Dynamic persistence of intracellular bacterial communities of uropathogenic *Escherichia coli* in a human bladder-chip model of urinary tract infections

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Abstract

Uropathogenic *Escherichia coli* (UPEC) proliferate within superficial bladder umbrella cells to form intracellular bacterial communities (IBCs) during early stages of urinary tract infections. However, the dynamic responses of IBCs to host stresses and antibiotic therapy are difficult to assess *in situ*. We develop a human bladder-chip model wherein umbrella cells and bladder microvascular endothelial cells are co-cultured under flow in urine and nutritive media respectively, and bladder filling and voiding mimicked mechanically by application and release of linear strain. Using time-lapse microscopy, we show that rapid recruitment of neutrophils from the vascular channel to sites of infection leads to swarm and neutrophil extracellular trap formation but does not prevent IBC formation. Subsequently, we tracked bacterial growth dynamics in individual IBCs through two cycles of antibiotic administration interspersed with recovery periods which revealed that the elimination of bacteria within IBCs by the antibiotic was delayed, and in some instances, did not occur at all. During the recovery period, rapid proliferation in a significant fraction of IBCs reseeded new foci of infection through bacterial shedding and host cell exfoliation. These insights reinforce a dynamic role for IBCs as harbours of bacterial persistence, with significant consequences for non-compliance with antibiotic regimens.

Keywords: bladder-chip, uropathogenic *Escherichia coli* (UPEC), intracellular bacterial communities (IBCs), bacterial persistence, antibiotic treatment, neutrophil swarms, neutrophil extracellular traps, shear stress, stretching, confocal live-cell imaging

Introduction

Urinary tract infections (UTIs), the second most-common cause for the prescription of antibiotics (Foxman, 2010) are characterized by the high frequency of recurrence, defined as a reappearance of infection within 12 months despite the apparently successful completion of antibiotic therapy. Recurrence occurs in about 25% of all UTIs (Foxman et al., 2000) and strongly impacts the cost of healthcare and reduces the quality of life, particularly since more than 60% of women are diagnosed with a UTI at least once in their lifetime (Klein and Hultgren, 2020). Uropathogenic *Escherichia coli* (UPEC), the causative agent for the majority of UTIs, exhibits a complex lifestyle in the bladder, with planktonic sub-populations within the urine co-existing with intracellular bacteria. UPEC invasion of the urinary bladder generates substantial changes to bladder morphology and a robust immune response. Much of our current understanding of early stages of UTI and the intracellular lifestyle is derived from studies in the mouse model (Anderson et al., 2003; Duraiswamy et al., 2018; Hannan et al., 2012; Hung et al., 2009; Justice et al., 2004; Schwartz et al., 2011; Yang et al., 2019). Examinations of mouse bladder explants via microscopy have revealed the formation of intracellular bacterial communities (IBCs) composed of thousands of bacteria within individual superficial bladder cells (Justice et al., 2004). IBCs also play a prominent role in clinical infection and have also been harvested from the urine of cystitis patients (Robino et al., 2013; Rosen et al., 2007). These structures are considered to have a linear progression from an early stage of colonization by single bacteria to an intermediate stage of biofilm-like communities culminating in the release of bacteria at the late stage. However, long-term imaging of infected animals or of explant-tissue is technically challenging and therefore it has been difficult to capture the dynamic changes that underlie the formation of these structures and their impact on infection and clearance by subsequent antibiotic treatment.

In addition, the bladder is an extremely complex organ; it has a stratified architecture with well-differentiated cell types; a lumen filled with urine whose composition and chemical properties can vary depending on the physiological state of the individual and is subjected to periodic and large changes in organ volume and surface area (Korkmaz and Rogg, 2007). These features may play important roles in infection, but they have been hitherto hard to capture outside of a whole animal model, where they are present in their entirety and cannot be dissected in a modular manner.

Organotypic models are well-suited to address these outstanding questions. A key strength of advanced organotypic models such as organs-on-chip (Benam et al., 2016; Huh et al., 2010a; Jang et al., 2013, 2019; Kim et al., 2016; Novak et al., 2020; Zhou et al., 2016) or organoids (Cakir et al., 2019; Clevers, 2016; Rossi et al., 2018; Sato et al., 2009) is that they increasingly recapitulate the complexity of host physiology. Organ-on-chip models have been developed for several organs either in isolation or in combination (Novak et al., 2020; Ronaldson-Bouchard and Vunjak-Novakovic, 2018). These systems are increasingly being used to model infectious diseases including viral and bacterial infections of the respiratory tract (Nawroth et al., 2020; Si et al., 2020; Thacker et al., 2020b, 2020a), gut (Jalili-Firoozinezhad et al., 2019; Kim et al., 2016; Shah et al., 2016; Tovaglieri et al., 2019), kidney (Wang et al., 2019), and liver (Kang et al., 2017). Recently, bladder organoids that mimic the stratified architecture of the urothelium have been used to study infections (Horsley et al., 2018; Smith et al., 2006; Sharma et al., 2020). However, the organoid model suffers from certain shortcomings inherent to the 3-D architecture such as the lack of vasculature, the inability to manipulate the cells mechanically, and the constrained volume of the lumen. In contrast, organ-on-chip models offer a complementary approach that does not suffer from these limitations. However, to our knowledge, there have

been no reports of a bladder-on-chip model. Although there are studies that have developed *in vitro* bladder models that recreate the stratified architecture of the bladder epithelium (Horsley et al., 2018; Smith et al., 2006; Suzuki et al., 2019), they have not been used to recapitulate the multiple stages of IBC formation. Similarly, while a few studies have visualized different stages of IBC development by culturing human bladder cells under urine flow, these models are restricted to monoculture experiments (Andersen et al., 2012; Iosifidis and Duggin, 2020). Furthermore, the lack of vasculature in these models restricts the extent to which immune cell components or drugs can be introduced in a physiologically relevant manner and none of the systems reported to date offer the possibility of mimicking the mechanics of filling and voiding in a functioning bladder (Andersen et al., 2012; Horsley et al., 2018; Iosifidis and Duggin, 2020; Smith et al., 2006).

Here we report the development and characterization of a bladder-chip model that mimics the bladder architecture by co-culture of a well-characterized human bladder epithelial cell line with bladder microvascular endothelial cells in a device geometry that allows the two cell types to be exposed to urine and nutritive cell culture media, respectively. The flow rates in the apical and vascular channels can be controlled independently, and multiple rounds of micturition are recreated via the application of a linear strain to the PDMS membrane that serves as the substrate for co-culture. Using this model, we show that diapedesis of neutrophils to sites of infection on the epithelial side can lead to the formation of neutrophil swarms and neutrophil extracellular traps (NETs), and that IBCs offer substantial protection to bacteria from antibiotic clearance. Our observations suggest that the role of IBCs in reseeding bladder infections upon cessation of antibiotic treatment or failure to complete a course of antibiotics might be more important than

previously assumed and therefore strategies aimed towards eradication of IBCs are very crucial for treatment efficacy.

Results

Reconstitution of bladder uroepithelium and bladder vasculature

We established a bladder-chip infection model by co-culturing HTB9 bladder epithelial cells (epithelial cells) and HMVEC-Bd primary human bladder microvascular endothelial cells (endothelial cells) in a novel bladder-chip approach (Fig. 1A). Immunostaining verified that the epithelial and endothelial cells formed confluent monolayers (cell densities in Table 1) with high expression of junction markers such as epithelial cell adhesion molecule (EpCAM) in the epithelial cell layer, and platelet endothelial cell adhesion molecule-1 (PECAM-1) and VE-cadherin in the endothelial cell layer (Fig 1B, C, additional images in Fig. S1A-H). Expression of these and other junction markers such as E-cadherin and zonula occludens-1 (ZO-1) was consistent across monocultures (Fig. S2A-G).

Similarly, a majority of the epithelial cells expressed cytokeratin 7 (CK7), a general uroepithelial marker and cytokeratin 8 (CK8), a differentiated uroepithelial marker both in monoculture (Fig. S2I, J) and on-chip (Fig. 1B, S1B, S1F). Some endothelial cells were also CK7+ (Fig. 1C, S2H). Co-culture of bladder epithelial and bladder endothelial cells in the human bladder-chip therefore did not alter the cellular expression patterns of these markers as compared to monocultures. We further characterized the HTB9 cell line in monoculture for markers for urothelial differentiation. HTB9 cells showed high expression of uroplakin-3a (UP3a) which has been shown to be essential for UPEC infection (Fig. S2K) (Martinez et al., 2000; Mulvey et al., 1998) but only a

small proportion of epithelial cells were positive for the basal cell marker cytokeratin1 (CK1), in agreement with the umbrella cell nature of the HTB9 cell line (Fig S2L, M) (Duncan et al., 2004; Smith et al., 2006). Overall, these observations confirmed that the bladder-chip is populated with cells that mimic the physiology of the bladder vasculature and the superficial urothelial cell layer. Further, the chip design enables the flow of media with different compositions through the epithelial and vascular channels. We used this feature to mimic bladder physiology by perfusion of diluted pooled human urine on the epithelial side and endothelial cell medium on the vascular side.

Modelling bladder filling and bladder voiding in the bladder-chip

The human bladder experiences vast changes in volume and surface area on a periodic basis. The first phase of this cycle, (*filling bladder state*), occurs through a slow and gradual increase in bladder volume due to addition of urine from kidney via the ureters, resulting in a large increase in bladder volume (Fig. 1D). At the level of the uroepithelium, these changes manifest as a 2-dimensional biaxial stretch of the bladder tissue. *Ex vivo* studies in rat bladders report that a maximum strain of 90% and 130% can be applied to bladder explants in the circumferential and longitudinal directions (Gloeckner et al., 2002; Parekh et al., 2010), although micturition *in vivo* is likely triggered before this maximum value is reached. Subsequently, volume growth slows, and the bladder attains a relatively constant volume, with the bladder epithelium in a corresponding state of maximal stretch, (*filled bladder state*). Voiding of the bladder through urination rapidly reduces bladder volume, (*voiding bladder state*) and removes the strain experienced by the bladder cells. The bladder epithelium, as a viscoelastic material, responds to

the removal of strain and relaxes over the subsequent period (Pascalis et al., 2018) where the bladder volume remains low (*‘voided bladder state’*) (Fig. 1D).

The architecture of the bladder-chip device allows for a linear strain to be applied to the porous membrane via negative pressure in the channels adjacent to the main channel of the device (*‘the vacuum channels’*) (Grassart et al., 2019; Huh et al., 2010b) (Fig. 1A). We characterized the linear strain experienced by epithelial cells due to application of negative pressure (Fig. S3). A plot of applied pressure vs. strain was linear, and we could achieve a dynamic range of linear strain (0 to 19 %) by application of negative pressure (0 to -900 mbar). High levels of applied strain were incompatible with long-term time-lapse microscopy as it generated a significant drift in the axial position of the membrane. We therefore limited the linear strain applied to a maximum of 10%, which is nevertheless a significant proportion of the typical strain experienced by the bladder tissue *in vivo*. We then modelled the bladder filling and voiding over a 6-hour duty cycle with different states: *filling bladder* (0 to 2 hours, 0 to 10% strain), *filled bladder* (2 to 4 hours, 10% strain), *voiding bladder* over a period of 2 minutes (4 hours to 4:02 hours, 10% to 0% strain) and *voided bladder* (4:02 hours to 6 hours, 0% strain) (Fig. 1D). This 6-hour duty cycle was then repeated for the remaining duration of each experiment. Overall, the bladder-chip model enables co-culture of two cell-types in nutritionally different microenvironments with a physiologically relevant level of applied strain that mimics bladder filling and voiding cycles.

UPEC infection of the epithelial layer under flow in the bladder-chip model

UPEC attachment and invasion of bladder epithelial cells has been shown to be sensitive to fluidic shear stress (Andersen et al., 2012; Zalewska-Piątek et al., 2020). Although UPEC infection in the bladder can occur with or without the presence of shear stress, we infected the

epithelial layer on the bladder-chip under flow conditions. The small volumes of the microfluidic chip motivated this approach, as rapid bacterial growth in the diluted human urine could lead to acidification of the medium. We therefore maintained a flow rate of 1.2 ml/hour for a period of 1.5 - 2 hours during infection of the epithelial layer of the bladder-chips with UPEC. Under flow conditions, an overwhelming majority of bacteria did not attach to the epithelial cells. Time-lapse microscopy showed that bacterial attachment to the epithelial cells increased steadily over this period, but that the typical infectious dose at the end of this period was low (<1 bacterium per epithelial cell, Fig. S4).

Accordingly, we established a 28-hour live-cell imaging experimental protocol as shown in the schematic in Fig. 1E and described in greater detail in the subsequent sections and in the Materials and Methods. Briefly, this consisted of an initial period of acclimatization, followed by UPEC infection, introduction of neutrophils, and two consecutive cycles of antibiotic treatment and recovery to monitor IBC dynamics at the single-cell level. This experimental protocol therefore mimicked key aspects of the host-pathogen interactions in early stages of UTIs as well as the response to antibiotic treatment.

