Matrix stiffness modulates infection of endothelial cells by *Listeria monocytogenes* via expression of cell surface vimentin

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ABSTRACT

Extracellular matrix (ECM) stiffness is one of many mechanical forces acting on mammalian

adherent cells that influence cellular function. We have addressed the open question of how

ECM stiffness might alter the susceptibility of host cells to infection by bacterial pathogens. We

manufactured hydrogels of varying physiologically-relevant stiffness and seeded human

microvascular endothelial cells (HMEC-1) on them. We then infected HMEC-1 with the bacterial

pathogen *Listeria monocytogenes* (Lm) and found that adhesion of Lm onto host cells increases

monotonically with increasing matrix stiffness, an effect that requires the activity of focal

adhesion kinase (FAK). We identified cell surface vimentin as a candidate surface receptor

mediating stiffness-dependent adhesion of Lm to HMEC-1, and demonstrated that bacterial

infection of these host cells is decreased when surface vimentin is perturbed. Our results

provide the first evidence that ECM stiffness can mediate the susceptibility of host cells to

bacterial infection.

INTRODUCTION

The extracellular environment of cells provides both chemical and mechanical stimuli to

influence cell behavior and function (Geiger et al., 2009, Chien et al., 2005). Extracellular matrix

stiffness (ECM), one of the many mechanical forces acting on cells, is an important determinant

of cellular behavior for most adherent mammalian cells (Gattazzo et al., 2014; Wells, 2008).

Cells can sense the stiffness of their matrix, which can vary over many orders of magnitude, and

accordingly alter their motility, adhesion, growth and differentiation (Discher et al., 2005;

Birukova et al., 2013). Yet the exact pathways whereby cells sense mechanical signals and

transduce them to generate biological signal cascades and specific cellular responses are not

yet fully understood (Trepat et al., 2008).

In the context of host-pathogen interactions, effects of matrix stiffness variation may be

most interesting for infectious agents that have the capacity to infect many different kinds of

tissues in the human body. One such agent is the food-borne facultative bacterial pathogen

Listeria monocytogenes (Lm). After initial invasion into the intestinal epithelium, Lm is able to

spread through the vasculature to distant organs, and can cause serious complications such as

meningitis and late-term spontaneous abortion by virtue of its unusual ability to penetrate and

cross a wide variety of endothelial barriers including the blood-brain barrier and the placenta

(Jackson et al., 2010; Vazquez-Boland et al., 2001). Lm has a broad range of susceptible host

animals, and uses multiple pathogenic strategies to achieve infection of a wide variety of tissues

within each host. It can directly adhere to and invade intestinal epithelial cells and hepatocytes

using bacterial surface proteins belonging to the internalin family, such as InlA, InlB and InlF,

which interact with host cell surface receptors (Mengaud et al., 1996; Shen et al., 2000; Kirchner

and Higgins, 2008). Lm can also directly adhere to and invade the vascular endothelial cells

(VECs) that line the inner lumen of blood vessels, using several distinct molecular mechanisms

that may vary depending on the subtype of VEC being infected (Drevets et al., 1995;

Greiffenberg et al., 1997; Wilson and Drevets, 1998; Greiffenberg et al., 1998; Parida et al.,

1998; Rengarajan et al., 2016).

Vascular endothelial cells (VECs) are known to be highly mechanosensitive. The

stiffness of the ECM surrounding blood vessels can vary significantly in space (location within

the vascular tree), in time (aging) and in pathophysiological conditions (e.g. arteriosclerosis,

cancer) (Chien et al., 2005; Collins et al., 2014; Krishnan et al., 2011; Volkman et al., 2002; Yeh

et al., 2012). These variations in stiffness can dramatically affect gene expression and barrier

integrity of VECs, thereby regulating the movement of vascular components from the

bloodstream into underlying tissues, including the dissemination of bacterial pathogens

(Lemichez et al., 2010). Clinical studies have shown that the local compliance of the basement

membrane of VECs in the brain tissue is as soft as 1 kPa, while bigger vessels such as the

aorta are as stiff as 20 kPa (Janmey and Miller, 2011; Kohn et al., 2015; Onken et al., 2014;

Wells, 2008; Wood et al., 2010), and their stiffness can increase up to 70 kPa due to aging

(Huynh et al., 2011) and in the context of cardiovascular diseases (CVDs), such as

atherosclerosis or hypertension (Blacher et al., 1999; Boutouyrie et al., 2002). VECs, like other

adherent cell types, probe features of their environment including its stiffness through integrins,

transmembrane receptors that allow attachment of the cells to their matrix through direct binding

to ECM ligand proteins (Schwartz, 2010; Senger et al., 2002). Integrin binding to the ECM leads

to recruitment of additional proteins and to formation of focal adhesions that in turn relay

information to the actin cytoskeleton and to various signaling molecules, modulating cellular

adhesion, shape, contractility, gene expression and fate in general (Pelham and Wang, 1997).

Focal adhesion kinase (FAK) is a non-receptor tyrosine kinase that has been established as a

key component of the signal transduction pathways triggered by integrins. The expression

and/or activity of FAK is dependent on ECM rigidity, showing decreased expression and/or

activation on softer matrices for certain cell types and can influence cell adhesion and motility

(Du et al., 2016; Higuita-Castro et al., 2014; Khatiwala et al., 2006; Provenzano et al., 2009).

However, no studies have previously addressed if and how VEC matrix stiffness sensing

through focal adhesions might affect host cells' interactions with bacterial pathogens.

Bacterial adhesion to the surface of cells is typically the initial event in the pathogenesis

of infection and can occur through receptor-mediated interactions between the host cell and the

pathogen (Pizarro-Cerdá and Cossart, 2006). Vimentin is generally an intracellular cytoskeletal

protein that forms intermediate filaments in many mesoderm-derived cells (Clarke and Allan,

2002). Vimentin can also be localized on the surface of cells for a variety of cell types, although

the precise mechanism whereby vimentin is delivered to the surface of cells is not yet fully

understood (Mitra et al., 2015; Mor-Vaknin et al., 2003; Päll et al., 2011; Rohrbeck et al., 2014;

Shigyo et al., 2015). Recent studies have shown that various bacteria as well as viruses use

surface vimentin as attachment receptor to facilitate entry into host cells (Bhattacharya et al.,

2009; Du et al., 2014; Garg et al., 2006; Mak and Brüggemann, 2016; Rohrbeck et al., 2014;

Yang et al., 2016; Yu et al., 2016; Zou et al., 2006). However, little is known about what

modulates the amount of vimentin exposed on the surface of cells and whether regulation of its

surface presentation potentially mediates bacterial uptake.

To assess whether ECM stiffness could mediate infection susceptibility of host cells, we

used Lm as our model pathogen and examined *in vitro* Lm infection in endothelial cells derived

from the microvasculature (human microvascular endothelial cells, HMEC-1) cultured on

matrices of varying stiffness. Subendothelial stiffness depends on the blood vessel's location

within the body, on the size of vessel, on age and on physiological or pathophysiological

conditions and so we chose our substrates' stiffness to span over a large range of stiffnesses,

from 0.6 kPa to 70 kPa (Kohn et al., 2015; Stroka and Aranda-Espinoza, 2011). We found a

two-fold increase in bacterial adhesion when cells reside on stiff as compared to soft matrices.

We also found that Tyr397 phosphorylation of FAK was higher for VECs residing on stiff

matrices, and furthermore that knockdown of FAK or treatment of VECs with FAK inhibitors led

to a decrease in bacterial infection. When we searched for candidate VEC surface receptors

differentially modulated depending on FAK activity, we identified surface vimentin as a

candidate, and found that decreasing the amount of host surface vimentin leads to a

concomitant decrease in Lm infection. Taken together, our findings provide evidence that

environmental stiffness of VECs, a previously unappreciated factor, plays an important role in

mediating infection susceptibility to Lm through differential activity of FAK that in turn affects the

amount of surface vimentin.

RESULTS

Uptake of *Listeria monocytogenes* by HMEC-1 is more efficient when cells reside on stiff

substrates.

Substrates on which vascular endothelial cells (VECs) are cultured *in vitro*, commonly

glass or tissue culture (TC) polystyrene, are approximately six orders of magnitude stiffer than

the natural ECM of human VECs (Dussurget et al., 2004; Sperling and Friedman, 1969). To be

able to recapitulate *in vivo* conditions and determine in a systematic way the effect of the VECs'

matrix stiffness on the efficiency of *Listeria monocytogenes* (Lm) infection, we developed an

assay based on manufacturing thin polyacrylamide hydrogels of varying stiffness ranging from

0.6 to 70 kPa on multi-well glass-bottom plates (Ahmed, 2015; Georges et al., 2006; Mih et al.,

2011) (Suppl. Fig. 1A). To enable cell adhesion, hydrogels were surface-coated with collagen I,

using a consistent density of collagen independent of hydrogel stiffness, as reported in previous

studies (Huang et al., 2013; Tse and Engler, 2010; Yeung et al., 2005). Human microvascular

endothelial cells (HMEC-1) seeded for 24 h on the hydrogels formed monolayers with

comparable densities regardless of substrate stiffness, similar to growth of these cells on TC

polystyrene (Suppl. Fig. 1B)

In order to measure the efficiency of bacterial infection quantitatively, we infected

HMEC-1 with a strain of Lm lacking expression of the ActA protein, which is necessary for intra-

and inter-cellular spread of this bacterium. In that way, we could attribute changes in the

number of infected cells directly to initial invasion events and not to spread of the bacteria from

cell to cell. We also confirmed that adhesion and invasion of wild-type Lm into HMEC-1 is

similar to that of Δ*actA* Lm, consistent with previous studies on other host cell types (Brundage

et al., 1993; Kocks et al., 1992), suggesting that ActA is not involved in adhesion or invasion

(Suppl. Fig. 1 D-F). The Δ*actA* Lm strain we used also expresses a fluorescent protein under a

promoter that is activated several hours after exposure of the bacteria to the host cell cytosol

(actAp::mTagRFP) (Zeldovich et al., 2011), allowing reliable fluorescence-based detection only

of bacteria that have successfully invaded the host cells. We determined the fraction of HMEC-1

infected with Lm in each well using flow cytometry (Fig. 1A-D). At a constant multiplicity of

infection (MOI) and constant host cell density, we found a monotonic increase (strictly

increasing relationship) in the number of VECs infected by Lm with increasing hydrogel stiffness

that was highly reproducible among biological replicates (Fig. 1E and Suppl. Fig 1C). The

overall efficiency of infection on the stiffest hydrogel substrates tested, 70 kPa, was comparable

to the efficiency of infection for the same cells grown on TC polystyrene, suggesting that above

a certain level of stiffness the infection efficiency does not change (Suppl. Fig 1C). Compared to

this maximum level of infection for HMEC-1 cultured on the stiffest substrates, infection

efficiency on the softest substrates decreased about two-fold (Fig. 1E and Suppl. Fig 1C).

HMEC-1 on soft hydrogels show decreased FAK activity and decreased FAK activity

leads to less efficient Lm infection.

Focal adhesion kinase (FAK) has been established as a key component of the signal

transduction pathways triggered by integrins binding to the ECM, and for some cell types FAK

expression and/or phosphorylation on residue Y397 have been shown to depend on mechanical

cues sensed by cells, such as shear stresses imposed by fluid flow and/or ECM rigidity (Du et

al., 2016; Higuita-Castro et al., 2014; Khatiwala et al., 2006; Mathieu et al., 2010; Provenzano et

al., 2009). We therefore sought to determine whether FAK expression or activity could be

modulated depending on the substrate stiffness where HMEC-1 reside. To that end, HMEC-1

were grown on soft 3 kPa hydrogels, stiff 70 kPa hydrogels and TC polystyrene substrates

treated with vehicle control or PF573228 FAK inhibitor. Cells were then harvested and total

amounts of FAK as well as pY397-FAK were determined using Western blot analysis. We found

that increasing the stiffness of the underlying substrate from 3 kPa to 70 kPa resulted in

increasing levels of pY397-FAK, but the levels of total FAK remained largely unchanged (Fig.

