



The Life & Health Risk Monitor is a periodic review of the latest developments affecting mortality and morbidity risk for the clients of Risk Management Solutions.

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CATASTROPHIC LOSS IN EMERGING LIFE MARKETS

The China earthquake of May 12 could exceed 80,000 deaths. It is the latest in a sequence of high fatality events to strike developing countries and illustrates the potential for emerging life insurance markets to experience excess mortality levels with a frequency and severity beyond those seen in the developed world life insurance markets.

Large fatality events in natural disasters have tended to cause very low losses to the insurance industry – underdeveloped countries with poor quality building stock have had very low insurance penetration. However as globalization shifts labor-intensive processes to developing economies, the life insurance penetration is growing, leading to exposure by international life insurers to natural catastrophes. The humanitarian disasters have dominated the news, but these also have significant implications for the future growth of international life insurers.

Insurance will pay only a small fraction of the overall property and economic losses from the Sichuan province earthquake in China on May 12, but initial estimates by the China Insurance Regulatory Commission show that the life insurance payouts will be many times larger than the property claims. The Sichuan region is an area of heavy industry and manufacturing whose economy has grown rapidly as production businesses have expanded in the region, many of them providing modest group life savings and protection plans as benefits for employees. The massive death toll – likely to exceed 80,000 – contains many workers who were at their factories when the earthquake struck at 1 pm local time. The total life insurance payouts will be relatively minor by Western standards – only tens of millions of dollars – but they indicate that extreme mortality events are a significant risk in these emerging life markets.

Recent years have seen a number of very high fatality events in emerging market regions. The Sichuan earthquake followed only days after the cyclone in Myanmar claimed possibly as many as 128,000 lives. In Northern India and Pakistan the earthquake of October 8, 2005 killed over 79,000 people. The tsunami of December 26, 2004 hit coastlines throughout Southeast Asia killing more than 225,000 people in 11 countries.

Cities throughout Asia are growing very rapidly. The scale of urbanization in the past three decades in China, Indonesia, India and several other rapidly developing countries surpasses anything seen during the historical urbanization of Western countries during the 19th century. China is currently adding 9 million people to its cities each year and now has 90 urban centers of more than a million people. By 2020, estimates suggest there will be 27 cities in the world with populations of more than 10 million – only 7 of them will be in the established economies of today's OECD nations.

The catastrophe potential for cities emerging through rapid economic development is becoming clearer. Cities also are not randomly impacted. Recent studies have shown that along the central Asian plateaus, cities are located where historical trade routes, water sources, and agriculture provided favorable sites – locations dictated by the topography created and controlled by fault movement in earthquakes: positioning cities exactly in seismic areas. Coastal cities sited for ports and river access are most at risk from the cyclones and storm surges and tsunamis that threaten certain shorelines.

Insurers can manage the potential for extreme losses in their rapidly-growing life insurance portfolios in emerging markets through the simple expedient of monitoring their geographical exposure. Knowing total policy numbers in a certain city or region, and knowing the potential for extreme events in these regions, enables accumulation management for extreme mortality events in emerging markets.

DISEASE OUTBREAKS FOLLOWING MAY 2008 DISASTERS

Outbreaks of infectious diseases in the aftermath of disasters can compound the morbidity and mortality and increase the difficulty of recovery. Myanmar's Cyclone Nargis and China's Sichuan earthquake illustrate the potential of post-disaster epidemics.

