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A multiple regression assessment of the biomineral urease activity from urine drainpipes of California public restrooms

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Abstract

Clogging and odor is strongly associated with ureolytic biomineralization in waterless and low-flow urinal drainage systems in high usage settings. These blockages continue to hinder widespread waterless and low-flow urinal adoption due to subsequent high maintenance requirements and hygiene concerns. Through field observations, hypothesis testing, and multiple regression analysis, this study attempts to characterize, for the first time, the ureolytic activity of the biomineralization found in alternative technologies located at 9 State-owned restrooms. Multiple regression analysis ($n = 55$, $df = 4$, $R^2 = 0.665$) suggests that intrasystem sampling location ($\hat{\beta} = 1.23$, $p < 0.001$), annual users per rest area ($\hat{\beta} = 0.5$, $p = 0.004$), and the volatile solids to total solids mass fraction ($\hat{\beta} = 0.59$, $p = 0.003$), are statistically significant influencers of the ureolytic activity of biomineral samples ($p < 0.05$). Conversely, *ureC* gene abundance ($p = 0.551$), urinal type ($p = 0.521$) and sampling season ($p = 0.956$) are not significant predictors of biomineral ureolytic activity. We conclude that high concentrations of the urease alpha subunit, *ureC*, which can be interpreted as proxy measure of a strong, potentially ureolytic community, does not necessarily mean that the gene is being expressed. Future studies should assess *ureC* transcriptional activity to measure gene expression rather than gene abundance to assess the relationship between environmental conditions, their role in transcription, and urease activities. In sum, this study presents a method to characterize biomineral ureolysis. This study establishes baseline values for future ureolytic inhibition treatment studies that seek to improve the usability of urine collection and related source separation technologies.

Keywords: Ureolysis, Urine source-separation, Biomineralization, Ureolytic activity

1 Introduction

Waterless and low-flow urinals reduce water consumption, improve hygiene with touchless operation, and can be used for source separation of urine; additionally, waterless systems require less plumbing than conventional systems. However, these source-separation technologies are susceptible to biomineralization [1, 2]. Biomineralization, usually of a mixed composition of struvite, calcium phosphate, calcium oxalate, and calcium carbonate, has plagued urine diversion projects

since the earliest projects were studied, leading to clogging, odor, and overall user dissatisfaction [1–4].

Researchers have described the formation of biomineralization in terms of (a) cellular activities, (b) passive formation of crystals caused by biofilms, and (c) biological and chemical facilitation of crystal supersaturation conditions [5–7]. Biomineralization in urine source-separation contexts is likely governed by a combination of mechanisms.

Urease and its ureolytic activity are measures of biomineralization potential because the rate of precipitation is dependent, in part, on the rate of increase of media pH, which depends on the rate of ureolysis. The elevated pH resulting from ureolysis plays a critical role in the

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supersaturation crystal formation process. Because urinals are subject to intermittent supplements of a urea and an ion source, urinals and urine drainage traps become a selective breeding ground for ureolytic organisms that cause an increase in the pH of collected urine and facilitate mineral precipitation as has been observed in urological devices [8]. Ureolytic bacteria responsible for the biomineralization use the nickel-dependent metalloenzyme, urease, to catalyze the hydrolysis of urea into ammonia and bicarbonate which in turn raises the pH and creates conditions favorable of precipitation [4]. In a past catheter study, researchers have demonstrated that rates of calcium and magnesium encrustation caused by various ureolytic bacteria isolates are correlated with an increase in ureolytic activity [9]. An elevated pH promotes calcium phosphate and oxalate stone formation due to a shift in phosphate speciation from HPO_4^{2-} to PO_4^{3-} and the decomposition of ascorbic acid into oxalate—both cases represent an increase in ion concentrations that lead to elevated encrustation rates found in catheters [10]. Ureolysis also results in carbonate and bicarbonate ion formation which can further contribute to biomineralization as the urine becomes supersaturated [11]. Researchers similarly showed that greater ureolytic rates from bacterial urease are correlated with greater rates of calcium carbonate precipitation [12–14]. Studies using *Proteus mirabilis* have shown that urease defective mutants fail to form crystalline biofilms in laboratory models, demonstrating the key role of pH and urease activity in crystal formation [15]. In dental plaque studies, researchers suggest that ammonia generating capacity in a mixed-species model of ureolytic oral biofilms is essential for the stabilization of microbial communities in ureolytic environments [16]. Losses of sufficient quantities of urease resulted in the acidification of biofilms and a decrease in community diversity [16].

Through multiple linear regression modelling, this study will be the first of its kind to: (a) model biomineral enzyme activity in terms of both categorical and quantitative predictors, (b) examine biomineral enzyme activity from urine source-separation technology, and (c) do so on a geographic scale with a sufficiently large sample size. This study also builds upon previous works describing soil or biofilm ureolytic activity that (a) use small sample sizes in parametric hypothesis tests ($n = 6$) or multiple regression ($n = 4$), (b) neglect discussion of model validation beyond the coefficient of determination (R^2), (c) do not discuss whether their data fits assumptions required for application of a statistical test, and (d) mention statistical significance, but not practical significance, i.e., the magnitude of effect [17–20].

Finding a link between environmental parameters such as intrasystem sampling location, usage frequency,

seasonality, gene abundance found through quantitative polymerase chain reaction (qPCR), and urinal types with the enzymatic activity of the biomineral samples will be useful in understanding the effects of restroom configuration on ureolytic activity. Understanding the effect of seasonality and sampling locations within a urine drainage system where ureolytic activity is highest may be insightful when predicting locations and times of year where the components of the urine collection system are most susceptible to biomineral fouling.