2A-C). In addition, the levels of pFAK-Y397 were similar for cells residing on stiff 70 kPa

hydrogels as compared to TC polystyrene substrates (Fig. 2A-C). Treating cells residing on

polystyrene with the specific FAK inhibitor PF573228 led to a significant decrease of pY397-

FAK while total FAK levels remained unchanged as compared to controls (Fig. 2A-C). Our

results suggest that FAK phosphorylation at Y397 is modulated by the stiffness of the substrate

on which HMEC-1 reside and therefore by different levels of cell–ECM interaction-induced focal

adhesion signaling.

To address whether reduced Lm uptake as observed for HMEC-1 residing on soft

matrices can be attributed at least in part to reduced FAK activity, we treated HMEC-1 residing

on polystyrene substrates with FAK inhibitors FAK-14 or PF573228 for one hour prior to

infection. We then measured the efficiency of infection with Lm as described above, and found

that both FAK inhibitors caused a similar dose-dependent inhibition of Lm infection (Fig. 2D).

We then transfected HMEC-1 with commercial non-targeting control siRNA (siNT) or siRNA

targeting FAK (siFAK) (Table S2) and total FAK expression was found to be about five-fold

reduced for the FAK knockdown cells as compared to controls as determined by

immunofluorescence (Suppl. Fig. 2A) and RT-PCR (Suppl Fig. 2B). We found a significant

approximately 2-fold decrease in Lm infection efficiency for the FAK knockdown cells as

compared to control cells (Fig. 2E; Suppl. Fig. 2C-D). Taken together these results are

consistent with the hypothesis that decreased bacterial infection of HMEC-1 residing on highly

compliant soft matrices may be in part due to decreased FAK activity.

To address whether elevating FAK activity can lead to increased bacterial uptake we

pre-treated cells for varying times with vasoconstrictor peptide hormone Angiotensin II, which

has been shown to induce an increase in phosphorylation of FAK *in vivo* in murine aortas (Louis

et al., 2007) and also shown *in vitro* to lead to enhanced phosphorylation of FAK at Y397 for a

variety of cell types (Greco et al., 2002; Torsoni et al., 2005; Weng and Shukla, 2002), including

endothelial cells (Montiel et al., 2005). We first treated HMEC-1 with 100 nM Angiotensin II for

varying times and then lysed the cells and used Western blotting to assess FAK expression and

phosphorylation of FAK at Y397 (Fig. 2F and Suppl. Fig. 2F). Interestingly, we found that

although FAK expression did not change upon treatment with Angiotensin II, phosphorylation of

FAK at Y397 increased substantially for cells treated with Angiotensin II for more than 30 min.

Since FAK activity was shown to be elevated for cells pretreated for more than 30 min with

Angiotensin II, we then asked whether that would be sufficient to lead to increased infection

susceptibility. When we infected HMEC-1 cells seeded on polystyrene substrates and

pretreated with 100 nM of Angiotensin II, we observed a modest but significant 23% increase in

infection susceptibility as compared to control cells (Fig. 2G and Suppl. Fig. 2E). We then

seeded HMEC-1 cells on soft 3 kPa and stiff 70 kPa hydrogels and pretreated cells with or

without 100 nM Angiotensin II for 2 h. We found a much stronger effect of Angiotensin II

increasing infection for cells plated on soft substrates than on stiff substrates; indeed, treatment

of cells on 3 kPa substrates with 100 nM Angiotensin II for 2 h was sufficient to raise the level of

infection to be approximately equal to infection on 70 kPa substrates (Suppl. Fig. 2G). This

result further supports the hypothesis that a primary determinant of the relatively inefficient

infection of HMEC-1 on soft substrates is the relatively low level of FAK activity in this

environmental condition.

Adhesion but not invasion efficiency is increased when Lm infect HMEC-1 residing on

stiff substrates.

Decreased infection efficiency of Lm in HMEC-1 residing on soft matrices or treated with

FAK inhibitors could be due to quantitative changes at several different steps in the infection

process, for example decreased bacterial adhesion onto HMEC-1, or decreased invasion of the

adhering bacteria into the HMEC-1, or a combination of both. To help identify the exact step in

infection that is sensitive to substrate stiffness, we used a constitutively GFP-expressing strain

of Lm to infect HMEC-1 residing on either soft 3 kPa hydrogels or stiff 70 kPa hydrogels, and

treated with vehicle control or PF573228. Samples were fixed shortly after infection and bacteria

that were attached to the cell surface but not yet internalized were specifically labeled with

antibodies under non-permeabilizing conditions. This inside/outside labeling method allows us

to distinguish between bacteria that are adhered but not internalized (GFP-positive and labeled

with the antibody) and those that are fully internalized by the HMEC-1 (GFP-positive but not

labeled with the antibody). We found that both the total number of bacteria per host cell and the

number of internalized bacteria per cell are significantly increased when HMEC-1 reside on stiff

70 kPa hydrogels as compared to soft 3 kPa hydrogels (Fig. 3A-B). However, importantly, the

invasion efficiency (ratio of internalized bacteria to total bacteria) did not differ between HMEC-1

residing on stiff as compared to soft matrices, suggesting that it is specifically the adhesion of

bacteria to the surface of host cells that is increased when the matrix stiffness is elevated and

which leads to increased Lm infection efficiency for cells residing on stiffer matrices (Fig. 3C).

Interestingly, we found a decrease in both Lm adhesion and invasion efficiency irrespective of

hydrogel stiffness for the cells treated with the FAK inhibitor (Fig. 3), suggesting that FAK

activity levels modulate both adhesion and invasion efficiency of Lm in HMEC-1, while substrate

stiffness affects adhesion only.

InlB contributes to Lm infection of HMEC-1 but is not modulated by substrate stiffness.

Our data indicate that lower FAK activity as it occurs when HMEC-1 are seeded on

softer hydrogels leads to decreased Lm adhesion onto the surface of HMEC-1. This finding led

us to hypothesize that a receptor at the surface of cells could be differentially regulated

depending on substrate stiffness, leading to decreased bacterial adhesion. To examine whether

any of the Lm internalins known to play a role in adhesion or invasion of other cell types,

including VECs, is implicated in infection of HMEC-1 and responsible for the matrix stiffness

dependent susceptibility to infection, we infected HMEC-1 with mutant strains deficient in each

of the internalin-encoding genes *inlA*, *inlB* or *inlF* (Fig. 4A and Table S1). We found a two-fold

decrease in bacterial infection when InlB was not present, suggesting that InlB is one of possibly

multiple bacterial factors that contribute to Lm infection of HMEC-1. In contrast to the effect of

the deletion in the *inlB* gene, deletion of *inlF* had no effect in bacterial infection of HMEC-1.

Deletion of *inlA* resulted in very modest but reproducible reduction in infection as reported

previously for human brain microvascular endothelial cells infected with Lm (Greiffenberg et al.,

1998).

The importance of InlB for initial invasion of Lm into HMEC-1 was further confirmed by

infecting HMEC-1 with a different strain that had deletions in both *inlB* and *actA* so that bacteria

could not spread from cell to cell. Consistent with our previous findings, we observed a two-fold

decrease in bacterial uptake for a series of different multiplicities of infection (MOI) when *inlB*

was knocked out (Fig. 4B). Importantly, bacteria carrying a deletion of *inlB* still exhibited a

strong monotonic dependence of infection efficiency on substrate stiffness (Fig. 4C). This

finding indicates that, while InlB contributes to some step in the infection of HMEC-1 by Lm, it is

not governing the step that is sensitive to substrate stiffness.

We confirmed this conclusion using four different lines of experimentation. First, we

directly assessed the effect of *inlB* deletion on bacterial adhesion and invasion of HMEC-1 using

inside/outside labeling as described above. We found that the total number of bacteria

associated with HMEC-1 cells was the same for wild-type bacteria as compared to an isogenic

ΔinlB strain (Fig. 4D), that is, adhesion to the host cell surface is indeed unchanged. However,

the number of internalized bacteria per cell and therefore the overall invasion efficiency was

significantly decreased for the *ΔinlB* strain (Fig. 4E-F). Second, we examined the effect of

inhibiting the host cell binding partner for InlB, the receptor tyrosine kinase Met (also known as

the hepatocyte growth factor receptor), on bacterial invasion. We confirmed that HMEC-1

express Met (Suppl. Fig. 3A), and then treated the cells with varying concentrations of the highly

selective Met inhibitor SGX-523 prior to infection (Buchanan et al., 2009). We found that only

uptake of the control Δ*actA* strain of Lm decreased with increasing concentration of SGX-523,

while uptake of the isogenic Δ*actA*/Δ*inlB* Lm did not change substantially as a function of SGX-

523 concentration (Fig. 4G). Third, when we then transfected HMEC-1 with commercial non-

targeting control siRNA (siNT) or siRNA targeting Met (siMet) and then infected HMEC-1 with

Lm, we found a significant 2-fold decrease in Lm infection efficiency for the Met knockdown cells

as compared to control cells (Fig. 4H; Suppl. Fig. 3B-C), while confirming that Met expression

was five-fold reduced for the Met knockdown cells as compared to controls through RT-PCR

(Suppl. Fig. 3D and Table S2). When we then infected transfected siNT and siMet HMEC-1 with

Δ*actA*/Δ*inlB* Lm, we found no significant difference in infection Lm uptake between the two

conditions, consistent with the previous results of cells pretreated or not with the SGX-523 (Fig.

4G and Suppl. Fig. 3E). These results confirm that InlB most likely contributes to Lm invasion

into HMEC-1 by interacting with host Met, as has been shown for other cell types (Bierne and

Cossart, 2002; Parida et al., 1998). However, Lm invasion into HMEC-1 treated with SGX-523

still retains a strong dependence on substrate stiffness (Fig. 4I), just as we found for the Δ*inlB*

strain. Fourth, we found that infection of HMEC-1 with the Δ*actA*/Δ*inlB* strain of Lm is still highly

sensitive to inhibition of FAK with PF573228, showing a dose-response curve that parallels that

of the control Δ*actA* strain (Fig. 4J).

So far we can conclude that substrate stiffness affects the adhesion of Lm to the surface

of HMEC-1 such that bacterial adhesion to host cells residing on soft substrates is about two-

fold less than to host cells residing on stiff substrates. The well-characterized InlB-Met

interaction appears to contribute to invasion of adherent bacteria into HMEC-1, and is

responsible for about half of the invasion efficiency for Lm infecting these cells, however this

interaction does not govern bacterial adhesion per se, is not sensitive to substrate stiffness, and

is orthogonal to the FAK signaling axis. We therefore sought to identify alternative possible host

cell receptors for adhesion of Lm to the surface of HMEC-1 that might be responsible for the

stiffness-dependent effects we consistently observe.

Inhibiting FAK activity leads to a reduced amount of cell surface vimentin for HMEC-1.

Since the decreased FAK activity associated with growth of HMEC-1 on softer hydrogels

leads to decreased Lm adhesion onto the surface of host cells, we attempted to identify

candidate host surface receptors whose amount is modulated by FAK activity and which

mediate bacterial adhesion. Since manufacturing soft and stiff PA hydrogels with large

dimensions is both technically challenging and costly, we instead grew cells on large TC

polystyrene plates and treated them with vehicle control or the FAK inhibitor PF573228. We

then biotinylated the cell surface-exposed proteins using membrane-impermeable EZ-Link

Sulfo-NHS-SS-Biotin and isolated them by affinity chromatography with streptavidin-agarose

beads (Fujimoto et al., 1992; Nunomura et al., 2005). Isolated surface proteins were then run in

2D-PAGE gels to allow separation of proteins according to both their isoelectric points and their

molecular weight (Elia, 2012). Gels were silver stained and comparison between gels was

performed by marking the spots that differed in intensity (Fig. 5A-B). We found a spot at

approximately 55 kDa consistently differing in two independent experiments between the control

sample and the sample treated with the FAK inhibitor PF573228 (see circles in Fig. 5A-B). In a

third replicate experiment of surface protein isolation, 2D-PAGE gels were Coomassie stained

and that specific 55 kDa spot that differed as a function of FAK inhibitor treatment was excised

and further analyzed by nanoliquid chromatography tandem mass spectrometry (nanoLC-

MS/MS). We identified this spot as the protein vimentin (accession number: gi|340219, Mascot

identification score: 788, number of identified peptides: 87, mass: 53752, isoelectric point: 5.05,

sequence coverage: 61%). Vimentin is a major component of the cytoskeleton forming

intermediate filaments, but exists also in soluble form and has been previously found to localize

at the cell surface for a wide variety of cells including VECs (Du et al., 2014; Fuchs and Weber,

1994; Mitra et al., 2015; Yu et al., 2016; Zou et al., 2006).

