## Innovation spread: lessons from HIV

KRISTINA TALBERT-SLAGLE<sup>1</sup>, DAVID BERG<sup>2</sup> AND ELIZABETH H. BRADLEY<sup>1</sup>

<sup>1</sup>Yale School of Public Health, New Haven, CT, USA, and <sup>2</sup>Yale School of Medicine, New Haven, CT, USA

Address reprint requests to: Kristina Talbert-Slagle, Yale University Global Health Leadership Institute, 2 Whitney Avenue, Suite 401, New Haven, CT 06520, USA. Tel: +203-432-6058; E-mail: kristina.talbert-slagle@yale.edu

Accepted for publication 15 April 2013

#### Abstract

Efficient spreading of evidence-based innovations among complex health systems remains an elusive goal despite extensive study in the social sciences. Biology provides a model of successful spread in viruses, which have evolved to spread with maximum efficiency using minimal resources. Here we explore the molecular mechanisms of human immunodeficiency virus (HIV) spread and identify five steps that are also common to a recent example of spread in complex health systems: reduction in door-to-balloon times for patients with ST-segment elevation myocardial infarction (STEMI). We then describe a new model we have developed, called AIDED, which is based on mixed-methods research but informed by the conceptual framework of HIV spread among cells. The AIDED model contains five components: Assess, Innovate, Develop, Engage and Devolve, and can describe any one of the following: the spread of HIV among cells, the spread of practices to reduce door-to-balloon time for patients with STEMI and the spread of certain family health innovations in low- and middle-income countries. We suggest that by looking to the biological sciences for a model of spread that has been honed by evolution, we may have identified fundamental steps that are necessary and sufficient for efficient, low-cost spread of health innovations among complex health systems.

Keywords: innovation diffusion, HIV, evidence-based medicine, virus spread

Breakthroughs in medicine and public health often require decades and significant input of resources to spread. Considerable social science literature has explored how and why innovations diffuse [1, 2], yet the spread of good ideas from bench to bedside for maximum benefit at low cost remains a central challenge. We propose addressing this challenge by looking outside of the traditional innovation diffusion disciplines to a biological model of successful spread: viruses.

Viruses have evolved to spread with maximum efficiency using minimal resources. All viruses are parsimonious, containing far fewer genes and proteins than the cells they target, and yet they spread efficiently. We suggest, therefore, that the mechanism of spread used by viruses may provide a model for the low-cost spread of a novel agent—in this case a health innovation—among complex systems. To explore this concept, we looked to a notorious virus example: HIV.

## Five steps of spread from HIV

The human immunodeficiency virus-1 (HIV) spreads efficiently among cells containing  $\sim 20\,000$  genes [3] using only 9 of its own viral genes [4]. The virus uses five essential steps to infect and spread among comparatively far more complex human cells. HIV: (i) binds to pre-existing receptors, (ii) overcomes resistance, (iii) makes its message readable and actionable while introducing slight changes for adaptability, (iv) integrates into

International Journal for Quality in Health Care vol. 25 no. 4

© The Author 2013. Published by Oxford University Press.

the cellular DNA and (v) spreads via existing networks with the help of changes in the environment (Table 1). Here we first describe in detail the process of HIV infection to illuminate these five steps of spread, and then we apply them to the spread of a specific health innovation: hospital practices to reduce treatment delays for patients with ST-segment elevation myocardial infarction (STEMI). We then explore whether, through this comparison, we have identified essential components of effective spread that can be applied more generally to facilitate the spread of innovations in complex health systems. To address this possibility, we describe a model that we have developed using HIV spread as a conceptual framework combined with evidence from the scale up of family health innovations in low- and middle-income countries. We propose that this model for scale up may provide a powerful and practical new tool to facilitate spreading of innovations among complex human systems, since it follows a biological example that has evolved to spread efficiently: HIV.

