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The Genome of the Black Death

Genome wide data from ancient microbes may help to understand mechanisms of pathogen evolution and adaptation for emerging and re-emerging disease. Using high throughput DNA sequencing in combination with targeted DNA enrichment we have reconstructed the ancient genome of *Yersinia pestis* from skeletons securely dated to the Black Death pandemic from the East Smithfield cemetery in London, England, 1348 – 1350. Phylogenetic analysis indicate that the ancient organism is ancestral to most extant *Y. pestis* strains and falls very close to the ancestral node of human infectious *Y. pestis* that had their genome sequenced. Temporal estimates suggest that the Black Death of 1346 – 1351 was the main historical event responsible for the introduction and worldwide dissemination of currently circulating *Y. pestis* strains pathogenic to humans, and further indicates that contemporary *Y. pestis* epidemics have their origins in the medieval era. Comparisons against modern genomes reveal no unique derived positions in the medieval organism, suggesting that the perceived increased virulence of the disease during the Black Death may not have been due to bacterial physiology. These findings support the notion that factors other than microbial genetics, such as environment, vector dynamics, and host susceptibility should be at the forefront of discussions regarding emerging *Y. pestis* infections.

When: Thursday 17th, May, 2012  
Where: Benham Lecture Theatre  
Time: 3pm for 3:10pm start - 4pm.

All Welcome