Given the high validity of identification, we sought to confirm whether vimentin is

expressed at the surface of HMEC-1 by performing immunostaining of non-permeabilized

HMEC-1 seeded on collagen I-coated glass substrates followed by epifluorescence imaging

(Fig. 6). For negative controls, cells were incubated with secondary antibody alone. The anti-

vimentin H-84 antibody stained the vimentin intermediate filaments of permeabilized cells very

well (Fig. 6A-B). Non-permeabilized cells showed surface staining of vimentin near cell-cell

junctions and very low background staining was observed for cells incubated with secondary

antibody alone (Fig. 6C-D). This localization confirmed that cell surface vimentin could be a

plausible candidate responsible for adhesion of Lm to HMEC-1.

HMEC-1 surface vimentin contributes to Lm uptake.

To determine whether surface vimentin specifically contributes to Lm adhesion and

thereby infection of HMEC-1, we used three independent methods to decrease the availability of

cell surface vimentin for bacterial adhesion. First, we pretreated HMEC-1 with varying

concentrations of H-84 anti-vimentin antibody prior to infection with Lm, and found a dose-

dependent decrease in infection efficiency (Fig. 7A). We found a maximum two-fold decrease in

Lm infection when incubating cells with 80 μg/ml anti-vimentin antibody, while increasing further

the concentration of the antibody did not lead to further decrease in Lm uptake (Suppl. Fig. 3A).

Second, HMEC-1 were transfected with commercial non-targeting control siRNA (siNT)

or siRNA targeting vimentin (siVIM) and total vimentin expression was found to be five-fold

reduced for the vimentin knockdown cells as compared to controls through RT-PCR and

reduced total vimentin expression was also confirmed through immunofluorescence (Suppl. Fig.

4A –B and Table S2). We found a significant decrease (about 30%) in Lm infection efficiency for

the vimentin knockdown cells as compared to control cells, while confirming that cell confluency

under both conditions was similar (Fig. 7B; Suppl. Fig. 4C-F).

Third, we treated HMEC-1 cells with varying concentrations of withaferin, a natural

product known to bind the soluble form of vimentin (Bargagna-Mohan et al., 2013; Bargagna-

Mohan et al.; Chi et al., 2010). We found a dose-dependent decrease in infection efficiency for

Lm in withaferin-treated cells, again finding a maximum two-fold decrease when cells were

treated with 5-10 μM of withaferin prior to infection (Fig. 7C). Higher concentrations of withaferin

disrupted HMEC-1 cell-substrate adhesion. Overall these results are consistent with the

hypothesis that cell surface vimentin is responsible for about half of the amount of adhesion of

Lm to the HMEC-1 surface, and that vimentin presentation on the cell surface is sensitive to

substrate stiffness.

As an additional control to confirm that anti-vimentin antibodies and withaferin treatment

inhibit Lm uptake due to effects on surface vimentin and not to non-specific effects, we

transfected HMEC-1 with commercial non-targeting control siRNA (siNT) or siRNA targeting

vimentin (siVIM) and then blocked cells for 1h with the H-84 anti-vimentin antibody. We then

infected the host cells with constitutively GFP-expressing Lm and fixed samples shortly after

infection. Through quantitative microscopy we observed no significant change in infection

susceptibility for vimentin knock-down cells blocked with anti-vimentin antibodies prior to

infection as compared to vimentin knock-downs alone, confirming that the antibodies inhibit

uptake due to effects on vimentin and not to non-specific effects (Suppl Fig. 4G). Similarly,

when HMEC-1 transfected with siNT or siVIM were pretreated with our without withaferin we

found a significant decrease in bacterial adhesion only for the control cells treated with

withaferin and not for the vimentin knock-down cells (Suppl Fig. 4H). Finally, we hypothesized

that if vimentin localizes at cell-cell junctions, and given that perturbing the amount of surface

vimentin leads to up to a 2-fold decrease in infection susceptibility, then we should expect that

when infecting HMEC-1 with Lm half of the bacteria should adhere at cell-cell junctions and half

of the bacteria could adhere anywhere else. Indeed, when we infected HMEC-1 with Lm, fixed

the samples and then immunostained for VE-cadherin as a proxy for cell-cell junctions (Suppl.

Fig. 5A), we observed that quite often bacteria were found adhering at cell-cell junctions. This

was not the case for vimentin knockdown cells where bacteria where found all across the apical

surface of cells (Suppl. Fig. 5B).

To examine any possible interaction between the contribution of vimentin-based

adhesion and the contribution of InlB/Met-based invasion of Lm infecting HMEC-1, we

pretreated HMEC-1 with withaferin or vehicle control and then infected with either Δ*actA* or

Δ*actA/* Δ*inlB* Lm over a range of multiplicities of infection (MOI). Consistent with our results

described above, we found a two-fold decrease in Lm uptake when cells were pretreated with

withaferin and infected with Δ*actA* Lm or when cells were not treated with withaferin but were

infected with Δ*actA/* Δ*inlB* Lm (Fig. 7D). When cells were both pretreated with withaferin and

infected with Δ*actA/* Δ*inlB* Lm, infection was decreased four-fold relative to control (Fig. 7D) , i.e.

InlB/Met and vimentin contribute independently to infection efficiency. However, under all

conditions there was still residual infection, suggesting that Lm uses additional strategies to

achieve uptake by HMEC-1, other than interactions with surface vimentin for bacterial adhesion

and with Met for increased bacterial internalization.

Uptake of *Listeria innocua* but not carboxylated latex beads by HMEC-1 depends on cell

surface vimentin.

Our results demonstrate that the vimentin-dependent adhesion of Lm to HMEC-1 is

sensitive to substrate stiffness and is not mediated by the bacterial internalins InlA, InlB, or InlF.

In order to gain insight into whether vimentin-based bacterial adhesion is a result of a non-

specific stickiness or a specific host-bacterium interaction, we measured the influence of cell

surface vimentin on adhesion of other bacteria and of non-biological particles. *Listeria innocua*

(Li) is a bacterium closely related to Lm that is considered non-pathogenic in that it lacks the

putative internalin family members and other virulence factors that Lm carries (Glaser et al.,

2001; Lauer et al., 2002). When we infected HMEC-1 with comparable loads of Lm and Li, we

found that adhesion of both bacteria is comparable (Fig. 8A). We also found that treating

HMEC-1 with FAK inhibitor PF537228 or blocking HMEC-1 with anti-vimentin antibody H-84

reduces adhesion of both Lm and Li onto HMEC-1 by similar amounts (Fig. 8A). Next, to

examine whether a bacterial factor common in Lm and Li could responsible for surface vimentin

mediated adhesion, we blocked HMEC-1 with anti-vimentin antibody and exposed cells to 2 μm

carboxylated latex beads, which are efficiently taken up by VECs. We found that uptake of

beads did not vary with antibody concentration and was identical to uptake of cells treated with

isotype control (Fig. 8B). Our results suggest that cell surface vimentin is a common receptor for

both Lm and Li in the context of adhesion to HMEC-1, but uptake of nonbiological particles such

as carboxylated latex beads does not depend on surface vimentin.

DISCUSSION

Bacterial infection of VECs depends on the stiffness of the matrix on which cells reside.

Our study provides the first evidence that ECM stiffness is a crucial determinant in modulating susceptibility of host cells to infection by bacterial pathogens. Using HMEC-1 cells as model host adherent cells and Lm as model bacterial pathogen, we demonstrated that host cell susceptibility to Lm infection increases with increasing ECM stiffness. Mechanosensitive cells, such as VECs, can "feel" a variety of physical cues such as fluid shear stresses, cyclic mechanical strains, matrix stiffness and respond to them by altering their morphology, gene expression and function (Kohn et al., 2015; Reinhart-King, 2008). Interestingly, many signaling pathways involved in mechanotransduction are common irrespective of the exact mechanical stimulus (Li et al., 1997; Zebda et al., 2012). For instance, exposure of VECs to laminar shear stress leads to recruitment of FAK at focal adhesions and to an increase in the phosphorylation at Y397 (Li et al., 1997). Consistent with FAK activity being sensitive to mechanical stimuli, we found that FAK activity is increased when cells reside on stiffer matrices. Concurrently, we observe a decrease in Lm uptake when FAK activity is reduced or inhibited. It is possible that enhanced FAK activity for VECs exposed to shear stresses, might also lead to increased Lm uptake, but this still remains to be investigated (Li et al., 1997). In our study, we only focused on the effect of ECM stiffness on host cell infection susceptibility and did not consider in our model additional mechanical cues that host cells experience (Shi and Tarbell, 2011). Based on our findings and on recent studies on shear flow-exposed endothelial cells infected with pathogens *B. burgdorferi* or *S. aureus*, we speculate that similar to matrix stiffness it is plausible that additional mechanical cues could also play an important role in mediating susceptibility of adherent host cells to bacterial infection (Claes et al., 2014; Niddam et al., 2017). Therefore, the development of organotypic models for studying bacterial infection, that take into account all of the different *in vivo* mechanical cues sensed by cells, is pertinent and will aid our emerging understanding of the biomechanics of host-bacteria interactions as well as the design of more

effective therapeutic interventions that take into consideration the local cellular mechanical

micro-environment.

Our findings suggest that together with biochemical cues, the stiffness of the

environment where cells reside is an additional variable worth considering since it affects

cellular behavior and susceptibility to bacterial infection. In traditional studies of bacterial

infection of host cells' ECM stiffness is not taken into account and such studies are commonly

performed on non-physiological glass or polystyrene surfaces. Our study on how HMEC-1

interact with Lm when varying subendothelial stiffness was designed with the intent to mimic

variations that occur in physiological conditions depending on the precise anatomic location of

the vessel, in aging and during pathophysiological conditions such as cardiovascular disease

(Zieman et al., 2005) or cancer (Acerbi et al., 2015). Our lower range of subendothelial matrix

stiffness (0.6 kPa) could be relevant for the brain microvasculature where the blood vessel

microenvironment is very soft whereas stiffer values are more relevant for bigger vessels or

aged/diseased vasculature (Kohn et al., 2015; Stroka and Aranda-Espinoza, 2011). For

instance, clinical studies on arteries of atherosclerotic mice have shown that vessel stiffness for

diseased mice can increase from 5 kPa to up to 28 kPa (Kothapalli et al., 2012). Similarly, injury

can increase vessel stiffness as has been shown for injured femoral artery whose stiffness

increases from 3 kPa to 10 kPa (Klein et al., 2009). Finally, studies have shown that aging can

lead to significant vessel stiffening with studies suggesting that the aorta stiffness due to aging

can raise from 20 kPa to 70 kPa (Huynh et al., 2011). We showed that subendothelial stiffness

changes the amount of surface vimentin expressed by VECs, therefore affecting critically how

much host cells will be susceptible to bacterial infection. That is atherosclerotic vessels or aged

vessels might be more susceptible to infection based on our findings, while VECs lining healthy

and softer vessels should be less susceptible to infection by Lm. It is plausible that low degree

of stiffness might be a host mechanism to protect against infection. For the purpose of the

present study we just examined how subendothelial stiffness modulates bacterial adhesion on

previously uninfected VECs. However, it is very possible that once bacteria infect their hosts

they might have developed ways to circumvent such a host mechanism by somehow altering

matrix stiffness, *i.e.* by reprogramming host cells to alter their production of ECM proteins or

matrix-degrading enzymes, which could lead to alterations in subendothelial stiffness and

subsequently VEC biomechanics and contractility, critically impacting infection. Future studies

should address how host cell biomechanics change upon infection and how bacterial infection

changes susceptibility of host cells to further infection.

