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SOCIAL AND ENVIRONMENTAL VULNERABILITY TO EMERGING INFECTIOUS DISEASES

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1. Introduction

Emerging Infectious Diseases (EIDs) have been broadly defined as 'diseases that have recently increased in incidence or geographic range, recently moved into new host populations, recently been discovered or are caused by newly-evolved pathogens' (Daszak *et al.*, 2001). In the past three decades, at least 40 EIDs have been identified, not including the regional resurgence of the widespread endemic diseases of the tropics (malaria, dengue fever, leishmaniasis, etc.) and the new antibiotic-resistant strains of bacterial infections (tuberculosis, staphylococcus, etc.) and protozoans (malaria).

There have been several papers and reports dealing with factors involved in the emergence (IOM, 1992; 2003; Molyneux, 2003; Mayer, 2000; Patz *et al.*, 2000; Daszak *et al.*, 2000; Wilson *et al.*,1994; Morse, 1993; 1995; Taylor *et al.*, 2001) as well as discussions on the technical, political and institutional responses to the EIDs (Broome, 1998; Binder *et al.*, 1999; Plotkin & Kimball,1997; Winch, 1998; LeDuc & Tikhomirov, 1994; Heymann & Rodier, 2001).

In this paper we use updated information on diseases that have emerged in the past few decades and discuss aspects of the contemporary social and environmental vulnerability to the emergence of infections. We present a conceptual framework to the study of the EIDs and we apply the concept of vulnerability to the study of the emergence and global dissem-

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ination of infections. Also, via a case study we discuss some aspects of the global interconnection of social and environmental drivers for the emergence/dispersal of infectious and parasitic diseases. Special emphasis is placed on how mechanisms of emergence are determined by vulnerability factors; on what makes an emerging infection capable of global spread, and the current characteristics of urban structures that make large settlements places for reception and global dispersal of EIDs.

2. Disease Emergence in the Past Three Decades

In regard to the EIDs identified in the last thirty years we can make these general statements:

1. For many of these EIDs the basic drivers and mechanisms of emergence are not known. For several others, solid hypotheses are accepted. Also, the exact place of first emergence and the year that the phenomenon has occurred can rarely be tracked (years in the table refer to the first isolation of the agent).

2. Disease processes have emerged due to several drivers and mechanisms, both in developed as well as in developing countries. In developed countries, among the six major categories of drivers identified by the IOM (1992, 2003), those associated with changes in technology/industry, microbial adaptation and change, and international travel and commerce tend to predominate. On the other hand, those EIDs clearly identified as originating in low income countries have usually been associated with the encroachment of agriculture on natural systems (land use changes); with direct contact with infected animals; and with the breakdown of public health measures and changes in demographics and human behavior.

3. The more immediate drivers and mechanisms can be discerned with some reliability or at least hypothesized. However, the more distant drivers are rarely discussed or even sought. Emergence is associated with disturbances of previously stable microbiological equilibria caused by various social and environmental activities by humans. The primary drivers of change (social, economic, cultural, political and behavioral) have so far received little research attention.

4. There is a variable epidemiological pattern in the EIDs. Some have become widespread pandemics (AIDS, cholera); others are globally distributed but occurring at low levels or as eventual outbreaks (Campylobacter; Rotavirus; E. coli, Legionella, etc.); while a few are restricted to groups of

countries (SARS, West Nile Virus fever, HTLV-1, Monkeypox). A few others have been reported occasionally from restricted localities (Nipah, Hendra, Pfiesteria, Avian Influenza, Guanarito, etc.), though some, such as avian influenza, seem to be developing the capacity to spread widely.

3. Vulnerability to Emerging Infectious Diseases

Vulnerability is a concept derived from geography and social sciences and, as far as human well-being is concerned, it has been developed initially to study the impacts of natural disasters upon human communities. It has been defined as 'the characteristics of a person or group related to the capacity to resist, cope with, and recover from the impacts caused by hazards' (Blaikie *et al.*, 1994). Another definition is 'the differential capacity of groups and individuals to deal with hazards based on their positions within the physical and social worlds' (Dow, 1992).