Diapedesis of neutrophils across the epithelial-endothelial barrier in response to UPEC infection in the bladder-chip

The bladder-chip platform enables continuous imaging while maintaining flow in both epithelial and vascular channels and mechanically stretching the membrane as part of the bladder voiding cycle. At the start of each live-cell imaging experiment, bladder epithelial cells in an initial relaxed state were perfused with sterile pooled human urine diluted in PBS on the epithelial side

and endothelial cell medium on the vascular side respectively (Fig. 2A1, B1, S5A1). The epithelial side was inoculated with a low dose of UPEC in diluted urine and infection was performed under flow (Fig. 2A2, B2, S5A2) for ca. 1.5 to 2 hours. The first bladder duty cycle also initiated at this timepoint. We maintained the optical focus of the microscope on the epithelial layer over the subsequent course of infection. UPEC attachment was evident during this infection phase by visual inspection (Fig. 2B2, S5A2).

After this period of infection, unattached bacteria in the epithelial channel were removed by perfusion of diluted urine. Our aim was to study the interaction of UPEC with host cells, therefore this perfusion was maintained throughout the experiment. Continuous perfusion reduced the accumulation of bacteria in the urine and enabled imaging of intracellular bacteria without large background noise in the fluorescence channels from planktonic bacteria. We subsequently performed a series of interventions that mimic the course of UTI infections and used time-lapse imaging to monitor the simultaneous changes in host-pathogen interaction dynamics. To mimic the host response, immune cells were introduced into the vascular channel. Among innate immune cells, neutrophils are the first line of defense in UTIs (Haraoka et al., 1999). We isolated neutrophils from human blood and verified that the isolation procedure yielded neutrophils with a high degree of purity (Son et al., 2017) through immunostaining for CD15, a neutrophil specific marker (Zahler et al., 1997) (Fig. S6). To enable identification and tracking of neutrophils, they were pre-labelled with CellTracker™ Deep Red dye, which stains the cytoplasm of these cells.

Neutrophils were subsequently introduced in the bladder-chip devices through the vascular channel, mimicking the natural route of immune cell migration into the bladder (schematic in Fig. 2A3-A5, snapshots in Fig. 2B3-B5, S5A3-A5). We used a cell concentration of ca. 2 million

cells/ml similar to the neutrophil concentration in human blood (Hsieh et al., 2007). During this period, the flow rate through the vascular channel was increased to 3ml/hour to provide a shear stress $\eta = 1$ dyne/cm², which aids neutrophil attachment to endothelial cells (Alon et al., 1995). In uninfected control chips, neutrophil attachment to the endothelial layer was minimal (Fig. S7A, B) and diapedesis of neutrophils to the epithelial layer was rare (Fig. 2C, S8A). In stark contrast, infection of the epithelial layer with UPEC elicited a robust attachment of neutrophils to endothelial cells (Fig. S7C, D), along with rapid diapedesis across to the epithelial side (Fig. 2B2-B4, S5A2-A4, S8C). We confirmed that neutrophil diapedesis was also stimulated in the absence of infection, upon exposure to a gradient of pro-inflammatory cytokines that are typically upregulated during UTIs (Agace et al., 1993; Hedges et al., 1992; Nagamatsu et al., 2015; Song et al., 2007) (interleukin-1 α , interleukin-1 β , interleukin-6 and interleukin-8 each at 100 ng/ml) across the epithelial-endothelial barrier (Fig. S8B). However, neutrophil diapedesis was more robust upon infection as compared to the cytokine gradient, with a higher number of neutrophils observed across multiple fields of view on the epithelial side (Fig. S8B-D). These results suggest that infection on-chip generates a strongly pro-inflammatory environment locally and that neutrophil diapedesis is further stimulated by the presence of UPEC (Agace et al., 1995; Oliveira et al., 2016).

Using time-lapse imaging, we were also able to quantify the kinetics of neutrophil migration with a temporal resolution of up to 7.5 minutes. Neutrophil diapedesis to the epithelial sites of infection was detected as early as ca. 15-17 minutes post-introduction into the vascular channel (Fig. 2B3, S5A3, supplementary movie SMov1, SMov2). Neutrophils that migrated to the epithelial side aggregated on the epithelial cells (Fig. 2B4-2B5, S5A4-A5, supplementary movie

SMov1, SMov2) In some cases, these neutrophils were able to control bacterial growth (Fig. 2B4-2B5, solid yellow boxes) whereas in others, bacterial growth was uncontrolled (Fig. 2B4-2B5, dashed white boxes). Diapedesis was observed in every field of view examined across n=4 infected chips, whereas diapedesis occurred infrequently in uninfected controls (Fig. 2C). Furthermore, the size of these aggregates was significantly larger in infected bladder-chips vs. uninfected controls, with the aggregates in case of infected-chips exhibiting the characteristic features of neutrophil swarms (Kienle and Lämmermann, 2016; Kreisel et al., 2010; Lämmermann et al., 2013). We quantified the size of the swarms formed by either estimating the maximum number of neutrophils observed in fields of view on the epithelial side (Fig 2D) or by measuring the total volume occupied by neutrophils normalized to the volume of a 3D field of view (Fig 2E). Using either metric, infection generated large swarms that did not occur in uninfected bladder-chips. The dynamics of swarm formation across n=51 and n=40 fields of view in two infected bladder-chips are shown in Fig. 2F. In infected bladder-chips, swarm formation was rapid, and swarms reached their maximum size typically between 60- and 90-minutes post-introduction of neutrophils (Fig. 2G).

Neutrophil extracellular traps (NETs) formation in response to UPEC infection

Neutrophils have complex responses to infections (Oliveira et al., 2016), including the formation of neutrophil extracellular traps (NETs) that occur by the release of cytosolic azurophilic granules around a scaffold of decondensed chromatin and potentially serves to trap and kill extracellular bacteria (Brinkmann et al., 2004). NETs have been shown to consist of antimicrobial granules such as myeloperoxidase (Metzler et al., 2011) and neutrophil elastase (Papayannopoulos et al., 2010) and have been observed in urine harvested from UTI patients (Yu

et al., 2017). Interestingly, we observed NET formation by neutrophils in the infected bladder-chip. We verified the formation of NETs on the epithelial layer through immunostaining of infected bladder-chips at 3.5 hours post-infection and 2 hours post-introduction of neutrophils in the vascular channel using antibodies against neutrophil myeloperoxidase (Fig 2H, S9A1-A3) and neutrophil elastase (Fig 2I, S9B1-B3). In each case, areas on the epithelial layer with strong immunostaining were observed (Fig. 2H3, 2I3). Neutrophils in these areas were typically in large numbers, characteristic of swarms. In addition, by this stage of the experiment, neutrophils that had high levels of myeloperoxidase or elastase typically did not retain strong expression of the cytoplasmic CellTracker dye used for identification of neutrophils in live imaging (cf. Fig. 2H2 and 2H3, 2I2 and 2I3). For each example, a zoomed-in image clearly shows long filament-like structures that extend between cells and are either myeloperoxidase positive (Fig. 2H5) or neutrophil elastase positive (Fig. 2I5), strongly suggestive of NETs (Brinkmann et al., 2004; Metzler et al., 2011; Papayannopoulos et al., 2010). NET formation was also observed in some instances by neutrophils in some locations on the endothelial channel, although large swarms did not form here (Fig. S9B1-B3).

To further characterize these structures, we imaged the epithelial layer of uninfected and infected bladder-chips with or without the addition of neutrophils using scanning electron microscopy (SEM). Representative images of the epithelial layers of uninfected bladder-chip controls (Fig. S10A) contrast with those from infected bladder-chips after neutrophil diapedesis (Fig. 2J1-J4, S10C) and clearly highlight the distinctive features of NET formation. In Fig. 2J1, neutrophils on the surface of the epithelial layer are clearly distinguishable by their distinctive spherical morphology and size (amber arrowheads). Thick bundles consisting of many thinner NETs formed between these neutrophils are shown by white arrowheads and appear to extend between

adjacent neutrophils, as is also evident in Fig. S10C. A majority of the epithelial cells have a characteristic flattened morphology with cell appendages that can extend between cells (cyan arrowheads); an example of a highly infected epithelial cell that is spherical in shape and with bacteria attached to its surface is indicated with a purple arrowhead (Fig. 2J1). A series of higher-magnification images in Fig. 2J2-2J4 show the structure of NETs in greater detail. Many individual UPEC bacteria (green arrowheads) are captured in these NETs (Fig. 2J2-2J4), which are themselves composed of many individual thinner fibres (indicated by yellow arrowheads in Fig. 2J2-2J4). These structures did not form in infected bladder-chips without the introduction of neutrophils (Fig. S10B), confirming their identity as structures identified as NETs via immunofluorescence (Fig. 2H, I). NET formation was a direct response to UPEC and not caused by hyperactivation of neutrophils due to experimental handling. To verify this, we collected the neutrophils that passed through an infected bladder-chip without attachment. Even upon infection, an overwhelming majority of the cells perfused into the chip flow out without adhering, because of the geometry of the channels in the device. NET formation in these samples was not observed unless the neutrophils were themselves infected by UPEC shed from the bladder-chip (Fig. S11). The bladder-chip model is therefore able to recapitulate key aspects of the host response to the early stages of UPEC infection while demonstrating that intracellular bacteria were substantially protected from neutrophil-mediated killing.

Heterogenous dynamics of intracellular bacterial communities within urothelial cells

Urinary tract infections that do not resolve upon intervention by the host immune system often require treatment with antibiotics. Antibiotics have complex pharmacokinetic and pharmacodynamic profiles *in vivo*, which we attempted to model through two successive rounds

of high dose administration of antibiotics (ampicillin at 40x MIC, Fig. S12A), on both the epithelial and vascular side, interrupted by periods with no antibiotic (schematics in Fig. 3A, 1E). Continuous time-lapse imaging over this entire period allowed us to capture the responses of bacteria to this simplified model of antibiotic profiles and to study the persistence of UPEC upon antibiotic treatment in the different physiological niches (Fig. 3 and Fig. 4).

A consequence of the first cycle of antibiotic administration under flow was the elimination of planktonic bacterial growth in the media in the apical channel, as is observed within the lumen of the bladder *in vivo*. Many bacteria that were still intact at the end of the antibiotic treatment intact did not regrow after the antibiotic was removed (Fig. S12 B). Regrowth commenced in only a small fraction of bacteria (Fig. S12C) after a variable lag phase (Fig. S12D) and rapid regrowth was highly correlated with intracellular location of bacteria within epithelial cells. These subsequently proceeded to form intracellular bacterial communities (IBCs), with a variable lag period. An example of an early stage of the IBC formation is shown in the timeseries in Fig. 3B1-B5, supplementary movie SMov3. This IBC was initially seeded with few bacteria that are present in Fig. 3B1 and clearly visible in Fig. 3B2. At the end of the timeseries, the entire host cell was packed with bacteria (Fig. 3B5). The exponential increase in bacterial numbers frequently led to the saturation of the 8-bit images in the bacterial channel. We therefore examined similar structures in separate bladder-chips via immunofluorescence (Fig. 3C, S13) staining. Zooms of two of the four IBCs highlighted in Fig. 3C show numerous tightly packed bacteria within epithelial cells that are both CK7+ (Fig. 3C) and CK8+ (Fig. S13). These bacterial morphologies are highly similar to early-stage IBCs observed in the bladder (Anderson et al., 2003; Duraiswamy et al., 2018; Justice et al., 2004). Higher resolution images of the biofilm-like structures within IBCs obtained via correlative light (Fig. 3D) and transmission

electron microscopy (Fig. 3E) showed that bacteria in IBCs can be either coccoid or rod shaped, which is also evident in scanning electron micrographs of bacteria within IBCs (Fig. 3F). IBCs within bladder-chip model therefore show many of the distinctive morphological features reported from images of infected bladders in the mouse model (Anderson et al., 2003; Hunstad and Justice, 2010).