Population displacement following natural disasters increases the risk of infectious disease outbreaks and compounds the morbidity and mortality. The healthcare infrastructure of a region is often weakened under the massive pressure of a major disaster. Although crucial in preventing and containing outbreaks, surveillance systems and vector-control programs may fall lower in priority as resources are scarce following a disaster. In addition, poor sanitation, lack of safe drinking water, and crowding often create conditions favorable for disease transmission. Diarrheal disease outbreaks after floods are well documented, and include cholera outbreaks after flooding in Bangladesh in 2004 and in West Bengal in 1988. Clusters of hepatitis E are often seen in refugee camps and other crowded living conditions; cases were also noted after the 2005 earthquake in Pakistan and in Aceh after the 2004 Indian Ocean tsunami. Acute respiratory infections and bacterial meningitis, both associated with crowded conditions, were both documented in Aceh and Pakistan as well. Diseases involving contaminated wounds or exposure to pathogens normally present in soil are often reported following earthquakes. For example, deaths from tetanus were reported after the 2005 Pakistan Earthquake, and the 1994 Northridge Earthquake was associated with an outbreak of the fungal disease coccidiomycosis. In many developing countries and conflict-affected populations, the displacement of people that already were malnourished or had poor immunization coverage can exacerbate the potential for death from communicable diseases. Death rates as high as 60 times over the baseline rates have been recorded in displaced populations in conflict-affected areas, with a majority of these deaths caused by communicable diseases.

Cyclone Nargis. There have already been reports of diarrhea and respiratory illness in cyclone survivors living in the destroyed villages along Myanmar's Irrawaddy Delta. Sources of fresh water in Myanmar have been contaminated with human corpses and animal carcasses, as well as saltwater from when the cyclone struck. There are concerns about widespread outbreaks of cholera, which is caused by ingestion of food or water contaminated with the bacterium *Vibrio cholera* and can lead to severe diarrhea and death. In addition to the military regime's initial refusal of outside aid, attempts to get medical supplies, food, and water to the region have been hampered by heavy rains. These heavy rains also increase the risk of vector-borne diseases such as malaria and dengue, because of the creation of new mosquito-breeding sites. The risk of measles and other person-to-person transmissible diseases are increased in the crowded conditions where homeless people are taking shelter.

Sichuan Earthquake. The Chinese Center for Disease Control has reported 30 cases of gas gangrene, a deadly form of gangrene caused by *Clostridium perfringens* bacteria. *C. perfringens* is commonly found in soil and enters the body through traumatic wounds such as those sustained during an earthquake. More than 5 million people have been left homeless or displaced in the quake-devastated areas in China. Hundreds of thousands of villagers evacuated to overcrowded camps after threats of post-earthquake flooding are vulnerable to diseases such as hepatitis, respiratory infections, and tuberculosis. Health officials report that no major communicable disease outbreaks have occurred, but higher-than-normal rates of gastrointestinal problems and fevers have been reported among earthquake survivors.

The majority of disaster-associated deaths are caused by the traumatic impact of the disaster. However, disaster survivors have an increased risk of communicable disease, and it is important to consider infectious disease risk when modeling natural disasters.

H5N1 CASE OF HUMAN TO HUMAN TRANSMISSION

If the highly pathogenic H5N1 influenza virus adapts to become easily transmissible between humans, the resulting pandemic could be severe. A probable case in China of H5N1 being passed from one person to another has caused concern but does not appear to be the feared antigenic adaptation.

As of May 2008, there have been 382 confirmed human cases of avian influenza A (H5N1) causing 241 deaths since monitoring began in 2003. Human cases of H5N1 infection have occurred in 14 countries, including Indonesia, Vietnam, Egypt, China, Thailand, and Cambodia. The virus has spread rapidly throughout East and Southeast Asia and has become endemic in domestic birds in many countries. Human cases are mostly a result of direct contact with infected poultry, common in areas where humans have close contact with birds, such as domestically-reared poultry or in live poultry markets. Concerns about a pandemic arise from the possibility of mutations to the virus that would allow it to pass easily from human to human. The first sign of a mutation is likely to be a family cluster of cases.

A family cluster – a father and son infected with H5N1 – was identified in December 2007 in China. First, a 24-year old salesman from Nanjing in Jiangsu Province died from avian flu. He was most likely infected with H5N1 during a visit to a poultry market 6 days before he became ill. His father, aged 52, also became infected with H5N1 after nursing him throughout his illness. The father survived the infection, after being diagnosed early and receiving prompt antiviral treatment and plasma cells from a participant in a vaccine trial. It is possible that the father could have independently caught H5N1 from infected poultry, but he appears to have had no contact with birds.

