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Efficient Gene Transfer in Bacterial Cell Chains

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ABSTRACT Horizontal gene transfer contributes to evolution and the acquisition of new traits. In bacteria, horizontal gene transfer is often mediated by conjugative genetic elements that transfer directly from cell to cell. Integrative and conjugative elements (ICEs; also known as conjugative transposons) are mobile genetic elements that reside within a host genome but can excise to form a circle and transfer by conjugation to recipient cells. ICEs contribute to the spread of genes involved in pathogenesis, symbiosis, metabolism, and antibiotic resistance. Despite its importance, little is known about the mechanisms of conjugation in Gram-positive bacteria or how quickly or frequently transconjugants become donors. We visualized the transfer of the integrative and conjugative element ICEBs1 from a *Bacillus subtilis* donor to recipient cells in real time using fluorescence microscopy. We found that transfer of DNA from a donor to a recipient appeared to occur at a cell pole or along the lateral cell surface of either cell. Most importantly, we found that when acquired by 1 cell in a chain, ICEBs1 spread rapidly from cell to cell within the chain by additional sequential conjugation events. This intrachain conjugation is inherently more efficient than conjugation that is due to chance encounters between individual cells. Many bacterial species, including pathogenic, commensal, symbiotic, and nitrogen-fixing organisms, harbor ICEs and grow in chains, often as parts of microbial communities. It is likely that efficient intrachain spreading is a general feature of conjugative DNA transfer and serves to amplify the number of cells that acquire conjugative mobile genetic elements.

IMPORTANCE Conjugative elements contribute to horizontal gene transfer and the acquisition of new traits. They are largely responsible for spreading antibiotic resistance in bacterial communities. To study the cell biology of conjugation, we visualized conjugative DNA transfer between *Bacillus subtilis* cells in real time using fluorescence microscopy. In contrast to previous predictions that transfer would occur preferentially from the donor cell pole, we found that transfer of DNA from a donor to a recipient appeared to occur at a cell pole or along the lateral cell surface of either cell. Most importantly, we found that when acquired by 1 cell in a chain, the conjugative DNA spread rapidly from cell to cell within the chain through sequential conjugation events. Since many bacterial species grow naturally in chains, this intrachain transfer is likely a common mechanism for accelerating the spread of conjugative elements within microbial communities.

Review

Horizontal gene transfer is an important factor in evolution, enabling bacteria to acquire new characteristics (1–4). Conjugative plasmids and integrative and conjugative elements (ICEs) are found in many bacterial species and are key mediators of horizontal gene transfer (4–7). ICEs normally reside integrated in the host genome but can excise to form a double-stranded DNA circle. Some and perhaps most ICEs undergo autonomous plasmid-like replication after excision (8, 9). ICEs can mediate their transfer by conjugation to other cells, where they can then integrate into the recipient genome.

ICEBs1 (Fig. 1) is an ~20-kbp integrative and conjugative element found integrated in the 3’ end of a leucine-tRNA gene in several strains of *Bacillus subtilis* (10–12). ICEBs1 genes required for excision and mating are derepressed during the RecA-dependent SOS response following DNA damage or when the sensory protein RapI is expressed and active (11, 13, 14). Overproduction of RapI causes ICEBs1 to excise in >90% of cells in a population (11, 13, 15, 16), greatly facilitating the characterization of this mobile genetic element. ICEBs1 can transfer into various *Bacillus* and *Listeria* species (11) and perhaps other organisms as well.

Many microbes, including *B. subtilis*, grow in chains, often in communities of cells, e.g., biofilms (17). The presence of conjugative elements in cells can contribute to the formation of such communities, and conjugation in these communities has been observed (18–20). During conjugation, there are potential donors that harbor a mobile element and potential recipients (here simply referred to as donors and recipients, respectively). A recipient that receives a mobile element is called a transconjugant and has the potential to become a donor. Very little is known about the relative orientation of cells during conjugation or how quickly or frequently transconjugants become donors. Some conjugation proteins localize to the cell periphery, predominantly at the poles, leading to the suggestion that DNA transfer occurs predominantly from a donor pole (21–24). However, in the case of ICEBs1 from *B. subtilis*, our results indicate otherwise.
We visualized the transfer of ICEBs1 in living cells in real time using fluorescence microscopy. We found that transfer of ICEBs1 from a donor to a recipient appeared to occur at a cell pole or along the lateral cell surface of either cell, in contrast to previous predictions. Furthermore, transconjugants often became donors, and this was especially evident in cell chains. We found that when cells grow in chains, there is efficient and successive transfer to neighboring cells in a chain, likely accelerating the spread of conjugative elements in microbial communities.

