Lilly Pfister

10/21/22

Dr. Tamara Davis

Biology 110

How the Black Death Changed Our Genome

In the mid-thirteen hundreds, the bubonic plague, commonly known as the Black Death, killed 30-50% of Afro-Eurasia, leaving a mark on both the human genome and history. Researchers led by Jennifer Klunk analyzed the extent of ~~this mark~~ it's influence after uncovering medieval remains of people before, during, and after the plague. They ~~then~~ continued to examine~~d~~ ~~if~~ the survivors of the Black Death to see if they carried mutations ~~to~~ that protected them from infection.

To do this, Klunk and her team used samples from three cemeteries in London and five cemeteries in Denmark. Researchers found 245 immune gene variants that rose or fell in response to the Black Death. Four highly differentiated candidate loci were chosen from the variants and suggested positive selection, ~~which is~~ the process where advantageous genetic variants sweep a population. These four loci were the mutations that most likely gave individuals a selective advantage.

The gene that stood out the most, ~~however,~~ was ERAP2. Previous work has shown that ERAP2 works in the immune response, highlighting ~~its~~ the importance of it's role against infection. Individuals with more copies of ERAP2 were better able to restrict the intracellular replication of Y. pestis, the bacterium that caused the plague. This implies that changes in ERAP2 allele frequencies during the Black Death were probably due to Y. pestis-induced natural selection.

Two variants of ERAP2 were found in the samples; one that encodes for a full length ERAP2 protein and one that encodes for a truncated, or shortened, one. Individuals who were homozygous for the full-length protein had an increased chance of surviving the plague by 40% compared to individuals with the truncated one. The full-length protein can increase ERAP2 expression and increase the expression of antibodies against Y. perstis.

Londoners carrying copies of the protective ERAP2 variant increased from 40% to 50% before and after the plague while in Denmark the proportion rose from 45% to 70%. Researchers have never documented a surge in natural selection in humans as strong as this one. As geneticist Luis Barreiro says, "A 10% change in allele frequency in only three to four generations is highly unusual". The protective variant is still found in 45% of British people today, which given its risk for autoimmune disorders, suggests that it was favored by natural selection until recently.

Though individuals with the advantageous haplotype are better at limiting bacterial growth, they typically have a weaker cytokine response to infection. The full-length ERAP2 gene is associated with autoimmune disorders such as Crohn's disease and rheumatoid arthritis.

While these results are incredible for illustrating the influence infection has over natural selection, the sample size for the study was relatively small. Only 206 individuals were deemed to have suitable DNA for data collection and only two areas (London and Denmark) were examined. The Black Death spanned across Europe, Africa and Asia and further studies could look into how more populations were impacted by Y. pestis.

despite ing

Though this study, examined a relatively small number of remains, researchers expect the

only

results to hold up as the criteria for the study were extremely thorough to ensure genetic changes were due exclusively to Y. pestis and not all infections. The findings are fascinating and the implication that natural selection can work as quickly as it did shows that genetic shifts might have saved people from the Black Death, not just improved cleanliness.

any examples of implications ?

overall: well written, diction can improve in some areas and i don't think it should be broken into so many tiny paragraphs. longer paragraph would make it feel more concise.