Vulnerability is broadly defined in terms of exposure, capacity and potentiality (Watts & Bohle, 1993), and is also distinguished as both a biophysical condition (geographic space) and defined by political, social and economic conditions of society (Liverman, 1990). In general it is recognized that the most vulnerable social groups are those that experience the most exposure to a hazard; that are the most sensitive to it (e.g., the most likely to suffer from it), and who have the weakest capacity to respond and ability to recover.

In relation to EIDs the concept of vulnerability can be applied to three different levels: drivers and mechanisms of emergence; dissemination of infections; and the social responses to control them. This expanded framework of vulnerability to biological hazards (EIDs) should include the characteristics of societies that produce the drivers and mechanisms of emergence and also render the receptive populations exposed to and sensitive to the infections. It would also include the conditions that facilitate the amplification of infections as well as those that determine the capacity of the social groups to respond to these hazards in a timely and effective way. By drivers we mean the social, economic and cultural dynamics that direct the human interventions in the physical world. By 'mechanisms' of emergence we consider the ensuing reactions in the environment and in the microbial world.

At the ecological level, mechanisms of emergence always involve the transfer of a pathogen from an 'extra-human' environment (biophysical

environment; domestic or wild animal) to the human hosts ('host transfer' in Figure 1). The early process of emergence of novel human infections can be approached from different perspectives: biological, ecological, geographical, social and behavioral. Vulnerability factors may operate in different moments of emergence: microbial changes, human exposure, human infection and local dissemination of the infection (Figure 2).

At the level of microbial changes human interference can facilitate genetic shifts through the use of drugs for therapy (microbial resistance) or by facilitating the interchange of agents between different hosts, such as the case of avian influenza, or by changing the natural ecosystems, such as the case of deforestation and the outbreaks of Venezuelan equine encephalitis (Brault *et al*., 2004).

Human contact with potentially novel pathogens (= exposure) may be determined by a host of factors, which range from the place of settlement, feeding habits (e.g., bushmeat), behavior (e.g., HIV) and medical and other technologies (e.g., blood transfusion, etc.).

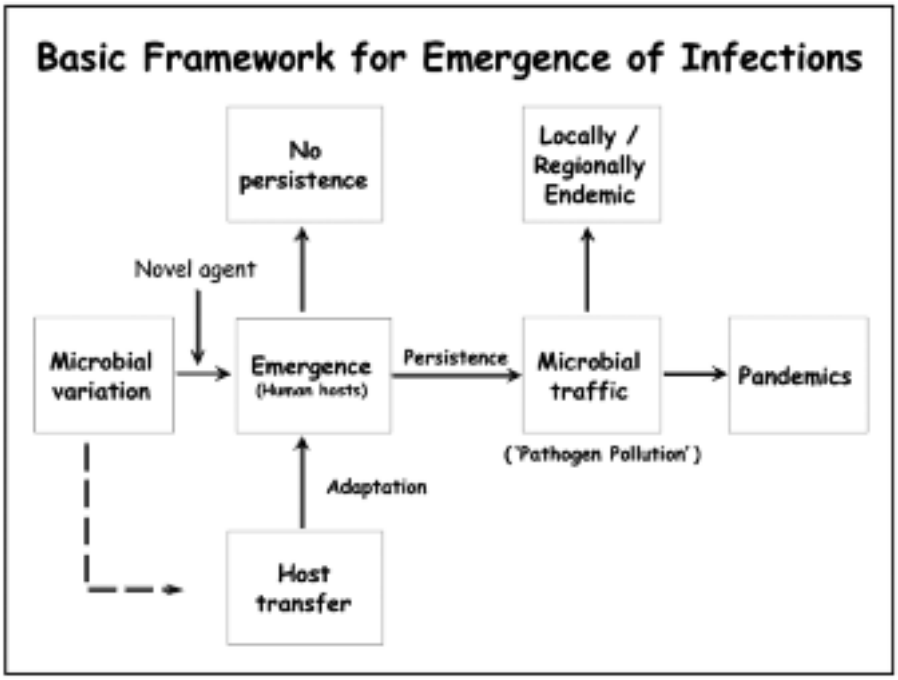

Figure 1. Basic framework for the emergence of infections.

