

Synopsis

EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS

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DOMESTICATED PLANTS , FOOD FOR THE FUTURE

The production of food (mainly grains) will have to increase 70% to feed the more than 9 billion people on the planet by 2050, according to the United Nations Food and Agriculture Organization (FAO).

Over the past half century, the world population has doubled and grain yield has tripled. Improvements to production have been achieved, in part, by using more farmland, water and fertilizer. With the changing climate, we will no longer be able to use these techniques, forcing us to use other tools such as improvements in the basic knowledge of plant genetics.

Top global experts in agrigenomics presented their work in this field at [B-Debate](#), an initiative of [Biocat](#) and the [“la Caixa” Foundation](#) to promote scientific debate, in conjunction with the [Center for Research in Agricultural Genomics](#) (CRAG) and with support from the [National Science Foundation](#) (United States).

CONCLUSIONS:

- ✓ Food production will have to increase up to 70% to feed the world population by 2050. With climate change and the impossibility of continuing to use more farmland, water and fertilizer, **better knowledge of plant genetics is key to applying other improvements.**
- ✓ The first plant genome was published in 2000. Today we have the full genome of more than 80 species and thousands of varieties: for example, up to 3,000 varieties of rice. As this technology becomes cheaper, the amount of data in this field will continue to grow, but researchers **are working to understand this information and its possible applications.**
- ✓ **The plants we feed ourselves with today are the result of genetic modifications they have been subjected to by human beings since the Neolithic era**, first intuitively and later with more precise techniques
- ✓ **GMOs are just the result of one of these techniques to genetically modify plants.** Knowledge acquired through agrigenomic research can be applied to other techniques.

1. PLANTS, BORN TO CHANGE

Since the advent of agriculture 10,000 years ago, we've transformed some species of plants and animals to such an extent that they would now be unable to survive in nature. "We feed ourselves with species invented by human beings, which are the fruit of genetic modifications, like corn," explains Josep Casacuberta, coordinator of the plant and animal genomics program at the [Center for Research in Agricultural Genomics \(CRAG\)](#) and scientific leader of this B·Debate.

"Genomes are designed to change"

Josep Casacuberta

The ability of living beings to adapt to their environment and, thus to survive depends in large part on their ability to evolve. In plants, there are two main mechanisms that allow for change: **polyploidy** and **transposons**.

Polyploidy, or adding chromosomes, leads to a mosaic of new combinations. Bringing together and regulating so much new information isn't easy, which leads plants to a stabilization process.

Kirsten Bomblies, professor at Harvard University, researches the mechanisms that make this possible.

"We've identified several genes that seem to be essential to this process, and many of them are related to meiosis: the process of separating chromosomes that allows sex cells to form," explains Bomblies. During meiosis, information is exchanged between chromosomes. This researcher's hypothesis is that plants, once stabilized, limit this

exchange, thus compensating for the excess of information. "If confirmed, this theory could have important repercussions on human health," believes Bomblies. Human beings generate variations in different ways than plants do, but the polyploidy process can generally be seen in cancer. So, understanding the mechanisms that can diminish that imbalance could lead to applications in oncology research.

THE GENETIC SHUFFLE

Polyploidy is the adding of chromosomes, whether by multiplying those a plant already has or merging its chromosomes with those of another species. **Transposons** are a very different mechanism: they are mobile elements, small fragments of DNA that can move around, travel to other parts of the chromosome or to other chromosomes, and can create new traits on these excursions. They are, for example, responsible for the fact that some species of corn have different colored kernels: when a transposon controlling the color gene moves, the way it manifests externally also changes. And even though only some of them are active, they can comprise up to 80% of a plant's DNA.

In general, both mechanisms act like shuffling a deck of cards: polyploidy allows the plant to play with twice (or three or many times) as many cards; transposons allow it to change the order of the deck, trying out different combinations like a game of poker or as if searching for run.