RESULTS

lacO/LacI-GFP system to visualize conjugative transfer of ICEBs1. To monitor ICEBs1 DNA transfer, we engineered *B. subtilis* strains to distinguish donors from recipients and transconjugants (Fig. 2), using detection systems similar to those previously used to visualize conjugation (25, 26). Recipients did not contain ICEBs1 and had a relatively uniform green fluorescence (Fig. 2A) from expression of a green fluorescent protein (GFP) fused to the *Escherichia coli* Lac repressor (LacI-GFP). Donors had a relatively uniform red fluorescence from constitutively expressed mCherry (Fig. 2A). Donors also contained ICEBs1 with a lac operator array (lacO, to which the Lac repressor binds). When ICEBs1::lacO transfers to a recipient, LacI-GFP binds the lacO array and appears as a green focus in the transconjugant (Fig. 2B). We induced ICEBs1 gene expression, excision, and conjugation in donor cells by overproducing RapI. Donors and recipients were mixed and spotted onto agarose pads on a microscope slide. Images of cells were captured every 30 min for up to 3 h and then analyzed. Transconjugants were identified as cells with at least one green focus in the transconjugant and/or transfer of multiple copies from the donor.

We found that ICEBs1 mating occurred either at a donor cell pole or along the lateral surface. We monitored donors surrounded by recipients in various orientations. Of 109 mating events visualized, 81 appeared to occur from the side of the donor (Fig. 2A and B), and 20 appeared to occur from the donor pole (Fig. 2C and D). (In 8 cases, it was difficult to determine the orientation of the donor.) The orientations were determined from the relative positions of cells at the earliest time point, shortly after donors and recipients were mixed and placed on the microscope slide. This ~4:1 ratio corresponds to the approximate ratio of lateral to polar surface area of the rod-shaped bacilli, indicating that mating appears to occur randomly along the donor cell surface. These results contrast with previous predictions that conjugation would occur predominantly at a donor cell pole (23, 24), predictions that were based on observations that some conjugation proteins (including one ICEBs1 mating protein) appear concentrated at cell poles (21–24). Occasionally, we observed transfer from a donor that was internal in a chain of cells and flanked at the poles by other donors. That such a cell can serve as a donor is consistent with the conclusion that transfer need not occur at a donor pole.

Rapid and efficient transfer of ICEBs1 in cell chains. Like many bacteria, *B. subtilis* often grows in chains (≥4 connected cells). Each cell in a chain is distinct and surrounded by a membrane and cell wall, but the cells remain connected by the polar cell wall. We observed rapid spread of ICEBs1 to many cells in a chain when an initial transconjugant was part of the chain. Among 53 cases in which a single cell in a chain initially received ICEBs1 from a donor, 43 (81%) of the transconjugants became donors and

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**FIG 1** Map of ICEBs1 and the constructs used. (A) ICEBs1 is ~20 kb and inserted in the 3′ end of trnS-leu2. Large arrows indicate open reading frames and orientation. The shaded boxes with small arrowheads underneath at the ends of ICEBs1 represent the 60-bp direct repeats. Vertical lines with arrows between *immR* and *xis* represent the two promoters (P*immR*, P*xis*) that are controlled by the transcriptional repressor/activator ImmR. (B) Insertion of the lacO array and *kan* and concomitant removal of part of *rapI* through *yddM*. (C) Boundaries of the *conG* deletion. (D) Insertion of sspB and *kan* and deletion of *rapI-phrI*.
transmitted ICEBs1 to neighboring cells in the chain, often within 30 min (Fig. 3A to E). It appeared that ICEBs1 spread to cells preexisting in the chain before the initial transconjugant divided. In addition, the number of cells in a chain that acquired ICEBs1 was greater than 2^n (the number expected from ‘n’ cell divisions), indicating spread by a mechanism other than growth and division of the initial transconjugant. Two types of experiments, described below, verified that spreading through the chains was due to conjugation and not due to replication and segregation of the plasmid form of ICEBs1 during cell division, or some unforeseen property of LacI-GFP bound to ICEBs1::lacO.