Surface vimentin is a receptor for *Listeria* infection of VECs.

We found that lower FAK activity as occurs when HMEC-1 are seeded on softer

hydrogels leads to decreased Lm and Li adhesion onto the surface of HMEC-1 and that is

attributable to lower levels of cell surface vimentin. The role of cell surface vimentin as an

attachment receptor facilitating bacterial or viral entry has been previously documented for other

pathogens (Bhattacharya et al., 2009; Du et al., 2014; Garg et al., 2006; Mak and Brüggemann,

2016; Rohrbeck et al., 2014; Yang et al., 2016; Yu et al., 2016; Zou et al., 2006). VEC surface

vimentin in particular has been shown to be the receptor for attachment of *E. coli* K1 and

multiple viruses (Das et al., 2011; Du et al., 2014; Koudelka et al., 2009; Yang et al., 2016; Zou

et al., 2006). We speculate that matrix stiffness of VECs might possibly also affect uptake of the

above viruses and bacteria, since the amount of surface vimentin is reduced when FAK activity

is decreased as in the case of cells residing on highly compliant matrices.

Bacterial adhesion to the surface of cells is commonly required as a precursor to

invasion (Lebrun et al., 1996; Lecuit et al., 2000). Our finding that both Lm and Li adhesion is

reduced when HMEC-1 are blocked with anti-vimentin antibodies suggests that the possible

bacterial binding partner of vimentin might be expressed in both bacterial species. Surface

vimentin has been shown to possess lectin-like activity binding N-acetylglucosamine (GlcNAc),

a sugar that is also commonly found as a component of bacterial cell envelopes (Ise et al.,

2010; Konopka, 2012). Specifically, GlcNAc is found decorating the wall teichoic acids of Lm

serotype 1/2a strains, such as the 10403S strain used in this study (Fiedler, 1988). That implies

that bacterial carbohydrate-binding to host cell surface vimentin might also be a plausible

specific interaction.

Lm uses multiple pathogenic strategies to infect VECs, some of which are independent

of ECM stiffness.

We identified that the Lm virulence factor InlB contributes to invasion of HMEC-1 cells,

mostly likely via its well-characterized interaction with the host cell receptor Met. Similarly, Lm

uptake is decreased by two-fold when Met is inhibited. However deletion of *inlB* and decrease of

Met activity by siRNA knockdown or by pharmacological inhibition do not affect the ability of the

infection process to respond to changes in substrate stiffness. When we infected HMEC-1 with

Δ*actA*/Δ*inlB* Lm after treating host cells with withaferin that binds to soluble vimentin, we found a

four-fold decrease in infection relative to controls, indicating that the vimentin-dependent and

InlB-dependent pathways contribute to infection independently of one another; however, even

when both pathways were blocked there was still residual Lm infection. This residual Lm

infection suggests that there are additional InlB-independent and vimentin-independent

mechanisms that Lm leverage to infect HMEC-1.

Increased Lm adhesion onto HMEC-1 residing on stiff matrices could be attributed to

multiple factors. In this work, we investigated the possibility of a receptor at the surface of host

cells being differentially regulated when FAK activity is increased, as in stiff matrices, and

identified cell surface vimentin as a well-supported candidate receptor. However, it is also

possible that additional factors might also lead to the decreased adhesion of Lm onto HMEC-1

residing on softer matrices. It is plausible that the cell surface glycans of HMEC-1 might be

differentially regulated depending on the stiffness of the environment. For example previous

studies have suggested both a positive correlation between FAK activity and the heparan

sulfate portion of the glycocalyx (Gopal et al., 2010; Liu et al., 2002) and between the heparan

sulfate portion of the glycocalyx and Lm adhesion onto enterocytes (Henry-Stanley et al., 2003).

Another possibility could be the differential regulation of biophysical or mechanical properties of

the host cells depending on matrix stiffness (e.g. cell cortical stiffness, surface roughness,

membrane tension). For instance, studies on adhesion of bacteria onto hydrogel surfaces have

shown that adherence is increased on stiffer hydrogels (Kolewe et al., 2015), suggesting that if

cells become stiffer on stiffer hydrogels, cellular stiffness alone could lead to increased bacterial

adhesion (Higuita-Castro et al., 2014; Tang et al., 2012).

VEC origin and physical cues might explain discrepancy between previous studies on

VEC infection by Lm.

The endothelial lining of blood vessels displays remarkable spatiotemporal heterogeneity

and the basis of these morphological and functional differences are still unclear (Aird, 2007;

Aird, 2012; Ingram et al., 2004). It is well documented that mechanical and chemical cues

relayed to VECs by their environment can alter both function and gene expression of VECs

found at different tissues (Aird, 2012; Kohn et al., 2015). However, even when VECs from

different origins are placed *in vitro* in the same biochemical and mechanical environment, they

can still exhibit unique characteristics and behaviors that are intrinsic to the cells themselves

and are not determined by differential culture or environmental conditions (Craig et al., 1998;

Ostrowski et al., 2014; Stroka and Aranda-Espinoza, 2011; Ye et al., 2014). For example, the

response of human umbilical cord endothelial cells (HUVEC) to changes in curvature or shear

stress is completely distinct as compared to that of human brain microvascular endothelial cells

(HBMEC) (Ye et al., 2014). In accordance with the differences these two cell types exhibit in

response to geometrical constraints or mechanical stimuli, studies have also shown differences

with respect to Lm infection. Past studies suggest that HBMEC infection by Lm depends on InlB

(Greiffenberg et al., 1998), while HUVEC uptake of Lm appears to be independent of both the

internalins InlA and InlB (Greiffenberg et al., 1997; Rengarajan et al., 2016). These studies are

not necessarily conflicting but suggest that bacterial infection of VECs depends upon both the

environment and the particular origin of VECs and therefore conclusions should refer to the

exact cell type and not to endothelial cells in general. Since many pathological processes occur

at the microvascular level of organs, we chose in this study to use HMEC-1 as our model for

VECs. However, extrapolation from results obtained for HMEC-1 infection by Lm to other VECs

should be performed with caution. In a similar analogy, although Lm uptake by HMEC-1

increases with increasing subendothelial stiffness that relationship could be different if HMEC-1

were infected with different bacterial pathogens. We speculate that the relationship between

ECM stiffness and susceptibility to infection is likely host cell- and pathogen- specific.

In conclusion, our results provide the first strong evidence that the local mechanical

environment and in particular the matrix stiffness of VECs regulates susceptibility of VECs to Lm

infection. The novel mechanosensitive pathway we identified suggests that increased ECM

stiffness sensed by VECs leads to enhanced FAK activity that augments the amount of vimentin

exposed at the surface of VECs. Increased amount of surface vimentin in turn increases Lm

adhesion and subsequent uptake by VECs. Our studies on the effect of ECM stiffness in

bacterial uptake of VECs can have other significant implications, since they provide an example

of how mechanotransduction can be exploited in biology and medicine facilitating the

development of therapeutic interventions against bacterial infections and other diseases.

MATERIALS AND METHODS

Fabrication of thin two-layered polyacrylamide (PA) hydrogels on 24-well glass-bottom

dishes

PA hydrogel fabrication was done as previously described with a few modifications for

the specific experiments (Bastounis et al., 2011; Bastounis et al., 2014; Georges et al., 2006;

Vincent et al., 2013). 24-well glass bottom plates (MatTek, P24G-1.5-13-F) were incubated for 1

h with 500 μL of 2 M NaOH. Wells were rinsed with distilled water, and 500 μL of 2% 3-

Aminopropyltriethoxysilane (Sigma, 919-30-2) in 95% ethanol were added to each well for 5

min. Wells were rinsed again with water and 500 μL of 0.5% gluteraldehyde was added in each

well for 30 min. Wells were rinsed with water and dried at 60°C. To prepare hydrogels of varying

stiffness, mixtures containing 3–10% acrylamide (Sigma, A4058) and 0.06–0.6% bis-acrylamide

(Fisher, BP1404-250) were prepared. Specifically, 0.6 kPa hydrogels contained 3% acrylamide

and 0.06% bis-acrylamide, 3 kPa hydrogels contained 5% acrylamide and 0.1% bis-acrylamide,

20 kPa hydrogels contained 8% acrylamide and 0.26% bis-acrylamide, and 70 kPa hydrogels

contained 10% acrylamide and 0.6% bis-acrylamide. For each stiffness, two mixtures were

prepared the second of which contained 0.03% 0.1 μm diameter fluorescent beads (Invitrogen,

F8803). Mixtures were then degassed for 15 min to remove oxygen, which inhibits acrylamide

polymerization.

First, 0.06% APS and 0.43% TEMED were added to the solutions containing no beads

to initiate polymerization and then 3.6 μL of the mixture was added at the center of each well,

capped with 12-mm untreated circular glass coverslips and allowed to polymerize for 20 min.

The coverslips were then lifted with a syringe needle with a small hook at its tip and then 2.4 μL

of the mixture containing tracer beads was added, sandwiched again with a 12-mm untreated

circular glass coverslip, gently pressed downwards by means of forceps, and allowed to

polymerize for 20 min. 50 mM HEPES pH 7.5 was added in the wells, and coverslips were

removed using the syringe needle and forceps. PA hydrogels were UV-sterilized for 1 h.

Hydrogels were then activated by adding 200 µL 0.5% w/v heterobifunctional crosslinker Sulfo-

SANPAH (ProteoChem, c1111) in 1% DMSO and 50 mM HEPES pH 7.5 on the upper surface

of the hydrogels and exposing to UV light for 10 min. After activation, the hydrogels were

washed with 50 mM HEPES pH 7.5 to remove excess crosslinker and were coated with 200 µL

of 0.25 mg/mL rat tail collagen I (Sigma-Aldrich, C3867) in 50 mM HEPES overnight at room

temperature. Prior to seeding cells, hydrogels were incubated with cell media to allow

equilibration for 30 min.

HMEC-1 culture and infection with *Listeria monocytogenes* (Lm)

Human microvascular endothelial cells (HMEC-1, generous gift from Welch lab, UC

Berkeley) were maintained in MCDB 131 medium (Fisher Sci Co, 10372-019) supplemented

with 10% FBS (GemBio, 900-108), 10 ng/mL epidermal growth factor (Sigma, E9644), 1 µg/mL

hydrocortisone (Sigma, H0888), and 2mM L-glutamine (Sigma, 56-85-9).

HMEC-1 were infected as previously described with the following modifications

(Rengarajan et al., 2016). The day prior to infection, host cells were seeded at a density of

4×10^5 cells/well for cells residing on wells of 24-well plates or at a density of 1×10^5 cells/well for

cells residing on wells of 48-well plates, and grown for 24 h. Lm liquid cultures were started from

a plate colony, and grown overnight, shaking, at 30 °C in Brain Heart Infusion (BHI) media (BD,

211059) supplemented with 200 µg/mL streptomycin and 7.5 µg/mL chloramphenicol. The day

of the infection, the O.D.600 of the overnight cultures was measured and diluted to 0.1.

Samples were incubated for 2 h shaking, in the dark at 30°C in BHI media supplemented with

200 µg/mL streptomycin and 7.5 µg/mL chloramphenicol to allow the O.D. 600 to reach 0.2-0.3

and let bacteria enter the logarithmic growth phase. Bacteria were then washed 3 times with

PBS to remove any soluble factors and infections were performed in normal growth media

(Reed et al., 2014).

To synchronize invasion, Lm diluted in normal growth media were added on the HMEC-1

cells and samples were spun for 10 min at 200 x g prior to incubation. After 30 min of incubation

at 37 °C, samples were washed 4 times in PBS and after an additional 30 min, media was

replaced with media supplemented with 20 μg/mL gentamicin. Multiplicity of infection (MOI) was

determined by plating bacteria at different dilutions, on BHI agar plates with 200 μg/mL

streptomycin and 7.5 μg/mL chloramphenicol and measuring the number of colonies formed 2

days post-infection. A similar approach was followed when HMEC-1 were infected with *Listeria*

innocua (Li), except that BHI plates with no antibiotics were used. All bacterial strains used in

these studied are indicated in Table S1.

