

Can you really eat just one?

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A Kansas State University genomicist is hoping an old potato chip slogan -- "betcha can't eat just one" -- will become the mindset of researchers when it comes to sequencing insect genomes.

"I've made the joke that genomes are like Lay's [potato chips](#) -- no one can sequence just one," said Susan J. Brown, a professor of biology and director of the Arthropod Genomic Center at K-State. "The idea is that when you sequence one [genome](#), you want to sequence another that's closely related and compare them."

A genome is basically the blueprint of an organism. It's made up of [DNA sequences](#) and all of the organism's genes, which contains the [genetic information](#) for their traits. Consequently, genome databases have become an essential tool in 21st-century biology.

"In each genome there are all these genes that scientists know nothing about," Brown said. "But when, for example, you change an organism's [food source](#), you all of the sudden see these genes being expressed. So we can study that and try to figure out if the expression is for an enzyme to digest the food source, or if it's being used to protect the insect from something that's in the food source."

Brown studies the genome of *Tribolium castaneum*, the red [flour beetle](#), and has helped turn the beetle into a [model organism](#) for geneticists. Her expertise in entomological genomics and [bioinformatics](#) led to her being named a 2011 Fellow of the Entomological Society of America in July. It's also put her at the forefront of two major genome projects that were

launched in recent months.

I5k is an initiative to sequence the genomes of 5,000 insects and [arthropods](#) during the next five years. It was introduced in a letter to the editor in the March issue of Science magazine and has been called "the Manhattan Project of Entomology."

"Having the information available from all of the insect genomes will allow us to understand the basic biology of the insect better so we can try to control them," Brown said. I5k is expected to transform the study of insect, pest and vector biology, and also improve quality of life for humans, as many entomological species pose threats to health, food supplies and economics.

Though sequencing 5,000 new insect and arthropod genomes isn't a small number, current sequencing technology is faster and more affordable than it was even a decade ago, Brown said. This has increased the appeal of genome sequencing and has brought several new researchers and laboratories together in an effort to expand the entomology genome database.

Brown also recently helped start Agripestbase, an online database for researchers that contains the sequenced genomes of various pest insects. Researchers can download the sequence of genes, proteins or even a genome as well as post and edit information about specific genes -- similar to a sophisticated wiki, but tailored to the scientific community. The goal of Agripestbase is to aid laboratories in finding new and better methods for pest control.

Agripestbase currently includes the genomes of *Tribolium castaneum*, the red flour beetle; *Mayetiola destructor*, the Hessian fly; and *Manduca sexta*, the Tobacco hornworm.

Each insect in the database is linked to [entomology](#) research being done in various K-State laboratories -- several of which are studying and targeting insect immunity and the exoskeleton.

Brown said she ultimately wants the i5k and Agripestbase to inspire biologists, entomologists and researchers who may be unfamiliar with genomes and the sequencing process to try sequencing an insect.

Though once they do, she hopes they find it hard to sequence just one.

Provided by Kansas State University

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