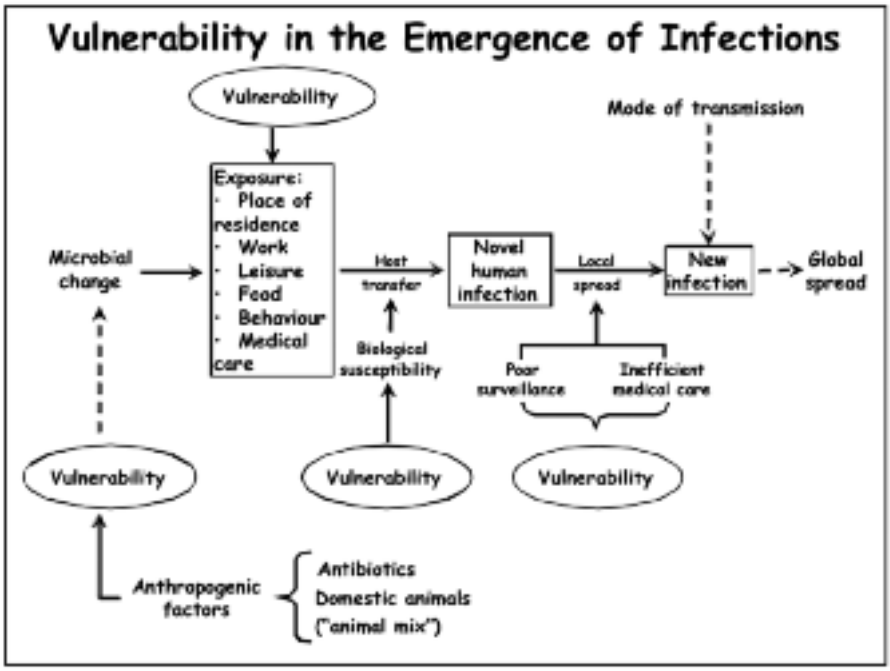

Figure 2. The role of vulnerability in the emergence of infections.

In the following step – host transfer (i.e., the invasion of human hosts) – vulnerability is determined basically by biological susceptibility (immunity). Local amplification of infection is primarily determined by the capacity of the organism to pass from one human host to another (infectivity) – but it is also a result of the capacity of the epidemiological surveillance systems to detect and control the spread of infection.

As for the phase of global (or regional) spread of EIDs, vulnerability is linked to the factors that cause people and goods to move from one geographical location to the other, either for economic reasons (commerce, work) or because of political factors (conflicts) and even tourism, an aspect which will be discussed later. In this regard, large metropolitan areas are especially vulnerable places as they are 'receptive' to the introduction and redistribution of pathogens undergoing global spread, also to be discussed in another section.

The capacity to respond to a disease emergence involves both the early detection of the disease and the implementation of control meas-

ures. This means a combination of clinical attentiveness, good laboratory facilities and comprehensive epidemiological surveillance systems for infections in both humans and animals (Desselberguer, 2000). Factors that may cause greater vulnerability in this area (= poor capacity to react) are political instability, lack of technical infrastructure and lack of professional expertise.

4. The Vulnerability of Developing Countries

Developing countries are especially vulnerable to the emergence and spread of novel human infections for several reasons, which can be summarized in Figure 3.