Numerous reports from the mouse model of infection have shown IBCs to be dynamic structures; growth in IBCs eventually culminates in bacterial shedding or the complete exfoliation of the IBC. The underlying dynamics of these phenotypes is hard to capture in the mouse model, but the bladder-chip model allowed us to track the dynamics of bacterial growth within individual IBCs over extended periods of time, providing information on bacterial dynamics within so-called early, middle, and late-stage IBCs. An example of the heterogeneity in growth rates is evident from the timeseries for three IBCs in Fig. 3G1-G5, supplementary movie SMov4. IBCs#1 and 2 subsequently began to shed individual bacteria (Fig. 3G4), a phenotype not observed in IBC#3. At a later timepoint (Fig. 3G5) the fates of all three IBCs were dramatically different – the cell containing IBC#1 had completely exfoliated and was removed from the field of the view by flow in the epithelial channel, IBC#2 continued to shed bacteria, whereas growth remained slow in IBC#3. We monitored the eventual fate of n=100 IBCs during the first and the second growth cycles which confirmed that shedding and exfoliation were not mutually exclusive. While some IBCs only shed bacteria (n=28) and others exfoliated without shedding (n=27), a substantial fraction of IBCs showed shedding prior to exfoliation (n=31) and some IBCs displayed neither phenotype (n=14). Furthermore, in addition to the coccoid and rod-shaped morphologies highlighted in Fig. 3C-F, time-lapse imaging also enabled us to capture

morphotypes that occurred relatively rarely such as the intracellular growth of filamentous forms of UPEC (Fig. 3H1-H5, S14, [supplementary movie SMov5](#), [SMov6](#)). In this time series, a filamentous bacterium can be seen and appears to encircle the inner boundary of the cell (Fig. 3H1-3H4) before filling the volume entirely (Fig. 3H5). Overall, time-lapse imaging confirms that a significant fraction of bacteria within IBCs can survive the first round of antibiotic treatment and are the source for reseeding of both the extracellular bacterial populations as well as the subsequent growth of IBCs in newly infected cells.

Dynamic persistence of intracellular bacterial communities within uroepithelial cells

A subsequent round of antibiotic treatment provided an opportunity to study the dynamic persistence of bacteria within IBCs in response to an antibiotic profile that was a closer mimic of the periodic antibiotic exposures *in vivo*. Furthermore, at this stage of the experiment, we were also able to study the responses of bacteria in intermediate and mature late-stage IBCs to antibiotic treatment, which was not possible during the first round of antibiotic administration early in the course of infection. In the examples highlighted in Fig. 4A1-A5 and [supplementary movie SMov7](#), bacterial growth after the first round of antibiotic treatment resulted in the formation of many large IBCs with tightly packed bacteria (Fig. 4A1-A2). Many of the bacteria within each of the four IBCs were eliminated by the antibiotic, but a substantial proportion of bacteria in each IBC nevertheless survived the antibiotic treatment (Fig. 4A3). Each of these IBCs subsequently regrows when the antibiotic is removed (Fig. 4A4-A5), and two additional IBCs are seeded during this time (white arrowheads in Fig. 4A5). Overall, the second round of antibiotic administration led to a sharp decline in instances of subsequent bacterial regrowth (Fig. S12C). In all instances, regrowth either occurred directly within IBCs, or was caused by the

shedding of bacteria from IBCs to repopulate the extracellular niche and seed new IBCs, highlighting the dynamic stability of this niche and its importance in establishing persistent infection. We therefore performed a careful analysis to quantify bacterial growth rate within IBCs. Growth within IBCs across different time periods was exponential (Fig. 4B). We were able to track a subset of IBCs across two growth cycles (examples in Fig. 4C). In a majority of instances these revealed exponential growth in the absence of antibiotic, delayed response to antibiotic, and a lag phase after the antibiotic was removed. In general, bacterial growth in IBCs in the second growth cycle was slower than in the first (Fig. 4D). However, this population level statistic may be influenced by the fact that many of the IBCs monitored in the second growth cycle had been exposed to two rounds of antibiotic treatment. For this sub-population, in n=16 out of n=18 IBCs, growth was slower after the second round of antibiotic administration (Fig. 4E).

Next, we examined the dynamics of bacterial growth within IBCs during the period of antibiotic treatment in greater detail. In the IBC shown in the timeseries in (Fig. 4F1-4F5, S15A1-A5, supplementary movie SMov8, SMov9), growth before antibiotic administration (Fig. 4F1, 4F2) continued for a considerable period after the antibiotic was administered (Fig. 4F3, Fig. 4F4, S15A1-S15A3). Eventually, a reduction in bacterial volume towards the end of the antibiotic administration period was observed (Fig. 4F5, S15A4-S15A5). In contrast, the relatively smaller IBC in the timeseries in Fig. 4G1-4G5, S15B2-S15B5, supplementary movie SMov10, SMov11 continued to grow throughout the period of antibiotic administration. These different dynamics are also captured in the plot of bacterial volume for multiple IBCs before, during, and after the antibiotic treatment (Fig. 4H). In all cases, bacterial volume continues to increase during a significant period of antibiotic administration and in 2 out of 18 cases, there was no decrease in

bacterial volume throughout this period (Fig. 4H). In contrast, extracellular bacteria likely adherent on the epithelial cells but not internalized within them were rapidly eliminated by combination of antibiotic treatment and flow (Fig. 4I), in all cases the bacterial volume reduced immediately upon antibiotic administration. This differential killing resulted in a significantly higher proportion of extracellular population of bacteria being killed (Fig. 4J). Elimination of bacteria within IBCs was highly heterogenous. Another consequence of this differential killing was that after the second round of antibiotic treatment, regrowth was observed in only a very small fraction of non-IBC UPEC (Fig. S12C). Protection of bacteria within IBCs therefore has a direct outcome of enabling the reseeding of infection at other locations within the epithelial monolayer.

Lastly, we sought to determine if the bladder duty cycle altered the dynamics of UPEC infection. A comparison between infected bladder-chips with and without the duty cycle (Fig. 4K, L, S16) revealed a significant increase in the bacterial burden when the duty cycle was implemented (Fig. 4M). These results suggest that the bladder filling and voiding cycle influence the uptake and proliferation of UPEC, possibly through physiological changes in the epithelial cells in response to applied strains (Apodaca, 2004; Carattino et al., 2013; Truschel et al., 2002; Wang et al., 2005). In turn, they suggest a deeper connection between the physiology of mechanically active organs such as the bladder and the processes of infection, which can be characterized in detail using this bladder-chip model.

Discussion

In our human bladder-chip model, we focused on recapitulating the key aspects of bladder physiology relevant to the study of the earliest stages of UPEC infection and IBC formation. Therefore, superficial bladder epithelial cells, the first cell-type usually infected by UPEC, were cultured both under flow in diluted pooled urine and in co-culture with bladder microvascular endothelial cells. The ability to apply a cyclic mechanical stretch to the PDMS membrane, originally designed to mimic the breathing motion in the lung (Huh et al., 2010b) or the peristaltic motion in the gut (Kim and Ingber, 2013), has been adapted here to mimic the slow expansion and rapid contraction of bladder volume. We demonstrate the ability to perform multiple duty cycles while simultaneously imaging the infected device via long-term time-lapse imaging, a technical advance that is difficult to achieve with bladder explants (Justice et al., 2004) or other *in vitro* studies of UPEC infection of bladder epithelial cells (Andersen et al., 2012; Horsley et al., 2018; Iosifidis and Duggin, 2020; Smith et al., 2006). Using this approach, we found that the total bacterial burden inside infected bladder-chips was significantly higher at a late stage of infection if a duty cycle was applied, unlike the non-significant influence of cyclic stretching on Shigella infection of intestinal-chips under flow conditions (Grassart et al., 2019). The exact mechanisms underlying this phenomenon remain to be explored, but there is an increasing understanding of the role of mechanical forces in regulating innate immune function (Solis et al., 2019). Our results showcase the ability of the bladder-chip model to capture these interactions between mechanical function, physiology, and infection, unlike other infection models reported thus far.

A primary focus of *in vitro* models developed so far has been to probe specific aspects of UPEC infection, such as the role of the stratified bladder architecture (Horsley et al., 2018) or the effects of micturition on IBC formation (Andersen et al., 2012; Iosifidis and Duggin, 2020).

However, the migration of immune cells into the bladder is difficult to reproduce in these models, and in many of these systems, live-cell imaging remains technically challenging (Horsley et al., 2018; Smith et al., 2006). Furthermore, the models do now allow mechanical manipulations of the cellular co-culture. In that sense, the bladder-chip model complements these existing approaches by providing these additional functionalities. Further development, potentially through the combination of organoid and organ-on-chip approaches, could lead to the development of a fully stratified uroepithelium on-chip.

Neutrophils are the first responders to UPEC infection (Abraham and Miao, 2015; Haraoka et al., 1999), and neutrophil migration involves a series of steps that commences with attachment to the endothelium under flow, migration on the endothelial surface, diapedesis across the epithelial-endothelial cell barrier and movement towards the site of infection (Ley et al., 2007; Nourshargh et al., 2010). Perfusion of the vascular channel with CD15+ neutrophils isolated from human blood shows that the bladder-chip model recapitulates all these phenotypes, with rapid diapedesis of neutrophils to sites of infection. There, neutrophils aggregate to form swarms (Hopke et al., 2020; Kienle and Lämmermann, 2016; Lämmermann et al., 2013; Reátegui et al., 2017) and subsequently, the formation of NETs (Branzk et al., 2014; Brinkmann et al., 2004; Metzler et al., 2011; Papayannopoulos et al., 2010) around extracellular bacteria is observed. Characterization of these structures via SEM shows that they can extend across many tens of microns and stain positive for myeloperoxidase (Metzler et al., 2011) and neutrophil elastase (Papayannopoulos et al., 2010), indicative of potent anti-microbial activity. However, neutrophil control of infection on-chip is partial; this is possibly due to the unrestricted growth of large numbers of extracellular bacteria and in some instances, exacerbated by the loss of some neutrophils due to flow in the

channel. Another contributing factor could potentially be the architecture of the PDMS membrane, which permits neutrophil diapedesis only at fixed spatial locations on-chip. Neutrophil migration may also be impacted by the relative stiffness of the PDMS membrane. Nevertheless, the demonstration of NET formation is consistent with the occurrence of these structures both in the mouse model (Ermer et al., 2009) as well as in the urine of infected patients (Yu et al., 2017) and suggests that the model is able to recapitulate important aspects of disease. It is also an important advance for the use of organ-on-chip approaches to recapitulate NET formation in infectious diseases.

IBC formation begins immediately after infection and is already underway upon neutrophil administration. However, clear demonstration of IBCs with a high degree of confidence was only possible after an initial treatment with a high dose of antibiotic that eliminated extracellular planktonic bacteria and improved the optical imaging of bacteria attached to or within epithelial cells. It enabled us to capture the full cycle of IBC growth from few bacteria to a large biofilm and subsequent release via shedding and filamentation. Importantly, the compact nature of the device allowed us to image multiple IBCs concurrently on the same chip with a high temporal resolution while simultaneously mimicking the bladder filling and voiding cycles, which is difficult to achieve in bladder explants (Justice et al., 2004) or bladder monoculture *in vitro* model systems (Andersen et al., 2012; Iosifidis and Duggin, 2020). Our observations reiterate the highly dynamic nature of these structures; growth was asynchronous and heterogenous and outcomes included bacterial shedding, exfoliation and filamentation (Hunstad and Justice, 2010; Justice et al., 2004; Scott et al., 2015). Notably, shedding and exfoliation were not mutually

exclusive for the time-period of our observations – we report examples of IBCs that shed bacteria and contract in volume before exfoliation.

While IBCs are clearly acknowledged as critical players in early infection, the contribution towards promoting persistence is not completely understood. For example, Blango *et al.*, (Blango and Mulvey, 2010) showed that incubation of bladder explants containing IBCs with a high dose of antibiotics for a period of 18 hours resulted in a substantial sterilization of these structures and concluded that other populations, notably quiescent reservoirs (Mysorekar and Hultgren, 2006) might play a greater role in the establishment of persistent populations. However, the pharmacokinetic profiles of most antibiotics in the host are not time invariant. In case of ampicillin, a standard regimen of ampicillin treatment is typically a bolus of 250-500 mg of antibiotic administered every 6 hours. Within the serum, ampicillin concentration peaks at a $C_{\max} \sim 3\text{-}40 \mu\text{g/ml}$, which is between 1.5 to 20-fold the MIC as measured in human serum (Bryskier, 2020; Putrinš *et al.*, 2015). We therefore chose concentrations that captured these antibiotic exposures (we used ampicillin at 40x MIC measured in the endothelial cell medium perfused in the vascular channel). Ampicillin concentrations in the blood rapidly decay with a half-life of between 60 and 90 minutes with a characteristic pharmacokinetic/pharmacodynamic profile. This period is modelled well by our experimental protocol where phases with high concentration of ampicillin are interspersed with periods with no antibiotic. We are therefore able to model the delivery of two consecutive doses of antibiotic and find that IBCs offer substantial protection against sterilization by a short duration of a high-dose antibiotic treatment and in many instances, bacterial regrowth after two successive rounds of antibiotic administration. Notably, in smaller ‘early IBCs’, bacterial growth continues throughout the

period of ampicillin administration, suggesting that the intact nature of the cell membrane likely diminishes the effect of the drug. Our results suggest that, IBCs may continue to play a role in reseeding sites of infection for a considerable period after the commencement of antibiotic treatment. This has particularly important implications with regard to the compliance of antibiotic use as proliferating IBCs could rapidly re-seed sites of infection throughout the bladder if antibiotic doses are missed. These unique capabilities of the bladder-chip to realistically model antibiotic treatment regimens for IBCs can be leveraged in the future to screen compounds (Spaulding et al., 2017) and identify optimal antibiotic treatments regimens that can eliminate persistent bacterial populations in IBCs or alter the host-pathogen interaction dynamic in UTIs.