2 Materials and methods

The coming subsections will describe the sampling procedures and locations followed by methods used in downstream analyses to quantify the environmental variables used in the statistical analyses. The R Markdown HTML output containing the script can be found in the Online Resources section. The raw environmental data can be found in the Dryad repository (DOI:<https://doi.org/10.25338/B82906>) as an RDS file.

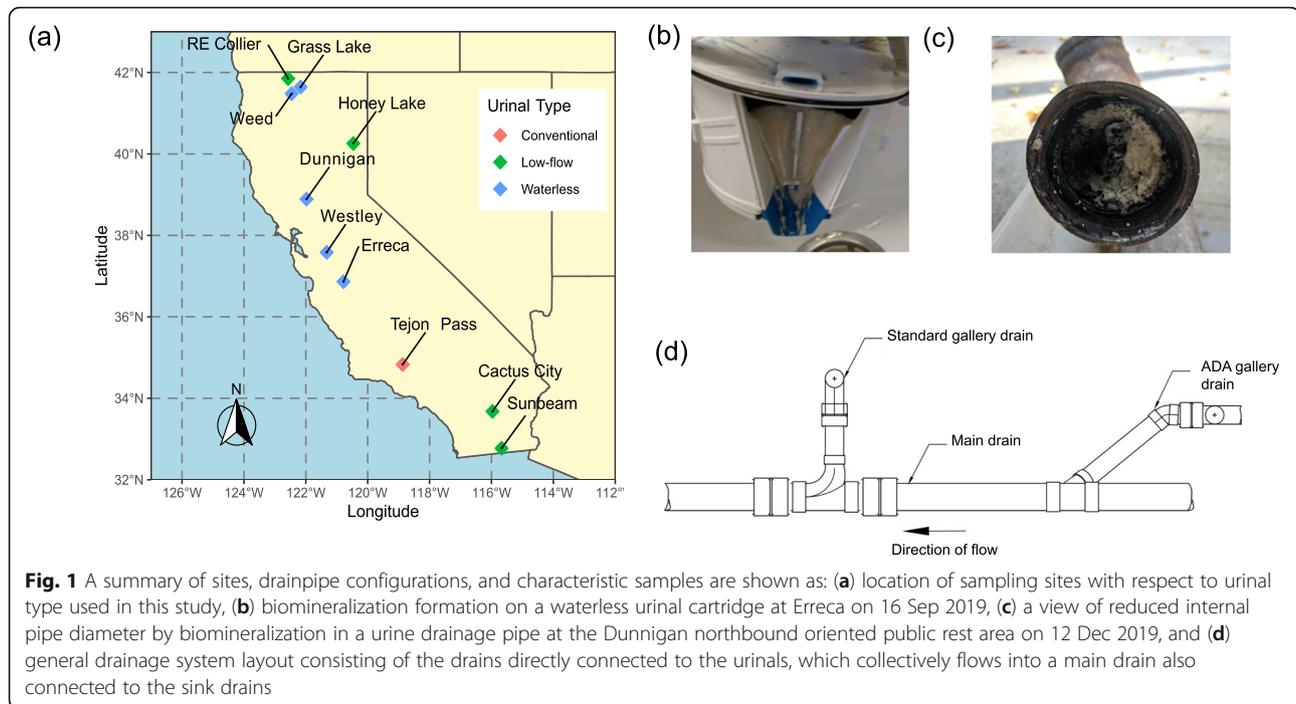
2.1 Sample collection

In the summer (July–August) and winter (December) of 2019, a total of 9 of public rest areas owned by the California Department of Transportation were sampled for ureolytic biomineralization. Due to poor pipe gallery design and lack of access points, no biomineral samples were collected from Honey Lake. The Honey Lake rest area, however, was assayed using the in-situ urease test to be discussed later. A summary map of the sampling sites is shown in Fig. 1.

These rest areas are situated throughout California along rest areas and had varying usage frequencies as estimated by California Department of Transportation using highway ramp volume counts [21]. Rest areas were categorized by the types of urinals installed: conventional ~ 1 gal per flush (3.78 L per flush), low-flow ~ 0.125 gal per flush (0.473 L per flush), and waterless (no flush).

Biomineralization deposits were scraped into sterile 50 mL conical tubes from fouled fixtures and drainage systems when available. A total of 2 conventional, 2 low-flow, and 5 waterless public restrooms along California highways, also known as rest areas, were observed in this study. The men's restrooms were typically fitted with two urinals at two different heights to conform to the American Disability Act.

All samples were stored in an ice chest after collection and processed within three days of sample collection. Previous work monitoring the ureolysis rate in soils have found that a distinct slowdown in ureolytic rate was not detected until 8 months of cooled storage [22]. As such, the sampling preservation measures were deemed adequate.



2.2 Biomineral ureolytic enzyme activity characterization

To compare enzymatic activities of biomineral samples *in vitro*, a known wet mass of the biomineral samples was suspended and mixed in a 100 mL volume of 7.3 pH 200 mM (4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid) (HEPES) buffer containing 2.5% urea m/m. The rate of increase in conductivity is proportional to that of urea hydrolysis and can be used as a surrogate measure for enzymatic activity [23]. As a comparative basis between samples, one unit of specific activity is defined as $\mu\text{S cm}^{-1} \text{min}^{-1} \text{g}^{-1}$ volatile solids (VS).