**Efficient transfer of ICEBs1 in cell chains depends on conjugation.** We found that efficient spreading of ICEBs1 in cell chains was dependent on conjugation. Null mutations in conG (yddG) of ICEBs1 prevent mating (C. T. Leonetti, M. A. Hamada, S. J. Lauer, A. D. Grossman, and M. B. Berkmen, unpublished results). We used a donor carrying ICEBs1::lacO ΔconG and a functional copy of conG+ elsewhere in the chromosome (see Materials and Methods), permitting the initial transfer of ICEBs1. However, transconjugants that receive ICEBs1::lacO ΔconG cannot retransfer the element because they lack conG. In 26 initial transconjugants that were each part of a chain, there was no detectable spreading of the ICEBs1::lacO ΔconG mutant to other cells in the chain, other than by cell division and segregation to daughters of the initial transconjugant (Fig. 3F to J). These results indicate that the rapid spreading of wild-type ICEBs1 through cells in chains is due to conjugation.

**Visualization of horizontal gene transfer using conditional protein degradation.** To further confirm that the spreading of ICEBs1 in chains was due to conjugation, we observed conjugation using a tracking system based on conditional protein degradation. Recipients expressed a fusion of GFP to a modified SsrA degradation tag (GFP-SsrA*). This fusion protein is rapidly degraded if cells produce SspB (29), a protein that delivers SsrA-tagged proteins to the cellular proteolytic machinery. Recipients did not produce SspB and were green (Fig. 3K). sspB was inserted into ICEBs1 (ICEBs1::sspB, without lacO) in a donor strain expressing mCherry (Fig. 3K to N). Transconjugants turn from green to dark due to the instability of GFP-SsrA* in the presence of SspB (29) expressed from newly transferred ICEBs1::sspB (Fig. 3K to N). When the initial transconjugant was in a chain of cells, the other cells in the chain (that were not contacting a red donor) also became dark (Fig. 3L to N), indicating the transfer of ICEBs1::sspB through the chain. These results also indicate that spreading was not due to growth and division, as once a transconjugant turns dark, all the progeny from division should initially be dark and should not start as green cells that subsequently turn dark. Based on these findings, we conclude that the initial transconjugants become donors and ICEBs1 rapidly spreads through cells in chains via efficient conjugation.

**DISCUSSION**

We used two different methods to visualize conjugative DNA transfer between donor and recipient cells. In one case, we visual-
ized the DNA that was transferred from cell to cell. In the second, we used conditional protein degradation to identify cells that acquired the horizontally transferred element. We found that successful conjugation of the integrative and conjugative element of \textit{B. subtilis}, ICE\textsubscript{Bs1}, occurred with no obvious orientation of the donor and recipient. That is, transfer of DNA from a donor into a recipient appeared to occur at a cell pole or along the lateral cell surface. Furthermore, when acquired by a cell in a chain of cells, ICE\textsubscript{Bs1} spread rapidly to other cells in the chain through sequential transfer events as transconjugants quickly became donors.

Integration and stable maintenance of ICE\textsubscript{Bs1} in the host chromosome requires repression of ICE\textsubscript{Bs1} gene expression from the 