In summary, the bladder-chip model incorporates aspects of bladder physiology highly relevant to early UPEC infection in a platform amenable to long-term live-cell imaging as well as for the administration of antibiotics and therapeutics in a physiologically relevant manner. Our results establish the suitability of this model for immunological and drug-delivery studies and show that IBCs are highly dynamic structures that offer substantial protection from antibiotic clearance for an extended period of time.

Figure 1: Human Bladder-chip model of UTI recapitulates the physiology of bladder filling and voiding.

(A) Schematic of the human bladder-chip with co-culture of the HTB9 human bladder epithelial cell line (epithelium, top) and primary human bladder microvascular endothelial cells (endothelial, bottom) on either side of the stretchable and porous membrane. Pooled human urine diluted in PBS and endothelial cell medium were perfused in the apical and vascular channels respectively to mimic bladder physiology. A negative pressure in the ‘vacuum’ channels (magenta) on either side of the main channel was applied to stretch the porous membrane to mimic stretching of the bladder. (B, C) Immunofluorescence staining of confluent epithelial and endothelial cell monolayers (anti-EpCAM (magenta) and anti-CK7 (yellow) for the epithelial cells and anti-PECAM-1 (green) for the endothelial cells) in an uninfected control chip. Some endothelial cells also stained positive for CK7. Cell nuclei were labeled with DAPI (azure). (D) Schematic of the reconstitution of the bladder filling and voiding cycle via stretching of the membrane with a duty cycle of 6 hours. The cycle consisted of a linear increase in strain through

547 stretching of the membrane (*filling bladder*, 0 to 2 hours), maintenance of the membrane under
 548 stretch (*filled bladder*, 2 to 4 hours), a quick relaxation of applied strain over 2 minutes (*voiding*
 549 *bladder*, 4:02 hours) and maintenance without applied strain (*voided bladder*, 4:02 hours to
 550 6hours). (E) An overview of the timeline of the experimental protocol including infection,
 551 addition of neutrophils via the vascular channel, and two cycles of antibiotic treatment
 552 interspersed by two bacterial growth cycles. The consecutive bladder duty cycles are indicated.
 553

Figure 2: Neutrophil diapedesis and NET formation on-chip.

(A1-A5) Schematic of the UPEC infection, introduction of neutrophils and diapedesis of neutrophils across the epithelial-endothelial barrier to sites of infection. Flow in the epithelial and endothelial channels is indicated by arrows; the flow rate was increased upon introduction of neutrophils in the vascular channel to increase attachment. **(B1-B5)** Snapshots from time-lapse imaging highlighting each stage in the infection cycle shown in **(A1-A5)**. Bladder epithelial cells (magenta) and neutrophils (amber) were identified with membrane (Cell Mask Orange) and cytoplasmic (Cell Tracker Deep Red) dyes, respectively. UPEC identified via constitutive expression of YFP are shown in green. Neutrophil swarms could either control bacterial growth (yellow dashed square, compare **B4** vs **B5**) or did not manage to restrict bacterial growth (white dashed square, compare **B4** vs **B5**). **(C)** Bar charts for relative frequency of neutrophil diapedesis (black) in n=3 uninfected control bladder-chips and n=4 infected bladder-chips. Data obtained from n=95 and n=116 fields of view, each of which was 206 x 206 μm^2 . **(D)** Quantification of the number of neutrophils detected on the epithelial layer, in control and infected bladder-chips. The red bar represents the median value, $p < 1\text{E-}15$. In many instances in the uninfected control bladder-chips, no neutrophil diapedesis is detected. Data obtained from n=95 and n=130 across 206 x 206 μm^2 fields of view. **(E)** A plot of the maximum neutrophil swarm volume on the epithelial layer normalized to the total volume for n=67 and n=118 fields of view on n=3 uninfected control and n=3 infected bladder-chips. The red bar represents the median value. $p < 1\text{E-}15$. **(F)** A plot of neutrophil swarm volume on the epithelial layer over time for n=51 and n=40 fields of view for n=2 technical replicates indicated by squares and circles. For each time profile, the volume is normalized to the maximum volume attained over the timeseries and t=0 refers to the timepoint at which neutrophils are introduced into the vascular channel **(G)** Plot of

the time to reach the maximum swarm volume in n=154 fields of view across n=4 infected bladder-chips. (**H1-H5, I1-I5**) NET formation by neutrophils on the epithelial layer. The neutrophils are identified by a cytoplasmic dye (CellTracker Deep Red, false coloured in amber) (**H2, I2**) and immunostaining with an anti-myeloperoxidase antibody (**H3**, zooms in **H5**) or an anti-neutrophil elastase antibody (**I3**, zooms in **I5**). Merged images in each case are shown in **H4** and **I4**. UPEC identified via YFP expression is shown in spring green. Nuclear labelling with DAPI is shown in azure. (**H5**) NETs, identified via anti-myeloperoxidase staining or anti-elastase staining are indicated with white arrows in (**H5**) and (**I5**) respectively. (**J1-J4**) Scanning electron micrographs of the epithelial layer of an infected bladder-chip 2 hours after the introduction of neutrophils in the endothelial channel. (**J1**) Neutrophils (amber arrowheads) are visible above a layer of epithelial cells. Thick bundles consisting of many thinner NET structures between neutrophils are indicated by white arrowheads, and examples of individual UPEC bacteria within the NETs are indicated by green arrowheads. A heavily infected epithelial cell with UPEC visible on the epithelial cell (purple arrowhead), and appendages between epithelial cells (cyan arrowheads) are also visible. (**J2**) Micrographs showing thick bundles consisting of many thinner NET structures (white arrowheads) that extend between cells and trap many individual bacteria. Thinner NET fibers (yellow arrowheads) are also visible. (**J3**) Zooms of the regions in **J2** identified by a yellow dashed square. Two bacteria held by a thick bundle composed of many thinner NET fibers are shown. (**J4**) Micrograph highlighting multiple bacteria trapped between NET bundles. p-values in **D** and **E** were calculated using a Mann-Whitney test. Scale bar = 50 μm in **B1-B5, H1-H5, I1-I5**.

Figure 3: Bladder-chip reveals dynamics of IBC growth, shedding and exfoliation.

(A) Schematics of the host-pathogen interactions within IBCs between successive rounds of antibiotic treatment with outcomes including shedding of bacteria and cell exfoliation shown. (B1-B5) Timeseries for the growth of an IBC from few bacteria (white arrowhead) after the first round of ampicillin treatment. Bacteria grow to completely fill the cell volume (B5). (C) Immunofluorescence characterization of two IBCs; the intracellular nature of growth is confirmed with staining with an anti-CK7 antibody. Correlative light (D) and transmission

608 electron micrographs (**E**) show two IBCs filled with both rod-shaped and coccoid-shaped
609 bacteria. (**F**) Coccoid-shaped bacteria (yellow arrowheads) and rod-shaped bacteria (magenta
610 arrowheads) are also visible in a scanning electron micrograph of an infected epithelial cell.
611 IBCs on infected bladder-chips shown in **C-F** were fixed 13 hours after UPEC infection and 6
612 hours into the first growth cycle. (**G1-G5**) Three examples of IBC growth, labelled 1 – 3 with
613 differing outcomes. Unrestricted bacterial growth is observed within all IBCs. In IBC#1 at
614 timepoint (**G4**) the IBC begins to shed bacteria into the surrounding medium. The cell exfoliates
615 in the time interval between (**G4** and **G5**). In IBC#2, bacterial shedding is visible at (**G4**) and
616 shedding continues until end of the timeseries with a reduction in bacterial volume. In contrast,
617 growth within IBC#3 is slower and neither shedding nor exfoliation occurs within the timeseries.
618 (**H1-H5**) Timeseries highlighting an example of filamentous UPEC growth within an IBC. Scale
619 bars, 10 μm in **B1-B5**, **G1-G5** and **H1-H5**.

Figure 4: IBCs offer a semi-protective niche that delays clearance of bacteria by antibiotics.

(A1-A5) Bacteria persist and grow in IBCs despite antibiotic treatment. Snapshots show the

growth of four IBCs with variable growth rates (A1-A2). Ampicillin treatment eliminates some

but not all of the bacteria within each IBC (A3). Growth resumes at all sites in (A4, A5),

formation of new IBCs in the second growth cycle is indicated by white arrowheads. (B) Plots of

logarithm of bacterial volume within five separate IBCs demonstrates exponential bacterial

627 growth. IBCs are seeded dynamically; growth can occur either in the first or second growth
628 cycle, or prior to the administration of antibiotic, or in few cases continues in the presence of the
629 antibiotic. **(C)** Plots of the logarithm of bacterial volume vs. time for n=8 IBCs tracked across
630 two growth phases with an intermediate period of ampicillin treatment. In the growth phases,
631 growth is exponential and bacterial volume continues to increase for up to ca. 120 minutes after
632 administration of antibiotic before declining due to loss of bacteria. In each case, growth resumes
633 after the antibiotic is removed. **(D)** Scatter plots of the doubling time of bacterial volume in IBCs
634 as measured in the first growth cycle (n=102) and the second growth cycle (n=59). Growth in the
635 second cycle is significantly slower ($p=4.7E-7$), red line represents the median value. **(E)**
636 Doubling time of bacterial volume in IBCs in the first and second growth cycle for some of the
637 IBCs in **(D)** that survived the antibiotic treatment. In n=16 out of 18 instances, growth is slower
638 in the second growth cycle. **(F1-F5)** High resolution time-series that highlights bacterial growth
639 within an IBC prior to **(F1, F2)** and after **(F3-F5)** administration of ampicillin. Some bacteria
640 within this IBC are subsequently eliminated **(F5)**. **(G1-G5)** High resolution time-series that
641 highlights bacterial growth within an IBC prior to **(G1, G2)** and after **(G3-G5)** administration of
642 ampicillin. The bacterial volume within this IBC is not diminished by antibiotic treatment **(G5)**.
643 **(H)** Plots of logarithm of bacterial volume within n=11 IBCs before, during, and after the second
644 round of antibiotic treatment. **(I)** Plot of the volume of extracellular bacteria upon antibiotic
645 administration from n=103 across 206 x 206 μm^2 field of view from n=3 bladder-chips. The
646 bacterial volumes are normalized to the volume immediately prior to the antibiotic
647 administration. **(J)** Scatter plot of the extracellular bacterial volume (n=105) and bacterial
648 volume within IBCs (n=22) after antibiotic treatment as a fraction of the maximum bacterial
649 volume prior to antibiotic treatment. Red line represents the median value, $p=5.8E-6$ as

650 calculated by Mann-Whitney test. (**K, L**) Representative images from the epithelial face of the
 651 infected bladder-chips with or without duty cycle. (**M**) Scatter plots of the logarithm of the total
 652 bacterial area across n=14 from infected bladder-chips with (n=2) and without (n=2) duty cycle,
 653 $p = 8.6E-6$. Infected bladder-chips shown in **K, L** were fixed 13 hours after UPEC infection and 6
 654 hours into the first growth cycle. p-values calculated using a Mann-Whitney test. Scale bars, 10
 655 μm in panels **A1-A5, F1-F5, and G1-G5**.

656

Cell type	Cell density/ $10^4\mu\text{m}^2$
Epithelial	31.7 ± 5.1
Endothelial	4.0 ± 0.6

Table 1.

Characterization of epithelial and endothelial cell densities from a total of n=18 fields of view in both the epithelial and endothelial layers from n=2 bladder-chips.

660

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 670 optimizing the protocol for TEM of infected bladder-chip. The authors thank and credit
 671 BioRender.com for the illustrations and schematics used in this manuscript.

