-M2, in a macrobroth dilution assay. The MIC of CO2 was >100-fold higher than CO2-M2, suggesting that the *fabl* resistance gene found on pCO2 offered substantial protection from triclosan (Table 1). As pCO2 is a conjugative plasmid, we next sought to determine whether this resistance was transferrable. To this end, we examined the MICs of triclosan for a recipient strain as well as a pCO2 transconjugant in the same strain background. Similarly, we identified a >100-fold increase in triclosan resistance (Table 1). Together, these data indicated that pCO2 provided significant protection against triclosan and that this resistance was transferrable by conjugation.

The presence of two functional antiseptic resistance genes (*qacA* and *fabl*) on pC02 suggests that *S. aureus* is under increasing selective pressure from exposure to different antiseptic agents. Interestingly, these genes are adjacent to each other, which may increase the frequency of cotransfer via conjugation. To this end, in addition to being found on the fully conjugated pC02, both *fabl* and *qacA* are found on pERY (a partially transferred pC02 exconjugant plasmid) (Figure 1), which we previously demonstrated displayed an increased conjugative transfer frequency as compared to pC02 (LaBreck et al., 2019). However, the partially transferred



FIGURE 1 Conjugative Triclosan Resistance. (a) A simplified map of pC02 drawn to scale using AngularPlasmid (AngularPlasmid, 2015). The *oriT* sequences for conjugative transfer are designated by *oriT1* and *oriT2*. The conjugative cluster containing the genes for conjugation is outlined in green. The resistance region containing multiple antimicrobial resistance genes is outlined in blue. Outside of the plasmid backbone, which is shown in black, are gray open reading frames that correspond to the different resistance genes: *dfrC* encodes resistance to trimethoprim; *msrA* and *mphC* encode resistance to erythromycin; *qacA* and *qacR* (*qacA*'s regulator), denoted as *qacA/R*, encode reduced susceptibility to chlorhexidine; *fabl* encodes reduced susceptibility to triclosan; *blaZ*, *blaR1*, and *blaI*, shown as *blaZ* and *blaR1/l*, encode resistance to beta-lactams; *cad* confers resistance to cadmium. The TnSha1 element and two additional IS257 elements are highlighted in yellow. The two replication initiation genes are indicated in red. The partial conjugative transfer event that generates the pERY plasmid variant is outlined in dark blue

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pERY is unstable without selection, likely nonconjugative, and similar plasmids have not been deposited into the NCBI database (LaBreck et al., 2019). These data suggest the pERY plasmid variant is uncommon in nature if it exists at all. Furthermore, it is unlikely that *qacA* and its regulator *qacR* move with *fabl* on the TnSha1 element; no IS1272-associated inverted repeats are found near *qacA* or *qacR* (data not shown). Regardless, the presence of *qacA*, *fabl*, and additional resistance elements provides an example of resistance gene clustering on a plasmid.

The resistance cluster on pC02 is located within a region that encompasses ~45% of the total plasmid sequence (Figure 1). This region and the conjugative cluster comprise the 61,539 bp sequence of pC02, which is the 5th largest *S. aureus* plasmid in the NCBI database. Given the large size of pC02, we hypothesized that there could be a fitness cost associated with carriage of pC02. To assess the fitness cost of pC02, we determined the competitive index of C02 versus C02-M2 (pC02-cured C02) in a daily passaged mixed culture assay. In the absence of antimicrobial agents, there was a >10-fold fitness advantage for C02-M2 after 48 hr, and this difference was further exaggerated at 72 and 96 hr (Figure 2a). These data indicate that pC02 impacts host fitness in the examined growth conditions.