## HIV as a model for spread

To establish itself in a human cell, HIV first binds to two specific, pre-existing, boundary-spanning cellular receptors (Step 1) [5–7] and then delivers viral materials, including nine viral genes, into the cell [8]. To resist HIV infection, the cell deploys antiviral proteins to attack the virus. HIV overcomes

This is an Open Access article distributed under the terms of the Creative Commons Attribution Non-Commercial License (http://creativecommons.org/ licenses/by-nc/3.0/), which permits non-commercial re-use, distribution, and reproduction in any medium, provided the original work is properly cited. For commercial re-use, please contact journals.permissions@oup.com 352

Table I The five steps of spread

- 1 Bind to pre-existing receptors
- 2 Overcome resistance
- 3 Make the message readable and actionable while introducing slight changes for adaptability
- 4 Integrate into the DNA
- 5 Spread via existing networks with the help of changes in the environment

this resistance (Step 2) by tricking the cell into discarding its own resistance mechanisms [9]. HIV then translates its message from RNA into DNA, so that it can be read and used by the cell [10]. During this translation process, called reverse transcription, many small changes, or mutations, are introduced, which ultimately allow the virus to adapt to additional sources of resistance (Step 3), such as an immune response or antiretroviral drugs [11, 12]. The viral DNA then integrates into the cellular DNA (Step 4), making infection irreversible. After integration, HIV primarily utilizes extant, routine cellular processes to replicate its genetic material and make more viral material [13]. HIV then exits the cell and spreads, first to nearby susceptible cells [14, 15] and then, after immune activation changes the environment and makes many more cells susceptible, throughout the body using existing transit networks, such as the lymph and circulatory systems (Step 5) [15-17]. By extensively employing existing systems in and among cells while using very few of its own genes and proteins, HIV establishes itself and spreads efficiently using very few of its own tools or materials.

### Parallels in biological and health systems: a case study in effective spread

To explore the potential parallels between spread of HIV among cells and spread of innovation among complex human health systems, we have chosen a recent example of successful spread: hospital practices to promote prompt 'door-to-balloon time' by reducing delays from hospital presentation to percutaneous coronary intervention (PCI) for patients with STEMI [18, 19]. In 2005, less than half of US patients with STEMI had door-to-balloon times within the national guideline of 90 min [18, 20], even though prompt treatment is critical for survival of patients with STEMI [21]. By 2010, however, >90% of patients with STEMI had door-to-balloon times within 90 min [18]. How did this happen, and did the spread of 90-min door-to-balloon time parallel the spread of HIV?

To address these questions, we suggest the following analogy: the 'virus' in this example is the published scientific information on effective hospital practices to reduce door-toballoon time and tools for implementing changes, which were packaged in the D2B Alliance, a quality campaign initiated in 2006 to reduce delays between hospital arrival and PCI for STEMI [22]. The 'cells' are the hospitals that took up practices to reduce door-to-balloon time. We suggest that the innovations to reduce door-to-balloon time spread among hospitals throughout the USA through the five steps shown (Table 1) that are parallel to the spread of HIV infection.

Initially, the D2B Alliance bound to pre-existing 'receptors' in the hospital (Step 1), who were most commonly opinion leaders, such as influential cardiologists, nurses, or quality improvement directors charged with improving performance on publicly reported measures, including door-to-balloon time. Often, the 'receptors,' or what organizational theorists call 'boundary spanners' [23], had leadership roles in the hospital. Because recommended strategies to reduce door-to-balloon time involved new hospital practices and new roles for emergency department staff, resistance emerged from groups who preferred the status quo [24]. Multiple methods were used to address and overcome resistance (Step 2), including requiring the signature of the hospital chief executive officer on the D2B Alliance enrollment letter, which committed the hospital to meeting the goals of the D2B Alliance. To translate published scientific data into information that hospital staff could readily comprehend and use, the D2B Alliance provided a toolkit and change package with step-by-step instructions for new work processes, making the message of the innovation readable and actionable. During this process, slight changes were introduced (Step 3) as hospitals adapted the recommendations to their specific organizational contexts. Integration of new strategies into the routine practices, or 'DNA,' of the hospital (Step 4) occurred through adoption of new standard operating practices, routine use of door-to-balloon time data feedback processes and emerging organizational norms regarding 90-min door-to-balloon times. Changes in organizational culture [22] also indicated successful integration, as cardiologists, emergency medicine and Emergency Medical Services collaborated in new ways and shifted practice expectations about door-to-balloon times. Finally, the D2B Alliance utilized existing communication networks to spread information to receptive hospitals. This process was greatly aided by changes in the regulatory and financial environment, including public reporting of door-to-balloon times and pay-for-performance schemes, which increased the susceptibility of hospitals around the country to the new information of the D2B Alliance and facilitated its spread (Step 5).

