1. Introduction

Background information Tuberculosis (TB) is a disease caused by Mycobacterium tuberculosis (M. tuberculosis) and a number of other bacteria belonging to the Mycobacterium tuberculosis complex (MTBC). The causative agent of most human cases of TB was discovered by Robert Koch in 1882, for which he received the Nobel Prize. TB is a chronic and infectious disease which affects mainly the lungs, causing mild to severe pulmonary symptoms in addition to wasting and fever. In addition to the more common symptoms, an infection can, in rare cases, disseminate to other parts of the body, including the bones and soft tissues (Santos & Roberts, 2001).

Tuberculosis tends to be prevalent in patients under 5, between 15 and 30, and over 60 years of age (Roberts & Buikstra, 2003). These broad categories of vulnerable individuals make a deadly and pernicious disease, which can have significant impacts on health and longevity, all the more troublesome from the perspective of global health efforts. Despite these devastating effects, infection with members of the MTBC does not always result in the development of fullblown TB. According to previous research (Comstock, 1982), only a very small percentage of infected individuals will develop an active, full-blown form of the disease, and in many cases the disease will lay dormant in the individual’s body for a number of years. This dormancy can later be interrupted by events such as illness, distress to the immune system or malnutrition. This has lead tuberculosis to be considered a disease of the poor, tending to occur at a greater frequency in regions where inadequate sanitation, malnutrition and high population density are issues (World Health Organization, 2009).

To demonstrate the extent to which TB is a contemporary issue, the World Health Organisation (2009) estimates that 1.2 - 1.5 million people died from the disease and its related complications in 2008 alone, and additionally suggests that as many as one third of the world’s population may be infected with the bacteria at any one time. Of these, it is supposed that 0.35 million cases were patients suffering from human immunodeficiency virus (HIV), which weakens the immune system and renders people more susceptible to microbiological infections such as TB (Chaisson & Martinson, 2008). HIV is thought to be one of the key factors influencing the rise of tuberculosis in the modern world (Griffith & Kerr, 1996).

The resurgence of tuberculosis is an urgent problem in many parts of the world, and warrants extensive research into the historical migration and evolution of the disease (World Health Organization, 2009). It is of vital importance that scientists understand the reasons for disease outbreak and spread if we are to tackle microbiological diseases in the long term and, as is the ultimate goal, learn to predict future outbreaks and take adequate measures to protect those at the greatest risk. One possible explanation to this resurgence proposed is the development of resistance to antibacterial drugs – a problem that has been reported for mycobacteria and many other species (Farmer, 2001). Natural selection has the potential to mould bacteria into resistant strains, an outcome that is entirely probable due to the sheer numbers of bacteria in the environment and the prodigious ability of bacteria to adapt to environmental stressed at an alarming rate. As mentioned above, infection with HIV is another possible reason for the current rise of tuberculosis as it weakens the immune system, resulting in Acquired Immunodeficiency Syndrome (AIDS), which renders patients increasingly vulnerable to TB, who often lacking the necessary immune strength to combat the disease (Raviglione et al., 1995).

Tuberculosis is a historical as well as a modern disease. As such, the question of how the disease may have impacted on the lives of ancient humans at different points has been a focus of archaeological research (Chalke, 1959). Biomolecular archaeology aims to study the prevalence, evolution, and history of diseases in the ancient world using modern methods of biochemical analysis. Biomolecular archaeology tends to be most effective and informative when bone material is present due to the nature of DNA degradation, and the protective properties of the bone matrix on DNA (Redman et al., 2009) and other molecules. Tuberculosis, being primarily a pulmonary disease, yet disseminating to the bones in a small number of cases, provides molecular biologists with a key opportunity to study the disease (both specifically and as a model for other bacterial diseases) in ancient remains from a number of sites around the world.

The remainder of the introductory chapter will be dedicated to a detailed overview of TB, including the symptoms and epidemiology of the disease, in addition to the skeletal manifestations of the disease and their relevance to the study of the TB in the context of archaeology. A detailed analysis of prior research into tuberculosis DNA and especially lipids will follow, and many of the 12 techniques and principles of the present project will be assessed prior to a detailed documentation of procedures in the “materials and methods” chapter. Finally, the aims of the project will be laid out clearly

źródło tekstu: https://www.escholar.manchester.ac.uk/api/datastream?publicationPid=uk-ac-man-scw:244382&datastreamId=FULL-TEXT.PDF