672

673 Materials and Methods

Reagent or resource	Designation	Source or reference	Identifiers	Additional information
strain, strain background	Uropathogenic Escherichia coli (UPEC) strain CFT073	PMID: 2182540	NCBI: txid199310	originally isolated from a pyelonephritis patient and provided by Prof. H.L.T. Mobley, University of Michigan, USA
plasmid	pZA32-YFP	PMID: 9092630		(Lutz and Bujard, 1997)
strain, strain background	CFT073-pZA32-YFP	this paper		this study
cell line (human)	HTB-9 TM bladder epithelial cells	ATCC	Cat#:5637	
cell line (human)	HMVEC-Bd – Human Bladder Microvascular Endothelial Cells	Lonza	Cat#:7016	
other	RPMI-1640 medium	ATCC	Cat#:30-2001	
other	Gibco TM RPMI 1640 Medium, no phenol red	Thermofisher	Cat#:11835063	
other	Gibco TM Fetal Bovine Serum, Premium Plus	Thermofisher	Cat#: A4766801	
other	EGM TM -2 MV Microvascular Endothelial Cell Growth Medium-2 BulletKit TM	Lonza	Cat#:CC-3202	
other	EBM-PRF Endothelial Medium Phenol-red free, 500 ML	Lonza	Cat#:CC-3129	
other	EGM TM -2 Endothelial SingleQuots TM Kit	Lonza	Cat#:CC-4176	
other	Gibco TM Antibiotic-Antimycotic (100X)	Thermofisher	Cat#:15240062	
other	Gibco TM Trypsin-EDTA (0.05%), phenol red	Thermofisher	Cat#:25300054	
drug	Chloramphenicol	Sigma-Aldrich	Cat#:C1919-25G	34 mg/ml in ethanol (stored at -20 °C)
drug	Ampicillin	Sigma-Aldrich	Cat#: A9518-5G	50 mg/ml in ddH ₂ O (stored at -80 °C)
other	pooled human female urine	Golden West Diagnostics	Cat#: OH2010-pH	
other	Phosphate Buffered Saline	Thermofisher	Cat#: 10010056	
other	Gibco TM HEPES	Thermofisher	Cat#: F2006	
other	Invitrogen TM DAPI	Thermofisher	Cat#: D1306	5 mg/ml in DMSO
other	LB (Luria broth base, Miller's modified)	Sigma-Aldrich	Cat#: L1900-1KG	

other	Organ-chips (Standard Research Kit - 24 per Pack)	Emulate	RE1000001024	Emulate, Inc. 27 Drydock Ave, 5th Floor Boston, MA 02210
other	CellMask™ Orange Plasma membrane Stain	Thermofisher	Cat#: C10045	used at 1μM in respective cell medium
other	HCS CellMask™ Deep Red Stain	Thermofisher	Cat#: H32721	used at 2μM in PBS
other	CellTracker™ Deep Red Dye	Thermofisher	Cat#: C34565	used at 1μM in respective cell medium
other	Elveflow® OB1 Pressure Controller OB1 Base MkIII+	Elveflow	Cat#: OB1MKIII+-MIX-	connected to 6bar compressed air channel
other	Elveflow® OB1 Pressure Controller OB1 MkIII Channel-900/1000	Elveflow	Cat#: OB1-Dual-	connected to Elveflow® OB1 Pressure Controller OB1 Base MkIII+
other	Diaphragm moist gas vacuum pump	KNF Neuberger	Cat#:LABOPORT® UN 820.3 FT.40P	connected to Elveflow® OB1 Pressure Controller OB1 MkIII Channel-900/1000
antibody	Anti-EpCAM	abcam	Cat#: ab71916	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Rabbit secondary antibody, Alexa Fluor 647 (2μg/ml) and Alexa Fluor 568 (2μg/ml) in 1%BSA
antibody	Anti-PECAM1 or Anti-CD31	abcam	Cat#: ab24590	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Mouse secondary antibody, Alexa Fluor 647 (2μg/ml) and Goat anti-Mouse Alexa Fluor 488 (2μg/ml) in 1%BSA
antibody	Anti-CK7	abcam	Cat#: ab209599	used at 1:100 dilution in 1% BSA
antibody	Anti-CK8	abcam	Cat#: ab192468	used at 1:100 dilution in 1% BSA
other	Alexa Fluor™ 555 Phalloidin	Thermofisher	Cat#: A34055	used at 1μM concentration in PBS

antibody	Anti-VE-Cadherin	abcam	Cat#: ab33168	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Rabbit secondary antibody, Alexa Fluor 647 (2µg/ml) and Alexa Fluor 488 (2µg/ml) in 1%BSA
antibody	Anti-Uroplakin3a	Santa Cruz	Cat#: sc-166808	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Mouse secondary antibody, Alexa Fluor 647 (2µg/ml) in 1%BSA
antibody	Anti-CK1	Thermofisher	Cat#: MA1-06312	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Mouse secondary antibody, Alexa Fluor 647 (2µg/ml) in 1%BSA
antibody	Anti-E-Cadherin	Thermofisher	Cat#: MA5-14408	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Mouse secondary antibody, Alexa Fluor 647 (2µg/ml) in 1%BSA
antibody	Anti-ZO-1	abcam	Cat#: ab216880	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Rabbit secondary antibody, Alexa Fluor 647 (2µg/ml) in 1%BSA
antibody	Anti-myeloperoxidase	abcam	Cat#: ab9535	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Rabbit secondary antibody, Alexa Fluor 568 (2µg/ml) in 1%BSA
antibody	Anti-neutrophil elastase	abcam	Cat#: ab68672	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Rabbit secondary antibody, Alexa

				Fluor 568 (2µg/ml) in 1%BSA
antibody	Anti-CD15	abcam	Cat#: ab665	used at 1:100 dilution in 1% BSA, conjugated with Donkey anti-Mouse secondary antibody, Alexa Fluor 568 (2µg/ml) in 1%BSA
antibody	Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 647	Thermofisher	Cat#: A-31571	2 mg/ml
antibody	Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 647	Thermofisher	Cat#: A-31573	2 mg/ml
antibody	Goat anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 488	Thermofisher	Cat#: A-11029	2 mg/ml
antibody	Donkey anti-Rabbit IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 568	Thermofisher	Cat#: A10042	2 mg/ml
antibody	Donkey anti-Mouse IgG (H+L) Highly Cross-Adsorbed Secondary Antibody, Alexa Fluor 568	Thermofisher	Cat#: A10037	2 mg/ml
peptide, recombinant protein	Fibronectin from human plasma	Sigma-Aldrich	Cat#: F1056	500 µg/ml in ddH ₂ O
peptide, recombinant protein	Native Collagen, Bovine dermis	AteloCell	Cat#: IAC-50	5 mg/ml
peptide, recombinant protein	Human IL-1α, research grade	Miltenyi Biotec	Cat#:130-093-894	1 µg/ml
peptide, recombinant protein	Human IL-1β, research grade	Miltenyi Biotec	Cat#:130-093-895	1 µg/ml
peptide, recombinant protein	Human IL-6, research grade	Miltenyi Biotec	Cat#:130-093-929	1 µg/ml
peptide, recombinant protein	Human IL-8, research grade	Miltenyi Biotec	Cat#:130-122-354	1 µg/ml
commercial assay or kit	MACSxpress® Whole Blood Neutrophil Isolation Kit, human	Miltenyi Biotec	Cat#:130-104-434	
software, algorithm	Imaris 9.5.1	Bitplane		

other	Gas chamber for stages with k-frame insert (160x110mm) - magnetic model with sliding lid.	okolab	Cat#: H201-K-FRAME	
other	Custom holder for 24mm x 60mm coverslip	okolab	Cat#:1x24by60-M	
other	µ-Slide 8 Well	ibidi	Cat#:80826	
other	Masterflex PharMed tubing, 0.89mm ID, 100 ft	Cole-Palmer	Cat#:GZ-95709-26	
other	Masterflex® Transfer Tubing, Tygon® 0.76mm ID	Cole-Palmer	Cat#:GZ-06419-03	
other	1.30 x 0.75 x 10 mm metallic tubes	Unimed	Cat#:9084 / 200.010-A	
other	1.00/0.75 x 20mm metallic tubes	Unimed	Cat#:200.010-A	
other	Aladdin programmable pump	WPI	Cat#: PUMP-NE-1000	

674

675 **Cell culture of human bladder epithelial and bladder endothelial cells**

676 The HTB9 human bladder epithelial carcinoma cell line (procured from ATCC, 5637) was
677 cultured in RPMI 1640 medium supplemented with 10% Fetal Bovine Serum (FBS) as
678 recommended by the supplier. Human Bladder Microvascular Endothelial cells (HMVEC-Bd)
679 (procured from Lonza, CC-7016) were cultured in Lonza EGM-2 MV BulletKit medium. Both
680 the epithelial and endothelial cells were generally cultured in their respective medium
681 supplemented with 1X Antibiotic-Antimycotic. Epithelial cells were passaged by detachment
682 with 0.05% Trypsin at 37°C for 3-5 minutes followed by neutralization of trypsin with RPMI
683 1640 medium/10% FBS. Bladder endothelial cells were passaged and split as recommended by
684 the supplier. The cells used in all the experiments were at ten passages or fewer. The cell lines
685 were tested routinely for mycoplasma contamination during passaging.

686 **UPEC culture for infection of bladder epithelial cells in the bladder-chip**

687 Uropathogenic *Escherichia coli* (UPEC) strain CFT073 was originally isolated from a
688 pyelonephritis patient (Mobley et al., 1990) and provided by Prof. H.L.T. Mobley, University of
689 Michigan, USA. A derivative strain expressing yellow fluorescent protein (YFP) was generated

by electroporation of CFT073 with the episomal plasmid pZA32-YFP (Lutz and Bujard, 1997), as described earlier (Dhar et al., 2015). To induce expression of type 1 pili, UPEC was grown in LB media containing 25 µg/ml chloramphenicol under non-shaking conditions at 37 °C for 2 days prior to the experiment, to achieve a stationary phase culture (OD₆₀₀=1.5 and corresponding to a concentration of 1.5 x 10⁹ bacteria/ml). The bacteria were diluted 10-fold to a final concentration of 1.5 x 10⁸ cells/ml) and resuspended in a solution of pooled human female urine (procured from Golden West Diagnostics Catalogue OH2010-pH) diluted 10-fold in Phosphate Buffered Saline.

Recapitulation of human bladder physiology in human bladder-on-a-chip device

Bladder-chip devices made of polydimethylsiloxane (PDMS) were purchased from Emulate (Boston, USA). The dimensions of the microfluidic device were as follows: width of the channels- 1000 µm, height of the upper channel- 1000 µm, lower channel – 250 µm). For extracellular matrix (ECM) coating, a coating solution consisting of the ER-1 compound (Emulate) dissolved in ER-2 solution at 0.5 mg/ml (Emulate) was introduced in both apical and vascular channels and the chips were subsequently activated by exposing the bladder-chip for 20 minutes under UV light. The channels were then rinsed with fresh coating solution and the protocol was repeated once. The channels of the bladder-chip were then washed thoroughly with PBS before incubation with an ECM solution of 150 µg/ml bovine collagen type I and 30 µg/ml fibronectin from human plasma in PBS buffered with 15 mM HEPES solution for 1-2 hours at 37°C as described previously (Thacker et al., 2020b). If not used directly, coated chips were stored at 4°C and pre-activated before use by incubation for 30 minutes with the same ECM solution at 37°C. Three days before the day of the experiment, HMVEC-Bd cells were seeded

into lower channel of the inverted bladder-chip device at 0.5 million cells/ml. Two days before the experiment, HTB9 cells were seeded into upper channel at 5 million cells/ml. Prior to the infection experiment, bladder endothelial and bladder epithelial cells were cultured in their respective medium supplemented with the 1X Antibiotic-Antimycotic solution. The antibiotics were removed prior to the experiment.

Characterization and immunostaining of human bladder epithelial and human bladder epithelial cells in ibidi wells and human bladder-chip

Human bladder epithelial and bladder endothelial cells were cultured inside ibidi μ -Slide 8 wells for one day. The cells were subsequently fixed with 4% paraformaldehyde (PFA) for 1 hour at room temperature. Fixed cells were then washed three times with 200 μ l of PBS to remove residues of PFA, permeabilized with 0.15 % Triton X-100 for 15 minutes; washed three times with 200 μ l of PBS to remove residues of detergent and then incubated in a blocking solution of 1% BSA in PBS for 1 hour. The cells were then incubated with primary antibodies (anti-EpCAM, anti-PECAM-1, anti-CK7, anti-CK8, anti-VE-Cadherin, anti-Uroplakin3a, anti-CK1, anti-E-Cadherin, anti-ZO-1, anti-myeloperoxidase, anti-neutrophil elastase, anti-CD15) at a dilution of 1:100 in an antibody incubation buffer comprising 1% BSA and 0.01% Triton-100 in PBS. The ibidi 8-wells were subsequently washed three times with PBS for 10 minutes each. Incubation with secondary antibody (Donkey anti-Mouse Alexa Fluor 647, Donkey anti-Mouse Alexa Fluor 568, Goat anti-Mouse Alexa Fluor 488, Donkey anti-Rabbit Alexa Fluor 647, Donkey anti-Rabbit Alexa Fluor 568, Donkey anti-Rabbit Alexa Fluor 488) at a concentration of 2 μ g/ml in antibody incubation buffer was subsequently performed for 1 hour at room temperature. Excess antibody was removed by washing three times with PBS for 10 minutes

each. Cell nuclei were stained with DAPI (5 µg/ml) for 30 minutes. Ibidi 8-wells were washed three times to remove unbound DAPI. Cells were covered with appropriate volume of PBS until imaging. Cells were imaged with 63X oil objective on Leica SP8 confocal microscope. Images were deconvolved using SVI Huygens (Quality, 0.05; Iterations, 40).

