Waiting for a pandemic

Rino Rappuoli and Giuseppe Del Giudice

Novartis Vaccines and Diagnostics, Via Fiorentina 1, 53100 Siena, Italy

Abstract

After a quiet period of nearly 30 years, influenza strains with hemagglutinin types that have not been seen in humans previously started to jump from birds to man, suggesting the risk of a new influenza pandemic. However, in contrast to the situation with all the other influenza pandemics occurring in the 20th century and before, in the 21st century we have sophisticated technologies for diagnosis, therapy and prevention. Modeling of the possible spread of a pandemic suggests that vaccination is by far the only way to eliminate the risk of a new pandemic. In this chapter we review the development of new vaccines against H5N1 viruses, showing that effective vaccines adjuvanted with oil-in-water emulsion are about to be licensed and will soon be available. The race against an influenza pandemic has begun; it is a battle against time that mankind cannot afford to lose.

Introduction

Since 1580, at least ten influenza pandemics have occurred, with an average of one pandemic every 42 years. Analysis of the most recent and more accurate data predicts one pandemic every 30 years (see the chapter by Lattanzi). The last pandemic was in 1968, 40 years ago and therefore common sense and mathematical models predict that we should be prepared for a new pandemic. During the last 9 years, all the events that are expected to happen before a pandemic did happen. First, a new virus carrying the H5 antigen, that had never been in humans before jumped from chickens into man and killed six people in Hong Kong in 1997. This early outbreak was contained by culling chickens in the Hong Kong area. The virus momentarily disappeared and we forgot about it for a few years. However, the virus was not dead at all; it was successfully breading, multiplying and expanding in birds in South East Asia [1], until it suddenly blew up again with human cases in 2003 and 2004 in Vietnam, Thailand, Indonesia, and China. Clearly
the virus had escaped any control and was so widespread that since then culling hundreds of million of chickens in the areas of outbreak has provided only a temporary relief, but has never been able to control the spread of the virus. The virus, in fact, was spreading globally using migratory birds as vectors and soon appeared in the rest of Asia, Russia, Turkey, Egypt, and Nigeria. Today, the H5N1 virus is endemic in the bird population in Asia, Europe, and Africa. While spreading geographically, the virus has also been evolving and drifting antigenically, so that today we have many genetically distinct isolates of the H5N1 virus that can be classified into several clades and subclades (see Fig. 1). Up to 1 February 2008, the virus caused

Figure 1. Evolution and nomenclature of the H5N1 virus isolates. Bold face indicates the most commonly studied viruses. Bold numbers on the right hand side indicate the clades and subclades.