Gravimetric analyses followed standard methods for the examination of water and wastewater [24]. A mass balance was performed by comparing the wet solids mass with the dry mass following 105 °C desiccation and fixed mass after 550 °C ashing. VS can then be determined and represents the organic matter in a given sample. Each biomineral sample was analyzed in triplicate and then averaged.

2.3 qPCR

To examine the relationship between *in vitro* ureolytic activity and the genetic predispositions for ureolysis, the genomes of phylotype representatives for the presence of urease genes were examined by qPCR. A similar protocol was described previously [25]. The urease associated gene were designed on the urease alpha subunit encoding gene (*ureC*). Primer sequences were obtained from

the literature [26]. Sensitivity and efficiency were established from the y-intercept and slope of the standard curve, which was created by running triplicate, 10-fold serial dilutions of plasmid DNA containing the ligated amplicon of each gene (Eurofins Genomics LLC, Louisville, KY). The sensitivity of *ureC-F* (TGGGCCTTAAAA THCAYGARGAYTGGG) and *ureC-R* (SGGTGGTGGC ACACCATNANCATRTC) was < 4000 copies/qPCR reaction and the efficiency was 80.6% ($R^2 = 0.9974$). Poor sensitivity and low efficiency for *ureC* is expected due to the nature of SYBR degenerative primers and has also been previously observed by past research on detecting the *ureC* gene in groundwater [27]. Biomineral samples were kept frozen at -20 °C prior to DNA extraction. DNA was manually extracted from 0.25 g of sample using a commercially available kit following manufacturer recommendations and eluted in 100 μL of diethylpyrocarbonate (DEPC) treated water (Qiagen DNeasy Power Soil Kit, cat # 12888–50). Each 12 μL reaction contained 6 μL SYBR master mix (Applied Biosystems SYBR Green PCR Master Mix, cat # 4309155), 0.48 μL of a primer-water mixture (primers at final concentration of 400 nM), 4.52 μL of DEPC-treated water, and 1 μL of extracted DNA. qPCR was performed using an automated fluorometer (ABI PRISM 7900 HTA FAST, Thermo Fisher Scientific). Standard amplification conditions were used: 95 °C for 3 min, 40 cycles of 95 °C for 15 s, 52 °C for 30 s, and 72 °C for 30 s, with a melting curve at 95 °C for 15 s, 52 °C for 15 s, and 95 °C for 15 s.

Data was analyzed using Applied Biosystems SDS software, version 2.4. Fluorescent signals were collected during the annealing phase and quantitative cycle (C_q) values extracted with a threshold of 0.2 and baseline values of 3–10 for the *ureC* assay. Amplification specificity was verified using the dissociation temperature (T_m) of the qPCR amplicons specific to each gene. Acceptable T_m ranges were determined to be $\pm 2\%$ of the positive controls. For *ureC*, the acceptable T_m range was 80.8–84.1 °C. Samples with detectable amplification but with T_m 's outside of the acceptable ranges were considered false positives and were deemed negative for the gene of interest. The absolute copy numbers were also normalized in terms of VS mass present in the biomineral samples.

2.4 Statistical analyses

All statistical work and data visualization was done using R version 4.0.2. An a-priori power analysis was first used to inform the design of this study, suggesting that a linear model can sufficiently capture a large effect size ($f = 0.35$) at a level of significance of 0.05 for a power of 0.8 using 1 tested dependent variable and 5 total predictors with a minimum sample size of 25 [28]. After excluding sample rows missing data from low quality qPCR reads and samples that did not have enough mass for gravimetric analysis or biomineral enzyme activity, this randomly sampled, complete case analysis included a sample size of 55 from 9 different facilities. In the regression analysis, conventional urinals were aggregated with low-flow urinals because both urinal types include flush water. A stepwise forward variable selection method was used. A corrected Akaike information criterion (AICC) was also used to validate model selection [29]. The ordinary least squares (OLS) multiple regression analysis was performed assuming that a natural log-log transformed linear model is an adequate descriptor of the system, whereby normality was verified in the Supplementary Materials. A natural log-log transformed dataset (as represented in Fig. S1) enables for a practical interpretation of the effect size as a percent change, or in this case, the elasticity between two biological variables [30]. Regression coefficients were interpreted as natural log-level for categorical variables. For the coming subsections, unless specified, variables will be discussed in terms of natural logarithms.

2.5 Characterizing the ureolytic activity in urinal traps in situ

In situ urinal trap testing was conducted to characterize the ureolytic rate at the time of sample collection within the urine drain trap. In situ biomineral ureolytic activity was used to support the regression analysis derived from in vitro urease assays. The project team developed a

method using pH and conductivity meters to characterize the baseline ureolytic rates. A description of the trap testing is shown graphically in Fig. 2. The sampling dates and raw data are shown in Table S1.

The in-situ urinal trap procedure was conducted as follows: First, the urine drain trap is vacuumed out as shown in Fig. 2. Once emptied, a 200 mM 7.3 pH HEPES buffer containing 2.5% m/m urea is added until the drain trap is full; the volumes of HEPES added are based on the urinal model and the sampling site as detailed in Table S1. Logging pH and EC meters were submerged in the trap opening and recorded for a total of 10 min from which the ureolytic rate could be estimated using the rate of EC formation.