For characterization of the cell types on-chip, bladder-chips with co-culture of bladder epithelial and bladder endothelial cells were kept under pooled diluted urine and EBM2 medium using P200 pipette tips for 2 days prior to PFA fixation. The cells in the bladder-chip were then immunostained following the protocol described above. Images were acquired with Leica HC FLUOTAR 25X (NA 0.95) multi-immersion objective on Leica SP8 confocal microscope.

Characterization of strain-pressure curve in the bladder-chip model

Elveflow OB1 MK3 – Microfluidic flow control system was used to control the negative pressure applied to the human bladder-chip. The control system was connected to the compressed air line (6 bar) for the positive pressure and diaphragm vacuum pump for the negative pressure. A negative pressure (0 to -900 mbar) with a step function of -100mbar was subsequently applied to the vacuum channels in the bladder-chip using a Pressure Controller (Elveflow OB1 pressure controller). For these experiments, both bladder epithelial and endothelial cells were seeded on the respective sides in the devices. This experiment was performed with the chip maintained on the stage of the microscope and a brightfield image was acquired at each step increase of -100mbar, on Leica SP8 confocal microscope. The PDMS inter-pore-to-pore distance was measured for 14 pore-to-pore combinations at each input of negative pressure. Linear fitting was performed using GraphPad Prism (version 9).

Mimicking bladder filling and voiding cycle in human bladder-chip

The stretching of the human bladder-chip was done using the Elveflow OB1 MK3 – Microfluidic flow control system connected to the compressed air line (6 bar) for the positive pressure and diaphragm vacuum pump for the negative pressure. Human bladder-chip in the relaxed (*voided bladder*) state was slowly perturbed with a linear ramp function to reach a stretched (*filled bladder*) state over a period of 2 hours. This period corresponded to the *filling bladder* state in Figure 1D. Bladder-chip was kept under stretched (*filled bladder*) state over the subsequent 2 hours. Micturition or urination was recapitulated by rapidly reducing the applied strain on the bladder-chip from the stretched (*filled bladder*) state to relaxed (*voided bladder*) state over a period of 2 minutes. Subsequently, the bladder-chip was maintained with no negative pressure applied in the vacuum channel under relaxed (*voided bladder*) state from (4:02 hours to 6 hours). This 6-hour bladder filling and voiding cycle was repeated continuously for the rest of the experiment.

Experimental setup and imaging parameters for time lapse imaging for UPEC infection in the human bladder-chip devices

The medium perfusion inside the bladder-chip device was achieved with the Aladdin syringe pumps. The syringes with respective media were connected to the bladder-chip via gas impermeable PharMed® tubing (inner diameter =0.89 mm, Cole palmer GZ-95809-26) along with longer transparent Tygon tubings (internal diameter of 0.76mm, Masterflex transfer tubing, Cole palmer). The PharMed® tubing was connected to the inlet and outlet of the bladder-chip with 1.30 x 0.75 x 10 mm metallic tubes (Unimed) and transparent tubing with 1.00/0.75 x 20mm metallic tubes (Unimed). The bladder-chip connected to external sources of flow was then

mounted onto a 24 x 60 mm No. 1 glass coverslip for microscopy imaging. When required for stretching experiments, tubing was also connected to the stretching channels on either side of the main channel. The connected device was subsequently assembled inside a temperature-controlled microscope environmental chamber at 37°C supplemented with 5% CO₂ (OKO labs). Time-lapse imaging was conducted using a Leica HC FLUOTAR 25X (NA 0.95) multi-immersion objective within custom made environmental chamber set at 37°C for infusion with syringe pumps. Water was pumped to the ring around the water objective at 9 Hz with pumping duration of 9 seconds and pumping interval 30 minutes, controlled by SRS software (HRZ=9, VPP=95). The autofocus mode (best focus, steps =9, range = 30 µm) was used to maintain the optical focus on the apical side of the PDMS membrane. The experiments were monitored frequently to ensure that the optical focus was maintained, and the experiment was halted and restarted if the focus was lost.

To enable rapid 3-D imaging across multiple spatial locations on-chip, we utilized the capability of the white light laser on the Leica SP8 confocal microscope to image at multiple wavelengths simultaneously. The excitation wavelengths were grouped into two sequences to minimize the spectral overlap. In the first sequence, laser emission at 555 nm was used to excite the Calmest Orange stain in the bladder epithelial cells. In the second laser excitation sequence, laser emission at 500 nm and 630 nm were used to excite the YFP within the bacteria and the cytoplasmic CellTracker™ Deep Red in the human neutrophils. Images were acquired with a scan speed of 400-700 Hz and a zoom factor of 2.25 (206.67 µm x 206.67 µm) resulting in an XY resolution of 450 nm depending on the number of pixels acquired per field of view. Z-stacks were acquired with 1 µm step sizes. Time lapse images were acquired with interval duration of

ca. 15-17 minutes, in a subset of experiments this was further reduced to 7.5 minutes by imaging with the second sequence only at a z-step size of 2 μm .

Time lapse imaging for UPEC infections in the human bladder-chip devices

Pre-infection stage

The time-course of the entire experimental protocol is shown in a schematic in [Figure 1](#). The bladder-chip device was perfused with diluted urine in the apical channel and EBM Endothelium phenol-red free medium supplemented with EGM-2 endothelial SingleQuots kit in the vascular channel. Prior to the commencement of infection, the chip was maintained at homeostasis and the epithelial cells were imaged for a period of two hours.

Infection stage

Stationary phase UPEC in diluted pooled urine at a concentration of 150 million cells/ml were flowed through the apical channel of the device at 1200 $\mu\text{l}/\text{hour}$ for 1.5 hours. During this period, EBM2 media was flowed through the endothelial channel at 600 $\mu\text{l}/\text{hour}$.

Bacterial washout and neutrophil introduction stage

Next, the syringe connected to the apical channel was replaced with a fresh syringe containing pooled diluted urine, this solution was then flowed in the apical channel over the epithelial layer of the chip at a flow rate of 600 $\mu\text{l}/\text{hour}$ over the next 3 hours. This allowed for the continuous removal of extracellular planktonic bacteria in the apical channel. At the same time, human neutrophils were introduced into the endothelial channel of the bladder-chip via flow. A solution of human neutrophils at a density of 2 million cells/ml isolated via negative selection was flowed

through the vascular channel for 2 hours in EBM2 medium with at higher shear stress of $\eta=1.0$ dyne/cm² to enhance neutrophil attachment to endothelial cells.

Neutrophil diapedesis stage

Diapedesis of human neutrophils to epithelial side and subsequent interactions of neutrophils with UPEC was observed for the subsequent 3 hours since introduction of neutrophils into the vasculature side of the chip. During this period, the flow rate in the apical and vascular channels were maintained at 600 μ l/hour and 3000 μ l/hour, respectively. During this period, in a subset of experiments, only the channels that were part of the second laser scanning sequence were imaged. Images of the CellTracker Orange dye for epithelial cell identification were not acquired (first laser scanning sequence). This enabled a number of fields of view to be captured with an enhanced temporal resolution and a frame rate of up to 7.5 minutes. For experiments studying the formation of NETs, the experiment was halted at this stage and the infected chips were fixed, permeabilized, blocked, and immunostained with anti-myeloperoxidase (abcam) or anti-neutrophil elastase (abcam) antibodies using the procedure described earlier. For all other experiments, live imaging continued to the subsequent antibiotic treatment phase, Immunofluorescence for anti-myeloperoxidase and anti-neutrophil elastase was done as the procedure described previously.

Antibiotic treatment and growth cycles

Thereafter, syringes connected to both apical and vascular channels were changed and ampicillin at 250 μ g/ml (used at ~40-fold over the minimum inhibitory concentration (MIC) of ampicillin against UPEC grown in EBM2 medium) was introduced in the diluted urine and the EBM2

media perfused into the apical and vascular channels, respectively, for 3 hours at a flow rate of 600 μ l/hour. This was the first ampicillin treatment cycle; whose purpose was to eliminate extracellular bacteria in the apical channel and allow intracellular bacterial colonies (IBCs) to be identified. The medium was subsequently switched with antibiotic-free medium for next 8 hours to allow for IBC growth within epithelial cells. During this period, the flow within the apical channel was maintained, to remove bacteria that grew extracellularly either because they survived the antibiotic treatment or that were released from infected epithelial cells. The ampicillin and growth cycle were then repeated, to allow the assessment of the response of bacteria within IBCs to antibiotic treatment as well as characterize the subsequent regrowth.

Image analysis of confocal live-cell images

Image analysis was performed with Bitplane Imaris 9.5.1. The time-lapse imaging stack included five channels: uroepithelial cells (epithelial channel), transmitted light (bright field channel), UPEC (bacterial channel), neutrophils (neutrophil channel), and transmitted light (bright field channel). Neutrophils were identified via the spot detection algorithm in Imaris used on the images from the neutrophil channel with the following parameters (Size, 8 μ m; Quality, 4 to 8). Swarms of neutrophils generate dense aggregates that are ill-suited to quantification with the spot detection algorithm. To quantify the size of the swarms, we therefore segmented images in the neutrophil channel to generate surfaces via the automatic segmentation tool in Imaris with the following parameters (Threshold, 10; Smooth Surfaces Detail, 0.5 or 1.0 μ m). Unfortunately, the time resolution was insufficient to track individual neutrophils over time particularly since neutrophils formed small clumps and rapidly changed their cell shapes.

For UPEC volume inside IBCs, necessary 3D volume was cropped in Imaris to ease image analysis. Total bacterial volume inside IBC was detected by creating the surface (Threshold, 15; Smooth Surfaces Detail, 0.5 or 1 μm) on UPEC channel.

In cases of measuring extracellular UPEC growth, surface was generated (Threshold, 15; Smooth Surfaces Detail, 0.5 or 1 μm) on UPEC channel to calculate total extracellular volume in the field of view.

Isolation and Labelling of human neutrophils from fresh human blood

Primary human neutrophils were isolated via negative depletion method from human blood with MACSxpress® Whole Blood Neutrophil Isolation Kit (Miltenyi Biotec), following the manufacturer's instructions. Isolation was performed without the use of a density-based centrifugation method. Isolated human neutrophils were then incubated with a 1 μM solution CellTracker™ Deep Red in a serum free RPMI phenol red free medium for 30 minutes in a cell culture incubator maintained at 37 C and 5% CO₂. Labelled human neutrophils were then washed with 10ml of 20% FBS in RPMI phenol red free medium twice to remove the unbound dye. The human neutrophils were suspended in Lonza EBM2 medium at a cell density of 1 million cells/ml. In some instances, labelled human neutrophils were passed through a filter with 40 μm pores to remove neutrophil clusters that may have formed during the isolation process.

Scanning electron microscopy of human bladder-chip

UPEC within infected human bladder-chips were allowed to proliferate for 6 hours (14 hours from start of UPEC infection) until the end of the first IBC growth cycle. After 6 hours, human bladder-chip was fixed at room temperature for 1 hour with a mix of 1% glutaraldehyde and 2%

paraformaldehyde in 0.1 M phosphate buffer (pH 7.4). The fixed bladder-chip was kept in the fixative overnight (at 4°C). Post overnight fixation, human bladder-chip was cut open from the apical channel side. A scalpel was used to cut approximately in the middle of the apical channel side (height=1mm) to expose the bladder epithelial cells. The fixed chip was further fixed for 30 minutes in 1% osmium tetroxide in 0.1 M cacodylate buffer followed by washing with the distilled water. Next, the bladder-chip was dehydrated in a graded alcohol series and dried by passing them through the supercritical point of carbon dioxide (CPD300, Leica Microsystems). Finally, the bladder-chip was attached to an adhesive conductive surface followed by coating with a 3 – 4 nm thick layer of gold palladium metal (Quorum Q Plus, Quorum Technologies). Images of the cells were captured using a field emission scanning electron microscope (Merlin, Zeiss NTS).

Uninfected human bladder-chip controls were fixed at the same time point (14 hours from start of the experiment). For the case of NETs formed on epithelial layer, an uninfected human bladder-chip was fixed 2 hours after the introduction of neutrophils into the vascular channel of the chip.

Preparation for transmission electron microscopy (TEM)

UPEC within infected human bladder-chips were allowed to proliferate for 6 hours (14 hours from start of UPEC infection) during the first IBC growth cycle. After 6 hours, human bladder-chip was fixed at room temperature for 1 hour with a mix of 1% glutaraldehyde and 2% paraformaldehyde in 0.1 M phosphate buffer (pH 7.4). The fixed bladder-chip was kept in the fixative overnight (at 4°C). Post overnight fixation, human bladder-chip was cut open from the apical channel side. A scalpel was used to cut approximately in the middle of the apical channel

side (height-1mm) to expose the bladder epithelial cells. The bladder-chip was then washed in cacodylate buffer (0.1M, pH 7.4), postfixed for 40 minutes in 1.0 % osmium tetroxide with 1.5% potassium ferrocyanide, and then fixed again with 1.0% osmium tetroxide alone. The bladder-chip was finally stained for 30 minutes in 1% uranyl acetate in water before being dehydrated through increasing concentrations of alcohol and then embedded in Durcupan ACM (Fluka, Switzerland) resin. The bladder-chip was then placed in Petri dishes so that approximately 1 mm of resin remained above the cells, and the dish than left in an oven at 65°C for 24 hours. Regions on interest, and corresponding to structures imaged with light microscopy were trimmed from the rest of the device, once the resin had hardened, and thin, 50 nm-thick sections were cut with a diamond knife, and collected onto single-slot copper grids with a pioloform support film. These were contrasted with lead citrate and uranyl acetate, and images taken with a transmission electron microscope at 80 kV (Tecnai Spirit, FEI Company with Eagle CCD camera).