With respect to the biological processes involved, the probability that microbial change and adaptation will occur is higher in developing countries since they contain most of the existing natural systems in the world

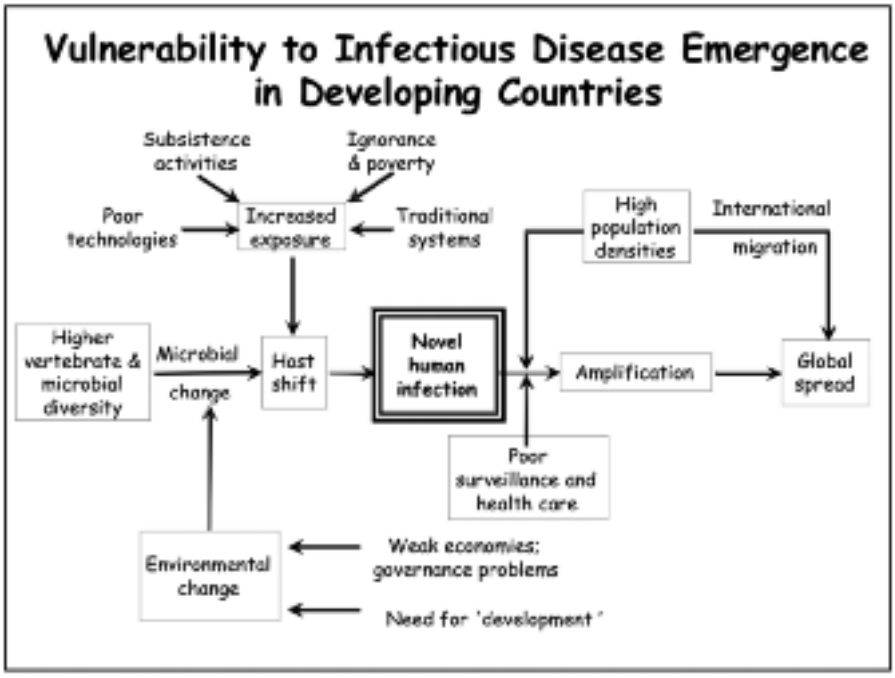

Figure 3. Vulnerability to emergence of infectious disease in developing countries.

that provide a rich environment for emergence, especially in the tropics, due to their high vertebrate and microbial biodiversity (Wolfe *et al.*, 2000). In this context the increased probability of a successful emergence event is determined by the intimacy and frequency of contact of people with the microbe-rich environment due to immediate subsistence needs, through direct contact with infected vertebrate animals, such as the case of bushmeat hunting (De Merode *et al.*, 2004). Human contact with potential new infections in these ecosystems can also be associated to the exposure to vectors during the human invasion of their established ecological niches, as part of their work. It has been demonstrated that environmental changes such as deforestation can result in microbial genetic and population shifts that may favor disease emergence (Borneman & Tripplet, 1997; Brault *et al.*, 2004). This is due to major shifts in the ecological niches of microbial populations and to changes in the selection pressures in the environment.

People are driven to enter these microbe-rich niches by their need for jobs (frequently 'unregulated'). The activity of exploitation of natural systems is often associated to international economic demands, especially for agricultural products and logging. However, traditional systems may also be associated with enhanced human-animal-environment contacts that may facilitate host transfer.

The major factors favoring the amplification of novel infections are demographic and those related to health systems. The new infection may escape early detection due to the chronic deficiencies in health surveillance in developing countries. On the other hand, high population densities (especially in urban areas) and migration (rural to urban; developing to developed countries) contribute to the spread of the pathogen on a wider scale.

The following case of the relationship between bovine spongiform encephalopathy (BSE) in Europe and the subsequent expansion of soybean cultivation in Brazil illustrates the vulnerability of developing countries to infectious disease emergence. It describes the possible linkages between disease-driven changes in livestock production systems in high-income countries and environmental changes favoring the emergence of infections in low-income countries.