Previous investigations of family clusters of cases in Indonesia and Thailand have been suggestive of person-to-person transmission of H5N1, but this study was the first one to obtain viral isolates from all cases. The viruses isolated from the father and son were nearly genetically identical. Scientists from the Chinese Centre for Disease Control and Prevention concluded that limited and non-sustained person-to-person transmission of the H5N1 virus within this family probably occurred.

Clinical and epidemiological data were also collected for 91 of the 100 identified contacts with close exposure to either of the two confirmed cases. 86% of these contacts received chemoprophylactic antivirals, and two (the 24-year old patient's girlfriend and his doctor) developed mild illness. Both of these ill contacts had normal chest x-rays and tested negative for H5N1. The scientists concluded that although the virus has not yet adapted enough to attain the ability to transmit more efficiently between humans, urgent epidemiologic investigation of avian flu clusters is necessary in order to monitor the appearance of H5N1 strains that are well-adapted to spread efficiently within humans.

In highly-pathogenic H5N1, the HA antigen can be cleaved by many tissue proteases, which results in systemic spread including respiratory and central nervous system infection. Infection with H5N1 typically occurs in the lower respiratory tract and results in a severe and aggressive illness with high mortality and complication rates, but the lack of upper respiratory involvement limits transmission.

RMS believes that if H5N1 mutates into a human-to-human transmissible form there is a high likelihood of it having significantly higher virulence than circulating strains of human flu. However, the likelihood of the H5N1 virus mutating is unknown and there is a significant probability that a yet unknown or variation on a currently circulating strain could be the next pandemic. The RMS model considers nearly 2,000 unique pandemic scenarios that include the presumption of human-to-human transmissibility.

PANDEMIC BUSINESS INTERRUPTION

The risk from infectious disease pandemics extends beyond life and health. Business interruption impacts are likely to be a primary driver of loss even with relatively mild pandemics. Pandemic business interruption is a quantifiable peril.

The threat to the insurance industry from infectious disease is not limited to life, health, and workers compensation losses. An event with little or no impact on these lines of business can still cause severe losses from business interruption (BI). Severe acute respiratory syndrome (SARS) was an example of an event with relatively minimal life and health impact, but significant economic losses due to business interruption. There has been one SARS outbreak, between November 2002 and July 2003, with 8,096 known infected cases and 774 deaths. Apart from the direct costs of intensive medical care and control interventions, SARS caused widespread social disruption and economic losses. Schools, hospitals, and some borders were closed and thousands of people were placed in quarantine. International travel to affected areas fell sharply by 50-70%. Hotel occupancy dropped by more than 60%. Businesses, particularly in tourism-related areas, failed, and some large production facilities were forced to suspend operations when cases appeared among workers. The estimated impact to the Asian economy was greater than \$50 billion. Canada, which had limited cases, had real GDP lowered by approximately \$1.5 billion for the year.

There is a growing supply of coverage being provided for pandemic BI, making it possible for companies to manage this risk. The RMS[®] Influenza Pandemic Risk model is a stochastic representation of many permutations of possible characteristics of influenza pandemics. By the addition of epidemic curves for each of the events, a probability distribution for pandemic business interruption can be developed. This produces the loss severity and duration for five components of business interruption coverages: absenteeism, civil authority, contingent BI, extra expense, and demand loss.

Absenteeism: The model can provide estimates of the number of the workers off sick, (or who may stay home to care for sick dependents) and how many are off at any one time, to estimate the resultant lost productivity. Insurance coverage can be provided based on thresholds of lost productivity, and sensible deductible levels set.