# Spread of innovation to improve health systems: what can we learn from HIV?

Efforts that reduce door-to-balloon time for patients with STEMI can be understood to spread among hospitals throughout the USA using the same five essential steps that HIV employs to spread among cells throughout the body (Table 1). The parallels are remarkable, highlighting the potential of this biological example to be more broadly applicable to the spread of innovations in health systems [25].

One potentially significant advantage to using HIV as a model for spread in social systems is that this virus has evolved over millennia to spread from cell-to-cell with incredible parsimony and efficiency. If we can envision HIV as analogous to an innovation that has been honed by evolution to fit its target, and the cell as a complex system that has evolved to maintain the *status quo* and resist change, then we may be able to look to HIV infection in order to identify key features and processes of an innovation and a target user group that are indispensible for successful spread.

With this conceptual framework in mind, we developed an evidence-based model with five, practical components to guide implementation and scale up of innovation in health systems [26]. Our model, which arose from a mixed-methods analysis combining systematic literature review and interviews with >33 key informants, describes features of scale up common to four different family health innovations in low- and middle-income countries: Depo-provera, exclusive breastfeeding, community health workers and social marketing. The model includes five nonlinear, interrelated components: Assess, Innovate, Develop, Engage and Devolve (AIDED) [26, 27]. Although the AIDED model was constructed using data from our mixed-methods analysis, its conceptual foundation is the biology of virus spread. In this model, the 'virus' is the innovation, and the 'cells' are the user groups for which the innovation is intended. Each component of the model therefore can be applied to describe not only the spread of an innovation among health systems, but also the spread of HIV among cells, providing a practical, evidence-based tool for innovation diffusion that is grounded in a biological model of efficient spread.

The first three components of the AIDED model, Assess, Innovate and Develop, emphasize the importance of developing an extensive understanding of the user group. By thoroughly assessing a user group to understand its environment, its receptivity and its potential resistance to the innovation, designers and funders of innovations can adapt the innovation for optimal fit, and develop support for the innovation in order to overcome resistance. For HIV, all of these processes have been accomplished by evolution, yielding a virus that can survive in the specific physiological environments where it encounters its target cells, bind to these target cells tightly via pre-existing, boundary-spanning receptors and overcome resistance (Table 1). The key learning of these first three components of the AIDED model is that a successful innovation will have evolved-or have been directed to evolve by the developers and funders-through a deliberate process of extensive assessment, trial-and-error and adaptation, so that it fits tightly and specifically to its target user group and successfully overcomes inevitable resistance.

The final two components of the AIDED model, Engage and Devolve, track very closely to the steps of spread described in Table 1. For the Engage component, the innovation must accomplish three distinct steps: first cross the boundary of the user group via boundary-spanning receptors, next translate the message of the innovation to make it accessible, with a high rate of adaptability, and finally integrate into the routines and norms, or 'DNA' of the user group. For Devolve, the innovation spreads along existing networks, often evolving as it goes. Our research on scale up of innovations in low- and middle-income countries indicated that by the time an innovation spreads, adaptations made by user groups change it, sometimes significantly and sometimes such that it fails [26]. The same proved to be true with practices to reduce door-to-balloon time, which were sometimes altered by hospital personnel to fit their needs and environment [24]. HIV, too, changes and adapts through mutation as it spreads, responding to pressures imposed by the immune system and antiretroviral drugs, ultimately generating many distinct variants in an infected individual, some of which are likely to be so altered that they fail to infect additional cells [11]. If the five steps in Table 1 are common to spread at both microscopic and macroscopic scales, then persistent blocking or omitting any one of these steps should lead to failure of innovation spread in the social world.