Analysis of infection via flow cytometry was performed at 7-8 h after exposure, unless

otherwise stated. For drug exposure experiments, unless otherwise indicated, media was

removed from the cells and replaced with media containing either the drug or vehicle control 1 h

prior to infection or 30 min prior to infection for the case of withaferin. Cells were cultured in the

drug-containing media for 1 h after infection. 1 h post-infection cells were washed four times and

drug-free gentamicin-containing media was added to the cells.

Antibodies and reagents

Hoechst (Thermofisher, D1306) was dissolved at 1 mg/mL in dimethyl formamide

(DMSO) and used at 1:1000. Drugs were dissolved in DMSO (Sigma, D2650) at the stock

concentrations indicated: 10 mM FAK inhibitor-14 (FAK-14) (Tocris Bioscience, 3414), 100 mM

PF573228 (Tocris Bioscience, 3239), 20 mM SGX 523 (Tocris Bioscience *5356*), 42 mM

withaferin (Sigma-Aldrich, W4394). Primary antibody used for staining of extracellular Lm was

rabbit polyclonal anti-*Listeria* genus specific antibody (ABCAM, ab35132). Primary antibody

used for staining Li was goat polyclonal BacTrace anti-*Listeria* genus specific antibody

(SeraCare Life Sciences Inc., 01-90-90). For incubation of cells with vimentin antibodies prior to

infection or immunostaining of surface vimentin, rabbit polyclonal H-84 vimentin antibody (Santa

Cruz Biotechnologies, sc-5565) was used. For isotype controls, cells were incubated with rabbit

IgG (Sigma, I5006). For western blotting the following antibodies were used: rabbit polyclonal

phospho-FAK Tyr397 (ThermoFisher, 44-624G), mouse monoclonal anti-FAK (EMD Millipore,

05-182), rabbit monoclonal anti-Met (cMet) antibody (Abcam, ab51067), anti-GAPDH antibody

(Cell signaling, 140C10).

Flow cytometry of HMEC-1 cells infected with Lm

7-8 h post-infection, infected HMEC-1 cells were detached from the substrate by

incubating them for 10 min with a mixture of 200 μL of 0.25% trypsin-EDTA and 0.05%

collagenase (Sigma, C0130). Solutions in each well were pipetted up and down 6 times to

ensure single cell suspensions, and 200 μL of complete media was added to inactivate trypsin

in each well. Solutions were transferred into 5 mL polystyrene tubes with a 35-μm cell strainer

cap (Falcon, 352235) and then samples were immediately analyzed by flow cytometry on the

Scanford FACScan analyzer (Custom Stanford and Cytek upgraded FACScan). 10,000-20,000

cells were analyzed per each replicate. To ensure analysis of single cells, the bulk of the

distribution of cell counts was gated using the forward versus side scatter plot. This gating

strategy ensures that single cells are analyzed and debris or cell doublets or triplets are

eliminated from the analysis. A second gating step was then performed to exclude cells that

autofluoresce by measuring the fluorescence of control-uninfected cells and gating the

population of infected cells so to exclude autofluorescence.

Immunostaining of extracellular adherent bacteria

HMEC-1 cells residing on either PA hydrogel substrates or glass collagen I-coated

coverslips were infected as described above with a Lm strain that constitutively expresses GFP.

20 min post-infection, 1 μg/mL Hoechst (Thermofisher, D1306) was added in each well to stain

the cells' nuclei. 30 min post-infection cells were washed 4 times in PBS and fixed with a non-

permeabilizing fixative for differential immunostaining for 20 min at room temperature (Yam and

Theriot, 2004). Fixative contained 0.32 M sucrose, 10mM MES pH 6.1, 138 mM KCl, 3 mM

$MgCl_2$, 2 mM EGTA and 4% formaldehyde EM grade. Following a wash with PBS, samples

were blocked for 30 min with 5% BSA in PBS and then incubated with anti-Lm primary antibody

(Abcam ab35132) diluted 1:100 in PBS containing 2% BSA for 1 h. Samples were washed in

PBS 3 times and then incubated with Alexa Fluor 546 goat anti-rabbit secondary antibody

(Invitrogen A-11035) diluted 1:250 in PBS containing 2% BSA for 1 h. Samples were washed 3

times in PBS and stored in 1 mL PBS for imaging. N > 1000 cells were analyzed per condition.

For imaging, we used an inverted Nikon Diaphot 200 with a CCD camera (Andor Technologies)

and a 40X air Plan Fluor NA 0.60 or a 100X oil objective. The microscope was controlled by the

MicroManager software package (Edelstein et al., 2014). For differential immunostaining, all

"green" bacteria associated with individual cells were counted as adherent; bacteria that were

both "green" and "red" (due to antibody binding) were counted as non-internalized. Nuclei

number was identified running a custom-made script in MATLAB (Mathworks Inc.) and the CellC

software was used for enumeration of the bacteria (Selinummi et al., 2005). For characterization

of total bacteria adhering to host cells (Lm or Li), same procedure was followed with the

exception that cells were permeabilized for 5 min in 0.2% Triton-X in PBS. Primary antibody

used was goat polyclonal BacTrace anti-*Listeria* genus specific antibody.

Immunostaining of surface vimentin

HMEC-1 cells residing on glass collagen I-coated coverslips were incubated at 37°C for

30 min with H-84 anti-vimentin antibody in 1:10 dilution in media. Cells were then washed three

times in PBS and fixed in 4% formaldehyde (EM grade) in PBS for 10 min at room temperature.

A blocking step with 5% FBS in PBS was followed for 30 min and then cells were incubated with

secondary goat anti-rabbit AlexaFluor-546 antibody diluted 1:250 in PBS containing 2% BSA for

1 h. For negative controls to ensure label is specific to primary antibody, cells with no primary

antibody were fixed and incubated for 1 h with secondary goat anti-rabbit AlexaFluor-546

antibody. As an additional control, cells were also fixed, permeabilized and stained for

intracellular vimentin. For imaging, we used an inverted Nikon Diaphot 200 with a CCD camera

(Andor Technologies) and a 100X oil objective.

HMEC-1 cell transfection with siRNA

678   For each well of a 24-well plate, $6x10^4$ HMEC-1 cells suspended in serum free media

were reverse-transfected with siRNAs at 20 nM final concentration using 0.25 µL lipofectamine

RNAiMAX (Invitrogen 13778075). The transfection mix was replaced by full media 8 h later.

Synthetic siRNA pools (including 4 distinct siRNA sequences for each gene) to target vimentin,

Met and FAK were purchased from Dharmacon (Table S2). HMEC-1 cells were treated with

control (non-targeting, siGLO and Kif11) or experimental siRNA in accordance with the

manufacturer instructions. Specifically, to demonstrate that transfection performed was sufficient

to get siRNAs into the cells, we transfected cells with synthetic siRNA, siGLO, that makes cell

exposed to it fluorescent 24 h post-transfection (Table S2). In addition to track a cell cycle

phenotype to verify that knockdown has occurred with our protocol, we transfected cells with

siKif11 that results in substantial cell death of transfected cells, approximately 24-48 h post-

transfection and can be verified on the TC microscope. Bacterial infections were performed

approximately 72 h after transfection

RT-qPCR

693   HMEC-1 cells were treated with control or experimental siRNA as described above.

mRNA was harvested using the RNeasy Micro Kit (Qiagen, 74004) and cDNA was prepared

using the Superscript III First-strand Synthesis SuperMix (ThermoFisher, 18080–400). qPCR

was performed using TaqMan PreAmp Master (Thermofisher, 4331182). Genes of interest were

amplified using primers Hs00958113_g1 for Vimentin (ThermoFisher, 4331182) and

Hs99999905_m1 for GAPDH (ThermoFisher, 4333764) on a StepOnePlus Real-Time PCR

System. Normalized relative quantity (NRQ) and error were calculated as previously described

[92]. GAPDH was used as control gene.

Western blotting of FAK and Met for HMEC-1 lysates coming from cells residing on

different substrates

For assessing FAK and Met phosphorylation and expression levels, cells were seeded

on different substrates for 24 h, and then lysed with a buffer containing 1% Nonidet P-40, 0.5%

sodium deoxycholate, and a protease inhibitor mixture (PMSF, leupeptin, aprotinin, and sodium

orthovanadate). The total cell lysate was separated by SDS/PAGE (10% running, 4% stacking)

and transferred onto a nitrocellulose membrane (Immobilon P, 0.45-µm pore size). The

membrane was then incubated with the designated antibodies. Immunodetection was performed

using the Western-Light chemiluminescent detection system (Applied Biosystems).

Cell surface protein isolation

The isolation of cell surface proteins was adapted according to (Karhemo et al., 2012)

and (Roesli et al.). Cells were plated on 10 x 15 cm cell culture dishes until reaching confluency

for each condition. Cells from 10 dishes were incubated with vehicle control (DMSO) containing

media and cells from other 10 dishes with 2 µM PF537228 FAK inhibitor for 1 h. Cells were then

washed three times with DPBS+ (PBS, 0.901 mM CaCl2, 0.492 mM MgCl$_2$, 2.667 mM KCl, 1.47

mM KH$_2$PO$_4$, 137.931 mM NaCl, 8.060 mM Na$_2$HPO$_4$-7H$_2$O, 5.555 mM D-Glucose, 0.327 mM

Sodium Pyruvate), and incubated for 30 min with 0.5 mM EZ-Link Sulfo-NHS-SS-Biotin

(APExBIO, 21331) in DPBS+ at 4°C. To quench any non-reacted biotinylation, 1 M Tris pH 8.0

at a final concentration of 50 mM was added on each plate for 10 min at 4°C. The solution was

then discarded and plates were rinsed twice in 1X TBS (50 mM Tris-Cl pH 7.2, 150 mM NaCl). 2

ml of TBS pH 7.2 with 1X protease inhibitor cocktail (1 mM EDTA, 10 µM E-64, 2 µg/ml

leupeptin, 15 µg/ml benzamidine, 0.1 mM PMSF) and with 1X phosphatase inhibitor cocktail (1

mM Na_3VO_4, 1 mM NaF) were added to each dish and cells were scraped into 40 ml falcon

tubes. Tubes were spun at 400 x g for 5 min and the supernatant was discarded. 10 ml of lysis

buffer (50 mM Tris-HCL pH 8.5, 150 mM NaCl, 2% NP-40, 0.25% Deoxycholate, 2x protease

inhibitor cocktail, 1x osphatase inhibitor cocktail) were added to each single pellet obtained from

10 x 15 cm plates, and cells were passed through a 25 G needle attached to a 10-mL syringe 3

times. Lysates were then sonicated for 5 min in a bioruptor with 30 sec ON/OFF cycle. 1 mM

$MgCl_2$ and 50 U/ml benzonase (Sigma, 9025-65-4) were added to the samples that were then

incubated at 4 °C for 2 h on a rotator. EDTA to a final concentration of 5 mM was added to each

sample and samples were spun in an ultracentrifuge (Rotor type 70.1 Ti; 33,000 rpm) at

100,000 x g for 60 min at 4 °C. Supernatants were then transferred into fresh 15 mL Falcon

tubes and protein concentration was estimated by the BCA protein assay (Thermo Fisher

Scientific, Pierce Rockford). Equal amounts of protein (~5 mg) from each extract were used for

cell surface protein isolation.

Streptavidin agarose beads (Pierce, 20347) were washed three times with lysis buffer.

50 µL per 5 mg/lysate were added for 2 h or overnight at 4 °C on a rotator. Samples were then

transferred to 2 ml gravity flow columns (BioRad) pre-equilibrated with 2 ml wash buffer I (50

mM Tris-HCL pH 8.5, 150 mM NaCl, 2% NP-40, 0.25% Deoxycholate, 0.5% SDS). The flow-

through was collected and stored at -80 °C. Columns were washed once with 2 mL lysis buffer

(excluding protease and phosphatase inhibitors), then with 2 mL wash buffer I, followed by a 2

ml wash with wash buffer II (50 mM Tris-HCL pH 8.5, 300 mM NaCl, 2% NP-40, 0.25%

Deoxycholate, 0.5% SDS) and then again with 2 mL wash buffer I. Beads were then transferred

to a fresh 1.5 mL Eppendorf tube and 3x volume of elution buffer (100 mM Tris-HCl pH 8.5, 2%

SDS, 100 mM DTT) was added and samples were incubated at 37 °C for 1 h on a thermomixer.