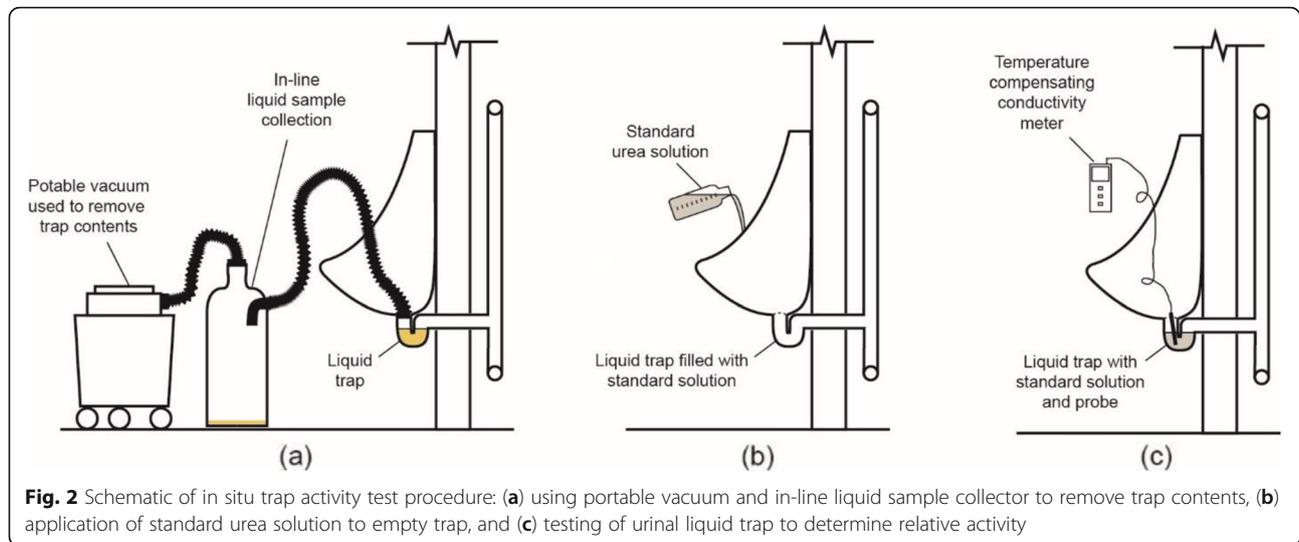
3 Results and discussion

After evaluating and selecting the most parsimonious multiple linear regression model composed of categorical and quantitative environmental variables, the observed influence, or lack thereof, of these variables will be discussed in the context of biomineral ureolytic activity.

3.1 Multiple linear model and validation

The multiple linear model composed of 55 observations is described in Tables 1 and 2. As shown in correlation heatmaps and residual analysis from Figs. S2, S3, and S4, the linear model is in agreement with the Gauss-Markov OLS regression assumptions, which require that: a) the expected value of the regression residuals tends towards zero, b) the residuals are homoscedastic, c) there is no autocorrelation between the regressors and the residuals such that exogeneity is upheld, d) the predictors are not multicollinear, and e) the residuals are also normal [30]. The residuals shown in Fig. S2 do not appear to have a trend based on the index plot, do not exhibit any correlation with each other from the autocorrelation plot, and appear homoscedastic from the fitted values vs. residuals plot. Finally, the residuals also appear normally distributed from the quantile-quantile plot in Fig. S2. As such, it was concluded that the natural log-log linear model appropriately describes natural logarithmically transformed data and that the model fits well with the data. The AICC model selection results are shown in Table S2, suggesting that the most parsimonious and probable model is Model 3 [29, 31].

The regression results describing the most probable model (Model 3) is shown in Tables 1 and 2, which also depicts the regression results from other tested models. The results presented in Tables 1 and 2 suggest that *ureC* gene concentrations (Model 4, $p = 0.551$), sampling season (Model 5, $p = 0.956$), and urinal types were statistically insignificant predictors of ureolytic activity ($p > 0.05$) and of low practical significance as indicated by



the relatively small regression coefficients (see Table 1). From Table 1, the strongest predictor of biomineral ureolytic activity was the sampling location, namely, those sampled from the main urinal drainage pipes exhibited the greatest enzymatic activity. In Model 3, the second strongest predictor was the VS/TS ratio. Annual number of users at a given rest area also positively influenced urease activity likely due to the increased loading and usage frequency resulting in a semi-constant stream of nutrients necessary for a strong ureolytic community to develop and thrive.

3.2 The influence of organic matter on ureolytic activity

Organic content is shown to be a significant ($p = 0.003$) and of sizeable effect ($\hat{\beta} = 0.59$) in predicting ureolytic activity (Table 1). This observation may be consistent with past findings from soil research which found correlations between organic matter concentrations and urease activity [13, 14, 32]. Others also observed that increased carbohydrate availability at neutral pH was correlated with increased *Actinomyces naeslundii* and *Sporosarcina pasteurii* urease activity [14, 17]. Liu et al., however, noticed that carbohydrate availability had no effect on *ureC* gene expression marked by through

reverse-transcriptase quantitative real-time PCR (RT-qPCR) mRNA transcripts [17]. Liu et al. hypothesizes that these observations were due to carbohydrate availability and pH modulation affecting the expression of genes other than *ureC* responsible for urease synthesis or apoenzyme activation [17].

