OMICS

Arabidopsis proteome v2.0

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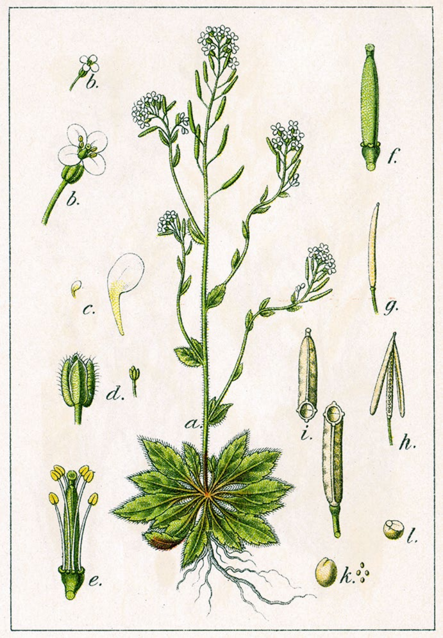

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The old debate between geneticists and biochemists has been a source of inspirational fun for decades. According to the familiar stereotypes, while geneticists think that the gene is the most fundamental heritable biological unit and the only worthy access point to understand the living world, biochemists are persuaded that proteins are the real functional actors at the heart of most biological functions that define life, and the rest does not really matter.

Of course, both approaches are important to fully understand complex organisms such as plants. We are all aware that the *Arabidopsis* reference genome published at the turn of the millennium was a giant leap for plant research. This milestone did not quench our thirst for knowledge, however, and was followed by the sequencing of hundreds of accessions to define a first pan-genome of the model species. On the more technically challenging protein front, an earlier try at mapping a global *Arabidopsis* proteome was published more than a decade ago and was badly in need of an update, which is exactly what a multi-lab team, mostly from Germany, has done in a recent study published in *Nature*.

The researchers generated an impressive amount of data, consisting of a full expression atlas combining state-of-the-art RNA-sequencing of the transcriptome and mass spectrometry of the proteome and phosphoproteome, freely accessible through web portals. The numbers are remarkable. Thirty different tissues were sampled and the dataset offers an unprecedented level of details on the inner working of plant cells. A little more than 18,000 proteins were detected, representing 66% of the annotated protein-coding genes, with measured levels spanning an extraordinary six orders of magnitude. Half of the identified proteins were phosphorylated. Similar mRNA levels can produce 100-fold differences in protein abundance. The 10 most abundant proteins represent a third of the total amount. Many more fascinating specific examples are given in the article.

This study might not settle the old argument between biochemists and geneticists, but it might unify all plant biologists who now have a novel tool to explore their favourite protein in the context of a striking dynamic proteome landscape in *Arabidopsis*.

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