Due to the emergence of the BSE in cattle in the UK (1986) and the subsequent discovery of the zoonotic aspect of the causative prion, producing the new variant Creutzfeldt Jakob Disease (Prusiner, 1998), new regulations for feeding cattle were enforced and rendered foods for animals were banned in Europe and elsewhere. This produced in the inter-

national market of agricultural commodities an increased demand for soybean grain, which is a 'clean' plant protein adequate to feed cattle and other domestic animals. Also, soy growing has been progressively transferred from temperate to tropical areas, where land is cheaper (Fearnside, 1999). In Brazil, one of the most important soybean producers in the world, this increased demand is causing the expansion of the soybean growing area in the central part of the country to the north, encroaching the Amazon forest. (Fearnside, *loc. cit.*). The country contains the largest block of original rainforest cover in the world and this poses a new risk of outbreaks of emergent arboviruses since this ecosystem is known to be rich in these microorganisms (Vasconcelos *et al.*, 2001), and environmental changes such as deforestation may place humans in contact with previously inaccessible pathogens (Figure 4).

This example illustrates the linkages between economic globalization and agricultural policies in developing countries and their adverse consequences for the natural systems and the resulting increase in the risk of disease emergence.

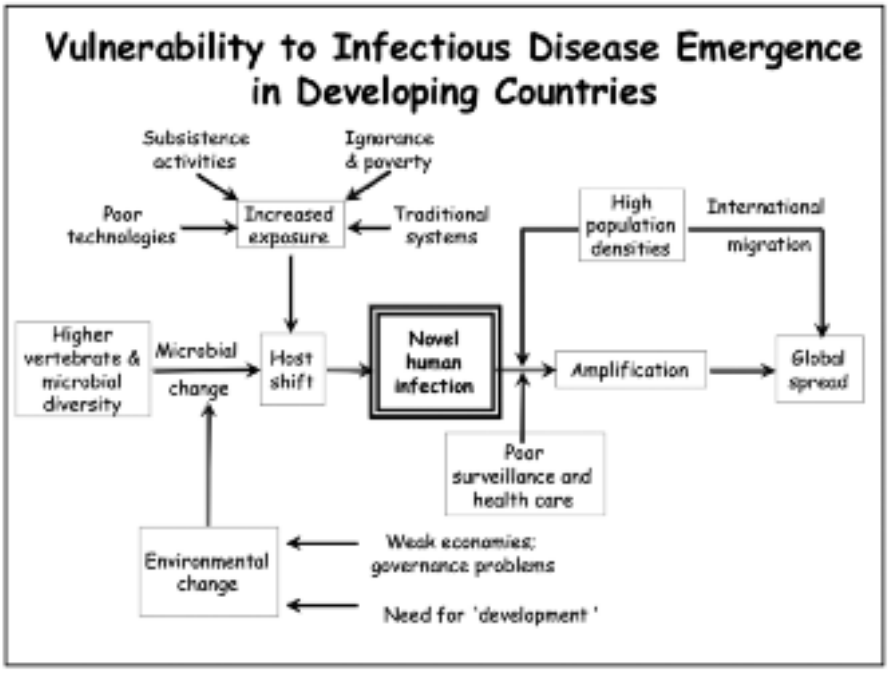

Figure 4. Soybean planting and disease risk in South America.

5. Globalization of Emerging Infections

Processes relevant to the globalization of infectious diseases, which is the last stage in the disease emergence process, will be discussed under these two general headings:

1) movement of humans and associated biological material;
2) trade.

5.1. *Movement of Humans and Associated Biological Material*

International travel and commerce facilitate rapid, massive, and global dispersal of biological material, including microbial genetic material. The scale, speed, and reach of movement of people and goods today is unprecedented and shapes the appearance, spread, and distribution of infectious diseases in humans, plants, and animals (Wilson, 1995a). Travel, trade, and the wide availability of mass transport have vastly expanded the movement of biological material that occurs naturally via migration of animals, flight of birds, movement of species such as insects, plant seeds, and marine life over land, in winds and air currents, and in streams and oceans.