Increasing the biomass of the inoculum by providing a carbon source in microbial induced calcite precipitation studies has been reported to promote the ureolytic activity [14]. Tobler et al. concluded that molasses supplementation selected for a larger microbial community that obtains their nitrogen from ureolysis, though there is no nitrogen limitation in urinals [14]. Others, who studied the environmental factors affecting microbially induced calcium precipitation concluded that increasing biomass may also increase ureolytic activity as there could be more active cells present [33]. Extracellular urease has also been suggested to be stabilized by adsorption to soil colloids, particularly organic matter, which may be similar to that observed in biomineral samples obtained from urine drain pipes [19].

One limitation of this study is that it is unclear what component of the organic fraction is correlated with increased ureolytic activity as VS is a bulk measurement encompassing any organic mass. Within the biomineral/

Table 1 Summary of effect sizes of significant predictors on biomineral ureolytic activity

Significant predictor variables	$\hat{\beta}$	CI (95%)	Effect on biomineral activity per g VS as elasticity ^a
Annual users per rest area	0.5	0.17, 0.82	A 25% increase in annual users per rest area corresponds to a 11.7% (3.9, 20.1) increase in biomineral activity
VS/TS (g g^{-1})	0.59	0.21, 0.97	A 25% increase in VS/TS (g g^{-1}) corresponds to a 14.1% (4.8, 24.2) increase in biomineral activity
Intrasystem location: main drain	1.24	0.83, 1.64	Compared to samples obtained from cartridges, those obtained from the gallery main drain had a 245% (129, 416) larger geometric mean in biomineral activity

^aParenthetical contents represent effect sizes at limits of confidence intervals

Table 2 Multiple regression summary of model predicting biomineral ureolytic activity

	Model 1	Model 2	Model 3	Model 4	Model 5	Model 6
Predictor variables	Estimates	Estimates	Estimates	Estimates	Estimates	Estimates
Intercept	-7.35(-12.80--1.90)**	-2.18(-6.92-2.57)	-0.55(-5.05-3.94)	-0.46(-5.00-4.08)	-0.56(-5.12-3.99)	-0.36(-4.92-4.20)
Annual users per rest area	0.96(0.56-1.37)***	0.57(0.22-0.92)**	0.50(0.17-0.82)**	0.47(0.14-0.81)**	0.49(0.16-0.83)**	0.49(0.16-0.82)**
Intrasystem location: gallery drain		-0.28(-0.62-0.07)	-0.19(-0.52-0.13)	-0.15(-0.51-0.21)	-0.19(-0.53-0.15)	-0.14(-0.50-0.22)
Intrasystem location: gallery main drain		1.02(0.61-1.43)***	1.24(0.83-1.64)***	1.26(0.85-1.68)***	1.24(0.83-1.65)***	1.23(0.82-1.64)***
VS/TS (g g ⁻¹)			0.59(0.21-0.97)**	0.57(0.19-0.96)**	0.58(0.17-0.99)**	0.56(0.18-0.95)**
ureC concentration (copy # g ⁻¹ VS)				0.01(-0.02-0.04)		
Sampling season					0.01(-0.31-0.33)	
Urinal type						-0.12(-0.49-0.25)
Observations	55	55	55	55	55	55
R ² /R ² adjusted	0.299/0.286	0.595/0.571	0.662/0.635	0.665/0.630	0.662/0.628	0.665/0.631

^aSignificance codes: 0 '****' 0.001 '***' 0.05 '*' 0.1 ''

stone matrix is also an organic fraction composed of carbohydrates, proteins, lipids, and dead cell mass that binds the mineral fraction of the precipitate [4]. Therefore, future research could evaluate different organic components such as carbohydrates, proteins, and exopolysaccharide substances.

3.3 The non-effect of urinal type and seasonality on ureolytic activity

In addition to the linear regression results, Kruskal-Wallis testing for biomineral ureolytic activity between waterless and low-flow urinals provides evidence that waterless and low-flow do not significantly differ in terms of biomineral activity ($p = 0.47$). While urinal type is not a statistically significant predictor of ureolytic activity, biomineral samples from waterless urinals have exhibited a greater maximum ureolytic activity than any biomineral sample obtained from low-flow urinals in this study, as shown in Fig. 3.

Finally, sampling season (as shown in Table 2) demonstrated no statistical ($p = 0.956$) or practical significance ($\hat{\beta} = 0.01$) in predicting biomineral activity. This may explain why fouling is a year-round phenomenon, as the biomineral ureolytic activity remains unaffected by seasonality, as the high urease activities year-round facilitate conditions necessary for precipitation to occur. Because seasonality does not seem to impact biomineral activity, future observations on the ureolytic activity of urine drainpipes may be performed without temporal confounding effects. Future microbial ecology studies can reveal more about the response of the bacterial