Data availability statement

The datasets generated during and analyzed during the current study are available from the corresponding authors on reasonable request and will be uploaded to Zenodo prior to publication.

Bibliography

- Abraham, S.N., and Miao, Y. (2015). The nature of immune responses to urinary tract infections. *Nat Rev Immunol* 15, 655–663.
- Agace, W.W., Hedges, S.R., Ceska, M., and Svanborg, C. (1993). Interleukin-8 and the neutrophil response to mucosal gram-negative infection. *J Clin Invest* 92, 780–785.
- Agace, W.W., Patarroyo, M., Svensson, M., Carlemalm, E., and Svanborg, C. (1995). *Escherichia coli* induces transuroepithelial neutrophil migration by an intercellular adhesion molecule-1-dependent mechanism. *Infect Immun* 63, 4054–4062.
- Alon, R., Hammer, D.A., and Springer, T.A. (1995). Lifetime of the P-selectin-carbohydrate bond and its response to tensile force in hydrodynamic flow. *Nature* 374, 539–542.
- Andersen, T.E., Khandige, S., Madelung, M., Brewer, J., Kolmos, H.J., and Møller-Jensen, J. (2012). *Escherichia coli* uropathogenesis in vitro: invasion, cellular escape, and secondary infection analyzed in a human bladder cell infection model. *Infect Immun* 80, 1858–1867.
- Anderson, G.G., Palermo, J.J., Schilling, J.D., Roth, R., Heuser, J., and Hultgren, S.J. (2003). Intracellular Bacterial Biofilm-Like Pods in Urinary Tract Infections. *Science* 301, 105–107.
- Apodaca, G. (2004). The Uroepithelium: Not Just a Passive Barrier. *Traffic* 5, 117–128.
- Benam, K.H., Villenave, R., Lucchesi, C., Varone, A., Hubeau, C., Lee, H.-H., Alves, S.E., Salmon, M., Ferrante, T.C., Weaver, J.C., et al. (2016). Small airway-on-a-chip enables analysis of human lung inflammation and drug responses in vitro. *Nat Methods* 13, 151–157.
- Blango, M.G., and Mulvey, M.A. (2010). Persistence of Uropathogenic *Escherichia coli* in the Face of Multiple Antibiotics. *Antimicrob Agents Ch* 54, 1855–1863.
- Branzk, N., Libode's, A., Hardison, S.E., Wang, Q., Gutierrez, M.G., Brown, G.D., and Papayannopoulos, V. (2014). Neutrophils sense microbe size and selectively release neutrophil extracellular traps in response to large pathogens. *Nat Immunol* 15, 1017–1025.
- Brinkmann, V., Reichard, U., Goosmann, C., Fauler, B., Uhlemann, Y., Weiss, D.S., Weinrauch, Y., and Zychlinsky, A. (2004). Neutrophil Extracellular Traps Kill Bacteria. *Science* 303, 1532–1535.
- Bryskier, A. (2020). *Antimicrobial Agents: Antibacterials and Antifungals*. pp. 113–162.
- Cakir, B., Xiang, Y., Tanaka, Y., Kural, M.H., Parent, M., Kang, Y.-J., Chapeton, K., Patterson, B., Yuan, Y., He, C.-S., et al. (2019). Engineering of human brain organoids with a functional vascular-like system. *Nat Methods* 16, 1169–1175.

968 Carattino, M.D., Prakasam, H.S., Ruiz, W.G., Clayton, D.R., McGuire, M., Gallo, L.I., and
969 Apodaca, G. (2013). Bladder filling and voiding affect umbrella cell tight junction organization
970 and function. *Am J Physiol-Renal* 305, F1158–F1168.

971 Clevers, H. (2016). Modeling Development and Disease with Organoids. *Cell* 165, 1586–1597.

972 Dhar, N., Dubée, V., Ballell, L., Cuinet, G., Hugonnet, J.-E., Signorino-Gelo, F., Barros, D.,
973 Arthur, M., and McKinney, J.D. (2015). Rapid Cytolysis of Mycobacterium tuberculosis by
974 Faropenem, an Orally Bioavailable β -Lactam Antibiotic. *Antimicrob Agents Ch* 59, 1308–1319.

975 Duncan, M.J., Li, G., Shin, J.-S., Carson, J.L., and Abraham, S.N. (2004). Bacterial Penetration
976 of Bladder Epithelium through Lipid Rafts. *J Biol Chem* 279, 18944–18951.

977 Duraiswamy, S., Chee, J.L.Y., Chen, S., Yang, E., Lees, K., and Chen, S.L. (2018). Purification
978 of Intracellular Bacterial Communities during Experimental Urinary Tract Infection Reveals an
979 Abundant and Viable Bacterial Reservoir. *Infect Immun* 86, e00740-17.

980 Ermert, D., Urban, C.F., Laube, B., Goosmann, C., Zychlinsky, A., and Brinkmann, V. (2009).
981 Mouse Neutrophil Extracellular Traps in Microbial Infections. *J Innate Immun* 1, 181–193.

982 Foxman, B. (2010). The epidemiology of urinary tract infection. *Nat Rev Urol* 7, 653–660.

983 Gloeckner, D.C., SACKS, M.S., FRASER, M.O., SOMOGYI, G.T., GROAT, W.C. de, and
984 CHANCELLOR, M.B. (2002). Passive Biaxial Mechanical Properties of the Rat Bladder Wall
985 After Spinal Cord Injury. *J Urology* 167, 2247–2252.

986 Grassart, A., Malardé, V., Gobba, S., Sartori-Rupp, A., Kerns, J., Karalis, K., Marteyn, B.,
987 Sansonetti, P., and Sauvonnet, N. (2019). Bioengineered Human Organ-on-Chip Reveals
988 Intestinal Microenvironment and Mechanical Forces Impacting Shigella Infection. *Cell Host*
989 *Microbe* 26, 435-444.e4.

990 Hannan, T.J., Totsika, M., Mansfield, K.J., Moore, K.H., Schembri, M.A., and Hultgren, S.J.
991 (2012). Host–pathogen checkpoints and population bottlenecks in persistent and intracellular
992 uropathogenic Escherichia coli bladder infection. *Fems Microbiol Rev* 36, 616–648.

993 Haraoka, M., Hang, L., Frendéus, B., Godaly, G., Burdick, M., Strieter, R., and Svanborg, C.
994 (1999). Neutrophil Recruitment and Resistance to Urinary Tract Infection. *J Infect Dis* 180,
995 1220–1229.

996 Hedges, S., Svensson, M., and Svanborg, C. (1992). Interleukin-6 response of epithelial cell lines
997 to bacterial stimulation in vitro. *Infect Immun* 60, 1295–1301.

998 Hopke, A., Scherer, A., Kreuzburg, S., Abers, M.S., Zerbe, C.S., Dinauer, M.C., Mansour, M.K.,
999 and Irimia, D. (2020). Neutrophil swarming delays the growth of clusters of pathogenic fungi.
1000 *Nat Commun* 11, 2031.

1001 Horsley, H., Dharmasena, D., Malone-Lee, J., and Rohn, J.L. (2018). A urine-dependent human
1002 urothelial organoid offers a potential alternative to rodent models of infection. *Sci Rep-Uk* 8,
1003 1238.

1004 Hsieh, M.M., Everhart, J.E., Byrd-Holt, D.D., Tisdale, J.F., and Rodgers, G.P. (2007).
1005 Prevalence of Neutropenia in the U.S. Population: Age, Sex, Smoking Status, and Ethnic
1006 Differences. *Ann Intern Med* 146, 486.

1007 Huh, D., Matthews, B.D., Mammoto, A., Montoya-Zavala, M., Hsin, H.Y., and Ingber, D.E.
1008 (2010a). Reconstituting Organ-Level Lung Functions on a Chip. *Science* 328, 1662–1668.

1009 Huh, D., Matthews, B.D., Mammoto, A., Montoya-Zavala, M., Hsin, H.Y., and Ingber, D.E.
1010 (2010b). Reconstituting Organ-Level Lung Functions on a Chip. *Science* 328, 1662–1668.

1011 Hung, C.-S., Dodson, K.W., and Hultgren, S.J. (2009). A murine model of urinary tract
1012 infection. *Nat Protoc* 4, 1230–1243.

1013 Hunstad, D.A., and Justice, S.S. (2010). Intracellular Lifestyles and Immune Evasion Strategies
1014 of Uropathogenic *Escherichia coli*. *Annu Rev Microbiol* 64, 203–221.

1015 Iosifidis, G., and Duggin, I.G. (2020). Distinct Morphological Fates of Uropathogenic
1016 *Escherichia coli* Intracellular Bacterial Communities: Dependency on Urine Composition and
1017 pH. *Infect Immun* 88.

1018 Jalili-Firoozinezhad, S., Gazzaniga, F.S., Calamari, E.L., Camacho, D.M., Fadel, C.W., Bein, A.,
1019 Swenor, B., Nestor, B., Cronic, M.J., Tovaglieri, A., et al. (2019). A complex human gut
1020 microbiome cultured in an anaerobic intestine-on-a-chip. *Nat Biomed Eng* 3, 520–531.

1021 Jang, K.-J., Mehr, A.P., Hamilton, G.A., McPartlin, L.A., Chung, S., Suh, K.-Y., and Ingber,
1022 D.E. (2013). Human kidney proximal tubule-on-a-chip for drug transport and nephrotoxicity
1023 assessment. *Integr Biol* 5, 1119–1129.

1024 Jang, K.-J., Otieno, M.A., Ronxhi, J., Lim, H.-K., Ewart, L., Kodella, K.R., Petropolis, D.B.,
1025 Kulkarni, G., Rubins, J.E., Conegliano, D., et al. (2019). Reproducing human and cross-species
1026 drug toxicities using a Liver-Chip. *Sci Transl Med* 11, eaax5516.

1027 Justice, S.S., Hung, C., Theriot, J.A., Fletcher, D.A., Anderson, G.G., Footer, M.J., and Hultgren,
1028 S.J. (2004). Differentiation and developmental pathways of uropathogenic *Escherichia coli* in
1029 urinary tract pathogenesis. *Proc National Acad Sci* 101, 1333–1338.

1030 Kang, Y.B. (Abraham), Rawat, S., Duchemin, N., Bouchard, M., and Noh, M. (2017). Human
1031 Liver Sinusoid on a Chip for Hepatitis B Virus Replication Study. *Micromachines-Basel* 8, 27.

1032 Kienle, K., and Lämmermann, T. (2016). Neutrophil swarming: an essential process of the
1033 neutrophil tissue response. *Immunol Rev* 273, 76–93.

1034 Kim, H.J., and Ingber, D.E. (2013). Gut-on-a-Chip microenvironment induces human intestinal
1035 cells to undergo villus differentiation. *Integr Biol* 5, 1130–1140.

1036 Kim, H.J., Li, H., Collins, J.J., and Ingber, D.E. (2016). Contributions of microbiome and
1037 mechanical deformation to intestinal bacterial overgrowth and inflammation in a human gut-on-
1038 a-chip. *Proc National Acad Sci* 113, E7–E15.

1039 Klein, R.D., and Hultgren, S.J. (2020). Urinary tract infections: microbial pathogenesis, host-
1040 pathogen interactions and new treatment strategies. *Nat Rev Microbiol* 18, 211–226.

1041 Korkmaz, I., and Rogg, B. (2007). A simple fluid-mechanical model for the prediction of the
1042 stress–strain relation of the male urinary bladder. *J Biomech* 40, 663–668.

1043 Kreisel, D., Nava, R.G., Li, W., Zinselmeyer, B.H., Wang, B., Lai, J., Pless, R., Gelman, A.E.,
1044 Krupnick, A.S., and Miller, M.J. (2010). In vivo two-photon imaging reveals monocyte-
1045 dependent neutrophil extravasation during pulmonary inflammation. *Proc National Acad Sci*
1046 107, 18073–18078.

1047 Lämmermann, T., Afonso, P.V., Angermann, B.R., Wang, J.M., Kastenmüller, W., Parent, C.A.,
1048 and Germain, R.N. (2013). Neutrophil swarms require LTB4 and integrins at sites of cell death
1049 in vivo. *Nature* 498, 371–375.