International travel is growing in numbers and speed. Today more than 1.4 million people cross international borders on airplane flights each day. In 1950 the number of international tourist arrivals was 50 million; in 2002 more than 700 million international tourist arrivals were registered (WTO, 2003). Although most travel occurs along well-established corridors, more travelers are reaching remote areas where they may have contact with potentially pathogenic microbes that are not yet well characterized in animals or environmental reservoirs. In 1999, more than 75 million people traveled from industrialized to developing countries. By the 1990s more than 5000 airports had regularly scheduled international flights. This means that dense urban centers throughout the world are connected by a steady flow of humans.

Migrating humans (soldiers, merchants, explorers, refugees, missionaries, others) have long played a role in the introduction and spread of infectious diseases. (Berlinger, 1992; Bruce-Chwatt, 1968; Crosby, 1989). The difference today is the scale, speed, and reach of interconnections. A human can be viewed an interactive biological unit, carrying an assemblage of microbial genetic material and immune responses and immunological memory that reflect past exposures (Wilson, 2003). Travelers often spend time in a sequence of shared environments (e.g., bus, train, terminal, plane,

ship, etc.), which link the traveler to a wide network of contacts. Relevant exposures can occur in transit as well as at the final destination. Travelers can pick up, carry, and transmit microbial genetic material during and after travel – in some instances long after travel. Microbes transmitted from person to person (especially respiratory pathogens and sexually transmitted infections) can be carried to any part of the world by travelers. HIV is a prominent contemporary example of an infection that was carried by humans and transmitted widely, primarily via sexual contact.

Humans who are sick often attract attention (and medical interventions), but humans can carry pathogens and transmit them in the absence of symptoms. Examples include asymptomatic infection with HIV and hepatitis B virus. Pathogens that regularly colonize mucosal surfaces (e.g., *Neisseria meningitidis, Streptococcus pneumoniae, Staphylococcus aureus*) may be carried (often transiently) and transmitted by healthy people who have no awareness that they carry these potential pathogens (Wilder-Smith *et al.*, 2002). Humans can also carry resistance genes, sometimes found in commensal bacteria of the gut or skin, which may be transferred to other microbes (O'Brien, 2000; Okeke, 2001). A carrier who introduces a pathogen, a new clone, or a resistance gene into a community may never experience any illness. Some infections, such as HIV, can remain asymptomatic for prolonged periods, allowing transmission to occur repeatedly, over a long period of time, and in places remote from the site of acquisition.

5.2. *Global Trade and the Spread of Diseases*

Global trade is another mechanism for the worldwide dispersal of pathogens (that can infect humans, plants, and animals), insect vectors (such as mosquitoes), and intermediate hosts. Imported food now comprises a substantial part of the diet for many populations, especially in North America and parts of Europe. For example, the U.S. imports more than 30 billion tons of food per year, including fruit, vegetables, meat, and seafood (Murphy, 1999). The food chain has become very long; fresh produce may be grown and packed thousands of kilometers from where it is consumed. Mass production and mass processing of many foods and wide distribution networks mean that microbial contamination at one point in the production site or during processing may reach thousands or millions of people in multiple countries. Contamination can occur because of human ignorance or error, breakdown in equipment, or it may be introduced intentionally.

Trade in exotic animals is huge, much of it illegal; animals may be sought as pets or for food. In the U.S. the annual trade in illegal plants and animals is estimated at US$3 billion, a significant portion of it from trade in exotic reptiles (for pets). In one port (Miami) in one year (1996) more than 30 million animals were legally imported. Among the arrivals were 28.6 million fish, 1.1 million reptiles, 108,000 amphibians, 70,000 mammals, and 1,400 birds.[1] In 1999, the year that an outbreak of West Nile virus (WNV) was first identified in the U.S., with its epicenter in New York, 2,770 birds legally entered the country through JFK International Airport in New York. In addition, almost 13,000 birds passed through this airport in transit (Rappole, 2000).

Multiple wildlife species, many of them exotic and rare, are often collected from diverse, remote areas and kept in close proximity in zoos or wildlife conservation parks, adjacent to large human populations. These captive wildlife populations undergo inconsistently intense observation and monitoring. They are occasional sources of infection but can also serve usefully as sentinel populations for new events. In the WNV outbreak in New York, testing of stored and newly collected sera suggested that birds newly introduced to the Bronx Zoo were not the source of infection, that WNV infection had not been present before 1999, and that it spread widely in the zoo bird population and to a lesser extent in mammals (Ludwig *et al.*, 2002).