Beads were then spun down and supernatant was collected and 5% aliquoted for gel-analysis

(2.5% elution for Western Blot and 2.5% elution for Silver staining of 1D-PAGE gels) and the

rest was put in a fresh 1.5 mL Eppendorf tube and stored at -80°C.

2D SDS-PAGE electrophoresis and staining

Two-dimensional electrophoresis was performed according to the carrier ampholyte

method of isoelectric focusing (Burgess-Cassler et al., 1989; O'Farrell, 1975) by Kendrick Labs,

Inc. (Madison, WI) as follows: Isoelectric focusing was carried out in a glass tube of inner

diameter 2.3 mm using 2% pH 3-10 Isodalt Servalytes (Serva, Heidelberg, Germany) for 9600

volt-h. 1 µg of an IEF internal standard, tropomyosin, was added to the sample. This protein

migrates as a doublet with lower polypeptide spot of MW 33,000 and pI 5.2. The enclosed tube

gel pH gradient plot for this set of Servalytes was determined with a surface pH electrode. After

equilibration for 10 min in Buffer 'O' (10% glycerol, 50 mM dithiothreitol, 2.3% SDS and 0.0625

M Tris, pH 6.8), each tube gel was sealed to the top of a stacking gel that overlaid a 10%

acrylamide slab gel (0.75 mm thick). SDS slab gel electrophoresis was carried out for about 4 h

at 15 mA/gel. The following proteins (Sigma Chemical Co., St. Louis, MO and EMD Millipore,

Billerica, MA) were used as molecular weight standards: myosin (220,000), phosphorylase A

(94,000), catalase (60,000), actin (43,000), carbonic anhydrase (29,000) and lysozyme

(14,000). These standards appear along the basic edge of the silver-stained (Oakley et al.,

1980) 10% acrylamide slab gel. The gels were dried between sheets of cellophane with the acid

edge to the left.

Manual comparisons of patterns of silver-stained 2D gels

Each gel for comparison was overlaid with a transparent sheet for labeling polypeptide

spot differences without marking the original gel. Two experienced analysts manually compared

protein patterns and polypeptide spots that were unique to or differed between controls and

PF537228 samples were outlined.

Protein digestion and peptide extraction

Proteins that were separated by SDS-PAGE/2D-PAGE and stained by Coomassie dye

were excised, washed and the proteins from the gel were treated according to published

protocols (Darie et al., 2011; Shevchenko et al., 1996; Sokolowska et al., 2012c). Briefly, the gel

pieces were washed in high purity, high performance liquid chromatography HPLC grade water,

dehydrated and cut into small pieces and de-stained by incubating in 50 mM ammonium

bicarbonate, 50 mM ammonium bicarbonate/50% acetonitrile, and 100% acetonitrile under

moderate shaking, followed by drying in a speed-vac concentrator. The gel bands were then

rehydrated with 50 mM ammonium bicarbonate. The procedure was repeated twice. The gel

bands were then rehydrated in 50 mM ammonium bicarbonate containing 10 mM DTT and

incubated at 56 ^{o}C for 45 min. The DTT solution was then replaced by 50 mM ammonium

bicarbonate containing 100 mM Iodoacetamide for 45 min in the dark, with occasional vortexing.

The gel pieces were then re-incubated in 50 mM ammonium bicarbonate/50% acetonitrile, and

100% acetonitrile under moderate shaking, followed by drying in speed-vac concentrator. The

dry gel pieces were then rehydrated using 50 mM ammonium bicarbonate containing 10 ng/µL

trypsin and incubated overnight at 37 ^{o}C under low shaking. The resulting peptides were

extracted twice with 5% formic acid/50 mM ammonium bicarbonate/50% acetonitrile and once

with 100% acetonitrile under moderate shaking. Peptide mixture was then dried in a speed-vac,

solubilized in 20 µL of 0.1% formic acid/2% acetonitrile.

Liquid chromatography and tandem mass spectrometry (LC-MS/MS)

The peptide mixture was analyzed by reverse phase liquid chromatography (LC) and MS

(LC-MS/MS) using a NanoAcuity UPLC (Micromass/Waters, Milford, MA) coupled to a Q-TOF

Ultima API MS (Micromass/Waters, Milford, MA), according to published procedures (Darie et

al., 2011; Sokolowska et al., 2012a; Sokolowska et al., 2012b; Spellman et al., 2008). Briefly,

the peptides were loaded onto a 100 µm x 10 mm NanoAquity BEH130 C18 1.7 µm UPLC

column (Waters, Milford, MA) and eluted over a 150 min gradient of 2-80% organic solvent

(ACN containing 0.1% FA) at a flow rate of 400 nL/min. The aqueous solvent was 0.1% FA in

HPLC water. The column was coupled to a Picotip Emitter Silicatip nano-electrospray needle

(New Objective, Woburn, MA). MS data acquisition involved survey MS scans and automatic

data dependent analysis (DDA) of the top three ions with the highest intensity ions with the

charge of 2+, 3+ or 4+ ions. The MS/MS was triggered when the MS signal intensity exceeded

10 counts/sec. In survey MS scans, the three most intense peaks were selected for collision-

induced dissociation (CID) and fragmented until the total MS/MS ion counts reached 10,000 or

for up to 6 sec each. The entire procedure used was previously described (Darie et al., 2011;

Sokolowska et al., 2012a; Sokolowska et al., 2012b). Calibration was performed for both

precursor and product ions using 1 pmol GluFib (Glu1-Fibrinopeptide B) standard peptide with

the sequence EGVNDNEEGFFSAR and the monoisotopic doubly-charged peak with m/z of

785.84.

LC-MS/MS data processing and protein identification

The raw data were processed using ProteinLynx Global Server (PLGS, version 2.4)

software as previously described (Sokolowska et al., 2012a). The following parameters were

used: background subtraction of polynomial order 5 adaptive with a threshold of 30%, two

smoothings with a window of three channels in Savitzky-Golay mode and centroid calculation of

top 80% of peaks based on a minimum peak width of 4 channels at half height. The resulting pkl

files were submitted for database search and protein identification to the public Mascot

database search (www.matrixscience.com, Matrix Science, London, UK) using the following

parameters: databases from NCBI (bacteria), parent mass error of 1.3 Da, product ion error of

0.8 Da, enzyme used: trypsin, one missed cleavage, propionamide as cysteine fixed

modification and Methionine oxidized as variable modification. To identify false negative results,

we used additional parameters such as different databases or organisms, a narrower error

window for the parent mass error (1.2 and then 0.2 Da) and for the product ion error (0.6 Da),

and up to two missed cleavage sites for trypsin. In addition, the pkl files were also searched

against in-house PLGS database version 2.4 (www.waters.com) using searching parameters

similar to the ones used for Mascot search. The Mascot and PLGS database search provided a

list of proteins for each gel band. To eliminate false positive results, for the proteins identified by

either one peptide or a mascot score lower than 25, we verified the MS/MS spectra that led to

identification of a protein.

Atomic force microscopy force-distance measurements for hydrogel stiffness

characterization

AFM force-distance beating were performed on PA hydrogel samples in 50mM HEPES

pH 7.5 buffer with a Park NX-10 AFM (Park Systems, Santa Clara, CA) using commercial silicon

nitride cantilevers CP-PNP-SiO with a sphere tip (sQube, 0.08 N/m stiffness, sphere radius ~ 1

micron) and gold coating on the reflective side. Temperature has been kept at 37 ˚C throughout

the experiment. Tip calibration curves were performed on glass substrate surface, which was

considered infinitely hard for the soft tips used. Two approach-withdraw cycles were performed

per cell. Data analysis of FD curves and calculation of Young's modulus was performed using

XEI software (Park Systems, Santa Clara, CA) and SPIP software (Image Metrology, Hørsholm,

Denmark).

Visualization and comparison of distributions

Distributions were visualized by using boxplots with the features indicated below. Bold

black line parallel to the x-axis indicates the median (second quartile) of the distribution and

boxplot's notched section shows the 95% confidence interval around the median (Wilcoxon–

Mann–Whitney nonparametric test). Regular black lines extended vertically below and above

the medians represent the first and third quartiles of the distribution. Lines extending vertically

from the boxplot (whiskers) represent the lowest datum within 1.5 IQR (interquartile range) of

the lower quartile and the highest datum within 1.5 IQR of the upper quartile. Data points

beyond the whiskers are considered outliers and displayed as circles. To assess whether the

differences between the medians of two distributions are significant we run a nonparametric

Wilcoxon rank sum test since the distributions are not normal. One or two asterisks denote

statistically significant differences between the medians of two distributions (<0.05 or <0.01,

respectively).

AUTHOR CONTRIBUTIONS:

E.E.B. and J.A.T. conceived the project and designed the experiments. E.E.B. performed

experiments and analyzed data. Y.Y. performed experiments. E.E.B. and J.A.T. wrote the

paper.

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was performed at the Stanford Shared FACS Facility and RT-qPCR was performed at the

Stanford PAN Facility.

FIGURE LEGENDS

Figure 1. Uptake of Lm by HMEC-1 depends on the stiffness of the matrix on which cells

reside.

HMEC-1 residing on PA hydrogels of varying stiffness coated with collagen I were infected with

Δ*actA* Lm (actAp::mTagRFP). Infection was analyzed by flow cytometry 7–8 h post infection.

Bacteria were added at a multiplicity of infection (MOI) between 30 to 50 bacteria per host cell.

(A-D) Histograms of the logarithm of bacterial fluorescence intensity per cell for HMEC-1 plated

on 0.6 kPa **(A)**, 3 kPa **(B)**, 20 kPa **(C)** and 70 kPa **(D)** PA hydrogels. Histograms for N=5

replicates are shown in different colors. Histogram of control uninfected cells is shown in purple.

Based on the autofluorescence of the control group a gate is defined (see black and red lines)

showing what is considered uninfected (left, black line) and infected (right, red line). **(E)**

Boxplots of percentage of HMEC-1 infected with Δ*actA* Lm versus hydrogel stiffness for the data

shown in panels A-D. Circles represent outliers, and the boxplots' notched sections show the

95% confidence interval around the median (Wilcoxon–Mann–Whitney test, for details about

boxplots see Materials and Methods). One or two asterisks denote statistically significant

differences between the medians of two distributions (<0.05 or <0.01, respectively; Wilcoxon

rank sum test).

Figure 2. FAK activity of HMEC-1 residing on soft PA hydrogels is decreased, as is Lm

uptake.

(**A)** Western blots from whole HMEC-1 lysates showing expression of phosphorylated FAK

(Tyr397) and total FAK for cells residing on soft gels (3 kPa), stiff gels (70 kPa) and TC

polystyrene substrates with or without 2 μM PF537228 FAK inhibitor. In each Western blot,

equal quantities of protein were loaded and equal loading was confirmed in relation to

glyceraldehyde 3-phosphate dehydrogenase (GAPDH) expression. In each case, the Western

blots shown are representative of 3 independent experiments. (**B-C)** Normalized ratio of

FAK/GAPDH **(B)** and pFAK (Tyr397)/GAPDH **(C)** for HMEC-1 residing on varying stiffness

substrates and treated or not with 2 µM PF537228 FAK inhibitor. Different color circles

correspond to data from 3 independent experiments. Black bars represent the mean of the 3

independent experiments. For each experiment values have been normalized relative to the

ratio for cells residing on polystyrene substrates. **(D)** Inhibition of bacterial uptake by FAK

inhibitors. FAK-14, PF573228 or vehicle control was added 1 h before addition of bacteria to

HMEC-1 residing on polystyrene substrates. Percentage of HMEC-1 infected with Δ*actA* Lm

(actAp::mTagRFP) as a function of inhibitor concentration (mean +/- SD, N = 4 replicates). x = 0

corresponds to cells treated with vehicle control. Inset shows the same data with concentration

on a log scale. Infection was analyzed by flow cytometry, 7–8 h after infection. MOI is 80.