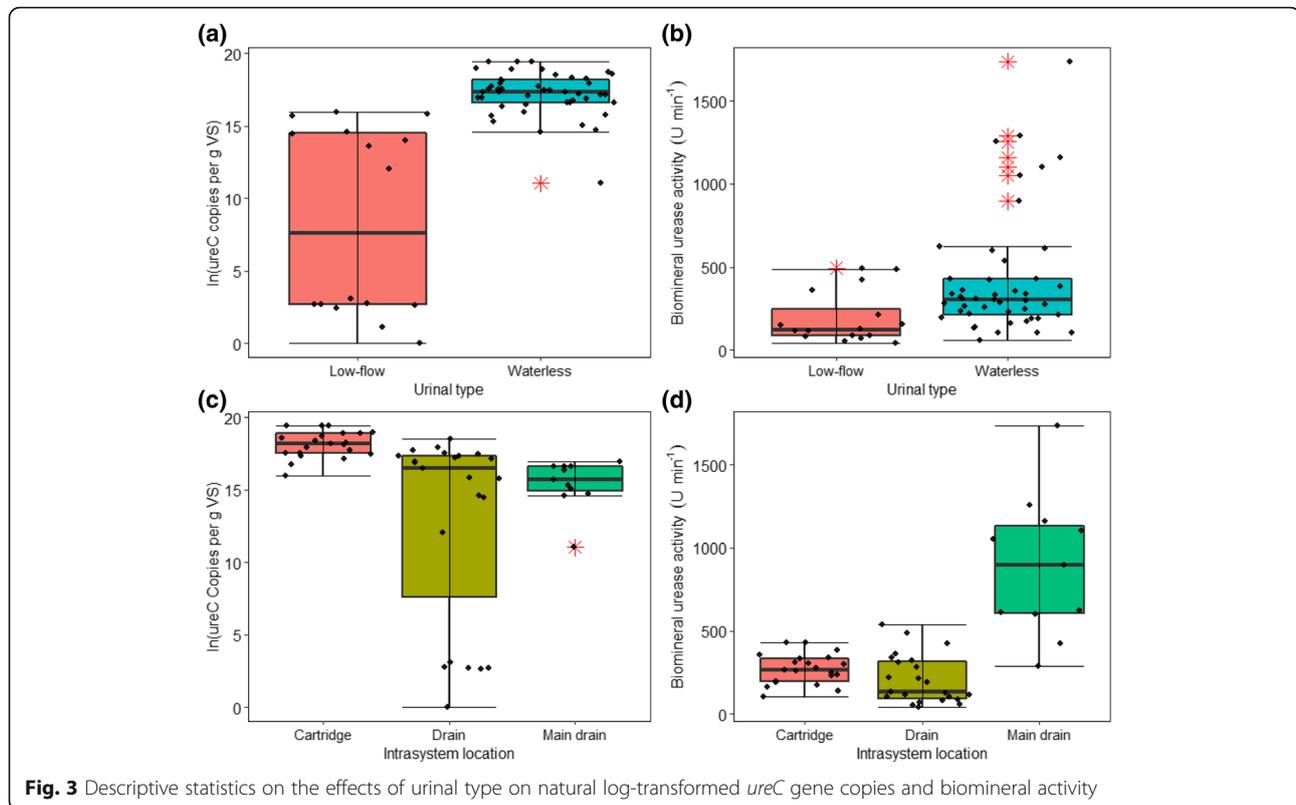
community structure to seasonality, which can then be cumulatively related to the biomineral ureolytic activity.

3.4 Effects of intrasystem sampling location on ureolytic activity

While the ureolytic activity of biomineral samples obtained from the drainage pipes immediately following the drain traps were not significantly different from those corresponding to samples obtained from waterless urinal cartridges (Pairwise Wilcoxon Rank Sum: $p = 0.053$), samples taken from the main drain lines which contacts handwashing water were significantly non-identical in terms of ureolytic activity (Kruskal-Wallis: $p < 0.001$; Pairwise Wilcoxon Rank Sum: $p < 0.001$). Within one system, cartridges and gallery drain lines immediately succeeding the urinal are exposed to the same urine feed without mixing with potable water and thus face similar environmental conditions that influence ureolytic activity [13]. Because drain line samples directly follow cartridge samples and are exposed to the same urine, the relative similarity in environmental conditions between cartridge and drain line samples may explain their different ureolytic rates compared to main drainpipe samples but not with each other.

3.5 Biomineral ureolytic activity may be predicted by transcriptional activity more than by urec and 16S rRNA gene abundance

Kruskal-Wallis testing results suggest that the *ureC* abundance between low-flow and waterless urinals are significantly nonidentical ($p < 0.001$), but there was no detected significant effect on biomineral ureolytic



activity as suggested by the multiple regression results shown in Table 2. The lack of statistical significance describing the relationship between *ureC* gene copies and ureolytic activities disagrees with bivariate correlation studies done by Sun et al. and Fisher et al., where it was found that soil ureolysis rates were significantly correlated with *ureC* gene copies [34, 35]. Notably, neither studies discussed effect size and used a small sample size ($n < 12$) for analyses describing individual soil horizons [34, 35]. Conversely, other soil urease studies have also found that ureolytic activities are correlated with total nitrogen, total carbon, and soil organic carbon concentrations, but not the abundance of *ureC* genes as in agreement with our study [36]. The regression results suggest that ureolytic gene abundance is insufficient in predicting ureolytic activity in a linear model.

