

Scientists discover common genes that defend coffee plants against devastating diseases



The Arabica coffee tree. Credit: NTU Singapore

Arabica coffee is the most economically important coffee in the world and accounts for 60% of the world's coffee products. But the plants it comes from are vulnerable to a disease that in the 1800s devastated Sri Lanka's coffee empire.

Today, an international team of researchers co-led by Nanyang Technological University Singapore (NTU Singapore) has made a breakthrough that helps protect Arabica plants (Coffea arabica) against the fungal disease called coffee leaf rust.

The other co-leaders of the study, published in Natural geneticsare based at Nestlé, the world's largest food and beverage company, the University of Montpellier in France and the University at Buffalo in the United States.

Scientists have mapped in great detail all the genetic material – or genomes – of Arabica and two related coffee plants. This allowed the team to identify a new combination of genes shared by coffee leaf rust-resistant plants. Using genome data, other useful traits in coffee plants can also be identified.

The discovery of resistance genes paves the way for better protecting coffee lovers' daily dose and maintaining the high-quality taste of their beverage, supporting an industry employing millions of workers. According to the International Coffee Organization, the livelihoods of 125 million people around the world depend on the coffee trade.

Coffee leaf rust has wreaked havoc in coffee-producing countries and continues to destroy coffee plantations today. The United States Agency for International Development estimated that between 2012 and 2014, an outbreak of coffee leaf rust caused approximately \$1 billion in economic damage in Latin America.

Assistant Professor Jarkko Salojarvi from NTU's School of Biological Sciences, who co-led the research team, said: "The high-quality genome sequences of the three plant species, as well as the candidate genetic sequences for resistance to coffee leaf rust, are the cornerstone of breeding new varieties of Arabica plants that are more adaptable to change and more resistant to diseases caused by pathogens such as fungi.

The project involved a large consortium of researchers and coffee breeders from Australia, Belgium, Brazil, Canada, China, Colombia, Finland, France, Germany, Indonesia, Italy, the Netherlands, South Africa, Spain, Switzerland, Uganda and the United States.

Dr Patrick Descombes, senior genomics expert at Nestlé Research and one of the co-leaders of the study, said: "While there are other public benchmarks for Arabica, the quality of our work team is extremely high. cutting-edge genomic approaches, including high-throughput long- and short-read sequencing, to create the most advanced, comprehensive and continuous Arabica reference to date.

## Low genetic variability

Arabica plants have low genetic diversity, making them susceptible to pests and diseases. Cultivated plants generally do not possess the genetic trait that confers resistance to coffee leaf rust, caused by the fungus Hemileia Vastatrix.

The fungi form orange-yellow spots on the leaves of coffee plants, which eventually wither and fall. Loss of leaves reduces the quality and quantity of berries from plants harvested for coffee preparation.

To avoid a potentially disastrous wipeout of Arabica plants worldwide due to coffee leaf rust, scientists studied the genomic origins and breeding history of the plant.

To do this, they mapped the highly detailed genome sequences of Arabica and two related coffeeproducing plants, Robusta (C. canephora) and C. eugenioides, which are the modern ancestors of Arabica.

This was achieved using advanced techniques, namely high-fidelity PacBio technology to sequence DNA with high precision, and high-throughput chromosome conformation capture to create detailed 3D maps of how different DNA segments interact. Genome data is publicly available.

Scientists' analysis suggests that Arabica's resistance to coffee leaf rust may have disappeared when Arabica plants became widely cultivated, because all Arabica coffee plants grown are from the same strain with very little genetic variability.

However, a hybrid of Arabica and Robusta resistant to the disease was found on the island of Timor in 1927. Unfortunately, resistance comes with a trade-off as the hybrid does not produce coffee as good as that other Arabica plants.

Without an alternative, the descendants of the hybrid Timor plant still form the basis of all leaf rustresistant variants of the coffee plant.

Previous research has discovered certain genes that potentially confer resistance to leaf rust in different coffee plants. But without a map of the genome of individual coffee plants, it was difficult to

precisely identify these genes and determine whether they were also present in other coffee plants, which would increase the chances that they code for resistance. The process of identifying genes was also slow.

However, thanks to new research mapping the genomes of different coffee plants in great detail, the identification of resistance genes will be faster and more precise.

Using the plants' genomic information, the researchers analyzed the most common cultivated coffee varieties, accounting for approximately 95% of global coffee production, and compared them to descendants of the Timor hybrid.

This allowed them to find a common region of DNA sequences among different leaf rust-resistant coffee plants, with a new combination of Robusta-based genes that can transmit resistance to Arabica plants in general. Knowing the existence of these shared genes greatly increases the likelihood that these genetic sequences can actually defend against leaf rust, and could allow breeders to select for them when growing new coffee varieties.

Through their analysis, the researchers also postulated that Arabica originated from a chance event 350,000 to 610,000 years ago, when Robusta and C. eugenioides plants were naturally cross-pollinated to create the first plants Arabica in the wild.

This dating falls between previous estimates, with an older one placing the chance event at just 20,000 years ago, while others push it back to a million years ago. The researchers said the discrepancy with earlier figures could be due to historical changes in the population sizes of wild and cultivated plants, as well as different sources and the limited amount of data used.

By comparing the high-quality genome sequences of Arabica with those of Robusta and C. eugenioides, the research team discovered that the three species are still very similar genetically. This suggests that for future breeding programs aimed at ensuring that Arabica plants are disease resistant, breeders may consider using other related coffee species, such as Robusta and C. eugenioides.

Using only Arabica plants to select for the resistance trait is problematic because the study found that even wild Arabica varieties, not just cultivated ones, have very low genetic diversity, making breeding more difficult. for disease resistance.

"The low genetic diversity of modern cultivated and wild Arabica plants constitutes an obstacle to their breeding using wild plant varieties. But the close similarities found between Arabica, Robusta and C. eugenioides plants are likely to facilitate the introduction of interesting traits from the latter two into Arabica," said Assistant Professor Salojarvi.

The highly detailed genome sequences mapped for the three coffee plants also mean that other useful traits could be identified in the future, such as drought resilience, higher crop yield and more aromatic coffee beans.

These traits can be identified using genetic markers, which can be used to predict the future performance of coffee plants, instead of waiting years for plants to mature and bear berries to find out.

Since the Timor leaf rust-resistant hybrid does not produce coffee as good as that of regular Arabica plants, the compiled genomic data now provides researchers with a fast route to breeding new disease-resistant plants that still retain their sublime, smooth appearance and the sweet taste of Arabica appreciated by coffee lovers around the world.

Plus d'information:

Jarkko Salojärvi et al, The genome and population genomics of the allopolyploid Coffea arabica reveal the diversification history of modern coffee cultivars, Natural genetics (2024). DOI : 10.1038/s41588-024-01695-w

The high quality genomes of Arabica, Robusta and C. eugenioides are available at this link: bioinformatics.psb.ugent.be/gdb/coffea\_arabica/

Journal information: Natural Genetics

https://news.india24.press/science/93990.html