\begin{figure}[h]
\centering
\includegraphics[width=\textwidth]{image}
\caption{Examples of ICE\textsubscript{Bs1} transferred to cells in chains. A time course is shown for three different matings. In all cases, the first panel of each set (A, F, K) is the first time point (time 0), followed by images of the same field of cells taken at 30-min intervals. Donors are red, and recipients are green. Arrows point to some of the foci of LacI-GFP in transconjugants. (A to E) Spread of ICE\textsubscript{Bs1} through a chain of cells. Donors contained ICE\textsubscript{Bs1} with a lacO array (red cells, strain AB86). Recipients expressed LacI-GFP (green cells, strain MMB849). Transconjugants have at least one focus of LacI-GFP. (F to J) Spreading requires conjugation functions. Donors contained ICE\textsubscript{Bs1} with a lacO array, a null mutation in conG (an ICE\textsubscript{Bs1} gene required for conjugation), and a copy of conG\textsuperscript{+} elsewhere in the chromosome (red cells, strain AB101). Recipients and transconjugants were as described above. (K to N) Spreading of ICE\textsubscript{Bs1} through a chain of cells visualized by conditional protein degradation. Images are merges of phase, green (GFP), and red (mCherry). Red donors (strain CAL1391) contained constitutively expressed sspB in ICE\textsubscript{Bs1}. Green recipients (strain CAL1379) expressed a GFP-ssrA\textsuperscript{*} fusion. Transconjugants turned from green to dark due to instability of GFP-SsrA\textsuperscript{*} in the presence of SspB (29) expressed from the newly transferred ICE\textsubscript{Bs1}.}
\end{figure}
Derepression of Pxis (Fig. 1). Derepression of Pxis leads to expression of genes needed for ICEBs1 excision and conjugation (11, 15). The excised circular form of ICEBs1 is required for its dissemination to recipients. Our results indicate that soon after receiving ICEBs1, a very high percentage of transconjugants become donors by expressing conjugation genes. The ability of a transconjugant to become a donor is likely influenced by the kinetics of repression of Pxis, which in turn is influenced by the kinetics of accumulation of the ICEBs1 repressor ImmR. ImmR both activates and represses its own expression, creating a homeostatic autoregulatory loop (15). Initially, there is no ImmR in a newly formed transconjugant, permitting transcription from Pxis and expression of ICEBs1 conjugation genes. However, in the absence of an inducing signal, expression and accumulation of ImmR in the transconjugant will eventually repress Pxis, allowing integration of ICEBs1 into the chromosome. This type of regulatory circuit is common in mobile genetic elements, notably in integration of ICEBs1 in the newly formed transconjugant, permitting transcription from Pxis and expression of ICEBs1 conjugation genes. However, in the absence of an inducing signal, expression and accumulation of ImmR in the transconjugant will eventually repress Pxis, allowing integration of ICEBs1 into the chromosome. This type of regulatory circuit is common in mobile genetic elements, notably in bacteriophage (30, 31), and is important in fate determination for such elements. In ICEBs1, this circuit likely allows switching between an active dissemination mode (excision and gene expression) and a quiescent inactive mode (integration and repression). Our studies indicate that a delay in ICEBs1 integration and transcriptional repression in transconjugants contributes to the spread of ICEBs1 in cell populations.

Much is known about conjugation and conjugative elements of both Gram-negative and -positive bacteria (4, 32, 33). In most cases, transfer efficiencies of a few percent are considered high. Our results indicate that conjugation efficiencies in cell chains can be >50%. A different mechanism for efficient dispersal of a mobile element has been described for Streptomyces ICEs that can exist as stable plasmids. Plasmid spreading through Streptomyces mycelia depends on spreading proteins (Spd) and is independent of conjugation proteins (summarized in references 32 and 34). In contrast, transfer of ICEBs1 to cells in a chain requires the conjugation machinery and is not due to replication and segregation of the plasmid form of ICEBs1.

Many bacterial species, including pathogenic, commensal, symbiotic, and nitrogen-fixing organisms, grow in chains and harbor conjugative elements. In addition, microbial biofilms are often composed of long chains or aggregates of connected cells (17). It seems likely that efficient intrachain spreading is a general feature of conjugative DNA transfer and probably serves to rapidly amplify the number of cells that acquire conjugative mobile genetic elements. When cells are present in a chain, they are in intimate contact with other cells in a pole-to-pole configuration. The high efficiency of intrachain conjugation is likely due to close and stable cell-cell contact. The high concentration of conjugation proteins at donor cell poles (21–24) might also contribute to the efficient pole-to-pole transfer in cell chains.

**MATERIALS AND METHODS**

**Bacterial strains and alleles.** The _B. subtilis_ strains used are listed (Table 1). All are derivatives of JH642 and contain thrC and pheA mutations (not indicated). Strains were constructed by standard procedures using natural transformation (35). Strains cured of (missing) ICEBs1 (11) are indicated as ICEBs1. RapI was overproduced from the xylose-inducible promoter _PsyI_ from _amyE_::(_PsyI-rap1)_spc as described previously (23).