Transposons —the small mobile fragments of “travelling” DNA— are also the focus of current research in agrigenomics. Some of these are more at risk of becoming activated, moving around the genome and causing changes. Marie Mirouze, researcher at the Montpellier Institute for Development Research, uses a technique to identify these elements that are “ready to jump”, which as a whole have come to be called the “mobilome”. To do so, she scans DNA circles,

or closed pathways the cell provokes in the transposons to prevent them from returning to the DNA once their copies have left it. One small error in that closing could allow them to return and transfer to the genome, provoking unpredictable changes.

2. HOW HAVE THE PLANTS WE EAT CHANGED?

Since the Neolithic era, humankind has selected the traits it most desired from each plant, thus guiding evolution in large part. Now, thanks to scientific research, there are many more precise improvement techniques, but for thousands of years these changes were carried out intuitively.

Studying these changes isn't easy. For example, to study the variations in Arabidopsis —the first plant genome to be deciphered— Oliver Loudet, head of the [INRA](#) research group, and his team have collected varieties from America, Sicily and even isolated areas (and therefore non-domesticated plants) like Tajikistan, in Central Asia.

From there, they study how the plants behave under stress, for example due to lack of water, and observe how they resist and grow and look for scientific (and epigenetic) explanations.

Carlos Alonso-Blanco, of the [Spanish National Center for Biotechnology](#), and his team do something similar in Madrid: studying varieties of the same plant and how they adapt to the seasons. In this search, they have found various regions associated with the flowering time, adaptation to high temperatures and even resistance to pollution.

3. PLANT BREEDING: PUTTING SCIENCE INTO PRACTICE

Once we know of these modifications, can they be used to improve crops? In 2000, the first plant genome was published; today we have the full genome of more than 80 species,

as well as the genome of different varieties of the same species: databases used continually by plant breeders .

“The use of GMOs is an option, but in no way is it the only one: the knowledge acquired can be applied to organizing crops, to implementing sequential planting or in cross-breeding”

Oliver Loudet,
Head of INRA research group

For Josep Casacuberta, scientific leader of the event and former member of the [European Food Safety Authority](#) (EFSA) Panel on Genetically Modified Organisms, GMOs are neither the only nor the whole solution, but he advocates calming the alarm generated by this type of crop. “GMOs are subject to strict risk controls and, furthermore, new techniques allow much closer control of the changes introduced,” he says. One of these techniques is called CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats), considered to be the great promise in gene therapy and whose use has even been proposed [to modify human embryos](#) and prevent genetic diseases.

As Casacuberta points out, “genomic variations have been brought about in plants consistently throughout history: in the 1950s, X-rays were used to provoke modifications currently found in many foods. **Without these advances,” he reiterates, “we wouldn’t be able to face the challenge of our future food needs and improving the species we eat.”**

James Giovannoni, researcher at the [Boyce Thompson Institute for Plant Research](#) (New York), presented the research that has allowed his team to analyze mutations and the epigenetics and metabolomics (all of the products derived from metabolism) of the tomato. “We’ve identified areas of the genome that affect color, texture, ripening and flavor,” he highlights.

Rod Wing, director of the [Arizona Genomics Institute](#), explained at the B-Debate how his work tackles head-on the problem of feeding a population that is growing with no end in sight. Therefore, his research focuses on rice, the most commonly consumed food on the planet. **“The inhabitants of societies that depend on rice will double by 2050,** and this grain is already the base of 50% of the world’s diet,” he points out. To improve it, “it must be more resistant, easier to grow and more nutritive,” he explains. So far, the genome of more than 3,000 varieties of rice have been sequenced, but now all of this information must be integrated and interpreted. To do this, Wing has helped set up the [International Rice Informatics Consortium](#), an initiative that aims to centralize and optimize all the work being done.

SWEETER MELONS THANKS TO THE GENOME

Jordi García Mas, CRAG researcher responsible for deciphering the melon genome, was one of the experts present at the B-Debate. His group has sequenced the genome of several melon varieties to study how they have evolved over time and how this has affected ripening. For example, some types of melon ripen when administered ethylene, a plant hormone. But the Christmas melon (the most common type in Spain) is immune to it and follows other pathways. Experts have identified an area of the DNA that seems to be directly involved in this process, and another that seems to be related to sugar accumulation and sweetness.