



SPECIAL SEMINAR ICVV 2017

TUESDAY, JUNE 6th, 2017

University of La Rioja

Complejo Científico Tecnológico (CCT)

Aula Magna

13:00

Genetics and epigenetics of adaptation to the environment

Detlef Weigel

Max Planck Institute for Developmental Biology, Germany



Detlef Weigel, a German-American scientist, is currently a director at the Max Planck Institute for Developmental Biology. He is a member of the US National Academy of Sciences, the German National Academy of Sciences Leopoldina and the Royal Society, and recipient of several scientific awards, most recently the GSA Medal.

The first major finding from his lab was that an *Arabidopsis thaliana* gene could dramatically accelerate flowering of trees; this established a proof of concept for Arabidopsis genetics as a platform for biotechnological discoveries. His group later discovered the first plant microRNA mutant and identified the factor that we now know to be the long sought-after mobile flower-inducing signal. Detlef was one of the first to exploit natural genetic variation for understanding how the environment affects plant development. In recent years, his work in evolutionary genetics and genomics has focused on plant immunity and epigenetics. In addition to hypothesis-driven research, his group has a long history of providing new technologies and resources to the community. This has culminated in an effort to sequence the genomes of over 1000 natural *A. thaliana* strains (The 1001 Genomes Project).

Detlef has an extensive record of service to the scientific community, having served on many editorial and advisory boards. He is a forceful advocate of open access publishing, and founding Deputy Editor of eLife. He is also a co-founder of three biotech startups.



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ABSTRACT

My group is addressing fundamental questions in evolutionary biology, using both genome-first and phenotype-first approaches:

1. Where do new genetic variants come from?
2. Why are some variants maintained for a much longer time than others?
3. And why are some combinations of variants incompatible with each other?

The background for these questions is our population genomic work in *Arabidopsis* and the related genus *Capsella*. In collaboration with our Bergelson, Ecker, Mott, Nordborg, K. Schmid and others, including Monsanto, we have been describing whole-genome variation in wild isolates of *A. thaliana* (<http://1001genomes.org>). This has, for example, led to the discovery of a Neanderthal-like group that has apparently survived since the Last Glacial Maximum. A similarly remarkable finding that emerged from the *Capsella* work with Neuffer, Slotte and Wright is the ubiquity of long-term balancing selection, specifically at immunity loci. On the other end of the spectrum, we are analyzing new DNA mutations and epigenetic variants that have arisen under laboratory conditions or in a natural mutation accumulation experiment. The latter studies, with Bergelson and Burbano, take advantage of an *A. thaliana* lineage that was apparently introduced to North America in historic times and accounts for about half the population there.

The ultimate goal of our top-down studies is to understand how genetic and epigenetic variation interacts with reassortment of variants after crosses and with natural selection to shape geographic patterns of diversity. One example is our work with Dangl on the evolution of immune receptors, which have evolved to be highly diverse because of pathogen pressure – which in turn can lead to paranoid plants that mount an immune response even though they are not even attacked by pathogens. A final example is our prediction of which *A. thaliana* populations will and which populations will not be able to adapt to climate change.

Additional information about our work can be found on our website, <http://weigelworld.org>.



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