(i) **ICEBs1::lacO/lacI-gfp.** A deletion-insertion in ICEBs1 was made by inserting an array of ~120 Lac operators (lacO) (36) along with _kan_ (kanamycin resistance), by double crossover, into the region of ICEBs1 from bp 879 (of 1176) at the 5' end of _rapI_ and leaving 156 bp (of 942 bp) at the 3' end of _yddM_ (Fig. 1). This allele, ICEBs1 [Δ(rapI-yddM)::lacO kan], is simply referred to as ICEBs1: lacO. The ICEBs1: lacO allele used here was present in donor strains in the absence of lacI-GFP. The presence of LacI-GFP (or LacI) interfered with kanamycin resistance, probably by silencing expression of the adjacent _kan_ gene.

The _lacO_ array contained on a plasmid was previously integrated into ICEBs1 by single crossover (23). We found that the single-crossover array was not transferred to recipients during conjugation, necessitating the integration of a _lacO_ array by double crossover.

LacI-GFP was produced from thrC::(_PsyI-rap1)_spc::(_PsyI-mCherry kan cat)_::pMMB1010 (Ppen-mCherry) as described previously (37). This construct fuses lacI-GFP to a constitutive promoter and is integrated at thrC (making the cells threonine auxotrophs). Strains containing this fusion without a _lacO_ array have relatively uniform green fluorescence. The presence of a _lacO_ array in a cell with LacI-GFP results in a green focus. Strains containing lacI-GFP were used as recipients in conjugation experiments with ICEBs1: lacO donors.

(ii) **Construction and complementation of _ΔconG_.** _ΔconG_ ( _yddG_ ) is an in-frame markerless deletion of codons 5 to 805 (of 815). It was constructed in a manner analogous to that constructed for _conEA_ (88-808) (23). _conG_ function was provided in trans by thrC::(_ICEBs1-311 [ΔattR100::tet _mls]_::PamyE ::(Ppen-mCherry)_::pMMB1010 (Ppen-mCherry) cat) as recipients in conjugation experiments with ICEBs1: lacO donors.

(iii) **Ppen-mCherry at _cgED_.** We used two different constructs that expressed a version of _mCherry_ (38) that was codon optimized for _E. coli_ (provided by S. Sandler) from the constitutive promoter _Ppen_. _Ppen_ was obtained from upstream of _lacI_ from a plasmid derived from pSF1-1 (35). Plasmid pMMB1010 contains Ppen-mCherry with a linked _kan_ flanked by sequences from _cgED_ in the pGEMCatt (35) backbone. This was integrated by single crossover into _cgED_, selecting for chloramphenicol resistance. This construct was used in donor strains AB86, AB101, and AB110 (Table 1).

We also used a Ppen-mCherry fusion at _cgED_ that is integrated by double crossover. This allele, Δ _cgED1388_::(_Ppen-mCherry)_ cat is an insertion-deletion containing Ppen-mCherry followed by _cat_ (chloramphenicol resistance) inserted between base pairs 160 and 490 of the 1,278-bp _gcED_ open reading frame. The inserted genes are cooriented with _cgED_ in the _B. subtilis_ chromosome. Ppen-mCherry was obtained from _B. subtilis_ strain MMB1023 containing _cgED_::(_Ppen-mCherry)_ kon as a double crossover from pMMB1010, as described above. _cat_ was obtained from pGEMCatt (35). The Δ _cgED1388_::(_Ppen-mCherry)_ cat was contained on plasmid pCAL1387 and was introduced into the _B. subtilis_ chromosome by transformation and double-crossover homologous recombination. This construct was used in donor strain CAL1391 (Table 1).

### TABLE 1. _B. subtilis_ strains used

| Strain (use) | Relevant genotype |
|--------------|-------------------|
| AB86 (donor) | ICEBs1 [Δ(rapI-yddM)::lacO kan] amyE::(_PsyI-rap1)_spc gde::pMMB1010 (Ppen-mCherry kon cat) |
| AB101 (donor) | ICEBs1 [Δ(rapI-yddM)::lacO kon conG A (5-805) (unmarked)] thrC325::[ICEBs1-311 [ΔattR100::tet _mls]_::PamyE::(_PsyI-rap1)_spc | gde::pMMB1010 (Ppen-mCherry kon cat) |
| AB110 (donor) | ICEBs1 [Δ(rapI-yddM)::lacO kon conG A (5-805) (unmarked)] amyE::(_PsyI-rap1)_spc gde::pMMB1010 (Ppen-mCherry kon cat) |
| CAL1379 (recipient) | ICEBs1 thrC::(_PsyI-gfp-sraA* _mls) |
| CAL1391 (recipient) | ICEBs1 Δ(rapI-phr1) 1366::[Ppen-sspB kon] amyE::(_PsyI-rap1)_spc gde::D1388::(_Ppen-mCherry)_ cat |
| MMB849 (recipient) | ICEBs1 thrC::(_Ppen-lacD111-gfpmut2 _mls) |