Representative data come from 1 of 3 independent experiments. (**E)** Boxplots of percentage of

HMEC-1 infected with Δ*actA* Lm (actAp::mTagRFP) for cells treated either with non-targeting

siRNA (siNT) or FAK siRNA (siFAK) (means +/-S.D., 3 independent experiments and N=6

replicates per experiment). MOI is 60 (gray) or 20 (green). Circles represent outliers, and the

boxplots' notched sections show the 95% confidence interval around the median (Wilcoxon–

Mann–Whitney test, for details about boxplots see Materials and Methods). One or two asterisks

denote statistically significant differences between the medians of two distributions (<0.05 or

<0.01, respectively; Wilcoxon rank sum test). **(F)** Normalized ratio of pFAK (Tyr397)/GAPDH for

HMEC-1 residing on polystyrene substrates and treated for varying amount of time (min) with

100 nM Angiotensin-II. Different color circles correspond to Western blot data from 3

independent experiments. In each Western blot, equal quantities of protein were loaded and

equal loading was confirmed in relation to glyceraldehyde 3-phosphate dehydrogenase

(GAPDH) expression. Black bars represent the mean of the 3 independent experiments. For

each experiment values have been normalized relative to the ratio for untreated cells (t = 0 min).

(**E)** Boxplots of percentage of HMEC-1 infected with Δ*actA* Lm (actAp::mTagRFP) for cells pre-

treated for 2 h either with vehicle control or 100 nM Angiotensin-II (means +/-S.D., 3

independent experiments and N=4 replicates per experiment). One or two asterisks denote

statistically significant differences between the medians of two distributions (<0.05 or <0.01,

respectively; Wilcoxon rank sum test).

Figure 3. Lm adhesion but not invasion efficiency is increased when HMEC-1 reside on

stiff hydrogels.

HMEC-1 residing on soft (3 kPa) or stiff (70 kPa) PA hydrogels and treated with vehicle control

or 2 µM PF537228 FAK inhibitor were infected with Lm (constitutively expressing GFP) at an

MOI between 1.5 to 15. 30 min post-infection samples were fixed, and immunostained, and

infection was analyzed by microscopy followed by image processing. Boxplots show: (**A**) total

bacteria per cell; (**B**) internalized bacteria per cell; (**C**) invasion efficiency (ratio of internalized

bacteria to total bacteria); (**D**) cells in the field of view. Representative data come from 1 of 3

independent experiments. N=800-1000 cells were analyzed for each condition. Two asterisks

denote statistically significant differences between the medians of two distributions (<0.01;

Wilcoxon rank sum test).

Figure 4. Infection of HMEC-1 by Lm is in part mediated by InlB in a manner independent

of matrix stiffness.

(**A**) Percentage of HMEC-1 infected with Lm as a function of the logarithm of MOI (mean +/- SD,

N = 4 replicates). HMEC-1 were infected with the indicated strains: wild type (circle); Δ*inlA*

(square); Δ*inlB* (cross); Δ*inlF* (diamond) (actAp::mTagRFP). The frequency of infected HMEC-1

was determined by flow cytometry 7–8 h post infection. Representative data come from 1 of 3

independent experiments. (**B**) Percentage of HMEC-1 infected with Lm as a function of the

logarithm of MOI (mean +/- SD, N = 4 replicates). HMEC-1 were infected with the indicated

strains: Δ*actA* (black circle); Δ*actA/*Δ*inlB* (gray square) (actAp::mTagRFP). The frequency of

infected HMEC-1 was determined by flow cytometry 7–8 h post infection. Representative data

come from 1 of 3 independent experiments. **(C)** Boxplots of percentage of HMEC-1 infected with

Lm as a function of substrate stiffness (N = 5-6 replicates). HMEC-1 were infected with the

indicated Lm strains: Δ*actA* (gray); Δ*actA/*Δ*inlB* (black) (actAp::mTagRFP) at an MOI of 20.

Infection was analyzed by flow cytometry, 7–8 h after infection. Representative data come from

1 of 3 independent experiments. One or two asterisks denote statistically significant differences

between the medians of two distributions (<0.05 or <0.01, respectively; Wilcoxon rank sum test).

(D-F) HMEC-1 residing on collagen I-coated glass substrates were infected with Lm

(constitutively expressing GFP) or Δ*inlB* Lm at an MOI of 3.5. 30 min post-infection samples

were fixed, immunostained and infection was analyzed by microscopy followed by image

processing. Boxplots showing: (**D**) total bacteria per cell; (**E**) internalized bacteria per cell; (**F**)

invasion efficiency (ratio of internalized bacteria to total bacteria). For each condition, 500-550

cells were analyzed in total. **(G)** Percentage of HMEC-1 infected with Lm as a function of SGX-

523 Met inhibitor concentration (mean +/- SD, N = 4 replicates). SGX-523 or vehicle control was

added 1 h before addition of bacteria. HMEC-1 were infected with the indicated strains: Δ*actA*

(black circle); Δ*actA/*Δ*inlB* (gray square) (actAp::mTagRFP) at an MOI of 75. Infection was

analyzed by flow cytometry, 7–8 h after infection. Representative data come from 1 of 3

independent experiments. **(H)** Boxplots of percentage of HMEC-1 infected with Δ*actA* Lm

(actAp::mTagRFP) for cells treated either with non-targeting siRNA (siNT) or Met siRNA (siFAK)

(means +/-S.D., 3 independent experiments and N=6 replicates per experiment). MOI is 60

(gray) or 20 (green). Circles represent outliers, and the boxplots' notched sections show the

95% confidence interval around the median (Wilcoxon–Mann–Whitney test, for details about

boxplots see Materials and Methods). One or two asterisks denote statistically significant

differences between the medians of two distributions (<0.05 or <0.01, respectively; Wilcoxon

rank sum test). **(I)** Boxplots of percentage of HMEC-1 infected with Lm as a function of substrate

stiffness (N = 5-6 replicates). HMEC-1 were treated with vehicle control or 1 μM SGX-523 Met

inhibitor for 1 h prior to infection and then infected with Δ*actA* Lm (actAp::mTagRFP). Infection

was analyzed by flow cytometry, 7–8 h after infection. MOI is 20. Representative data come

from 1 of 3 independent experiments. **(J)** Percentage of HMEC-1 infected with Lm as a function

of PF537228 inhibitor concentration (mean +/- SD, N = 4 replicates). PF537228 or vehicle

control was added 1 h before addition of bacteria (see Suppl. Fig. 1D). HMEC-1 were infected

with the indicated strains: Δ*actA* (black circle); Δ*actA/*Δ*inlB* (gray square) (actAp::mTagRFP) at

an MOI of 75. Infection was analyzed by flow cytometry, 7–8 h after infection. Representative

data come from 1 of 3 independent experiments. Inset shows the same data with concentration

on a log scale.

Figure 5. Lower FAK activity leads to reduced amount of cell surface vimentin.

(A-B) 2D-PAGE gels of plasma membrane proteins of HMEC-1 grown on TC polystyrene

substrates treated for 1 h with vehicle control **(A)** or 2 µM PF537228 FAK inhibitor **(B).** pH

increases from left to right. Gels were silver stained and one isoelectric point marker

(tropomyosin), added to each sample as an internal standard, is marked with a black arrow. The

one spot that differed consistently between 3 independent experiments is indicated with a black

circle and corresponds to vimentin (55 kDa).

Figure 6. Surface vimentin is localized along the periphery of HMEC-1.

(A-D) Cells were stained for vimentin using the rabbit anti-vimentin H-84 antibody. For negative

controls, cells were stained with secondary anti-rabbit IgG antibody alone. Representative

phase image of cells (left column), image of the nuclei (middle column) and H-84 anti-vimentin

antibody fluorescence (right column) are shown for: **(A)** Permeabilized HMEC-1 strained for

intracellular vimentin; **(B)** Permeabilized HMEC-1 incubated with anti-rabbit IgG alone as

negative controls. **(C)** Non permeabilized HMEC-1 stained for surface vimentin; **(D)** Non

permeabilized HMEC-1 incubated with anti-rabbit IgG alone as negative controls. Scale bar

shown in white is 20 μm. White arrows point at the localization of surface vimentin at cell-cell

junctions.

1005

Figure 7. Surface vimentin of HMEC-1 is implicated in Lm uptake. (**A**) Decrease in bacterial

uptake after blocking HMEC-1 with anti-vimentin antibody H-84. Barplots of percentage of

HMEC-1 infected with Δ*actA* Lm (actAp::mTagRFP) as a function of antibody concentration

(means +/-S.D. and N=6 replicates per experiment). Representative data come from 1 of 3

independent experiments. Infection was analyzed by flow cytometry, 7–8 h after infection. (**B**)

Barplots of percentage of HMEC-1 infected with Δ*actA* Lm (actAp::mTagRFP) for cells treated

either with non-targeting siRNA (siNT) or vimentin siRNA (siVIM) (means +/-S.D., and N=6

replicates per experiment). Representative data come from 1 of 3 independent experiments.

MOI is 50 (black barplots) and 17 (gray barplots). (**C**) Decreased uptake of Lm when HMEC-1

are treated with withaferin that captures soluble vimentin 30 min prior to infection. Barplots of

percentage of HMEC-1 infected with Δ*actA* Lm (actAp::mTagRFP) as a function of withaferin

concentration (means +/-S.D. and N=6 replicates per experiment). Representative data come

from 1 of 3 independent experiments. Infection was analyzed by flow cytometry, 7–8 h after

infection. (**D**) Percentage of HMEC-1 infected with Lm as a function of the logarithm of MOI

(mean +/- SD, N = 4 replicates). HMEC-1 were infected with the indicated strains: Δ*actA* (black);

Δ*actA/*Δ*inlB* (gray) (actAp::mTagRFP) and HMEC-1 were treated with vehicle control (circle) or

withaferin (diamond) for 30 min prior to infection. The frequency of infected HMEC-1 was

determined by flow cytometry 7–8 h post infection. Representative data come from 1 of 3

independent experiments. MOI ranged from 50 to 120. One or two asterisks denote statistically

significant differences between the medians of infection fraction of control versus all other

groups (<0.05 or <0.01, respectively; Wilcoxon rank sum test).

1027

Figure 8. Blocking HMEC-1 with anti-vimentin antibody reduces Li adhesion onto HMEC-1

but not uptake of beads.

(A) Boxplots showing the number of bacteria per cell, for HMEC-1 residing on glass substrates

and treated with vehicle control, 2 µM PF537228 FAK inhibitor, or 80 µg/mL H-84 anti-vimentin

antibody prior to infection. Cells were infected with Lm or Li at an MOI of 4. 30 min post-infection

samples were fixed, immunostained and adhesion of bacteria was analyzed by microscopy

followed by image processing. For each condition, 2300-2600 cells were analyzed in total and

data refer to 1 of 2 independent experiments. Two asterisks denote statistically significant

differences between the median values of control cells versus all other groups <0.01; Wilcoxon

rank sum test). **(B)** HMEC-1 residing on TC polystyrene substrates and blocked for 1 h with

varying concentrations of H-84 anti-vimentin antibody or isotype control were "infected" with 2

µm beads at different concentrations. The frequency of micro-bead uptake by HMEC-1 was

determined by flow cytometry 2 h post addition of beads. Plot shows percentage of cells that

internalized beads as a function of the beads/cell added for different H-84 antibody

concentrations (mean +/- SD, N = 4 replicates).

1043

 SUPPORTING INFORMATION CAPTIONS

Figure S1. Lm infection of VECs residing on hydrogels of varying stiffness.