1050 Ley, K., Laudanna, C., Cybulsky, M.I., and Nourshargh, S. (2007). Getting to the site of
1051 inflammation: the leukocyte adhesion cascade updated. *Nat Rev Immunol* 7, 678–689.

1052 Lutz, R., and Bujard, H. (1997). Independent and Tight Regulation of Transcriptional Units in
1053 *Escherichia Coli* Via the LacR/O, the TetR/O and AraC/I1-I2 Regulatory Elements. *Nucleic*
1054 *Acids Res* 25, 1203–1210.

1055 Martinez, J.J., Mulvey, M.A., Schilling, J.D., Pinkner, J.S., and Hultgren, S.J. (2000). Type 1
1056 pilus-mediated bacterial invasion of bladder epithelial cells. *Embo J* 19, 2803–2812.

1057 Metzler, K.D., Fuchs, T.A., Nauseef, W.M., Reumaux, D., Roesler, J., Schulze, I., Wahn, V.,
1058 Papayannopoulos, V., and Zychlinsky, A. (2011). Myeloperoxidase is required for neutrophil
1059 extracellular trap formation: implications for innate immunity. *Blood* 117, 953–959.

1060 Mobley, H.L., Green, D.M., Trifillis, A.L., Johnson, D.E., Chippendale, G.R., Lockatell, C.V.,
1061 Jones, B.D., and Warren, J.W. (1990). Pyelonephritogenic *Escherichia coli* and killing of
1062 cultured human renal proximal tubular epithelial cells: role of hemolysin in some strains. *Infect*
1063 *Immun* 58, 1281–1289.

1064 Mulvey, M.A., Lopez-Boado, Y.S., Wilson, C.L., Roth, R., Parks, W.C., Heuser, J., and
1065 Hultgren, S.J. (1998). Induction and Evasion of Host Defenses by Type 1-Piliated Uropathogenic
1066 *Escherichia coli*. *Science* 282, 1494–1497.

1067 Mysorekar, I.U., and Hultgren, S.J. (2006). Mechanisms of uropathogenic *Escherichia coli*
1068 persistence and eradication from the urinary tract. *Proc National Acad Sci* *103*, 14170–14175.

1069 Nagamatsu, K., Hannan, T.J., Guest, R.L., Kostakioti, M., Hadjifrangiskou, M., Binkley, J.,
1070 Dodson, K., Raivio, T.L., and Hultgren, S.J. (2015). Dysregulation of *Escherichia coli* α -
1071 hemolysin expression alters the course of acute and persistent urinary tract infection. *Proc*
1072 *National Acad Sci* *112*, E871–E880.

1073 Nawroth, J.C., Lucchesi, C., Cheng, D., Shukla, A., Ngyuen, J., Shroff, T., Varone, A., Karalis,
1074 K., Lee, H.-H., Alves, S., et al. (2020). A Microengineered Airway Lung Chip Models Key
1075 Features of Viral-induced Exacerbation of Asthma. *Am J Resp Cell Mol* *63*, 591–600.

1076 Nourshargh, S., Hordijk, P.L., and Sixt, M. (2010). Breaching multiple barriers: leukocyte
1077 motility through venular walls and the interstitium. *Nat Rev Mol Cell Bio* *11*, 366–378.

1078 Novak, R., Ingram, M., Marquez, S., Das, D., Delahanty, A., Herland, A., Maoz, B.M., Jeanty,
1079 S.S.F., Somayaji, M.R., Burt, M., et al. (2020). Robotic fluidic coupling and interrogation of
1080 multiple vascularized organ chips. *Nat Biomed Eng* *4*, 407–420.

1081 Oliveira, S. de, Rosowski, E.E., and Huttenlocher, A. (2016). Neutrophil migration in infection
1082 and wound repair: going forward in reverse. *Nat Rev Immunol* *16*, 378–391.

1083 Papayannopoulos, V., Metzler, K.D., Hakkim, A., and Zychlinsky, A. (2010). Neutrophil
1084 elastase and myeloperoxidase regulate the formation of neutrophil extracellular traps. *J Cell*
1085 *Biology* *191*, 677–691.

1086 Parekh, A., Cigan, A.D., Wognum, S., Heise, R.L., Chancellor, M.B., and Sacks, M.S. (2010).
1087 Ex vivo deformations of the urinary bladder wall during whole bladder filling: Contributions of
1088 extracellular matrix and smooth muscle. *J Biomech* *43*, 1708–1716.

1089 Pascalis, R.D., Parnell, W.J., Abrahams, I.D., Shearer, T., Daly, D.M., and Grundy, D. (2018).
1090 The inflation of viscoelastic balloons and hollow viscera. *Proc Royal Soc* *474*, 20180102.

1091 Putrinš, M., Kogermann, K., Lukk, E., Lippus, M., Varik, V., and Tenson, T. (2015). Phenotypic
1092 Heterogeneity Enables Uropathogenic *Escherichia coli* To Evade Killing by Antibiotics and
1093 Serum Complement. *Infect Immun* *83*, 1056–1067.

1094 Reátegui, E., Jalali, F., Khankhel, A.H., Wong, E., Cho, H., Lee, J., Serhan, C.N., Dalli, J.,
1095 Elliott, H., and Irimia, D. (2017). Microscale arrays for the profiling of start and stop signals
1096 coordinating human-neutrophil swarming. *Nat Biomed Eng* *1*, 0094.

1097 Ronaldson-Bouchard, K., and Vunjak-Novakovic, G. (2018). Organs-on-a-Chip: A Fast Track
1098 for Engineered Human Tissues in Drug Development. *Cell Stem Cell* *22*, 310–324.

1099 Rossi, G., Manfrin, A., and Lutolf, M.P. (2018). Progress and potential in organoid research. *Nat*
1100 *Rev Genet* *19*, 671–687.

1101 Sato, T., Vries, R.G., Snippert, H.J., Wetering, M. van de, Barker, N., Stange, D.E., Es, J.H. van,
1102 Abo, A., Kujala, P., Peters, P.J., et al. (2009). Single Lgr5 stem cells build crypt-villus structures
1103 in vitro without a mesenchymal niche. *Nature* 459, 262–265.

1104 Schwartz, D.J., Chen, S.L., Hultgren, S.J., and Seed, P.C. (2011). Population Dynamics and
1105 Niche Distribution of Uropathogenic *Escherichia coli* during Acute and Chronic Urinary Tract
1106 Infection. *Infect Immun* 79, 4250–4259.

1107 Scott, V.C.S., Haake, D.A., Churchill, B.M., Justice, S.S., and Kim, J.-H. (2015). Intracellular
1108 Bacterial Communities: A Potential Etiology for Chronic Lower Urinary Tract Symptoms.
1109 *Urology* 86, 425–431.

1110 Shah, P., Fritz, J.V., Glaab, E., Desai, M.S., Greenhalgh, K., Frachet, A., Niegowska, M., Estes,
1111 M., Jäger, C., Seguin-Devaux, C., et al. (2016). A microfluidics-based in vitro model of the
1112 gastrointestinal human–microbe interface. *Nat Commun* 7, 11535.

1113 Si, L., Bai, H., Rodas, M., Cao, W., Oh, C.Y., Jiang, A., Nurani, A., Zhu, D.Y., Goyal, G.,
1114 Gilpin, S.E., et al. (2020). Human organs-on-chips as tools for repurposing approved drugs as
1115 potential influenza and COVID19 therapeutics in viral pandemics. *Biorxiv* 2020.04.13.039917.

1116 Smith, Y.C., Grande, K.K., Rasmussen, S.B., and O’Brien, A.D. (2006). Novel Three-
1117 Dimensional Organoid Model for Evaluation of the Interaction of Uropathogenic *Escherichia*
1118 *coli* with Terminally Differentiated Human Urothelial Cells. *Infect Immun* 74, 750–757.

1119 Solis, A.G., Bielecki, P., Steach, H.R., Sharma, L., Harman, C.C.D., Yun, S., Zoete, M.R. de,
1120 Warnock, J.N., To, S.D.F., York, A.G., et al. (2019). Mechanosensation of cyclical force by
1121 PIEZO1 is essential for innate immunity. *Nature* 573, 69–74.

1122 Song, J., Duncan, M.J., Li, G., Chan, C., Grady, R., Stapleton, A., and Abraham, S.N. (2007). A
1123 Novel TLR4-Mediated Signaling Pathway Leading to IL-6 Responses in Human Bladder
1124 Epithelial Cells. *Plos Pathog* 3, e60.

1125 Spaulding, C.N., Klein, R.D., Ruer, S., Kau, A.L., Schreiber, H.L., Cusumano, Z.T., Dodson,
1126 K.W., Pinkner, J.S., Fremont, D.H., Janetka, J.W., et al. (2017). Selective depletion of
1127 uropathogenic *E. coli* from the gut by a FimH antagonist. *Nature* 546, 528–532.

1128 Suzuki, K., Koyanagi-Aoi, M., Uehara, K., Hinata, N., Fujisawa, M., and Aoi, T. (2019).
1129 Directed differentiation of human induced pluripotent stem cells into mature stratified bladder
1130 urothelium. *Sci Rep-Uk* 9, 10506.

1131 Thacker, V.V., Sharma, K., Dhar, N., Mancini, G.-F., Sordet-Dessimoz, J., and McKinney, J.D.
1132 (2020a). Rapid endothelial infection, endothelialitis and vascular damage characterise SARS-
1133 CoV-2 infection in a human lung-on-chip model. *Biorxiv* 2020.08.10.243220.

- 1134 Thacker, V.V., Dhar, N., Sharma, K., Barrile, R., Karalis, K., and McKinney, J.D. (2020b). A
1135 lung-on-chip model of early M. tuberculosis infection reveals an essential role for alveolar
1136 epithelial cells in controlling bacterial growth. *Elife* 9, e59961.
- 1137 Tovaglieri, A., Sontheimer-Phelps, A., Geirnaert, A., Prantil-Baun, R., Camacho, D.M., Chou,
1138 D.B., Jalili-Firoozinezhad, S., Wouters, T. de, Kasendra, M., Super, M., et al. (2019). Species-
1139 specific enhancement of enterohemorrhagic E. coli pathogenesis mediated by microbiome
1140 metabolites. *Microbiome* 7, 43.
- 1141 Truschel, S.T., Wang, E., Ruiz, W.G., Leung, S.-M., Rojas, R., Lavelle, J., Zeidel, M., Stoffer,
1142 D., and Apodaca, G. (2002). Stretch-regulated Exocytosis/Endocytosis in Bladder Umbrella
1143 Cells. *Mol Biol Cell* 13, 830–846.
- 1144 Wang, E.C.Y., Lee, J.-M., Ruiz, W.G., Balestreire, E.M., Bodungen, M. von, Barrick, S.,
1145 Cockayne, D.A., Birder, L.A., and Apodaca, G. (2005). ATP and purinergic receptor–dependent
1146 membrane traffic in bladder umbrella cells. *J Clin Invest* 115, 2412–2422.
- 1147 Wang, J., Wang, C., Xu, N., Liu, Z.-F., Pang, D.-W., and Zhang, Z.-L. (2019). A virus-induced
1148 kidney disease model based on organ-on-a-chip: Pathogenesis exploration of virus-related renal
1149 dysfunctions. *Biomaterials* 219, 119367.
- 1150 Yang, E., Chee, J.L.Y., Duraiswamy, S., Chen, S., Lees, K., and Chen, S.L. (2019). Isolation of
1151 Single Intracellular Bacterial Communities Generated from a Murine Model of Urinary Tract
1152 Infection for Downstream Single-cell Analysis. *J Vis Exp Jove*.
- 1153 Yu, Y., Kwon, K., Tsitrin, T., Bekele, S., Sikorski, P., Nelson, K.E., and Pieper, R. (2017).
1154 Characterization of Early-Phase Neutrophil Extracellular Traps in Urinary Tract Infections. *Plos*
1155 *Pathog* 13, e1006151.
- 1156 Zahler, S., Kowalski, C., Brosig, A., Kupatt, C., Becker, B.F., and Gerlach, E. (1997). The
1157 function of neutrophils isolated by a magnetic antibody cell separation technique is not altered in
1158 comparison to a density gradient centrifugation method. *J Immunol Methods* 200, 173–179.
- 1159 Zalewska-Piątek, B., Olszewski, M., Lipniacki, T., Błoński, S., Wieczór, M., Bruździak, P.,
1160 Skwarska, A., Nowicki, B., Nowicki, S., and Piątek, R. (2020). A shear stress micromodel of
1161 urinary tract infection by the Escherichia coli producing Dr adhesin. *Plos Pathog* 16, e1008247.
- 1162 Zhou, M., Zhang, X., Wen, X., Wu, T., Wang, W., Yang, M., Wang, J., Fang, M., Lin, B., and
1163 Lin, H. (2016). Development of a Functional Glomerulus at the Organ Level on a Chip to Mimic
1164 Hypertensive Nephropathy. *Sci Rep-Uk* 6, 31771.

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