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 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 Netherlands Institute of Ecology in Wageningen. And, Richards adds, “people are really stubborn about accepting that’s possible.”

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

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