In our research on scale up of family health innovations in low- and middle-income countries, [26] we found a few examples of failure resulting from incompletely accomplishing or omitting one of the five components of the model [27], although failures may be under-represented due to publication bias. We are unaware of systematic empirical tests of failures to spread innovations due to omitting or blocking one of the steps listed in Table 1. For this question, however, we can turn to the biological model for insight. With HIV, each of the steps described in Table 1 is required for successful spread: the virus cannot infect cells that lack at least one of the specific, pre-existing receptors it targets [7], nor can it spread among cells with certain types of internal resistance that the virus is not equipped to counter [28]. Many antiretroviral drugs block the spread of HIV by interrupting either the boundary-crossing process, translation of the message, integration or spread after release from an infected cell [29]. This observation at the biological level, bolstered by our research on family health innovations in health systems, suggests that, in theory, the five steps of spread in Table 1 are critical, although we have yet to demonstrate this conclusion empirically.

The existing literature on diffusion of innovation is vast, replete with models, theories and frameworks that describe many factors and contingencies for promoting spread. Many of these models incorporate some of the specific features described in Table 1. For example, Rogers [2] describes certain features of innovations that could also be used to describe HIV, such as reinvention (or adaptability), being simple to use (such as having only nine genes) and the concept of 'innovation-system fit,' (could also be virus-cell fit). These features also proved important for the spread of practices to reduce door-to-balloon time in US hospitals and for the scale up of family health innovations in low- and middle-income countries that we studied [24, 26]. Greenhalgh et al. [30] have identified additional features of an innovation that also strikingly parallel those of HIV, including the idea of a 'hard core,' which contains the key knowledge of the innovation, and a 'soft periphery,' which is important for the fit of the innovation to the target. The hard, or firm, core of HIV is the viral genes, which contain the biological information that allows the virus to infect and spread, while the soft periphery is the exterior shell of the virus, which allows it to bind and fuse with the cells it targets. For the door-to-balloon innovation, the firm core was the published scientific information on effective hospital practices to reduce door-to-balloon time and tools for implementing changes, packaged in the soft periphery of the D2B Alliance, a quality campaign [22].

Given that the model for spread described here is founded on an example of spread in a biological system, direct comparison with existing models for innovation diffusion is difficult. We note, however, that some features of the AIDED model are common in other published models, including the 'Conceptual Model for Considering the Determinants of Diffusion, Dissemination and Implementation of Innovations in Health Service Delivery and Organization' developed by Greenhalgh et al. [30] as well as intervention mapping, first described by Bartholomew et al. [31]. Like the AIDED model, these other models emphasize the importance of a thorough assessment to evaluate many features of the potential user, including needs as well as behavioral and environmental factors. All of these models indicate that the implementation and/or spread of a new idea is a complex, nonlinear, iterative process. In addition, the model developed by Greenhalgh et al. describes the importance of several of the features identified as important in the AIDED model (among many others), including system readiness, which involves 'receptive context for change,' boundary spanners, with 'ties both inside and outside the organization,' and spread along existing networks [30]. Despite these intriguing similarities, the AIDED model differs from existing models of innovation diffusion because it is based on virus spread-a process honed by evolution for maximum efficiency using minimal resources-and because it contains only five practical components that may be necessary and sufficient for spread in complex systems.