Greater abundances of potentially ureolytic bacteria indicated by proxy of sample *ureC* gene concentrations, may not be correlated with biomineral ureolytic rates as suggested by the regression results. That *ureC* was detectable indicates that part of the bacterial community in the biomineral samples has the urease-positive genotype, but not all bacteria with the *ureC* may be displaying a urease-positive phenotype [37]. This is because urease activity may not be expressed under the growth conditions found in urine drain pipes, and may explain why

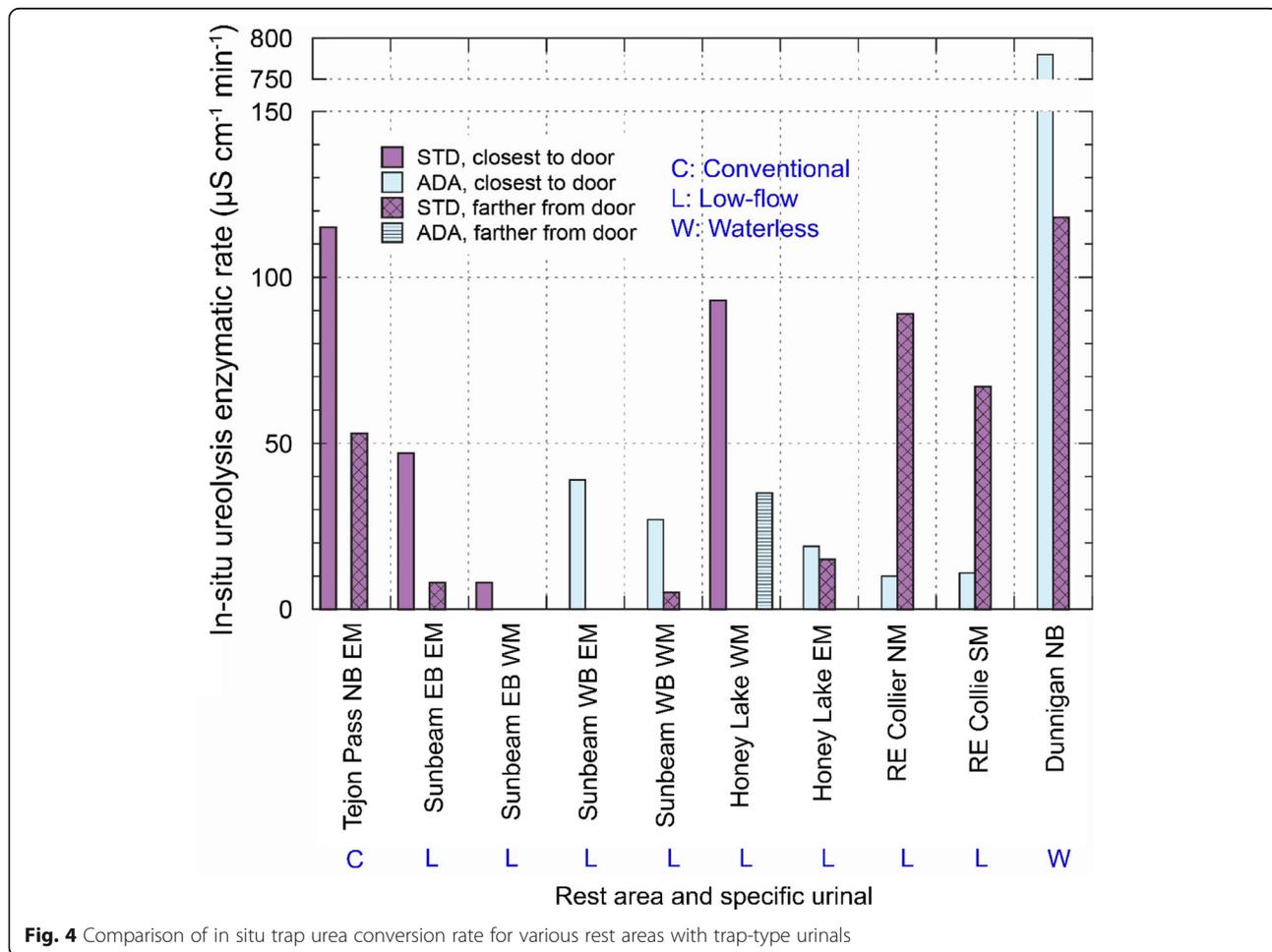
urease activities did not differ significantly when grouped by urinal type [37]. Expression of the urease-positive genotype and the eventual translation into the urease protein is regulated at the transcriptional level rather than at the genomic level [38–40].

That *ureC* gene abundance is not a statistically significant predictor of biomineral ureolytic activity is likely due to the need for environmental conditions that would induce certain microbial transcriptional responses that cause an increase in urease activity. When comparing *ureC* copies per g VS, values grouped by intrasystem sampling location differed significantly between cartridge vs. gallery drain (Kruskal-Wallis: $p < 0.001$; Wilcoxon Rank Sum: $p < 0.001$) and cartridge vs. gallery main drain (Kruskal-Wallis: $p < 0.001$; Wilcoxon Rank Sum: $p < 0.001$). However, Fig. 3 reinforces hypothesis testing results in that samples from the main drain with the lowest functional gene concentrations exhibited maximal ureolytic activity of all samples as predicted by the multiple regression model. One possible explanation is that the main drains and low-flow urinal drain lines are exposed to flush and sink water, which leads to a decrease in nitrogen concentrations in the stream contacting the biofilm due to dilution. In response, the ureolytic ammonia oxidizing bacterial community

may be upregulating *ureC* transcription to produce more urease to convert the urea into ammonia at a faster rate for pH regulation or to acquire ammonia for biomass production or energy generation [41].

Further regression testing by adding the 16S rRNA gene concentration as a variable to the most probable model (Model 3) also suggests that the 16S rRNA gene concentrations in the biomineral samples are not a strong ($\hat{\beta} = 0.13$) or significant ($p = 0.127$) predictor of ureolytic activity. This suggests that a greater bacterial load within a sample, estimated by proxy of gene concentration may not correspond to greater ureolytic rates in a given biomineral sample. Our observations on the lack of correlation between 16S rRNA gene abundance and ureolytic activity disagrees with Wang et al.'s study, where they found a statistically significant correlation between urease activity and 16S rRNA copies via automatic linear modeling [32]. However, such discrepancies in results may be due to distinct environmental conditions between soil samples and ureolytic biomineralization from drain pipes which could influence the expression of the urease gene and its eventual translation.