Antiseptic compounds are used daily in hospitals and communities. After their application, the majority of antiseptic compounds are disposed of in wastewater and then accumulate at subinhibitory

concentrations in the environment (Mulder et al., 2018; Zhang et al., 2015). To this end, subinhibitory concentrations of chlorhexidine in sludge and influent wastewater have been measured at 7.6 µg/ml and 0.001185 µg/ml, respectively (Östman, Lindberg, Fick, Björn, & Tysklind, 2017). Similarly, triclosan has been shown to be present in influent wastewater at concentrations of 0.0038-0.0166 µg/ml (McAvoy, Schatowitz, Jacob, Hauk, & Eckhoff, 2002). To determine whether subinhibitory concentrations of antiseptics could reduce the relative fitness cost of pC02, we repeated the mixed culture experiment in subinhibitory concentrations of two antiseptics. In the presence of subinhibitory chlorhexidine (0.1 μ g/ml) or triclosan (0.0015 μ g/ml), the fitness cost of harboring pC02 was partially or fully negated throughout the entire 96 hr (Figure 2a). To determine whether the phenotype was similar in different concentrations of subinhibitory chlorhexidine and triclosan, we tested two additional concentrations for each antiseptic (Figure 2b). Again, the fitness cost associated with pC02 carriage was ameliorated in 0.05 µg/ml chlorhexidine or 0.003 µg/ml triclosan. However, this amelioration was not seen in chlorhexidine and triclosan at 0.01 μ g/ml and 0.00075 μ g/ml, respectively (Figure 2b); thus, a minimum concentration threshold of each antiseptic was required to eliminate the fitness cost associated with carriage of pC02. Together, these data indicate that biologically relevant subinhibitory concentrations of antiseptic compounds can select for strains that carry antiseptic resistance plasmids.



FIGURE 2 Fitness Cost of pC02 in Mixed Culture. Strains C02 and C02-M2 were inoculated at similar CFU and passaged every 24 hr. The competitive index was calculated at 24, 48, 72, and 96 hr by dividing the ratio of C02-M2 to C02 at output time points by the ratio of C02-M2 to C02 at the input time point. (a) Strains were grown in MHB, MHB + 0.1 µg/ml chlorhexidine or MHB + 0.0015 µg/ml triclosan. Statistically significant differences are indicated as determined by twoway ANOVA with Dunnett's multiple comparison test. (b) Strains were grown in MHB supplemented with either $0.05 \,\mu g/ml$ chlorhexidine, $0.01 \,\mu g/ml$ chlorhexidine, 0.003 µg/ml triclosan, or 0.00075 µg/ml triclosan. Statistically significant differences are indicated as determined by two-way ANOVA with Tukey's multiple comparison test. For both A and B, graphed values represent at least three independent replicates for each strain and the bar indicates the geometric mean. Limit of detection data points are plotted as outlined symbols

Antiseptics have become an integral component in many healthcare and common use consumer products. When applied at recommended concentrations, they are effective at inhibiting microbial contamination. However, given their increasing applications, antiseptic compounds have inevitably accumulated in the environment at subinhibitory concentrations (Mulder et al., 2018; Zhang et al., 2015). Toxicities from QACs and triclosan have been demonstrated for various aquatic organisms (Dann & Hontela, 2011; Di Nica, Gallet, Villa, & Mezzanotte, 2017; Zhang et al., 2015). However, little is known about the effects of subinhibitory concentrations of antiseptics in wastewater. Other groups have demonstrated increased plasmid stability in subinhibitory concentrations of metals and antiseptics, as well as cross-resistance development in subinhibitory antibiotic concentrations (Braoudaki & Hilton, 2004; Buffet-Bataillon et al., 2012; Gullberg et al., 2014; Kampf, 2018; Wand, Bock, Bonney, & Sutton, 2017). Outside of the aquatic environment, subinhibitory concentrations of antiseptics can also be found on surfaces, which provide similar selective pressures (Bashir et al., 2019; Ribič, Klančnik, & Jeršek, 2017). Herein, we showed that subinhibitory concentrations of antiseptics negated the fitness cost associated with carrying a large plasmid in S. aureus (Figure 2), and in doing so coselected for the presence of multiple antimicrobial resistance genes on pC02. En masse, the data support the need for greater antiseptic stewardship.