In an example of the triumph of trade pressures over good sense, distributors of exotic animals have exported prairie dogs from the U.S. to multiple other countries even though prairie dogs can be infected with the bacteria that cause tularemia, plague, and other potentially life-threatening infections in humans. An outbreak of tularemia in prairie dogs at a distribution center in Texas, which exported these animals to at least 10 states and seven countries, highlights this risk. Microbes in imported animals can be a source of human disease and may also threaten domestic and local wildlife populations (Daszak *et al.*, 2000). In the spring of 2003, prairie dogs housed with exotic African rodents became infected with monkeypox virus (from Africa), resulting in subsequent transmission to humans (Guarner *et al.*, 2004).

A UK government report estimated that in 2003 more than 11.5 tons of bushmeat (including monkey, rat, bat, gorilla, camel, and elephant) were smuggled into the UK (*The Telegraph*, 5 Sept 2004, reported on ProMED). In Africa, the establishment of networks, improved infrastruc-

[1] Stephanie Ostrowski, Division of quarantine, CDC; verbal communication.

ture, and especially the building of roads for logging and other development has facilitated the trade in bushmeat (Nisbett *et al*., 2001).

Simian immunodeficiency viruses (SIVs) are widespread in primate species. In one study of blood and tissue samples in Cameroon, from 788 monkeys (bushmeat and pet animals), 16.6% of plasma samples tested strongly positive for HIV antigens (Peeters, 2002). There is good evidence that the AIDS pandemic in humans originated from multiple introductions of related SIV viruses from African apes and monkeys and the subsequent evolution of these viruses (Hahn *et al*., 2000; Sharp *et al*., 2001). Contact with primates as pets or with primate tissue through butchering animals could allow transfer of SIVs to humans. A recent survey of inhabitants in rural Cameroon found that more than 60% reported contact with fresh blood or body fluids from nonhuman primates, primarily through hunting and butchering chimpanzees, monkeys, or gorillas (Wolfe *et al*., 2004). Further testing of humans with contact showed evidence of infection with simian foamy virus, a retrovirus endemic in African primates. Although this virus is not known to cause disease in humans, its presence in humans confirms ongoing transmission of primate viruses to humans.

Arthropods that can serve as vectors of human, animal, and plant diseases are regularly transported around the world by ships, planes or other vehicles. They may become established and spread in the new area (Bram *et al*., 2002; Lounibos, 2002). Historically, water tanks in boats provided a suitable environment for the survival of mosquitoes traveling across oceans. *Aedes albopictus*, a mosquito competent to transmit dengue fever virus and other viral pathogens, was introduced into North America in the 1980s, probably via used tires imported from Asia. It was first identified in Texas and spread to 678 counties in 25 states within 12 years (Moore *et al*., 1997). Of note, its dispersal followed interstate highways. It has also been introduced into several countries in Latin America. *Aedes albopictus* is the vector implicated in an outbreak of dengue serotype-1 that started in Hawaii in 2001.

Introduced exotic species threaten local populations and ecosystems. Ships used to transport cargo carry all types of biological life in ballast water and have been the source of introductions of invasive, exotic species into ports around the world (Carlton & Geller, 1993). Infectious diseases also threaten plants and animals and thereby have a major economic impact. Examples include bovine spongiform encephalopathy (BSE) in the UK and subsequently in many other countries, and foot and mouth disease, especially in the UK. Infectious diseases in plants and animals may also

have both direct and indirect consequences to human health. The transnational movement of people and goods facilitates the introduction of plant pathogens and their vectors into new communities. Infectious diseases of plants such as Karnal bunt of wheat, potato late blight, and citrus tristeza affect large, commercially important crops (Bandyopadhyay & Frederiksen, 1999). The destruction by disease of major food crops such as rice, wheat, and potatoes, could affect food security.