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(iv) ICEBs1: [(P[ppn-sspB] kan) and gfp-ssrA]. The allele Δ(rapI-pphr1)1366::[(P[ppn-sspB] kan) [simply ICEBs1: (P[ppn-sspB])] is an insertion-deletion, removing the region of ICEBs1 from 100 bp upstream of the rapI open reading frame through the stop codon of pphr1 (Fig. 1). E. coli sspB fused to the constitutive promoter Pppn is inserted in this region, followed by kan. The inserted genes are cooriented with downstream yidM (Fig. 1). sspB with a ribosome-binding site was obtained from pKG1266 (29). kan was obtained from pGK67 (39). Δ(rapI-pphr1)1366::[(P[ppn-sspB] kan) was constructed as a linear PCR product and introduced into ICEBs1 in the B. subtilis chromosome by transformation and homologous recombination.

gfp-ssrA expressed from a constitutive promoter and integrated at thrC was described previously (29). Some strains containing insertions in thrC also require methionine to grow, likely due to the effects of the insertion at thrC on the adjacent hom gene, needed for methionine biosynthesis.

Media and growth conditions. E. coli and B. subtilis cells were grown in LB medium for routine cloning and strain constructions. Strains for experiments were grown in defined 57 minimal salts medium (containing 50 mM MOPS [morpholinepropanesulfonic acid] supplemented with 1-arabinose (1%), phenylalanine (40 µg/ml), tryptophan (40 µg/ml), threonine (200 µg/ml), and methionine (40 µg/ml), as needed. Xylose (1%) was added to induce expression from PxyI-rapI.

Live-cell imaging and mating conditions. Donors and recipients were colony purified from frozen (~80°C) stocks on LB plates with the appropriate antibiotic. Cells from a single colony were inoculated into liquid LB medium and grown to an optical density at 600 nm (OD600) of ~0.2 to 0.8. Cells were then diluted into defined minimal medium with arabinose as the carbon source to an OD600 of ~0.02. After at least 3 to 4 generations, cells were diluted into defined minimal medium with arabinose as the carbon source and an OD600 of ~0.2. After at least 3 to 4 generations (OD600 of ~0.2), expression of rapI from PxyI-rapI, was induced by addition of xylose to the donors. Cells were grown for another hour to allow for ICEBs1 gene expression and excision. Donors and recipients were mixed at a ratio of ~1 donor per 10 recipients at a concentration of ~10^6 cells per ml. Two microliters of cells were placed on a slide of agarose (1.5% UltraPure agarose; Invitrogen) dissolved in defined minimal growth medium. The approximate dimensions of the agarose slice were 0.25 mm in height by 15 mm in length by 5 mm in width.

The agarose slice was placed on a standard glass coverslip (VWR), with the cells between the agarose and the coverslip. The agarose slice (with coverslip) was placed in a homemade incubation chamber made by stacking three sealable Gene Frames (ABgene) and mounting them on a standard microscope slide (VWR). Two small pieces of filter paper soaked in water were placed in the edges of the chamber to prevent evaporation and drying of the agarose slice. We found that under these conditions, cells grew and mated successfully. The chamber was mounted on the motorized stage of a Nikon Ti-E inverted microscope placed in the temperature-controlled box (Nikon) at 37°C. Fluorescence was generated using a Nikon Intensilight mercury illuminator through appropriate sets of excitation and emission filters (filter set 49008 for mCherry and filter set 49002 for GFP; Chroma). Acquisition of images was performed using a Cool- Snap HQ camera (Photometrics) and processed using NIS-Elements Advanced Research 3.10 software. Typically, 50 to 100 fields of cells of appropriate density were chosen for automated imaging, and images were captured every 30 min for up to 3 h.

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