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CONFLICT OF INTEREST

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AUTHOR CONTRIBUTION

Patrick T LaBreck: Investigation; Methodology; Writing-original draft; Writing-review & editing. D. Scott Merrell: Investigation; Methodology; Resources; Writing-original draft; Writing-review & editing.

ETHICS STATEMENT

None required.

DATA AVAILABILITY STATEMENT

All data are provided in the manuscript. Original raw data are available by request. GenBank accession numbers for *S. aureus* 2014.C02 ____MicrobiologyOpen

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and pC02 are CP012120.2 (https://www.ncbi.nlm.nih.gov/nucco re/CP012120.2) and CP012121.2 (https://www.ncbi.nlm.nih.gov/ nuccore/CP012121.2), respectively.

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REFERENCES

- Andersson, D. I., & Hughes, D. (2010). Antibiotic resistance and its cost: Is it possible to reverse resistance? *Nature Reviews Microbiology*, 8, 260–271. https://doi.org/10.1038/nrmicro2319
- AngularPlasmid. (2015). AngularPlasmid, on Vixis. Retrieved from http:// angularplasmid.vixis.com/about.php
- Bashir, M. H., Hollingsworth, A., Schwab, D., Prinsen, K. S., Paulson, J. E., Morse, D. J., & Bernatchez, S. F. (2019). Ex vivo and in vivo evaluation of residual chlorhexidine gluconate on skin following repetitive exposure to saline and wiping with 2% chlorhexidine gluconate/70% isopropyl alcohol pre-operative skin preparations. The Journal of Hospital Infection, 102, 256–261.
- Braoudaki, M., & Hilton, A. C. (2004). Adaptive resistance to biocides in Salmonella enterica and Escherichia coli O157 and cross-resistance to antimicrobial agents. Journal of Clinical Microbiology, 42, 73–78. https ://doi.org/10.1128/JCM.42.1.73-78.2004
- Buffet-Bataillon, S., Tattevin, P., Bonnaure-Mallet, M., & Jolivet-Gougeon, A. (2012). Emergence of resistance to antibacterial agents: The role of quaternary ammonium compounds-a critical review. *International Journal of Antimicrobial Agents*, 39, 381–389. https://doi. org/10.1016/j.ijantimicag.2012.01.011
- Dann, A. B., & Hontela, A. (2011). Triclosan: Environmental exposure, toxicity and mechanisms of action. *Journal of Applied Toxicology*, 31, 285–311. https://doi.org/10.1002/jat.1660
- Di Nica, V., Gallet, J., Villa, S., & Mezzanotte, V. (2017). Toxicity of quaternary ammonium compounds (QACs) as single compounds and mixtures to aquatic non-target microorganisms: Experimental data and predictive models. *Ecotoxicology and Environmental Safety*, 142, 567–577. https://doi.org/10.1016/j.ecoenv.2017.04.028
- Foster, T. J. (2017). Antibiotic resistance in Staphylococcus aureus. Current status and future prospects. FEMS Microbiology Reviews, 41, 430–449. https://doi.org/10.1093/femsre/fux007
- Furi, L., Haigh, R., Al Jabri, Z. J., Morrissey, I., Ou, H.-Y., León-Sampedro, R., ... Oggioni, M. R. (2016). Dissemination of novel antimicrobial resistance mechanisms through the insertion sequence mediated spread of metabolic genes. *Frontiers in Microbiology*, 7, 1008. https:// doi.org/10.3389/fmicb.2016.01008
- Gullberg, E., Albrecht, L. M., Karlsson, C., Sandegren, L., & Andersson, D. I. (2014). Selection of a multidrug resistance plasmid by sublethal levels of antibiotics and heavy metals. *mBio*, 5, e01918–e2014. https ://doi.org/10.1128/mBio.01918-14
- Johnson, R. C., Schlett, C. D., Crawford, K., Lanier, J. B., Merrell, D. S., & Ellis, M. W. (2015). Recurrent methicillin-resistant *Staphylococcus aureus* cutaneous abscesses and selection of reduced chlorhexidine susceptibility during chlorhexidine use. *Journal of Clinical Microbiology*, 53, 3677-3682. https://doi.org/10.1128/JCM. 01771-15
- Kampf, G. (2018). Biocidal agents used for disinfection can enhance antibiotic resistance in gram-negative species. *Antibiotics*, 7. https://doi. org/10.3390/antibiotics7040110
- LaBreck, P. T., Li, Z., Gibbons, K. P., & Merrell, D. S. (2019). Conjugative and replicative biology of the *Staphylococcus aureus* antimicrobial resistance plasmid, pC02. *Plasmid*, 102, 71–82. https://doi. org/10.1016/j.plasmid.2019.02.006
- LaBreck, P. T., Rice, G. K., Paskey, A. C., Elassal, E. M., Cer, R. Z., Law, N. N., ... Ellis, M. W. (2018). Conjugative transfer of a novel staphylococcal