Civil Authority: Some types of business will suffer losses incurred from mandatory suspension due to governmental interventions. Periods of suspension of public activities and governmental institutions (such as schools) are mandated in U.S. Centers for Disease Control (CDC) guidelines for combating a pandemic.

Contingent BI: The effect of illness in a supplier's workforce can also be assessed for its impact on contingent BI cover. In most cases, if the supplier is located in the same city or region as the business, then their illness wave will be at the same time as the business. However, if the supplier is located in a different region – or even in a different country – then the supplier failure could occur at a different time as the workforce sickness, compounding the length of time that the business is disrupted.

Extra Expense: Direct costs incurred, such as hiring additional staff, buying emergency supplies, increasing work-from-home capabilities, or increasing salaries to decrease fear-based absenteeism from critical staff members.

Demand Loss: Demand drop reduction for a company's products or services is related to sickness levels in the general population and specifically in the customer base. Precedents show that the fear of infection tends to be the cause of much of the drop in demand, particularly for the more virulent diseases. Some industries, like IT, healthcare, and mail service may actually experience an increase in demand due to a pandemic.

The quantification of risk in these areas can help with determining the probability of exceeding certain levels of loss, how to structure pandemic response plans, and understanding the need for risk transfer mechanisms. RMS modeling provides the ability for insurers to quantify coverage for a company's business impacts from infectious disease.

TAMIFLU RESISTANCE IN H5N1 AND SEASONAL INFLUENZA

Recent research has shown that both circulating seasonal influenza strains and some strains of H5N1 have shown signs of resistance to the antiviral drug Tamiflu. Tamiflu is a critical component of most influenza pandemic response plans and the resistant strains are being closely monitored.

Tamiflu (oseltamivir phosphate), an oral antiviral drug for the treatment of uncomplicated influenza, can be effective in reducing the burden of flu in susceptible viruses when administered within two days of symptoms appearing. Tamiflu can also be used to reduce the chance of infection in people aged 1 year and older who have increased risk of flu because of close contact or community outbreaks. The potential preventative benefits are an important component of most countries' pandemic response plans.

Influenza viruses are RNA viruses, which means they are prone to rapid mutation and are known to mutate more quickly than most other viruses. As these mutations occur, some strains build up a resistance to antivirals commonly used to treat influenza. The level of antiviral resistance may vary by strain. Recently, both circulating strains of seasonal flu and some strains of H5N1 (avian flu) have shown resistance to Tamiflu.

A report on the seasonal influenza strains circulating in Europe reveals that some H1N1 viruses show signs of resistance to Tamiflu. Nineteen of 148 influenza A H1N1 samples from 10 European countries tested positive for resistance to oseltamivir. The Tamiflu-resistant variant has a H274Y mutation. However, this strain is sensitive to other antivirals including zanamivir, amantadine, and rimantadine. The European Centre for Disease Prevention and Control reported rates of Tamiflu resistance as high as 70% in a viral strain circulating in Norway. A similar mutation is being seen in other regions of the world. Almost 10% of cultured strains in the United States showed resistance to Tamiflu.

Several strains of the H5N1 virus have also shown Tamiflu resistance. Resistance has been observed in several countries and may contribute to the higher-than-average mortality rates in some countries (Vietnam, Indonesia, and Egypt). The resistance level has been primarily mild, but this has raised some questions about the potential efficacy in using Tamiflu as the primary line of defense for H5N1 and has increased emphasis on non-pharmaceutical interventions.

It is likely that the resistant strains will continue to spread and more strains will evolve resistance. However, the level of resistance varies considerably. Tamiflu may still be effective in limiting the severity of illness or reducing the potential for infection, but less so than in non-resistant strains. Many circulating strains are still susceptible to Tamiflu and it is efficacious in reducing the severity of illness as well as preventing infection.