To illustrate the applicability of the AIDED model to the process of spread in complex health systems, we return to the door-to-balloon example. As described above, the large-scale diffusion of best practices to improve door-to-balloon time spread among hospitals via similar steps as does HIV when spreading among cells, likely involving some quality improvement work within each hospital. We believe that the AIDED model could be employed by quality improvement teams for similar initiatives, as follows. The quality improvement team would assess their environment in terms of its capabilities and challenges, design the intervention (for instance, a set of improved procedures) so that it would fit a receptive user group (for instance, a nursing unit), be adaptable to the particular needs and preferences of each receptive user group (for instance, allowing certain procedures to be altered slightly) and overcome resistance, develop support among the staff on the unit to facilitate take up and further overcome resistance, engage one or more boundary spanners (perhaps a nurse manager), translate the materials into language the unit staff understand easily (for instance, making instructions in pictorial form), embed the new procedures into routines (potentially revising job descriptions and data feedback processes to integrate the new procedures) and then use common networks (for instance, cross-unit, departmental staff meetings or hospital-wide quality meetings) to devolve the improved procedures to staff that are within the professional network of those in the initial unit. The quality improvement team would also need to invest in ongoing assessment and adaptation throughout the devolution of the innovation.

To address the persistent challenge of spreading evidencebased innovations among complex health systems, we have looked outside of the social science disciplines to biology, in which we found an example of efficient spread: HIV. Like all viruses, HIV spreads efficiently through comparatively far more complex systems using very few of its own resources, providing a potentially powerful, evolutionarily-honed example of efficient spread. If HIV can indeed serve as a model for spread, then close observation of its processes could yield potent lessons for health professionals. We suggest that further exploration of the parallel between virus spread and innovation diffusion may provide key insight into processes necessary and sufficient for the efficient spread of parsimonious innovations in complex human systems.

#### **Authors' contribution**

All authors contributed equally to the intellectual content, conceptual development and design of this manuscript. K.T.S. wrote the section describing the molecular steps of HIV infection; E.H.B. wrote the section describing the spread of best practices through the D2B Alliance. All authors co-wrote the remaining sections and edited the entire document.

#### Funding

This work was supported by a T32 training grant from the Agency for Healthcare Research and Quality [5T32HS017589] and the Gates Foundation [contract 5216]. Funding to pay the Open Access publication charges for this article was provided by the Global Health Leadership Institute (GHLI) at Yale University.

#### References

- Greenhalgh T, Robert G, Bate P et al. Diffusion of Innovations in Health Service Organisations: A Systemic Literature Review (Studies in Urban and Social Change). Malden, MA: Blackwell Publishing Ltd, 2005.
- 2. Rogers EM. *Diffusion of Innovations*, 5th edn. New York, NY: Simon and Schuster, Inc, 2003.
- International Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature* 2004;431:931–45.
- Frankel AD, Young JA. HIV-1: fifteen proteins and an RNA. *Annu Rev Biochem* 1998;67:1–25.
- Alkhatib G, Combadiere C, Broder CC *et al.* CC CKR5: a RANTES, MIP-1alpha, MIP-1beta receptor as a fusion cofactor for macrophage-tropic HIV-1. *Science* 1996;**272**:1955–8.
- Bowers K, Pitcher C, Marsh M. CD4: a co-receptor in the immune response and HIV infection. Int J Biochem Cell Biol 1997;29:871–5.
- Lusso P. HIV and the chemokine system: 10 years later. EMBO J 2006;25:447–56.

