

MEDIA RELEASE

UP researchers decode genome of king protea

University of Pretoria (UP) researchers are at the forefront of a very special first for South African plant sciences. They have unravelled the precise genetic make-up of the country's national flower, the king protea (*Protea cynaroides*). It is the first plant that's unique to South Africa – and the species-rich fynbos biome in particular – to have its entire genome sequenced in-depth.

“The project is also very special because most of the work was done in South Africa, one of the world's most biodiverse countries,” says project leader Professor Eshchar Mizrahi of UP's Department of Biochemistry, Genetics and Microbiology and its Forestry and Agricultural Biotechnology Institute (FABI).

Researchers from FABI, the Department of Biochemistry, Genetics and Microbiology, and UP's Department of Plant and Soil Sciences worked together on the resulting paper, which was published in The Plant Journal. They collaborated with plant genome evolution expert Prof Yves van de Peer's research group at Ghent University and the VIB Centre for Plant Systems Biology in Belgium. Prof Van de Peer also holds joint appointments at UP and the Nanjing Agricultural University in China.

Tissue from the “Little Prince” variety of king protea was used in the analysis because it is readily available in nurseries and would make further research easier.

Based on the entire genome sequencing work done, the researchers found that the genome of *Protea cynaroides* contains 12 distinctive chromosomes. It is about 1.18 gigabases (Gb) long, which means it contains more than 1.18 billion “letters” of the DNA alphabet (A,C,T and G) across these 12 chromosomes. In comparison, the human genome is about 3.2 Gb long, while that of *Arabidopsis thaliana*, the first plant ever sequenced, is about 135 Mb, or 0.135 Gb.

Surviving mass extinctions

The information has allowed the researchers involved to shed light on the evolutionary past of the king protea and other members of the *Protea* genus and larger Proteaceae family. They now believe that ancestors of the Proteaceae family developed an identical, duplicate set of their entire genome about 68 million years (MYA) ago. This helped the family as a whole to survive the K-Pg boundary, a mass extinction period around the late Cretaceous period some 66 MYA ago. The extinction event saw 60% of all plant species and 80% of all animals (including non-avian dinosaurs) disappear from Earth.

This genome duplication event happened before all extant lineages that are part of the larger Proteaceae family diverged some 63 MYA into what is today around 1 600 species, most occurring in the southern hemisphere. The common ancestor of the approximately 100 species of *Protea* found in South Africa and Australia's related macadamia nut trees (such as *Macadamia integrifolia*) and waratah (*Telopea speciosissima*) dates back to when dinosaurs went extinct.

It supports research previously conducted separately by two members of the project team, Prof Van de Peer and Prof Nigel Barker of UP's Department of Plant and Soil Sciences, who is interested in the evolution of the Proteaceae family. They suggested independently that polyploidisation (the condition where cells in an organism have more than one pair of chromosomes) could have helped plants to survive environmental turmoil and similar extinction events.

Cluster roots

Proteas survive and thrive in the nutrient-poor soils of the Cape Floristic Region of South Africa, thanks, in part, to their adaptive cluster root system. This allows the plants to take up as many nutrients as possible from the soil. Notably, it helps them to better "mine" for growth-enhancing phosphorous in the soil, which is usually not easily available to most plants.

Most plants take up nutrients with the help of a symbiotic relationship with soil fungi (the so-called arbuscular mycorrhiza symbiosis, or AM symbiosis) growing on their root systems or by forming nodules that contain nitrogen-fixing bacteria (such as is the case for legumes).

The research team's analysis of the king protea's genome proves definitively – and for the first time – that plant species in the Proteaceae family cannot form any symbiotic relationship with soil fungi because they have lost the specific genes that are involved in this process.

"The loss of these key genes ultimately caused the loss of AM symbiosis," Prof Mizrachi explains. "However, it is still unclear whether this was followed or preceded by the emergence of cluster roots in the Proteaceae family as an alternative way to take up nutrients from the soil."

He sets out the long-term value of continuing fundamental plant biology research.

"If we can find out more about how this function evolved, one day it might be possible to engineer this ability into crops so that they would need less fertiliser to thrive."

Research applications

The two lead authors of The Plant Journal paper, Jiyang Chang of the University of Ghent and geneticist Prof Tuan Duong of UP's Department of Biochemistry, Genetics and Microbiology, say that knowledge about the Protea cynaroides genome paves the way for researchers to better understand the molecular mechanisms that underlie various critical ecological adaptations that Proteaceae possess. This includes the ability of the plants to survive fires, their specialised way of acquiring nutrients from the soil through cluster roots and their unique variety of flower styles.

"It can help us understand the variation underlying the immense floral diversity of the Cape Floristic Region, an area known for the huge variety of endemic plants only found there," the two researchers say. "It can empower new research in plant diversification, horticulture and how plants in particular adapt to nutrient-poor soils."

The king protea genome has a relatively stable structure, as there had not been much rearrangement of the genome, and because it diverged very early from most eudicots (a clade of flowering plants with two seed leaves upon germination).

"Therefore, we could use it to study and compare ancient whole genome duplications in other plant species and, for instance, noted it in the genus Papaver, of which the opium poppy is a member," Prof Mizrachi says. He would like to see more South African investment in the sequencing of the genomes of more local plants, and more genomic research as a whole, led by African researchers, on the continent.

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Caption for infographic: What do macadamias, artichokes, proteas and dinosaurs have in common?
University of Pretoria researchers find that the common ancestor of the approximately 100 species of Protea found in South Africa and Australia's related macadamia nut trees (such as Macadamia integrifolia) and waratah (Telopea speciosissima) dates back to when dinosaurs went extinct.

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ABOUT THE UNIVERSITY OF PRETORIA

The University of Pretoria (UP) is one of the largest contact and residential universities in South Africa, with its administration offices located on its Hatfield Campus in Pretoria. This 115-year-old institution is also one of the largest producers of research in South Africa.

Spread over seven campuses, it has nine faculties and a business school, the Gordon Institute of Business Science (GIBS). It is the only university in the country with a Faculty of Veterinary Science, which is ranked the best in Africa.

UP has 120 academic departments and 92 centres and institutes, accommodating more than 56 000 students and offering about 1 100 study programmes. It has the most academic staff with PhDs (70%), NRF-rated researchers (613).

The 2023 QS World University Rankings by Subject ranked UP first in South Africa in Accounting and Finance, Law, Economics and Econometrics, Mechanical Engineering, Electrical and Electronic Engineering, Chemical Engineering, Mathematics, and Veterinary Science.

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