Sequencing the Black Death Genome

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From 1347 through 1351, a vicious pandemic now colloquially known as the “Black Death” claimed the lives of approximately 30 million people, or an estimated 30 – 50% of the European population. In the last several decades, academic and biomedical interest in the causative agent of the pandemic fuelled controversial claims where the prevailing view that the disease was caused by an intense outbreak of Yersinia pestis (bubonic plague) was challenged based on historical descriptions of the disease that differed from modern accounts of bubonic or pneumonic plague infections. In recent years, ancient DNA data from victims of the medieval outbreak have strongly implicated Y. pestis as the responsible pathogen. DNA survives in the fossil record longer than theory predicts, the determinants of which are dependent upon a complex array of environmental factors that are difficult to model. Post mortem, DNA is cleaved to short fragment sizes that range between 30-60bp, the thermodynamics of which enhance preservation. We have used a novel enrichment technique to capture and sequence the genome of the bacteria 'responsible' for the Black Death. I will discuss the implications of this research in the context of understanding the evolution of virulence and the co-evolution of their hosts, namely humans.