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plasmid encoding the biocide resistance gene, *qacA*. *Frontiers in Microbiology*, 9, 2664. https://doi.org/10.3389/fmicb.2018.02664

- McAvoy, D. C., Schatowitz, B., Jacob, M., Hauk, A., & Eckhoff, W. S. (2002). Measurement of triclosan in wastewater treatment systems. Environmental Toxicology and Chemistry: An International Journal, 21, 1323–1329. https://doi.org/10.1002/etc.5620210701
- McCarthy, A. J., & Lindsay, J. A. (2012). The distribution of plasmids that carry virulence and resistance genes in *Staphylococcus aureus* is lineage associated. *BMC Microbiology*, 12, 104. https://doi. org/10.1186/1471-2180-12-104
- Mulder, I., Siemens, J., Sentek, V., Amelung, W., Smalla, K., & Jechalke, S. (2018). Quaternary ammonium compounds in soil: Implications for antibiotic resistance development. *Reviews in Environmental Science and Bio/Technology*, 17, 159–185. https://doi.org/10.1007/ s11157-017-9457-7
- Munita, J. M., & Arias, C. A. (2016). Mechanisms of antibiotic resistance. Microbiology Spectrum, 4, 1-24. https://doi.org/10.1128/microbiols pec.VMBF-0016-2015
- Östman, M., Lindberg, R. H., Fick, J., Björn, E., & Tysklind, M. (2017). Screening of biocides, metals and antibiotics in Swedish sewage sludge and wastewater. *Water Research*, 115, 318–328. https://doi. org/10.1016/j.watres.2017.03.011
- Pal, C., Bengtsson-Palme, J., Kristiansson, E., & Larsson, D. J. (2015). Cooccurrence of resistance genes to antibiotics, biocides and metals reveals novel insights into their co-selection potential. BMC Genomics, 16, 964.

- Ribič, U., Klančnik, A., & Jeršek, B. (2017). Characterization of Staphylococcus epidermidis strains isolated from industrial cleanrooms under regular routine disinfection. Journal of Applied Microbiology, 122, 1186–1196.
- Ventola, C. L. (2015). The antibiotic resistance crisis: Part 1: Causes and threats. *Pharmacy and Therapeutics*, 40, 277.
- Wand, M. E., Bock, L. J., Bonney, L. C., & Sutton, J. M. (2017). Mechanisms of increased resistance to chlorhexidine and cross-resistance to colistin following exposure of *Klebsiella pneumoniae* clinical isolates to chlorhexidine. *Antimicrobial Agents and Chemotherapy*, 61, 1-12. https://doi.org/10.1128/AAC.01162-16
- Zhang, C., Cui, F., Zeng, G.-M., Jiang, M., Yang, Z.-Z., Yu, Z.-G., ... Shen, L.-Q. (2015). Quaternary ammonium compounds (QACs): A review on occurrence, fate and toxicity in the environment. *The Science of the Total Environment*, 518–519, 352–362. https://doi.org/10.1016/j. scitotenv.2015.03.007

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