

Researchers sequence pepper genome, find jumping genes enhanced diversity

March 4 2014, by Marcia Malory



The image illustrates field performance of Zunla-1 at post-break stage. Credit: Cheng Qin

(Phys.org) —Cheng Qin of Sichuan Agricultural University in China and his colleagues have sequenced the genomes of wild and domesticated peppers and found that a large percentage of the pepper genome consists of transposons, "jumping genes" that change position within the genome.

These transposons probably were responsible for the pepper's great degree of genetic diversity. The research appears in the *Proceedings of the National Academy of Sciences*.

The pepper (genus *Capsicum*) is a member of the Solanaceae, or nightshade family, which also includes the tomato, potato and eggplant. At least 32 species of pepper are native to tropical America; Native Americans domesticated five of these around 6000 BC. Peppers adapt easily to different and agricultural and [climatic conditions](#); consequently, pepper cultivation spread throughout the world after Columbus reached the Americas. In 2011, the worldwide pepper harvest reached 34.6 million tons. Today, [peppers](#) come in a wide variety of size, shapes and colors. They range in taste from bland to extremely spicy. People use peppers as food, as spices, as medicine and as ornamental crops.

To gain a better understanding of pepper evolution, Qin's team generated and analyzed the genomes of two types of peppers: a cultivated pepper known as Zunla-1, and its wild ancestor, Chiltepin. The researchers discovered that more than 81% of the pepper genome consists of transposons. In comparison, transposons make up only 50.3% of the tomato genome and only 47.2% of the [potato genome](#).

The team found that most of the transposons in the pepper appeared about 300,000 years ago. They concluded that the pepper's genomic expansion would have begun then. When they created a phylogenetic tree by examining pepper, tomato, potato, grape, papaya and rock cress genes, they found that that the Solanaceae family first appeared almost 156 million years ago, and the pepper diverged from the tomato and potato about 36 million years ago. Thus, the expansion of the pepper genome occurred very late in the pepper's evolutionary history.

By resequencing the genomes of 18 different types of Zunla-1, two forms of Chiltepin and the semi-wild pepper *Capsicum chinense*, Qin's

team was able to identify genes, added to the [genome](#) after domestication, associated with seed dormancy, disease resistance and the ripening process, which affects shelf life. The researchers also identified the genes that affect the synthesis of capsaicin, the chemical that makes pepper spicy. The team believes these findings will benefit pepper breeding programs.

More information: "Whole-genome sequencing of cultivated and wild peppers provides insights into Capsicum domestication and specialization," by Cheng Qin et al. *PNAS*, www.pnas.org/cgi/doi/10.1073/pnas.1400975111

Abstract

As an economic crop, pepper satisfies people's spicy taste and has medicinal uses worldwide. To gain a better understanding of Capsicum evolution, domestication, and specialization, we present here the genome sequence of the cultivated pepper Zunla-1 (*C. annuum* L.) and its wild progenitor Chiltepin (*C. annuum* var. *glabriusculum*). We estimate that the pepper genome expanded ~0.3 Mya (with respect to the genome of other Solanaceae) by a rapid amplification of retrotransposons elements, resulting in a genome comprised of ~81% repetitive sequences.

Approximately 79% of 3.48-Gb scaffolds containing 34,476 protein-coding genes were anchored to chromosomes by a high-density genetic map. Comparison of cultivated and wild pepper genomes with 20 resequencing accessions revealed molecular footprints of artificial selection, providing us with a list of candidate domestication genes. We also found that dosage compensation effect of tandem duplication genes probably contributed to the pungent diversification in pepper. The Capsicum reference genome provides crucial information for the study of not only the evolution of the pepper genome but also, the Solanaceae family, and it will facilitate the establishment of more effective pepper breeding programs.

© 2014 Phys.org

Citation: Researchers sequence pepper genome, find jumping genes enhanced diversity (2014, March 4) retrieved 19 April 2024 from <https://phys.org/news/2014-03-sequence-pepper-genome-genes-diversity.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.