- Nisole S, Saib A. Early steps of retrovirus replicative cycle. *Retrovirology* 2004;1:9.
- Wissing S, Galloway NL, Greene WC. HIV-1 Vif versus the APOBEC3 cytidine deaminases: an intracellular duel between pathogen and host restriction factors. *Mol Aspects Med* 2010;**31**:383–97.
- Freed EO, Martin MA. HIVs and their replication. In: Knipe DM, Howley PM (eds). *Fields' Virology*. 5th ed. Philadelphia: Lippincott Williams & Wilkins, 2007, 2107–85.
- Coffin JM. HIV population dynamics in vivo: implications for genetic variation, pathogenesis, and therapy. *Science* 1995;**267**:483–9.
- Perelson AS, Neumann AU, Markowitz M *et al.* HIV-1 dynamics *in vivo*: virion clearance rate, infected cell life-span, and viral generation time. *Science* 1996;**271**:1582–6.
- Greene WC, Peterlin BM. Charting HIV's remarkable voyage through the cell: basic science as a passport to future therapy. *Nat Med* 2002;8:673–80.
- Martin N, Sattentau Q. Cell-to-cell HIV-1 spread and its implications for immune evasion. *Curr Opin HIV AIDS* 2009; 4:143–9.
- Douek DC, Picker LJ, Koup RA. T cell dynamics in HIV-1 infection. *Annu Rev Immunol* 2003;21:265–304.
- Zhang ZQ, Wietgrefe SW, Li Q et al. Roles of substrate availability and infection of resting and activated CD4+ T cells in transmission and acute simian immunodeficiency virus infection. Proc Natl Acad Sci USA 2004;101:5640–5.
- Haase AT. Targeting early infection to prevent HIV-1 mucosal transmission. *Nature* 2010;464:217–23.
- Krumholz HM, Herrin J, Miller LE *et al.* Improvements in door-to-balloon time in the United States, 2005 to 2010. *Circulation* 2011;**124**:1038–45.
- Bradley EH, Nallamothu BK, Herrin J et al. National efforts to improve door-to-balloon time results from the Door-to-Balloon Alliance. J Am Coll Cardiol 2009;54:2423–9.
- Bradley EH, Herrin J, Wang Y *et al.* Strategies for reducing the door-to-balloon time in acute myocardial infarction. N Engl J Med 2006;355:2308–20.

- 21. Antman EM, Anbe DT, Armstrong PW et al. ACC/AHA guidelines for the management of patients with ST-elevation myocardial infarction—executive summary: a report of the American College of Cardiology/American Heart Association Task Force on Practice Guidelines (Writing Committee to Revise the 1999 Guidelines for the Management of Patients With Acute Myocardial Infarction). Can J Cardiol 2004;20:977–1025.
- Krumholz HM, Bradley EH, Nallamothu BK et al. A campaign to improve the timeliness of primary percutaneous coronary intervention: Door-to-Balloon: an alliance for quality. JACC Cardiovasc Interv 2008;1:97–104.
- 23. Thompson JD. Organizations in Action: Social Science Bases of Administrative Theory: New York: McGraw-Hill, 1967.
- Bradley EH, Nembhard IM, Yuan CT *et al*. What is the experience of national quality campaigns? Views from the field. *Health Serv Res* 2010;45(6 Pt 1):1651–69.
- von Bertalanffy L. General system theory; a new approach to unity of science. 1. Problems of general system theory. *Hum Biol* 1951;23:302–12.
- Bradley EH, Curry LA, Taylor LA *et al.* A model for scale up of family health innovations in low-income and middle-income settings: a mixed methods study. *BMJ Open* 2012;2(4). doi: 10.1136/ bmjopen-2012-000987.
- Bradley EH, Curry L, Pérez-Escamilla R et al. Dissemination, diffusion, and scale up of family health innovations in low-income countries, 2011: http://www.gatesfoundation.org/global-health/ Documents/yale-global-health-report.PDF (30 January 2013, date last accessed).
- Malim MH, Bieniasz PD. HIV restriction factors and mechanisms of evasion. *Cold Spring Harb Perspect Med* 2012;2: a006940.
- Arts EJ, Hazuda DJ. HIV-1 antiretroviral drug therapy. Cold Spring Harb Perspect Med 2012;2:a007161.
- Greenhalgh T, Robert G, Macfarlane F et al. Diffusion of innovations in service organizations: systematic review and recommendations. *Milbank Q* 2004;82:581–629.
- Bartholomew LK, Parcel GS, Kok G. Intervention mapping: a process for developing theory- and evidence-based health education programs. *Health Educ Behav* 1998;25:545–63.