

## Press Release

### Large-scale gene expression data offer new clues for land plant evolution

*New work identifies similar gene expression patterns between equivalent organs of different land plants and suggests that novelties evolved via repurposing of pre-existing genes.*

**Oeiras, 12 July 2021** - Around 500 to 470 million years ago, plants started colonizing land. The earliest examples possessed a small axis terminated by a spore-forming structure, resembling to a certain extent nowadays mosses. From there, plant diversity on land exploded in a myriad of new species. Novel organs and structures allowed plants to dramatically alter the surface of our planet. Carbon dioxide levels decreased, oxygen abundance increased and terrestrial life flourished.

Evolving such a vast diversity of new organs, like roots, leaves, or immobile gametes, required coordinated genetic changes: appearance of novel genes, repurposing of genetic material, and development of new regulatory programs. “The activity of our genes is different in all our organs and many of them are only active in specific places. This is what makes each organ develop and fulfil its function. And it is no different in plants”, explains **Jörg Becker**, about the work developed as IGC principal investigator and member of GREEN-IT. Jörg is now the head of the Plant Reproduction and Evolution lab at ITQB NOVA, and signs this article with the double affiliation.

In a study published in **Nature Plants**, a consortium between Europe, including the team led by Jörg Becker, United States, and Singapore — introduces an atlas compiling gene expression data from ten land plant species—the largest collection to date. “We realized that collaboration between experts from different fields was a unique opportunity to maximize synergies and avoid duplication of research efforts”, Jörg highlights. Pivoting to a detailed analysis of the collected data, the team aimed at identifying novel components involved in forming organs and sexual cells. “Comparing data from such a diverse set of species allowed us to distinguish genes that play a role during reproduction in all land plants from genes that play a role only in flowering plants”, the researcher exemplifies.

The comparative analysis identified a large portion of the gene expression that has remained unchanged throughout evolution when looking at equivalent organs from

## Press Release

completely different species. “The main set of genes that are expressed tends to be similar across the analysed samples”, Jörg clarifies. Interestingly, the data hints yet at

another pattern, showing that the development of new plant organs was driven mainly through the repurposing of already existing genes. “We saw that many groups of genes appeared long before the corresponding organ, and this tells us that novelty in land plants relied a lot on repurposing existing genetic material”, explains the researcher.

Their vast expertise in the field of plant sexual reproduction prompted the team to also look for patterns in female and male gamete development. “We were particularly interested in comparing early land plants, which have swimming sperm and rely on water for sexual reproduction, with land plants with non-motile sperm cells, which are found inside the pollen grain and do not depend on water for mobility”, Jörg reveals. The team found that male reproduction seems more specialized than the female one, since male gametes express a higher number of unique genes. Among them were numerous transcription factors (proteins that regulate gene expression) and kinases (proteins that transfer phosphate to other proteins) that can be potentially important for pollen biogenesis and function.

Since around ten thousand years ago we have been making plants our main source of food and materials. But generating these valuable resources is getting increasingly harder. Human population expansion, competition for land use and global climate change put tremendous pressure on crop yield, and any step taken towards a comprehensive view of the inner workings of plants is thus invaluable. “Knowing which genes are important for the development and functioning of a specific organ gives us an indication of which genes we should manipulate to enhance its function. We are looking for the ones that make the development of sperm and eggs more resistant to heat stress, for example, and for ways to overcome fertilization barriers between plant species to obtain hybrids with superior qualities in the future”, Jörg remarks.

---

This study was developed at Instituto Gulbenkian de Ciência in collaboration with the EVOREPRO consortium (Gregor Mendel Institute, Austria, University of Regensburg, Germany, University of Leicester, UK, University of Warwick, UK, MPI Molecular Plant Physiology, Germany, now Nanyang Technological University (Singapore) and Brown University, US). Funding was granted by ERA-CAPS programme (FCT to JDB).

## Press Release

### Original paper

Irene Julca et al. **Comparative transcriptomic analysis reveals conserved programs underpinning organogenesis and reproduction in land plants.** Nature Plants.

DOI: <https://doi.org/10.1038/s41477-021-00958-2>

### More information

Ana Morais

Head of Institutional Communication

@: [anamorais@igc.gulbenkian.pt](mailto:anamorais@igc.gulbenkian.pt)

Contact: +351 965 249 488