(A) Young's moduli of hydrogels. Plot showing the expected Young's modulus of the hydrogels

given the amount of acrylamide and bis-acrylamide used versus the Young's modulus

measured through AFM (N=6). Stiffness of the 0.6 kPa could not be measured, as the

hydrogels were very soft and adhered to the AFM tip. **(B)** Fraction of cells passed through the

flow cell in 20 s for HMEC-1 residing on varying stiffness substrates. HMEC-1 were seeded on

0.6 kPa, 3 kPa, 20 kPa and 70 kPa PA hydrogels as well as TC polystyrene substrates for 24 h

at a starting concentration of $4x10^5$ cells per well for 24 h. Cells were then detached from their

matrix and number of cells per well passed through the flow cell in 20 s was measured using a

flow cytometry for cells coming from N=5-6 wells for each substrate stiffness. Results from 3

independent experiments were combined and for each experiment values were normalized

relative to the mean number of cells passed through the flow cell for cells residing on TC

polystyrene substrates. No significant differences were detected. **(C)** Boxplots of normalized

fraction of HMEC-1 infected with Δ*actA* Lm for cells residing on PA hydrogels of varying

stiffness or TC polystyrene. Stiffness (kPa) of each substrate is indicated. Boxplots refer to data

from 3 independent experiments, with N = 5-6 replicates per experiment. For each experiment

values have been normalized relative to the mean infection level of cells residing on polystyrene

substrates. (**D-F)** HMEC-1 residing on collagen I-coated glass substrates were infected with Lm

(constitutively expressing GFP) or Δ*atcA* Lm at an MOI of 2.7. 30 min post-infection samples

were fixed, immunostained and infection was analyzed by microscopy followed by image

processing. Boxplots showing: (**D**) total bacteria per cell; (**E**) internalized bacteria per cell; (**F**)

invasion efficiency (ratio of internalized bacteria to total bacteria). For each condition, 500-600

cells were analyzed in total. Representative data come from 1 of 2 independent experiments.

Circles represent outliers, and the boxplots' notched sections show the 95% confidence interval

around the median (Wilcoxon–Mann–Whitney test, for details about boxplots see Materials and

Methods). One or two asterisks denote statistically significant differences between the medians

of two distributions (<0.05 or <0.01, respectively; Wilcoxon rank sum test).

1072

Figure S2. FAK-dependent decrease in bacterial uptake. (A) HMEC-1 treated with 20 nM of

non-targeting siRNA (siNT, first row**)** or FAK siRNA (siFAK, second row**)** were stained for FAK

using an anti-FAK antibody. Representative phase image of cells (left column), superimposed

with the image of the nuclei (blue) and anti-FAK antibody fluorescence (purple, right column) are

shown. Scale bar shown in white is 23 µm. **(B)** Relative with respect to GAPDH gene

expression of FAK obtained by RT-qPCR. The levels relative levels of expression in each siRNA

treated sample (#1-#3) are expressed relative to the control siNT treated sample #2 (normalized

relative quantity, NRQ). N=3 replicates are shown for each group treated with either siNT or

siVIM. (**C-D**) Histograms of the logarithm of Lm fluorescence intensity per cell for HMEC-1

treated with 20 nM of non-targeting siRNA (siNT) **(C)** or FAK siRNA (siFAK) **(D)**. HMEC-1 were

infected with *ΔactA* Lm (actAp::mTagRFP) and infection was analyzed by flow cytometry, 7–8 h

after infection. MOI is 45. Histograms for N=6 replicates are shown in different colors. Control

uninfected cells' histogram is shown in purple. Based on the autofluorescence of the control

group a gate is defined (see black and red lines) showing what is considered uninfected (left,

black line) and infected (right, red line). **(E)** Increase in bacterial uptake by Angiotensin II.

Angiotensin II or vehicle control was added 2 h before addition of bacteria to HMEC-1 residing

on polystyrene substrates. Percentage of HMEC-1 infected with *ΔactA* Lm (actAp::mTagRFP)

as a function of inhibitor concentration (mean +/- SD, N = 4 replicates). Infection was analyzed

by flow cytometry, 7–8 h after infection. MOI is 70. **(F)** Western blots from whole HMEC-1

lysates showing expression of phosphorylated FAK (Tyr397) and total FAK for cells residing on

TC polystyrene substrates and treated for varying amount of time with 100 nM Angiotensin-II. In

each Western blot, equal quantities of protein were loaded and equal loading was confirmed in

relation to glyceraldehyde 3-phosphate dehydrogenase (GAPDH) expression. The Western

blots shown are representative of 3 independent experiments. **(G)** Boxplots of percentage of

HMEC-1 infected with Δ*actA* Lm (actAp::mTagRFP) for cells residing on soft (3 kPa) or stiff (70

kPa) hydrogels and pre-treated for 2 h either with vehicle control or 100 nM Angiotensin-II (N=6

replicates). MOI is 62.5. Two asterisks denote statistically significant differences between the

medians of two distributions (<0.01; Wilcoxon rank sum test).

1101

Figure S3. Met-dependent decrease in bacterial uptake. (**A**) Western blot from whole HMEC-

1 lysates showing expression of Met for cells seeded on soft (3 kPa), stiff (70 kPa) and TC

polystyrene substrates treated or not with 2 μM PF537228 FAK inhibitor. In each case, equal

quantities of protein were loaded and equal loading was also confirmed in relation to

glyceraldehyde 3-phosphate dehydrogenase (GAPDH) expression. (**B-C**) Histograms of the

logarithm of Lm fluorescence intensity per cell for HMEC-1 treated with 20 nM of non-targeting

siRNA (siNT) **(C)** or Met siRNA (siMet) **(D)**. HMEC-1 were infected with Δ*actA* Lm

(actAp::mTagRFP) and infection was analyzed by flow cytometry, 7–8 h after infection. MOI is

45. Histograms for N=6 replicates are shown in different colors. Control uninfected cells'

histogram is shown in purple. Based on the autofluorescence of the control group a gate is

defined (see black and red lines) showing what is considered uninfected (left, black line) and

infected (right, red line). **(D)** Relative with respect to GAPDH gene expression of Met obtained

by RT-qPCR. The levels relative levels of expression in each siRNA treated sample (#1-#3) are

expressed relative to the control siNT treated sample #2 (normalized relative quantity, NRQ).

N=3 replicates are shown for each group treated with either siNT or siVIM. **(E)** Boxplots of

percentage of HMEC-1 infected with Δ*actA*/Δ*inlB* Lm (actAp::mTagRFP) for cells HMEC-1

treated with siNT or siMet (N=4 replicates). MOI is 60.

1119

Figure S4. Knocking down vimentin decreases Lm uptake. (A) HMEC-1 treated with 20 nM

of non-targeting siRNA (siNT, **first row)** or VIM siRNA (siVIM, **second row)** were stained for VIM

using the H-84 anti-vimentin antibody. Representative phase image of cells (Phase, left

column), superimposed with the image of the nuclei (blue) and anti-vimentin antibody

fluorescence (green, right column) are shown. Scale bar shown in white is 35 µm. **(B)** Relative

with respect to GAPDH gene expression of vimentin obtained by RT-qPCR. The levels relative

levels of expression in each siRNA treated sample (#1-#3) are expressed relative to the control

siNT treated sample #2 (normalized relative quantity, NRQ). N=3 replicates are shown for each

group treated with either siNT or siVIM **(C-D)** Histograms of the logarithm of Lm fluorescence

intensity per cell for HMEC-1 treated with 20 nM of non-targeting siRNA (siNT) **(C)** or vimentin

siRNA (siVIM) **(D)**. HMEC-1 were infected with *ΔactA* Lm (actAp::mTagRFP) and infection was

analyzed by flow cytometry, 7–8 h after infection. MOI is 34. Histograms for N=6 replicates are

shown in different colors. Control uninfected cells' histogram is shown in purple. Based on the

autofluorescence of the control group a gate is defined (see black and red lines) showing what

is considered uninfected (left, black line) and infected (right, red line). **(E)** Number of HMEC-1

passed through the flow cell in 20 s, for N = 4 samples coming from wells treated with either

siNT or siVIM. **(F)** Boxplots of percentage of HMEC-1 infected with *ΔactA* Lm for the data shown

in panels C-D. One or two asterisks denote statistically significant differences between the

medians of two distributions (<0.05 or <0.01, respectively; Wilcoxon rank sum test). **(F)** HMEC-1

residing on collagen I-coated glass substrates, treated with siNT or siVIM were also blocked for

1 h with anti-vimentin antibodies prior to infection. Cells were infected with Lm (constitutively

expressing GFP) at an MOI of 1.25. 30 min post-infection samples were fixed, immunostained

and infection was analyzed by microscopy followed by image processing. Boxplots shows total

bacteria per cell for an average of N=650 cells analyzed per condition **(F)** HMEC-1 residing on

collagen I-coated glass substrates, treated with siNT or siVIM were also treated for 30 min with

vehicle control or 5 µM withaferin prior to infection. Cells were infected with Lm (constitutively

expressing GFP) at an MOI of 1.25. 30 min post-infection samples were fixed, immunostained

and infection was analyzed by microscopy followed by image processing. Boxplots shows total

bacteria per cell for an average of N=630 cells analyzed per condition.

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Figure S5. Fewer Lm localize at cell-cell junctions for siVIM treated HMEC-1. (A-B) HMEC-

1 treated with 20 nM of non-targeting siRNA (siNT, A**)** or vimentin siRNA (siVIM, B**)** were

infected with Lm at an MOI of 3. 30 min post-infection samples were fixed, stained for VE-

cadherin that localizes all throughout the cell-cell junctions using an anti-VE-cadherin antibody.

Representative phase image of cells (left column), superimposed with the image of the nuclei

(blue) and anti-VE-cadherin antibody fluorescence (white, right column) superimposed with

fluorescence of Lm (red). Scale bar is 23 μm. Two representative examples are shown for each

condition. Yellow arrows point at cell-cell junctions were bacteria are co-localized.

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1159   **SUPPLEMENTARY TABLES**

1160   **Supplementary Table 1. Bacterial strains used in this study.**

1161   **Supplementary Table 2. Synthetic siRNA pools used in this study.**

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Figure 1

Figure 2

Figure 3

Figure 4

Figure 5

A

HMEC-1 on polystyrene, vehicle control

[kDa]

Increasing pH

B

HMEC-1 on polystyrene, PF573228

[kDa]

Increasing pH

Figure 6

Figure 7

Figure 8

Suppl. Figure 1

Suppl. Figure 2

Suppl. Figure 3

A

B

C

D

E

Suppl. Figure 4

Suppl. Figure 5

siNT		siVIM	
Phase and nuclei	VE-cadherin (white) Lm bacteria (red)	Phase and nuclei	VE-cadherin (white) Lm bacteria (red)

Supplementary Table 1: Bacterial strains used in this study

Name and source	Species	Genotype/Description
JAT983 (100)	*L. monocytogenes* 10403S	LLO^{G486D} actAp::mTagRFP
JAT985 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔactA* actAp::mTagRFP
JAT1045 (100)	*L. monocytogenes* 10403S	LLO^{G486D} Consitutive sGFP
JAT1046 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔactA* Consitutive sGFP
JAT1063 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔactA/ΔinlB* actAp::mTagRFP
JAT1060 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔinlB* Consitutive sGFP
JAT1051 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔinlA* actAp::mTagRFP
JAT1062 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔinlB* actAp::mTagRFP
JAT1115 (100)	*L. monocytogenes* 10403S	LLO^{G486D} *ΔinlF* actAp::mTagRFP
JAT638 (DP-L392) (85)	*L. innocua*	

Supplementary Table 2: Synthetic siRNA pools used in this study

Accession number	Gene (Protein)	Product Name	Catalog Number
	Negative control	ON-TARGETplus Non-Targeting Pool	D-001810-10
NM_000942	siGLO	ON-TARGETplus siGLO Control Reagent	D-001610-01
NM_004523.3	Kif11	ON-TARGETplus Human KIF11 (3832) siRNA	L-003317-00-0005
NM_003380.3	VIM	ON-TARGETplus Human VIM	L-003551-00-0005
NM_000245.3	MET	ON-TARGETplus Human MET	L-003156-00-0005
NM_001199649.1	PTK2 (FAK)	ON-TARGETplus Human PTK2	L-003164-00-0005