

Polygenic plague resistance in the great gerbil uncovered by population sequencing

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Abstract

Pathogens may elicit a high selective pressure on hosts and can alter genetic diversity over short evolutionary timescales. Intraspecific variation in immune response can be observed as variable survivability from specific infections. The great gerbil (*Rhombomys opimus*) is a rodent plague host with a heterogenic but highly resistant phenotype. Here, we investigate if the most plague-resistant phenotypes are linked to genomic differences between survivors and susceptible individuals by exposure of wild-caught great gerbils from Northwest China to plague (*Yersinia pestis*). Whole genome sequencing of ten survivors and ten moribund individuals revealed a low genome-wide mean divergence, except for a subset of genomic regions that showed elevated differentiation. Gene ontology (GO) analysis of candidate genes within regions of increased differentiation, demonstrated enrichment of pathways involved in transcription and translation and their regulation), as well as genes directly involved in immune functions, cellular metabolism and the regulation of apoptosis. Differential RNA expression analysis revealed that the early activated great gerbil immune response to plague consisted of classical components of the innate immune system. Our approach combining challenge experiments with transcriptomics and population level sequencing, provides new insight into the genetic background of plague-resistance and confirms its complex nature, most likely involving multiple genes and pathways of both the immune system and regulation of basic cellular functions.

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