

Genome of American cockroach sequenced for the first time

March 23 2018, by Bob Yirka



A close-up image of the American cockroach. Credit: Sheng Li

A team of researchers with South China Normal University and the Chinese Academy of Sciences has for the first time sequenced the genome of the American cockroach. In their paper published in the journal *Nature Communications*, the group describes features of the genome likely to prove useful to the insect in adapting so well to human environments.

The American [cockroach](#), oddly enough, did not actually evolve in America; it arrived via ships from Africa hundreds of years ago. It is also closely related to termites. In this new effort, the research team describes their efforts in sequencing the cockroach [genome](#), and offers some insights regarding the findings.

They found the insect has approximately 20,000 genes, surprisingly near the number of [human genes](#). The genome is among the largest in the insect world, smaller only than that of the locust, though many of its segments, they found, appeared to be repetitive. But perhaps more importantly, the team found that the cockroach has genes that give it a strong sense of smell, some that help it combat infections (which helps it thrive in dirty places), and others that help it to detoxify itself when it consumes toxic food. It also has genes that confer immunity and help to metabolize a wide range of food, including, they note, some ingredients found in insecticides. They found it also had genes that ward off a variety of ailments and other genes that regrow lost limbs. The researchers also found a large number of [genes](#) related to physical development, which allows the insect to grow so large and to molt many times along the way.



A close-up image of the American cockroach colony. Credit: Sheng Li

The researchers suggest the American cockroach has a genome that provides it with the tools needs to exist in a host of sometimes hostile environments, which explains how it has become the largest insect that lives among humans. On a positive note, the researchers report that they

found no evidence indicating that the insect could survive a nuclear holocaust.

Sequencing the genome of the pest, the researchers note, is likely to offer many benefits, such as learning how it is able to survive in environments that would kill most other insects and animals, or how it is able to regenerate limbs. There is also the possibility that in studying the cockroach genome, scientists will one day find a way to eradicate them.

More information: Sheng Li et al. The genomic and functional landscapes of developmental plasticity in the American cockroach, *Nature Communications* (2018). [DOI: 10.1038/s41467-018-03281-1](https://doi.org/10.1038/s41467-018-03281-1)

Abstract

Many cockroach species have adapted to urban environments, and some have been serious pests of public health in the tropics and subtropics. Here, we present the 3.38-Gb genome and a consensus gene set of the American cockroach, *Periplaneta americana*. We report insights from both genomic and functional investigations into the underlying basis of its adaptation to urban environments and developmental plasticity. In comparison with other insects, expansions of gene families in *P. americana* exist for most core gene families likely associated with environmental adaptation, such as chemoreception and detoxification. Multiple pathways regulating metamorphic development are well conserved, and RNAi experiments inform on key roles of 20-hydroxyecdysone, juvenile hormone, insulin, and decapentaplegic signals in regulating plasticity. Our analyses reveal a high level of sequence identity in genes between the American cockroach and two termite species, advancing it as a valuable model to study the evolutionary relationships between cockroaches and termites.

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