Antiviral drugs are significantly more difficult to produce than antibacterial drugs because the virus life cycle is dependent on the host. It is quite easy to kill most viruses; however, these methods also kill the host cells as well, making them undesirable for widespread use. Researchers are currently focused on developing drugs that target molecular machinery unique to the virus. The more knowledge gained about the molecular structure of viruses, the closer we come to developing a successful drug. The ever-changing characteristics of viruses make this a monumentally difficult task and it is doubtful we will have a viral miracle drug in the near future, so we will continue to rely upon Tamiflu.

RMS incorporates the effectiveness of Tamiflu and its uncertainty, together with the stockpiles currently held by each country, in the modeling of the counter-measures to assess the likely losses to life and health portfolios in that country. Information suggesting lower Tamiflu efficacy increases the likelihood of more severe losses in the modeling.

INCREASED LONGEVITY MAY HAVE A LINK TO THE BODY'S GROWTH HORMONE PRODUCTION

New evidence confirms the link between genetic abnormalities affecting insulin-like growth factor 1 (IGF1) activity and longevity in humans. Combined with the current development of anti-cancer drugs that target the IGF1 receptor, the prospect of new treatments to prolong life suddenly appears credible.

In March this year, a team from the Albert Einstein College of Medicine (AECM) in New York published a paper identifying a link between reduced insulin growth factor-1 (IGF1) activity and longevity. They studied a group of centenarians of Ashkenazi Jewish descent and found evidence of partial loss-of-function mutations in IGF1 receptors. Their results add weight to previous research from the Leiden University Medical Centre in Holland, which found a correlation between low insulin/IGF1 signaling pathway activity and increased lifespan. The Leiden University study lacked controls, making it difficult to untangle association and causation. Getting matched controls for the extreme elderly is understandably very difficult, but the AECM researchers overcame this difficulty by including the children of the centenarians in their study. The serum IGF1 levels were compared between the children of the centenarians and their matched controls. The tests showed decreased IGF1 effectiveness in females of this long-lived cohort, but no real difference was seen in the men. The results are not a complete surprise, as there have been similar findings with various animals revealing a number of common links. Previous studies on fruit flies and mice showed the same gender effect.

Another factor is cell and body size. It is known that short stature is a predictor of longevity. Some of the longest-lived ethnic groups are also shorter than the average, relatively short-lived Westerner. In the AECM study, controls were over an inch taller than the progeny of centenarians, and studies in mice and fruit flies also show a size discrepancy corresponding to longevity. Caloric restriction has long been known to be associated with longevity, but researchers from the National Institute of Environmental Health Sciences in San Francisco in the early 1990s found that in mice, the effect could be abolished by correcting the calorie-induced reduction in IGF1 levels with supplementation. It seems that IGF1 activity is the common link between a number of different factors known to predict lower mortality rates, increasing confidence that it is the key to underlying mechanisms controlling longevity risk.

Why should the IGF1 under-activity result in longer life expectancy? The answer is probably a complex one involving reduction in death rates from various diseases and a slowing of the cell aging process. However, it has long been recognized that there is a clear reduction in cancer mortality with reduced IGF1 levels. This has led to a great deal of research into the potential role of IGF1 receptor blockers as treatments for cancer. Many cancers express IGF1 receptors on their surface, and lower cancer rates are seen with lower IGF1 serum levels.

One of the important things about this line of research is that it offers mechanisms for potential interventions designed to increase lifespan. Ultimately, genetic manipulation could lead to a new generation of humans that are longer-lived. It is now possible to interfere with the binding of IGF1 to its receptor in order to reduce IGF1 activity, a commonly exploited mechanism of drug action in treatment of various diseases. Concerns that IGF1R blocking agents might inadvertently cause diabetes have been allayed by clinical trials of an IGF1 receptor blocker in 2007. While these are currently intended as cancer treatments, they open up the possibility of specific 'longevity' drugs being available in the future.

The genetics of IGF1 activity is one of the many genetic links to longevity currently being explored by researchers. Further understanding of the genetics of longevity and the creation of targeted 'longevity' drugs could significantly increase human lifespan. RMS is monitoring advancements in longevity research and exploring the impact of this and other advancements in the development of a longevity modeling solution.