6. Global Cities and Disease Emergence

Attributes of the world's populations today that favor the emergence and spread of infectious diseases include size, density, location, mobility, vulnerability, inequities, and demographic shifts (Wilson ME, 1995b). The human population is larger than ever in history. Most of the population growth in the coming decades is projected to be in developing countries. Populations of domestic animals are also larger than ever in the past; densely concentrated populations of animals may grow under conditions that favor spread of infections.

More people live in urban areas than ever in history, and urbanization is expected to increase. The most rapidly growing segment in the world is the urban population in developing countries (UN, 2001). Megacities, defined as urban areas with a population greater than 10 million, have increased from 5 in 1975 to 19 in 2000. Most of the new megacities are located in low latitude areas and in developing countries.

Several research programs have compared megacities in the more developed countries, focusing on the paradigm of the success of the global city (Sassen, 1991). However, comparisons of megacities that are at different development levels may also be informative, either to understand better their specific characteristics as highlighted via the contrast, or to investigate common processes that seem to affect them.

The widespread segregation of rich and poor, within cities, is increasingly recognized as a public policy crisis that assails low-cost housing projects in outlying urban areas. This 'dualization' problem can be viewed as the spatial translation of social exclusion. This isolation of underprivileged segments has been criticized for two reasons: first, due to the negative effects of regrouping poverty-stricken communities – resulting in a cumulation of material difficulties and socialization problems, with the risk that the immigrants will return to communitarianism that then hampers their integration

as citizens; and second, the negative physical characteristics of these neighborhoods – decaying buildings, excessively dense and 'inhuman' town-planning, enclaves, and a lack of safety and security. There is increasing awareness that segregation is becoming more marked, with two-tier cities appearing, characterized by a gap between the excluded and the others.

In many cases, the spatial dualization hypothesis applied to megacities is based on specific areas that constitute particularly striking examples: fashionable boroughs and gentrified neighborhoods on the one hand, with decaying downtown areas or huge outlying townships assailed by unemployment and poverty on the other. Although striking, these examples of marked contrasts do not offer an overall view of the development of the urban system, and do not confirm that this situation of opposites is due to the dualization process of the urban system as of a whole.

The relationships between EIDs and these recent societal developments in cities deserve more research attention, especially since significant alterations in the differential use of space by different social groups in cities have been occurring at increasingly rapid rates from the 1970s onwards. Of practical epidemiological importance is the fact that many of the large urban areas in developing countries are surrounded by peri-urban slums characterized by poor infrastructure, absence of clean water, inadequate waste disposal and sanitation, poor housing, and close contact between animal and human populations. Many people dwelling in these peri-urban slums have relatives in rural communities. Frequent contact between residents of peri-urban and rural areas offers opportunities for passage of microbes into and out of the urban areas. Medical care may be limited, allowing infections and other medical problems to go undiagnosed, untreated, and unreported.

7. Conclusions

Infectious disease emergence is a complex phenomenon, involving different types of drivers at different stages in the process of emergence. These range from the biological susceptibility of hosts to the economically-driven environmental changes caused by humans and the efficiency of health-care systems. The combination of these factors that influence disease emergence differs in developing and developed countries. In the former we find more often the combination of conditions most conducive to disease emergence, making those countries more vulnerable.

Although not all emergent diseases are able to 'go global' in today's world, international movements of humans and associated biological material as well as the global trade have been important mechanisms for the dissemination of pathogens and vectors around the world. Urbanization is expected to increase globally, especially in the developing world, and segregation within cities (that is, the isolation of underprivileged social segments) is becoming more marked, both in developing as well as in developed countries. The recent examples of SARS and avian influenza point to the role played by large cities in the amplification of emergent infectious diseases. As central nodes in the international network of travelers and of the exchange of goods, as well as densely populated by humans living under conditions of inequality, the global cities have become a matter of special concern in the epidemiology of disease emergence.

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