

PLANT BIOLOGY

Evolution Heresy? Epigenetics Underlies Heritable Plant Traits

LISBON—For some evolutionary biologists, just hearing the term epigenetics raises hackles. They balk at suggestions that something other than changes in DNA sequences—such as the chemical addition of methyl groups to DNA or other so-called epigenetic modifications—has a role in evolution. All of which guarantees that a provocative study presented at an evolutionary biology meeting* here last month will get close scrutiny. It found that heritable changes in plant flowering time and other traits were the result of epigenetics alone, unaided by any sequence changes.

The result could be a milestone in the debate, says Oliver Bossdorf, a plant evolutionary ecologist from the University of Tübingen in Germany. “I expect this will become a landmark paper.” At the very least, it will stoke one of the hottest topics in evolutionary biology. Nontraditional mechanisms of inheritance were the focus of three symposia at the meeting, two with standing room only attendance. “It’s an exploding field,” says Etienne Danchin, an evolutionary biologist at CNRS, the French national research agency, in Toulouse.

For 50 years, changes in an organism’s DNA sequence have been considered the sole currency of evolution. Epigenetic mechanisms—methylation and other chemical modifications that do not alter the sequence of DNA bases—can also influence a trait, by suppressing or promoting a gene’s activity. But those changes were thought to be too ephemeral to affect evolution. Although a few researchers have shown that epigenetic modifications can persist through several generations, critics would point out that these studies couldn’t rule out undiscovered genetic variation might really be in play. “The burden of proof is on the epigeneticist,” Bossdorf says.

Now, quantitative geneticist Frank Johannes of the University of Groningen in the Netherlands has tried to provide it. At the meeting, he described how he and colleagues tied DNA methylation patterns to heritable variation in flowering time and root length in different strains of the model plant *Arabidopsis thaliana*. The team was able to home in on differentially methylated DNA regions that were responsible for the variation—and

*The XIV Congress of the European Society for Evolutionary Biology was held 19–24 August.

to show that DNA sequences near and far from those sites were almost identical in all the lines.

The origins of Johannes’s analysis lie in work by Vincent Colot from the Institut de Biologie de l’Ecole Normale Supérieure in Paris and Philippe Guerche and Frédéric Hospital, colleagues from the



Epi-evolution? Hundreds of specially bred lines of *Arabidopsis* (bottom) reveal that epigenetic modifications underlie heritable variation in flowering time.

French agricultural research agency, INRA. Seven years ago, they crossed two nearly genetically identical *Arabidopsis* strains, one normal and the other lacking a gene whose protein helped maintain methylation. Through further breeding, the researchers created 500 *Arabidopsis* strains with distinct patterns of low and high methylation sites in their genomes—a catalog of epigenetic variation that researchers could then study for links to physical traits in the plant

lines. “To create these lines was really brilliant,” Bossdorf says.

In 2009, Johannes and his colleagues reported that some methylation patterns in these lines were stable over the eight generations tested. They also noticed differences in the plants’ flowering times and heights. Since then, Colot, Johannes, and their colleagues managed to pinpoint a few regions on the plant chromosomes that control flowering time and root length—and established those same sites had differences in methylation among the various plant lines.

Colot and his collaborators sequenced the genomes of 80 of the *Arabidopsis* lines studied, and with Johannes, have found almost no differences in the DNA at those same sites. The researchers also ruled out that the trait changes were caused by transposable elements, rogue DNA that’s typically held in check by methylation. “So the heritable basis [of the traits] had to be due to differential methylation,” Johannes concluded.

The study is “a huge step forward in showing that [methylation] has an impact in phenotype and matters in natural variation,” says Christina Richards, an evolutionary ecologist from the University of South Florida in Tampa.

Yet she and others note the work has limitations. “The source of variation was very artificial” in the lab-made strains, Richards notes, and *Arabidopsis*, with its unusually small plant genome, may not reflect what happens in other plants. “We still need more evidence that these are true effects and that this is something that influences evolution in natural populations,” adds Jon Ågren, an evolutionary ecologist at Uppsala University in Sweden.

Johannes says his team found similar connections between methylation and flowering time in natural strains of this plant, indicating that the laboratory study has some relevance to wild populations. But the experiment doesn’t address the most controversial aspect of epigenetics and evolution—whether an environmental stress can alter an organism’s epigenetic markings and lead to a permanent trait change that’s acted upon by natural selection—a notion that, to some, sounds suspiciously like Lamarckism.

“A lot more hard evidence is necessary before one can claim that epigenetics plays a very important role in evolution,” says ecological geneticist Koen Verhoeven at the Netherlands Institute of Ecology in Wageningen. And, Richards adds, “people are really stubborn about accepting that that’s possible.”

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