From Fig. 4, the observation that conventional and low-flow urinals can have similar in situ ureolytic rates with those from waterless urinals is consistent with the regression results where it was found that urinal type is neither a significant ($p = 0.521$) and practical ($\hat{\beta} = -0.12$) predictor of the in vitro biomineral ureolytic activity. While low-flow urinals constitute most fixtures described in Fig. 4 due to drain trap inaccessibility for other urinal types, Fig. 4 demonstrates that Dunnigan northbound, a waterless urinal site, exhibited the greatest maximum in situ ureolytic rates of all drain traps tested. Conversely, the standard urinal at Tejon Pass ranked 2nd of all sites screened for in situ ureolytic rate. The Tejon Pass urinal exhibited a similar rate ($115 \mu\text{S cm}^{-1} \text{min}^{-1} \text{VS}$) compared to that of the Dunnigan northbound standard height urinal ($118 \mu\text{S cm}^{-1} \text{min}^{-1} \text{VS}$). Urinals in the same study sites also appear to exhibit different urea conversion rates. One possible explanation is that there simply may be less ureolytically active biomineral mass in one drain trap compared to the urinal adjacent to it at the time of sampling. It



cannot be guaranteed that there is sufficient biomineral mass within a given drain trap at any given time, which could be affecting the in situ ureolytic rates. Ideally, a larger sample size for the in-situ tests could alleviate any ambiguity from this confounding factor, and so further research with increased sample size is needed. Regardless of this confounding factor, the in-situ tests demonstrate that it is possible for the ureolytic activity of biomineral samples from urinals with high flush water volumes to match that from waterless urinals. Raw urease activity values grouped by sampling sites can be found in Table S1.

4 Conclusions

In conclusion, *ureC* gene abundance was not a strong and significant predictor of biomineral urease activity. More so, the regression model suggests that rest areas with greater user frequencies and organic content represented by VS exhibited greater biomineral urease enzyme activities. Where one samples within a urine drainage system also appears to affect the strength of the enzyme activity. Conversely, urease activities did not appear to differ based on the seasonality of the sampling period or the urinal type. One limitation of the sampling methodology is that the age of the biomineral samples was uncontrolled largely due to different cleaning and maintenance frequencies at each rest area examined. Though, it would be impractical to impose strict cleaning routines for dozens of laborers who maintain these rest areas statewide. Currently it is unclear how age could affect the strength of the urease activity of biomineral samples, but future studies should explore such effects.

Our findings indicate that flush water alone may not be an adequate preventative measure for preventing ureolytic biomineralization. Urease activity can be as strong in conventional and low-flow biomineralization as it is in waterless biomineralization, even if there is a smaller ureolytic community in flush type urinals as indicated by low relative *ureC* gene concentrations shown in Fig. 3. It is also possible that flush water may also influence the precipitation chemistry in drain lines, as flush water containing elevated magnesium and calcium concentrations may contribute to crystallization. While the smaller abundance of *ureC* gene concentrations in low-flow urinal samples is insufficient in accounting for the similar ureolytic activities exhibited by the two urinal types and intrasystem sampling locations, the differences in *ureC* gene concentrations grouped by urinal type shown in Fig. 3 may likely be due to a difference in community structures. Future next-generation-sequencing and microbial ecology studies should visualize the potentially ureolytic microbial community structure by sequencing the *ureC* gene in addition to 16S rRNA to

visualize the total bacterial community to find relationships between the bacterial community, environmental factors, and ureolytic activity.

In conjunction with measuring bulk parameters such as pH, future studies should incorporate RT-qPCR to determine the effects of nutrient concentrations, sampling locations, and urinal types on urease gene expression at the transcriptional level. A future RT-qPCR experiment on ureolytic biomineral samples can reveal how the effects of varying dilution rates between low-flow and waterless urinals affects the transcriptional activity of a gene of interest and its relationship with ureolytic activity.

5 Supplementary Information

The online version contains supplementary material available at <https://doi.org/10.1186/s42834-021-00114-7>.

Additional file 1: Supplementary materials. Table S1 Summary of *in situ* trap test data. **Table S2** Akaike information criterion results model selection. **Fig. S1** Histograms depicting the data distribution of natural logarithmically transformed data set. **Fig. S2** The residuals of the hypothesized model including *ureC* gene concentration as a predictor (model 4) demonstrates adherence to the Gauss-Markov assumptions of the linear model described in the manuscript. **Fig. S3** A correlation heatmap without distribution was used as guidance to avoid multicollinearity in models. **Fig. S4** The correlation matrices suggest that the independent variables included in the multiple regression analysis is not affected by multicollinearity and that confounding factors are not observed

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Data/code availability

The raw data can be found in the Dryad repository (DOI:<https://doi.org/10.25338/B82906>). The preprint can be found on BioRxiv (DOI: <https://doi.org/10.1101/2021.02.18.431895>).

Authors' contributions

Kahui Lim performed the statistics, lab analysis, and field sampling. Harold Leverenz provided editorial review and performed the field sampling. Samantha Barnum and Cara Wademan performed qPCR. All authors read and approved the final manuscript.

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Declarations

Competing interests

The authors declare no competing financial interest.

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