OTHER DEVELOPMENTS IN BRIEF

H7N2 strain of Influenza identified as a pandemic candidate

Recent research by a team led by Terrence Tumpey at CDC has identified that some H7 strains of influenza, mainly found in birds, have evolved some of the traits they would need to become infectious between humans. In 2003 the strain H7N7 hit poultry in the Netherlands and less severe forms, H7N2 and H7N3 have caused several outbreaks between 2002 and 2003. Several human cases have been tracked, but symptoms have been mainly mild, with only one human death. Analysis of a human case in 2003 shows that the H7N2 is capable of replicating in the respiratory tract of mammals, which is unusual for an avian virus, and indicates the potential for it to evolve into a humanly transmissible form, for which the population has no immunity, causing a pandemic.

Quitting smoking follows social network patterns

Longevity and health studies try to estimate the numbers of smokers in a portfolio of insureds or pension holders. A recent study published in the New England Journal of Medicine explores the patterns of how people give up smoking, and shows that it spreads like an infectious disease, with the chances of an individual smoking decreasing if their spouse gave up (67%) , or their friends quit (36%), or co-workers (34%) or siblings (25%). Neighbors quitting had negligible impact, suggesting that the phenomenon of giving up smoking is a response to a cultural shift, passing through a social network. Portfolios that contain social networks – or work groups – may have a high correlation of non-smokers that is unrepresentative of the population at large.

New pre-pandemic vaccine approved

GlaxoSmithKline won European Union approval in May 2008 for a vaccine against multiple strains of avian influenza. This would be useable against a range of potential strains that could emerge as a humanly transmissible virus. The vaccine depends on a new type of adjuvant (a booster to the effectiveness of the antigens that are produced). The adjuvant is an oil-in-water emulsion so powerful that only a twentieth of the usual amount of antigen is needed.

Second genetic link to weight and obesity

A genome-wide search for type 2 diabetes-susceptibility genes identified a common variant in the FTO gene that predisposes to diabetes through an effect on the Body Mass Index, which is a standard measure of obesity. This first genetic link to obesity was published last year. On May 4, 2008, a study was published in Nature Genetics uncovering new genetic variants that influence fat mass, weight and risk of obesity. The variants act in addition to the variants of the FTO gene. Adults carrying variants in both genes are, on average, 3.8 kg (or 8.5 lb) heavier. The variants map close to a gene called MC4R: mutations in this gene are the most common genetic cause of severe familial obesity.

RISK MANAGEMENT SOLUTIONS FOR THE LIFE & HEALTH INSURANCE INDUSTRY

Risk Management Solutions, Inc., (RMS) applies the latest science in analytical tools for making risk management decisions in the life and health insurance industry, including management of excess mortality, excess morbidity and longevity risk.

RMS licenses its models in software to clients, and also provides consulting services, technical support, model outputs, and other applications of its research and development.

RMS has a suite of catastrophe risk models to assess the frequency and severity of excess mortality in life insurance portfolios resulting from a number of potential causes of high fatality events. RMS models are stochastic, objective, and transparent, derived from scientific analysis of each of the threat phenomena. The models provide an independent assessment of risk metrics for use in portfolio management, pricing, and risk transfer decision making.

PROBABILISTIC MODELS

- Influenza Pandemic
- Other Infectious Disease Pandemics
- Terrorism Mortality and Morbidity
- Earthquake Casualty
- Other Natural Catastrophes

CONSULTANCY SERVICES

RMS provides consulting services to help life and health insurers across many areas of risk management. Projects include balance sheet analyses and implementation of regional portfolio management, specific loss liability areas, business continuity management, insurance product design, alternative risk transfer, and reinsurance optimization. RMS has provided risk management services for a number of the leading life and health insurers worldwide.

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RMS Pandemic Influenza Model Overview factsheet

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